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Ernesto Fattorusso
William H. Gerwick
Orazio Taglialatela-Scafati
Editors

VOLUME 1

Handbook of Marine Natural Products

 Springer

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Handbook of Marine Natural Products

With 691 Figures and 45 Tables

 Springer

Editors

Ernesto Fattorusso
Dipartimento di Chimica delle Sostanze Naturali
Università di Napoli Federico II
Via Montesano 49
80131 Naples
Italy

William H. Gerwick
Scripps Institution of Oceanography
Skaggs School of Pharmacy and Pharmaceutical Sciences
University of California
San Diego, CA 92093
USA

Orazio Tagliatela-Scafati
Dipartimento di Chimica delle Sostanze Naturali
Università di Napoli Federico II
Via Montesano 49
80131 Naples
Italy

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Preface

The field of marine natural products is nearing the 50 year mark since its origin in the 1960s with pioneering studies in Japan by Toshi Irie and in the United States by Paul Scheuer. Since that time and their early studies to describe the fundamental organic chemistry of marine organisms, it has grown and evolved to be highly multidisciplinary, integrating methods development in organic structure analysis, pharmacology, synthetic and medicinal chemistry, toxicology, biosynthesis and mechanistic bioorganic chemistry, and genomics. Indeed, the field is reaching a maturity in approach and societal significance that could only be guessed at in the early days, and several marine-derived or marine-inspired drugs are now on the market (7) or in various stages of clinical trial (13). Of equal significance, more than 120 marine natural products are articles of commerce for their utility as reference standards and pharmacological probes of cell biology. However, with this maturity comes a responsibility on the part of students and researchers in the marine natural products sciences to know the history and origins of the field, and so enabled, to keep vital and current the subject through innovation and creative new science.

A number of reviews and multi-author monographs have appeared in this field with the primary objective of providing a scholarly perspective on some dimension of marine natural products as well as an entry point to the relevant literature. Most notably, the book series championed by Paul Scheuer and the yearly scholarly reviews by Faulkner and subsequently by the Munro and Blunt team have served our community well in these regards. However, except for early texts by Scheuer and Pietra, and various specialty volumes such as that of Valerie Paul on Marine Chemical Ecology, comprehensive textbooks covering this field have not appeared which are suitable as an introduction to the field or a companion to an advanced undergraduate/graduate university course on the topic. This has been a shortcoming which has both made teaching of this subject difficult in the classroom and complex to articulate the scope and nature to those outside of the field.

It is with this goal and vision in mind that the editors first came together in 2008 at a Marine Natural Products Gordon Research Conference in Ventura, California, to begin organizing a textbook in this field of marine natural products science. At that time we outlined a volume of considerable scope, divided into six sections, which would provide a comprehensive overview of this highly diverse field.

We next identified potential leaders in the field to provide chapters on specific topics within each of these sections. We were highly gratified that almost all contacted authors were able to accept our invitation to contribute to this handbook, and, subsequently, to receive their inspiring and scholarly chapters. Without the efforts and dedication of these many authors, this volume clearly would not have been possible, and we thank them all most sincerely. We believe that it was the shared vision of all of the authors that provided the motivation to contribute to a textbook that would help define the field as well as provide a contemporary guide to those entering this exciting branch of science.

A unique feature of this volume is the inclusion of a series of thought-provoking study questions at the end of each chapter. Some of these will aid in understanding the principles and concepts presented in each chapter, whereas others represent actual topics for further research. A careful consideration of these questions by interested students will certainly enhance the level of understanding of the material presented as well as stimulate new ideas suitable as actual research projects.

Upon receipt of the various chapters the editors undertook the multistage process of editing, improving consistency between chapters, and identifying index terms. We thank the multitude of people at our respective institutions for their contributions to various aspects of this lengthy process. We also thank the several key people at Springer who have helped this volume become a reality. And finally, we thank our families for their understanding during the many early mornings and late evenings that we were engaged in the writing and editorial process. However, if we reach our vision to have provided a truly useful text for those entering the field of marine natural products science, then, indeed, it will all have been worthwhile. To the readers of this volume, we sincerely wish that you will find knowledge, perspective, and inspiration in your scholarly pursuit of the marine natural products sciences. We hope that this volume will assist you as you continue the tradition of innovation and creativity that has characterized this field over its first 50 years.

Ernesto Fattorusso
William H. Gerwick
Orazio Tagliatela-Scafati
February 2012

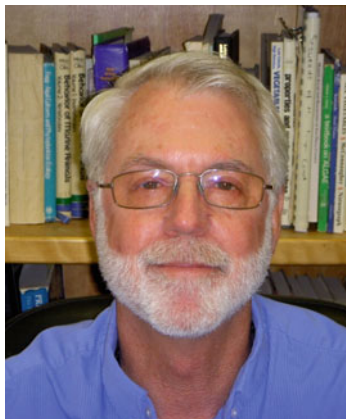
About the Editors



Ernesto Fattorusso

Dipartimento di Chimica delle Sostanze
Naturali
Università di Napoli Federico II
Via Montesano 49
80131 Naples
Italy

Ernesto Fattorusso graduated in Chemistry in 1960 and got *Libera Docenza* in Natural Products Chemistry in 1967. He was assistant professor at the University of Naples (1963–1975); in 1975, he became full Professor of Organic Chemistry at the Faculty of Science. In 1980, he moved to the Faculty of Pharmacy, where he was elected Dean twice. Since 2011, he is Professor Emeritus of Organic Chemistry of the University of Naples Federico II. He has published more than 400 scientific papers and on 2008 edited the book *Modern Alkaloids*. His research activity started by studying the structure and biogenesis of melanins, and, since the end of 1960s, he has pioneered the chemical investigation of marine metabolites. He has won the *A. Quilico Award* (2002) of Italian Chemical Society, the *P. Scheuer Award* (2004) of Akademie of Erfurt, and the *P. Scheuer Award* (2010) of University of Honolulu Foundation. Since 2005, he is Editor of *Steroids*.

**William H. Gerwick**

Scripps Institution of Oceanography
Skaggs School of Pharmacy and
Pharmaceutical Sciences
University of California
San Diego, CA 92093
USA

William Gerwick holds a Ph.D. from Scripps Institution of Oceanography, University of California San Diego (1981) where he described the unique organic secondary metabolites of several marine macroalgae. His postdoctoral research focused on the biosynthesis of microbial natural products at the University of Connecticut. He was an assistant professor of Chemistry at the University of Puerto Rico in 1982–1983, and then professor of Pharmaceutical Sciences at the Oregon State University College of Pharmacy for over 20 years. In 2005, he returned as Full Professor to Scripps and the newly formed Skaggs School of Pharmacy and Pharmaceutical Sciences, UCSD, and in 2011 was named Distinguished Professor of Oceanography and Pharmaceutical Sciences. He has served as president of the American Society of Pharmacognosy, a member for the NIH scientific review committee on natural products chemistry, and holds affiliate positions at several other universities and institutions around the world. In 2011, he was awarded the UC San Diego Chancellor's Associates Award for Excellence in Engineering and Scientific Research. He has served on several scientific and review panels in the USA and abroad, including his current role on the Oceans and Human Health National Advisory Committee. His research fuses marine natural products drug discovery research with biosynthetic investigations at the chemical, biochemical, and genetic levels, and he has pioneered the integrated use of advanced analytical instrumentation in this area of scientific research.

**Orazio Tagliatela-Scafati**

Dipartimento di Chimica delle Sostanze
Naturali

Università di Napoli Federico II

Via Montesano 49

80131 Naples

Italy

Orazio Tagliatela-Scafati holds a Ph.D. in Bioactive Natural Products (1997) from the University of Naples Federico II. He was appointed as Assistant Professor of Organic Chemistry in 1999 and, since 2004, he is Associate Professor in Organic Chemistry at Faculty of Pharmacy, University of Naples Federico II.

He has served on several scientific and review panels and he is member of the Editorial Board of the scientific journals *Steroids* and *Marine Drugs*. His research activity focuses on isolation, stereostructural elucidation, and semi-synthetic transformation of bioactive secondary metabolites (especially with antitumor, antimalarial, and anti-inflammatory activities) from marine invertebrates and terrestrial plants. He is the author of about 100 research papers and the editor of the books *Flavour and Fragrance Chemistry* and *Modern Alkaloids*.

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List of Contributors

Anna Aiello Dipartimento di Chimica delle Sostanze Naturali, Università degli Studi di Napoli “Federico II”, Naples, Italy

Raymond J. Andersen Departments of Chemistry and Earth & Ocean Sciences, University of British Columbia, Vancouver, BC, Canada

Giuseppe Bifulco Department of Pharmaceutical and Biomedical Sciences, University of Salerno, Fisciano (Salerno), Italy

John Blunt Department of Chemistry, University of Canterbury, Christchurch, New Zealand

John Buckingham Dictionary of Natural Products, CRC Press/Informa, London, UK

Maria Giovanna Chini Department of Pharmaceutical and Biomedical Sciences, University of Salerno, Fisciano (Salerno), Italy

Hyukjae Choi Scripps Institution of Oceanography, Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California, San Diego, CA, USA

M. Letizia Ciavatta Istituto di Chimica Biomolecolare – Consiglio Nazionale delle Ricerche, Pozzuoli (Naples), Italy

Patrizia Ciminiello Dipartimento di Chimica delle Sostanze Naturali, Università degli Studi di Napoli “Federico II”, Naples, Italy

Guido Cimino Istituto di Chimica Biomolecolare – Consiglio Nazionale delle Ricerche, Pozzuoli (Naples), Italy

Gordon M. Cragg Natural Products Branch, Developmental Therapeutics Program, National Cancer Institute, NCI-Frederick, Frederick, MD, USA

Phillip Crews Department of Chemistry and Biochemistry, University of California, Santa Cruz, CA, USA

Adele Cutignano Istituto di Chimica Biomolecolare – Consiglio Nazionale delle Ricerche, Pozzuoli (Naples), Italy

Cecilia D'Angelo National Oceanography Centre Southampton, University of Southampton, Southampton, UK

Carmela Dell'Aversano Dipartimento di Chimica delle Sostanze Naturali, Università degli Studi di Napoli "Federico II", Naples, Italy

Simone Di Micco Department of Pharmaceutical and Biomedical Sciences, University of Salerno, Fisciano (Salerno), Italy

Sherif S. Ebada Institute of Pharmaceutical Biology and Biotechnology, Heinrich-Heine University, Duesseldorf, Germany; Department of Pharmacognosy and Phytochemistry, Faculty of Pharmacy, Ain-Shams University, Cairo, Egypt

Ernesto Fattorusso Dipartimento di Chimica delle Sostanze Naturali, Università di Napoli Federico II, Naples, Italy

Jörg Feldmann Marine Biodiscovery Centre, Department of Chemistry, University of Aberdeen, Old Aberdeen, Scotland, UK

William Fenical Center for Marine Biotechnology and Biomedicine, Scripps Institution of Oceanography, University of California, San Diego, CA, USA

Angelo Fontana Istituto di Chimica Biomolecolare – Consiglio Nazionale delle Ricerche, Pozzuoli (Naples), Italy

Martino Forino Dipartimento di Chimica delle Sostanze Naturali, Università degli Studi di Napoli "Federico II", Naples, Italy

Nobuhiro Fusetani Fisheries and Oceans Hakodate, Graduate School of Fisheries Sciences, Hokkaido University, 3-1-1, Minato-cho, Hakodate, Japan

Lu Gan National Research Center for Geoanalysis, Beijing, China

Margherita Gavagnin Istituto di Chimica Biomolecolare – Consiglio Nazionale delle Ricerche, Pozzuoli (Naples), Italy

William H. Gerwick Scripps Institution of Oceanography, Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California, San Diego, CA, USA

Deborah J. Gochfeld National Center for Natural Products Research, The University of Mississippi, Oxford, MS, USA

Kirk R. Gustafson Molecular Targets Laboratory, Center for Cancer Research, National Cancer Institute-Frederick, Frederick, MD, USA

Adrianna Ianora Functional and Evolutionary Ecology, Laboratory Stazione Zoologica Anton Dohrn, Naples, Italy

Marcel Jaspars Department of Chemistry, Marine Biodiscovery Centre, University of Aberdeen, Aberdeen, UK

Paul R. Jensen Center for Marine Biotechnology and Biomedicine, Scripps Institution of Oceanography, University of California, San Diego, CA, USA

Flora Katz John E. Fogarty International Center, National Institutes of Health, Bethesda, MD, USA

Jeffrey D. Kittendorf Life Sciences Institute and Department of Medicinal Chemistry, University of Michigan, Ann Arbor, MI, USA

Gabriele M. König Institute for Pharmaceutical Biology, University of Bonn, Bonn, Germany

Eva Krupp Department of Chemistry, Marine Biodiscovery Centre, University of Aberdeen, Old Aberdeen, Scotland, UK

Dehai Li Departments of Chemistry and Earth & Ocean Sciences, University of British Columbia, Vancouver, BC, Canada

Alfonso Mangoni Dipartimento di Chimica delle Sostanze Naturali, Università di Napoli Federico II, Naples, Italy

Emiliano Manzo Istituto di Chimica Biomolecolare – Consiglio Nazionale delle Ricerche, Pozzuoli (Naples), Italy

Marialuisa Menna Dipartimento di Chimica delle Sostanze Naturali, Università degli Studi di Napoli “Federico II”, Naples, Italy

Antonio Miralto Functional and Evolutionary Ecology Laboratory, Stazione Zoologica Anton Dohrn, Naples, Italy

Jonathan C. Morris School of Chemistry, University of New South Wales, Sydney, Australia

Jon Mortison Life Sciences Institute and Department of Medicinal Chemistry, University of Michigan, Ann Arbor, MI, USA

Werner E. G. Müller Institute for Physiological Chemistry, Medical Center of the Johannes Gutenberg University, Mainz, Germany

Murray Munro Department of Chemistry, University of Canterbury, Christchurch, New Zealand

Brian T. Murphy Center for Marine Biotechnology and Biomedicine, Scripps Institution of Oceanography, University of California, San Diego, CA, USA

Hiroshi Nagai Department of Ocean Science, Tokyo University of Marine Science and Technology, Minato-ku, Tokyo, Japan

Dale G. Nagle Department of Pharmacognosy, School of Pharmacy, The University of Mississippi, Oxford, MS, USA

Yoichi Nakao School of Advanced Sciences and Technologies, Waseda University, 3-4-1, Shinjuku-ku, Tokyo, Japan

David J. Newman Natural Products Branch, Developmental Therapeutics Program, National Cancer Institute, NCI-Frederick, Frederick, MD, USA

G. Ulrich Nienhaus Center for Functional Nanostructures, Karlsruhe Institute of Technology, Karlsruhe, Germany; Department of Physics, University of Illinois at Urbana-Champaign, Urbana, IL, USA

Matt Nodwell Departments of Chemistry and Earth & Ocean Sciences, University of British Columbia, Vancouver, BC, Canada

Franz Oswald Department of Internal Medicine I, University of Ulm, Ulm, Germany

Joseph R. Pawlik Department of Biology and Marine Biology, Center for Marine Science, University of North Carolina Wilmington, Wilmington, NC, USA

Alban R. Pereira Scripps Institution of Oceanography, Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California, San Diego, CA, USA

Andrew J. Phillips Department of Chemistry, Yale University, New Haven, CT, USA

Peter Proksch Institute of Pharmaceutical Biology and Biotechnology, Heinrich-Heine University, Duesseldorf, Germany

Pei-Yuan Qian KAUST Global Collaborative Program, Division of Life Science, Hong Kong University of Science and Technology, Clear Water Bay, Hong Kong, China

Andrea Raab Marine Biodiscovery Centre, Department of Chemistry, University of Aberdeen, Old Aberdeen, Scotland, UK

Christopher M. Rath Life Sciences Institute and Department of Medicinal Chemistry, University of Michigan, Ann Arbor, MI, USA

Raffaele Riccio Department of Pharmaceutical and Biomedical Sciences, University of Salerno, Fisciano (Salerno), Italy

Michel Roberge Department of Biochemistry & Molecular Biology, University of British Columbia, Vancouver, BC, Canada

Jaime Rodríguez Departamento de Química Fundamental, Campus da Zapateira. Universidade da Coruña, A Coruña, Spain

Giovanna Romano Functional and Evolutionary Ecology, Laboratory Stazione Zoologica Anton Dohrn, Naples, Italy

Joshua Rosenthal John E. Fogarty International Center, National Institutes of Health, Bethesda, MD, USA

Jamie B. Scaglione Life Sciences Institute and Department of Medicinal Chemistry, University of Michigan, Ann Arbor, MI, USA

Heinz C. Schröder Institute for Physiological Chemistry, Medical Center of the Johannes Gutenberg University, Mainz, Germany

David H. Sherman Life Sciences Institute and Department of Medicinal Chemistry, University of Michigan, Ann Arbor, MI, USA

Marc Slattery Department of Pharmacognosy, The University of Mississippi, Oxford, MS, USA; National Center for Natural Products Research, The University of Mississippi, Oxford, MS, USA

Edward G. Smith National Oceanography Centre Southampton, University of Southampton, Southampton, UK

Wendy Strangman Departments of Chemistry and Earth & Ocean Sciences, University of British Columbia, Vancouver, BC, Canada

Orazio Tagliatalata-Scafati Dipartimento di Chimica delle Sostanze Naturali, Università di Napoli Federico II, Naples, Italy

Wolfgang Tremel Institute for Chemistry, Johannes Gutenberg University Mainz, Mainz, Germany

Meg Upjohn Physical Sciences Library, University of Canterbury, Christchurch, New Zealand

Claudia Wagner Institute for Pharmaceutical Biology, University of Bonn, Bonn, Germany

Xiaohong Wang National Research Center for Geoanalysis, Beijing, China; Institute for Physiological Chemistry, Medical Center of the Johannes Gutenberg University, Mainz, Germany

J. Wiedenmann National Oceanography Centre Southampton, University of Southampton, Southampton, UK

Matthias Wiens Institute for Physiological Chemistry, Medical Center of the Johannes Gutenberg University, Mainz, Germany

Victoria L. Wilde Department of Chemistry, Yale University, New Haven, CT, USA

David E. Williams Departments of Chemistry and Earth & Ocean Sciences, University of British Columbia, Vancouver, BC, Canada

Stephen H. Wright Marine Biodiscovery Centre, Department of Chemistry, University of Aberdeen, Old Aberdeen, Scotland, UK

Sharon Ying Xu KAUST Global Collaborative Program, Division of Life Science, Hong Kong University of Science and Technology, Clear Water Bay, Hong Kong, China

Yu-Dong Zhou Department of Pharmacognosy, School of Pharmacy, The University of Mississippi, Oxford, MS, USA

Introduction

Ernesto Fattorusso, Willam H. Gerwick, and Orazio Taglialatela-Scafati

The use of both terrestrial and marine natural products (MNPs) as treatments for different ailments has accompanied humanity from its earliest civilizations. Nature represents an endless arsenal of new bioactive compounds and the study of these metabolites has historically proven to be of immense benefit in the drug discovery process.

The chemical investigation of terrestrial natural products can be dated back to the beginning of the nineteenth century, when organic molecules started to be studied with scientific rigour. Much younger is the chemical investigation of marine natural products (MNPs), now about 65 years old. Although approximately 70% of the earth's biosphere is made up by oceans, a unique environment that hosts a wealth of plants, animals, and microorganisms, a variety of reasons have hampered the development of MNP chemistry in the nineteenth and at the beginning of twentieth century. These are mainly related to technical constraints resulting from difficulties in the collection of marine organisms from the sea and, related to this, the relatively small amount of organisms that could be collected. As a result, this situation inevitably resulted in a very limited quantity of metabolites obtained from the extraction and purification processes.

Due to impressive progress in collection techniques (with the introduction of SCUBA), purification, and, above all, in structural studies through improvements in spectroscopic technologies, the last 40 years have witnessed an explosion of research focused on the immense biodiversity of the marine environment. This has resulted in a multidisciplinary endeavor involving natural product chemists, marine ecologists, pharmacologists and biochemists. The number of novel MNPs discovered to date has been recently estimated to be about 30,000, and their incredible diversity can be well appreciated by consulting the precious reviews published by the late D. J. Faulkner in *Natural Products Reports*, a series now continued by Blunt, Munro, and others. These annual reviews report all the new marine natural products emerging in the scientific literature and also give a fine idea of the relative prolificacy of the different organisms. Marine invertebrates (sponges, tunicates, soft corals, gorgonians, molluscs, echinoderms) are by far the most prolific producers of secondary metabolites, compared to fish and other vertebrates. This observation can have at least two possible explanations: (1) Their sessile and soft-bodied forms, combined with their consequent lack of mechanical or morphological weapons to be used as protection, force them to rely largely on a chemical

arsenal to deter predation from other reef organisms. Since the production of secondary metabolites has been selected by these organisms as a strategy for their survival, the greater is the number of secondary metabolites produced by an organism the greater are its chances in winning the evolutionary competition. (2) These marine invertebrates harbor in their tissue, in extra- and intracellular spaces, a great number of symbiotic and associated microorganisms and, thus, their biosynthetic potential is indirectly increased by the contribution of the biosynthetic machinery of the different symbiotic cells.

Thus, it is not surprising that one of the most recent trends in MNP chemistry, the direct chemical investigation of marine microbes (e.g., bacteria collected in the sediments and cyanobacteria), has revealed an incredible richness of interesting secondary metabolites. Moreover, some classes of marine microorganisms are actually responsible for the production of the toxic metabolites found in marine invertebrates, and several have been demonstrated to cause human intoxications of various levels of seriousness. The study of marine toxins was initiated at the very beginning of the MNP era, reaching milestones such as the isolation and structure elucidation of maitotoxin, the largest nonproteinaceous toxin known to date, and characterized by a skeleton of 164 carbon atoms.

With this wealth and variety of topics in mind, we decided to structure the present handbook with the aim of representing the different aspects of MNP science (i.e., ecology and pharmacology of bioactive compounds; recent advances in isolation, biosynthesis, and structural elucidation) in a volume which should provide representative examples of recent results as well as of the future outlook of this multidisciplinary branch of science. Obviously, this handbook is not intended as a comprehensive coverage of the entire field of MNP research, but we feel that through the diversity of topics treated, it can provide a good idea of its variety and richness. Thus, this handbook should be useful to a mixture of scientists and students in academia as well as industry that are interested in the most recent developments in this area. In addition, we have asked the authors to present their topics in a clear and didactic way, making a frequent use of examples and connections to their practical utility. Thus, we believe that this handbook will also serve as an excellent textbook for Ph.D. and postdoctoral students in several courses within the marine sciences. The study questions included at the end of each chapter are intended to be thought provoking stimuli to further deepen student knowledge and interest in the subject matter.

The handbook includes 30 chapters grouped into six sections. Section I provides an overall idea of the production and diversity of MNPs within some representative groups of marine organisms. Of course, the five chapters in this section do not aim at reporting all of the molecules isolated from each group, but rather, they describe the characteristics as well as unique carbon and heterocyclic skeletons and assorted functional groups. The astounding variety (and often complexity) of the chemical structures of MNP poses challenging problems to the chemists engaged in their stereostructural elucidation, which is also made more difficult by the small amounts commonly obtained from natural sources. In Sect. II, the reader will find described different aspects of the structural elucidation process with special attention given to

NMR spectroscopy. Recent advancements in NMR spectroscopy have allowed modern MNP laboratories to routinely solve structures on submicrogram quantities, and have undoubtedly fostered the recent explosion of novel marine compounds appearing in the literature. In the same section, a chapter by Blunt and Munro describes the importance of databases in the structural elucidation process while the chapter by Phillips et al. illustrates the elegance of several total syntheses of MNPs, highlighting also the role that these syntheses can play in confirming or revising the chemical structures assigned to marine compounds.

Section III illustrates the role of MNPs in chemical ecology, investigating the real purpose driving the production of MNPs and explaining how the coexistence and the interaction of an enormous number of species in the marine environment greatly rely on chemical signaling processes. Section IV is inherently connected to the previous one because it describes the biosynthetic origins of these metabolites, or how they can be acquired from dietary sources and/or symbiotic-associated organisms. A rapidly expanding number of MNP scientists have been investigating the molecular biology and genetics of marine secondary metabolite biosynthesis with the goal of understanding and manipulating their biosynthetic pathways (particularly polyketide and non-ribosomal peptide syntheses). If the development of this subdiscipline is able to attain its long-term goal, then the fermentation and cultivation of microbes could offer a practical solution to the problems of short supply of materials, a fundamental and significant issue which has long delayed and stalled the full development of MNP science.

Section V illustrates one of the most important applications of the MNP science, namely, the biomedical potential of small molecule natural products. Since Bergman's discovery of the antiviral and antitumor arabinose-containing nucleosides "spongothymidine" and "spongouridine" from *Cryptotethia crypta* in 1955, the potential of marine organisms in pharmaceutical applications has been the driving force of many of these scientific investigations. At the moment, five marine-derived drugs have been approved by the FDA or EMA (the EU agency), namely, two nucleosides (cytarabine and vidarabine), a polypeptide (ziconotide), the complex alkaloid trabectedin (ET-743), and the fantastically complicated synthetic derivative, Halaven, of the sponge metabolite halichondrin. Moreover, a further 15 compounds are in different phases of clinical trial and several hundred promising compounds are in preclinical stages. The eight chapters of Section V illustrate different aspects of the biomedical potential of MNPs, highlighting how this "natural library" can contain lead compounds to be used as an inspiration to design and develop new useful therapeutic agents, or to gain initial information about the pharmacophore and structure-activity relationships. ► [Chapters 20](#), ► [21](#), and ► [23](#) describe some specific pharmacological activities of small marine organic molecules, while ► [Chaps. 24](#) and ► [25](#) are focused on the potential use of marine macromolecules, fluorescent proteins, and biologically formed polymers of silica, respectively. The last two chapters of Section V discuss the long-standing and perplexing problem of compound supply, an inherent feature of working in the marine environment, and the legal and ethical issues connected to the exploitation of this environment. With the growing number of commercial

applications of MNPs, it is critical for practitioners of this field to possess a deep knowledge of intellectual property protection and constraints on public disclosure. Finally, Sect. VI includes two chapters reporting on marine toxins, one of the oldest fields of MNP chemistry but one still very active and interesting for its toxicological, pharmacological, and economic implications.

We cannot conclude this introductory chapter without thanking the friendly contributions of all of the colleagues that accepted the task of providing their invaluable expert knowledge through the preparation of the different chapters. We hope that this handbook on MNPs will succeed in further stimulating enthusiasm and interest in this relatively young but extremely dynamic and rapidly evolving discipline.

Part 1

Natural Product Trends in Different Groups of Marine Life

Taxonomy and Marine Natural Products Research

1

John Blunt, John Buckingham, and Murray Munro

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Abstract

A taxonomic overview of the marine environment is presented along with specifics on the key phyla. This is accompanied by a brief history of marine natural products research, the aspirations in this field of research, and an analysis, on a taxonomic basis, of the results of the past 60 years of marine natural products research. In the final sections of the chapter, conclusions are drawn from the work as to the phyla that might be of interest for future research.

J. Blunt (✉) • M. Munro

Department of Chemistry, University of Canterbury, Christchurch, New Zealand
e-mail: john.blunt@canterbury.ac.nz, murray.munro@canterbury.ac.nz

J. Buckingham

Dictionary of Natural Products, CRC Press/Informa, 1-4 Singer St., 4th Floor, London, UK
e-mail: johnbuckingham@blueyonder.co.uk

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1.1 Introduction

“Is it from pride, humour or irony that man has given the name “earth” to his own planet?” [1]

It was undoubtedly pride, not humor or irony, as Earth is the only planet of the Solar System not named from Greek or Roman mythology. Earth probably originates from the Middle English word, *erthe*, which can be traced back through Old English, Old High German, Greek to the Hebrew word *erez*, meaning ground [2]. It is however ironic and indeed humorous when Earth is viewed from space. The land masses our forbears took pride in are simply islands floating in enormous oceans. The 71% of the Earth’s surface that is the oceans is strikingly illustrated by the “Blue Marble” photo of earth taken from Apollo 17 [3] (Fig. 1.1). The oceans are a critical component of the Earth’s biosphere, unique in the Solar System and most probably among the several hundred other planetary systems throughout the Universe that have been identified in recent years.

The essential nonliving components of the biosphere are the atmosphere with its oxygen richness, the hydrosphere, predominantly saline, to an average depth of 3,800 m, and the land mass with its average height of 840 m [4]. In combination, these features support an amazing diversity of life forms.

1.2 How Many Species on Earth?

Systematics attempts to categorize this biological diversity on Earth and sort the various life forms into congruent groups, but there is no one single definition of what constitutes a species. Systematics has been influenced by the influx of new data and new methodology, particularly at the molecular level. As a consequence, taxonomy and recognition of groupings at the species level are constantly evolving. Taxonomists have attempted to impose a classification scheme on the whole of creation during an era of rapidly evolving knowledge. In the opinion of some, genomics will soon be capable of imposing an informatically robust relationship tree on all organisms. Most taxonomists beg to differ, claiming that changes and similarities are expressed through the phenotype not the genotype, and the genomic view disregards the possibility of convergent evolutionary pathways. What is true, however, is that in recent years there have been some major realignments of taxonomic groups based on genomic studies, even in such intensively studied and well-known groups as the higher plants.

The nineteenth-century high-level classification of organisms into plant and animal kingdoms has been abandoned since about the 1960s with the development of cladistic analysis. Since then it has become increasingly clear that certain groups of organisms, some of them previously little studied, such as the cyanobacteria or cyanophytes (so-called blue-green algae; more closely related to bacteria), the chromista (including the brown algae), and the archaeobacteria or archaea, show greater differences in both fundamental biochemistry and genetics from each other and from the so-called higher organisms than higher plants and animals show from each other. It was Whittaker



Fig. 1.1 A view of the earth taken from Apollo 17, December 7, 1972

in 1959 who proposed that the most fundamental division should be between the prokaryotes and the eukaryotes [5], a classification that has now been generally accepted but subsequently modified to include the discovery of the archaea in the 1970s [6].

Major projects are in place worldwide to collate information from available datasets and document the Earth's biodiversity. These include the *Global Biodiversity Information Facility* [7] and the *Species 2000/Integrated Taxonomic Information System* [8] responsible for the *Catalogue of Life*. In the 9th edition (2009), their Annual Checklist, with 1,160,711 distinct species being listed, was estimated to contain just more than one half of the known species [9]. The goal ultimately is to list every distinct species in each group of organisms. At present, some groups are globally complete, some are nearing completion, and others are partial only. At the top level of the taxonomic hierarchy *The Catalogue of Life* lists organisms, based on contemporary perspectives, as the prokaryotic Archaea and Bacteria and the eukaryotes organized as Animalia, Chromista, Fungi, Plantae, and Protozoa. This whole topic has been thoughtfully discussed by Gordon [10] as a management hierarchy or classification system for the *Catalogue of Life*. The partially rooted relationships between these groupings can be depicted diagrammatically in a phylogenetic tree of life [11] (Fig. 1.2).

Based on the known organisms there appears to be consensus [12–15] that the number of known species on Earth is 1.75–1.9 million. These numbers have modest certainty when dealing with the larger organisms or distinctive taxonomic groups, but there is considerable uncertainty when dealing with groups that are harder to classify,

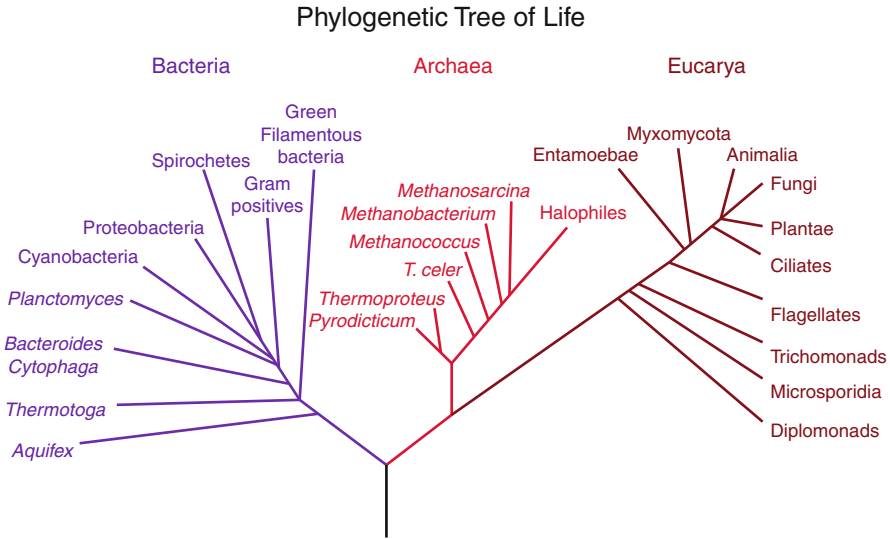


Fig. 1.2 A partially rooted phylogenetic tree of life

Table 1.1 Compilation of species numbers based on higher-order taxonomic groupings

	Total species			Marine species		
	Catalogue of Life [9]	Chapman [13] (<i>World accepted</i>)	Chapman [13] (<i>World estimate</i>)	WoRMS (2009) [16]	Bouchet (2006) [17]	Groombridge and Jenkins (2002) [4]
Archaea	281	–	–	0	0	?
Bacteria	9,773	10,307	~1,000,000	629	5,800	?
Fungi	44,669	98,998	1,500,000	1054	500	500
Protozoa ^a	6,866	28,871	>1,000,000	6,852	>14,800	12,500
Chromista ^a	7,901	~25,044	~200,500	4,098	7,600	1,500
Plantae	211,249	~310,129	~390,800	8,329	8,750	11,000
Animalia	953,661	1,424,153	~6,836,000	139,359	192,667	~205,000
	1,234,500	1,897,502	>10,900,000	160,319	>230,117	~250,000

^aFor comparative purposes the unicellular eukaryotic species have been partitioned between Chromista and Protozoa based on the systematics used by the *Catalogue of Life*. This should be considered speculative as not all databases or authors use these groupings, preferring instead Protocista. The *Catalogue of Life* places the Bacillariophyceae at a phylum level in the Plantae, but acknowledges this as a problem [10]

are microscopic, or are not economically important. It is likely to be many years before definitive answers emerge, but the total number of species will increase. Again estimates vary from 3–5 million [12] to 10–14 million [13, 15], or to 50 [14] to perhaps as many as 100 million species [15]. The breakdown of defined species in the *Catalogue of Life*, as of November 2009, is shown in Table 1.1. These numbers can

be contrasted with the 2009 compilation of world species by Chapman [13] who drew on information from systematists, the taxonomic literature, and previous compilations to arrive at an accepted number of species (~1.9 million) as well as providing an estimate of the total number of species on Earth (~11 million).

The contribution from the marine environment to the total species on Earth is relatively modest. At present the *World Register of Marine Species* (WoRMS) [16] lists 160,829 valid species (Table 1.1), 243,356 species names including synonyms, and 302,955 species to phyla. This data bank aims to capture all of the estimated 230,000 marine species by 2010. Two other sources [4, 17] have data on the estimated number of marine species (Table 1.1). Of the two sources, the data from Bouchet [17], who lists some 230,000 species, is the more definitive and thoughtful. Just as Chapman [13] extrapolated from the accepted number of world species to estimated world species and concluded that there were millions of Arthropod, Bacteria, Chromista, and Protozoa species yet to be characterized, Bouchet carried out a similar exercise for the marine world and speculated on the potential for greater numbers among the microbes and symbionts and the potential for the deep sea to produce a wide array of new species. There is clear evidence based on close field observations and culture-independent molecular techniques that the true number of marine species is considerably greater than that listed in Table 1.1.

The apparent lower species diversity between the terrestrial and hydrospheres (1.67 vs. 0.23 million) is a consequence of the overwhelming number of terrestrial arthropods (~1 million) for which there is no marine equivalent. In the marine world, species from Animalia are totally dominant accounting for 84% of the defined species (see Table 1.2 and Fig. 1.3).

All but one of the Animalia phyla have marine representation; the phylum Onychophora is the sole exception. The other notable feature is that the bulk of the Animalia phyla are exclusively, or nearly exclusively, marine, for example, Porifera, Echinodermata, and Bryozoa. Using data derived by May [14] on the relative numbers and distribution of the Animalia phyla this marine preference can be effectively depicted (Fig. 1.4). The aquatic and marine habitats are provided in the chart.

1.3 Marine Natural Products Chemistry

1.3.1 Historical

Rather surprisingly the natural products chemistry associated with marine species – marine natural products (MNP) – has only emerged over the past 75 years. This is in distinct contrast to the history of terrestrial natural products chemistry, which can readily be traced back to the earliest exponents of natural products chemistry at the start of the nineteenth century. For example, morphine was extracted and subsequently purified from the opium poppy plant about 1804 in Germany [18, 19]. However, the use of extracts from both terrestrial and marine sources as medicines, narcotics, or poisons stretches back to the earliest civilizations and is well documented in der Marderosian's 1969 review on marine pharmaceuticals [20].

Table 1.2 Suggested numbers for the marine phyla

Distribution of the marine phyla (Bouchet [17])			
Archaea	>0	Arthropoda (Chelicerata)	2,267
Archaea	–	Arthropoda (Crustacea)	44,950
		Brachiopoda	550
Bacteria	5,800	Cephalorhyncha (Priapulida; Loricifera; Kinorhyncha)	156
Cyanophyta	1,000	Chaetognatha	121
Bacteria	4,800	Chordata (Ascidiaceae)	4,900
		Chordata (Cephalochordata)	32
Fungi	500	Chordata (Mammalia)	110
Fungi	500	Chordata (Actinopterygi)	16,475
		Cnidaria	9,795
Protozoa	>14,800	Ctenophora	166
Ciliophora	?	Cycliophora	1
Sporozoa	?	Echinodermata	7,000
Euglenophyta	250	Echiura	176
Dinophyta (Dinomastigota)	4,000	Ectoprocta/Bryozoa	5,700
Radiolaria	550	Entoprocta/Kamptozoa	170
Foraminifera	10,000	Gastrotricha	395
		Gnathostomulida	97
Chromista	7,600	Hemichordata	106
Ochrophyta (Phaeophyceae)	1,600	Mesozoa (Rhombozoa; Orthonectida)	106
Ochrophyta (Chrysophyceae)	500	Mollusca	52,525
Haptophyta ^a	500	Nematoda	12,000
“Bacillariophyta”	5,000	Nematomorpha	5
		Nemertea	1200
Plantae	8,750	Onychophora	0
Chlorophyta	2,500	Phoronida	10
Magnoliophyta ^b	50	Placozoa	–
Rhodophyta	6,200	Platyhelminthes	15,000
		Porifera	5,500
Animalia	192,667	Rotifera	50
Acanthocephala	600	Sipuncula	144
Annelida	12,000	Tardigrada	212
Annelida (Pogonophora)	148		

^aFigure extracted from the *Catalogue of Life* [9]

^bBouchet had not included any members of the Magnoliophyta (mangroves, saltmarsh plants) in his estimates. The estimated figure for the Magnoliophyta from Groombridge and Jenkins [4] has been included

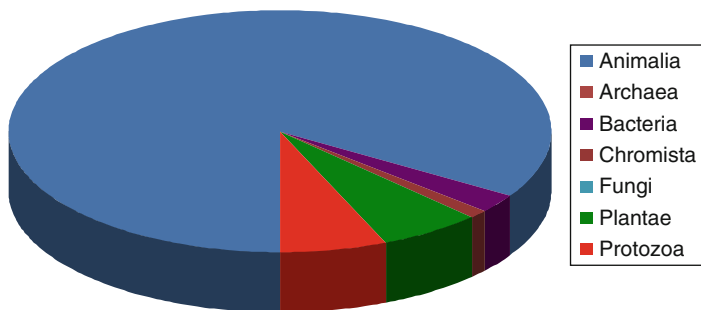


Fig. 1.3 Distribution of marine species by higher-order taxonomic grouping

This review is interesting as it surveyed this new and developing field from a taxonomic perspective. Of course at that stage relatively few compounds had been characterized and the emphasis was very much on toxins, pharmacology, and the biomedical potential for marine natural products. This emphasis was natural following on from Bergman's 1950s discovery of the non-ribose nucleosides spongthymidine and spongouridine from the West Indian sponge *Cryptotethia crypta* [21–25]. The subsequent evaluation of the biomedical potential of these arabinose-based nucleosides undoubtedly stimulated tremendous interest in the potential for pharmaceutical discoveries from the oceans. Bergman's first publication on marine organisms was in 1933 [26] while his 50th and last marine paper *Marine Products L, Phospholipides of Sponges* was in 1961 [27]. Over that 28-year period, Bergman studied sponges, sea anemones (cnidarians), and algae with a structural, not a biomedical, focus. In the 1950s, Nigrelli, Burkholder, and Ciereszko worked and commented specifically on biomedical aspects of marine natural products, for example, the neurotoxic effects of saponins from sea cucumbers, the antibiotic properties of sponge constituents and gorgonians, and antitumor activities associated with molluscs, echinoderms, and annelids [28–33]. In the meantime, work on toxins from marine vertebrates and invertebrates was initiated by Hirata, Scheuer, and Moore [34–38]. The first systematic study of a range of marine animals, both invertebrates as well as vertebrates, was reported in 1970 by Pettit who had collected from broad geographical areas [39]. This early systematic study was expanded by Rinehart with his bioassay-directed collections and onboard screening in the areas of Baja California (1974) and the Caribbean (1978) [40]. By the 1970s, species from across the marine phyla had been collected and were being studied. It was Faulkner, another early leader in the field, who commented that by 1975 there were already three parallel fields of study in marine natural products: marine toxins, MNP chemistry, and marine chemical ecology [41]. The distinct tracks, recognized over 30 years ago, continue today with systematic studies directed toward a particular phylum, toward a particular class of compounds, or following a particular bioactivity in the field of natural products chemistry. The study of marine toxins is still a dynamic aspect of the field and the role of MNPs in ecological studies has flourished. The major development of the past 20 years has

been the discovery and realization of the importance of marine-associated and marine-derived microorganisms. Led by Fenical, the study of marine microorganisms has rapidly become a major focus for a rapidly rising number of researchers [42]. Any survey would also have to note the rapid rise, since 2000, of studies associated with mangroves, whose habitats are right at the marine–terrestrial interface [43].

That study of just a few phyla by Bergman in the 1930s and 1940s was followed by a systematic exploration of the marine environment that has established the marine environment as a rich source of novel, bioactive compounds.

1.3.2 The Marine Resource

The marine environment is an extremely complex one, showing immense biodiversity. It is now clear that, while many marine natural products are located in the tissues of the larger marine animals and plants, and are thus genuine natural products of those organisms, many others are produced by associated endo- or epibiotic microorganisms. Most marine microorganisms have not yet been successfully cultured, and definitive proof of origin is in most cases currently lacking making it extremely difficult to distinguish between commensalism, saprophytism, symbiosis, or parasitism. These products produced by symbiotic, commensal, or epiphytic microorganisms appear in many cases to play a role in chemical defense mechanisms.

To better understand the depth of the marine resource, each of the major divisions/phyla is briefly described. The following descriptions of the characteristic features of each marine phylum have been condensed from the very full descriptions contained in the *Dictionary of Marine Natural Products* (DMNP) [44] which should be referred to for more detail. The DMNP descriptions also include more numerous examples of representative natural products from each phylum, and further surveys of the chemistry of some of the phyla are contained in subsequent chapters of this Handbook. Another particularly useful reference source is *Substances Naturelles d'Origine Marine* by Kornprobst [45].

Alternative taxonomic views are possible. In some groups of organism (e.g., molluscs) there is reasonable agreement among taxonomists about the major subdivisions of the phylum, but in others (e.g., Protozoa and Chromista) there are huge differences between alternative taxonomic schemes. For example, the Annual Checklist of the *Catalogue of Life* has an inconsistent treatment of diatoms and needs correcting. The diatoms appear in three places and it appears that two classification systems are in simultaneous use such that two diatom classes – Coscinodiscophyceae and Fragilariophyceae – are listed under phylum Ochrophyta in kingdom Chromista, whereas class Bacillariophyceae is listed as a phylum-rank entry under kingdom Plantae [10]. In this review of taxonomy and chemistry, the *Catalogue of Life's* higher taxa are used and in general the *Catalogue's* system of assigning phyla adhered to.

1.3.2.1 Archaea

The archaea are prokaryotic organisms inhabiting extreme environments, both marine and terrestrial, such as hydrothermal vents, and also highly saline regions.

There are three generally recognized groups: thermophiles (heat-tolerant), halophiles (tolerant of highly saline media such as in the Dead Sea; some species are also extremely alkali tolerant, growing in media up to pH 12), and methanogens (some species of which are also highly thermotolerant). It is also convenient to recognize a group of “psychrophiles” tolerant of cold Arctic and Antarctic conditions. Although only discovered in the 1970s [6], it now appears that the archaea are in fact the most abundant bacteria in the marine environment [46]. They show major differences from other prokaryotes in their genome, and these are carried through into fundamental differences in membrane structure and biochemistry. Their cell walls do not contain the glycopeptides found in the Bacteria. Stabilization of the membrane structure is effected by esters of glycerol with characteristic branched-chain terpenoid fatty acids, a role that in prokaryotes is performed by carotenoids and/or hopanoids and in eukaryotes by sterols.

1.3.2.2 Bacteria

The Bacteria are characterized by a cell wall structure based on a glycoprotein formed by (1 → 4) linked *N*-acetylglucosamine and *N*-acetylmuramic acid cross-linked by peptide side chains containing unusual amino acids which render different bacterial strains biochemically and immunologically distinct. In Gram-positive bacteria, the glycoprotein coat forms the outermost layer; in Gram-negative bacteria there is an outer membrane coat that prevents this layer being stained by the reagent. Bacteria may be photosynthetic or non-photosynthetic, and the photosynthetic bacteria may be anaerobic (sulfur bacteria) or aerobic (which includes the cyanobacteria). The former group utilizes the bacteriochlorophylls as photosynthetic pigments. Further major subdivisions such as alpha-, beta-, gamma-, and delta-proteobacteria have been delineated according to various schemes, but the overall picture is complex [47–49]. The majority of secondary metabolites are produced by the cyanobacteria and by the actinobacteria, which are described separately in the following sections.

Cyanobacteria

The older term blue-green algae is now considered a misnomer, and the cyanobacteria are considered a subdivision of the photosynthetic Bacteria. They are unicellular organisms that are both marine and terrestrial; some marine species also inhabit fresh water. Some are truly monocellular, but when found unassociated with other organisms, many species adhere via their mucilaginous coats into filaments or tufts visible to the naked eye. Cyanobacteria are among the earliest known organisms. Schemes for the subclassification of the cyanobacteria are based on their mode and degree of such association, or alternatively by the type of spores formed. Attempts have also been made to classify them chemotaxonomically. About 1,000 species have currently been described. Cyanobacteria are responsible for frequent algal blooms, the toxicity of which is associated with their high level of secondary metabolites [50, 51]. Cyanobacteria are present in the tissues of many sponges, often as a major component of the biomass. The most characteristic secondary metabolites are peptidic and are also characterized by a high degree of halogenation.

Actinobacteria

The Actinobacteria are a particular class of the Gram-positive Bacteria showing filamentous growth, and some similarities to fungi. (In the past they have often been classified as filamentous fungi and are sometimes called “higher bacteria.”) They also merit special treatment biochemically speaking because of their vast production of different types of natural products, many of them with strong antibiotic or other pharmacological activity. The most important genera, in terms of natural products, are *Streptomyces* and *Actinomyces*. Actinobacteria occur in marine sediments, and probably as endophytes in many marine organisms. The recent discovery of three marine genera is notable and already significant, and novel chemistry has come from these discoveries (*vide infra*) [52–56]. As a group they tolerate a wide range of salinities.

1.3.2.3 Protozoa

The term “protozoa” is difficult to define taxonomically and is subject to ongoing modification in the light of biochemical studies, which are leading to the reclassification of many groups. It was formerly used as a blanket term to describe almost any kind of unicellular organism, but it is now known that the dinoflagellates are more closely related to the brown algae (Chromista: Ochrophyta; Phaeophyceae) than to other unicellular organisms. The ciliate organisms, for example, *Paramecium*, can be placed here, although it now appears that they are biochemically closest to the dinoflagellates. It is convenient to recognize four subdivisions: flagellates, amoebae, sporozoans (Apicomplexa), and ciliates based on their modes of locomotion, but the reservations expressed above concerning their fundamental dissimilarities must be borne in mind, and a proper classification remains premature.

Dinophyta (Dinoflagellates)

These monocellular organisms are economically important as the causative agents of toxic “red tides.” Biochemical and other studies have shown clearly that they are more closely related to the ciliates and to certain other groups than they are to other flagellate organisms. About 4,000 species are known (Table 1.2). Only just over half are photosynthetic; some are carnivorous. Their main anatomical characteristic is the possession of two flagellae, one equatorial and one longitudinal. Most are unicellular but some are filamentous. They participate in a range of symbiotic associations, especially with corals and with molluscs. Those organisms which are photosynthetic contain chlorophylls *a* and *c*. They contain a range of xanthophylls. The characteristic steroids are a range of 4 α -methyl derivatives representing an intermediate stage between the tetracyclic triterpenoids and the cholestane/ergostane type predominant in the phaeophyta and relatives.

Many shellfish toxins are now known to be dinoflagellate metabolites but may not currently have been specifically described as such in the literature. The known toxins of dinoflagellates fall into two main groups, though the exact type of toxin produced is genus specific. The first main group is polyketide-derived, either long-chain with some cyclic ether formation (e.g., amphidinols [57, 58]) or with multiple ether rings (“polyether ladders”) (e.g., *brevetoxins* (see Fig. 1.5) [59, 60]).

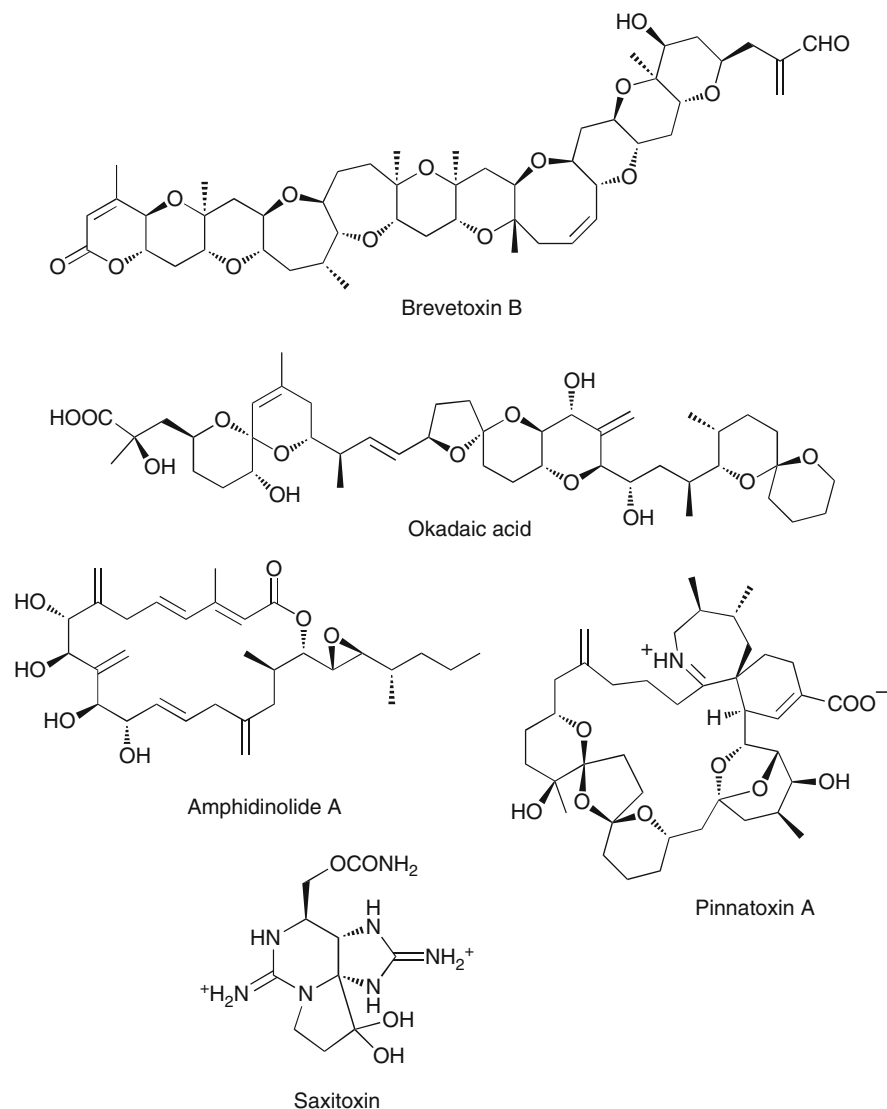


Fig. 1.5 Metabolites from protozoa

Another structural subtype is shown by *okadaic acid* [61], while other polyketides are macrolides such as the *amphidinolides* [62, 63]. Alicyclic nitrogenous polyketides, such as the *pinnatoxins* [64, 65] which have been isolated from shellfish are known to be dinoflagellate produced. It is notable that in known cases the biosynthesis of polyketides in dinoflagellates is by a totally different pathway from that in other organisms. The other main class is composed of nitrogenous guanidino toxins of which *saxitoxin* is the prototype [66].

Ciliophora (Ciliates)

Genera studied chemically include *Euplotes*, *Tetrahymena*, *Litonotus*, and *Pseudokeronopsis*. The ciliates are non-photosynthetic organisms but can often harbor photosynthetic algae as symbionts. Chemical studies have been fairly limited, but a range of sesquiterpenoids, and some highly unusual triterpenes, have been isolated.

1.3.2.4 Chromista

The term Chromista was first introduced in 1981 as a higher-order taxon and includes all algae whose chloroplasts contain chlorophylls *a* and *c* [67]. Previously, the photosynthetic chromists had been classified as plants, while non-photosynthetic chromists were classified with the fungi or animals with the close relationship among chromists not appreciated until the advent of ultrastructural and molecular studies. Chlorophyll *c* and a number of other pigments found in the Chromista are not found in any plant group, and it is these pigments which give them their characteristic brown or golden color. Within the Chromista, the phylum that has been of greatest interest to marine natural product chemists is the Ochrophyta which encompasses the class Phaeophyceae, or the “brown algae.”

Ochrophyta: Phaeophyceae (Brown Algae)

About 1,600 species of brown alga are known, almost exclusively marine. The term “phaeophyta” is to be preferred, even if it is depicted as being at a phylum level. Modern studies have shown that the phaeophyta are only very distantly related to the other algae and the term “brown alga” is therefore a misnomer, although it remains in widespread use. Together with the diatoms and the chrysophytes, they constitute what has been described as the Stramenopiles. Whereas the other two subgroups are entirely monocellular, the vast majority of brown algae are multicellular and macroscopic, sometimes attaining very large size. Most species inhabit cold and temperate, often rough, seas and are sessile, demonstrating a well-defined differentiation into a foot (holdfast), stem (stipe), and frond and growing in surface or relatively shallow waters. The exception is the brown algae of the Sargasso Sea, which are two free-floating *Sargassum* species inhabiting tropical waters. The photosynthetic pigments of all species within the Stramenopiles are chlorophylls *a*, *c*₁, and *c*₂ (characteristic absence of chlorophyll *b*). The carotenoid content is limited to fucoxanthin and lesser amounts of violaxanthin. Both the structural and the storage carbohydrates of the phaeophytes differ from those present in other classes of algae.

The range of sterols found is limited and mostly based on minor modifications of the fucosterol structure, which is the major steroid. There is a wide range of unusual oxylipins, for example, bridged epoxy compounds and prostanoid-like cyclopentanoids.

Brown algae contain a wide range of terpenoids, phenolics, and meroterpenoids, but a striking and somewhat unexpected feature is the paucity of halogenated compounds, and those that are found in small amounts are bromo- and iodo- rather than chloro-substituted. They are unique in their ability to concentrate iodine (and also arsenic) to concentrations of up to 1% dry weight, and although 99% of

the iodine in the tissues is inorganic, the other 1% finds its way into thyroxine and other iodinated tyrosines and a small number of miscellaneous phenolics. The major secondary metabolite content of brown algae is represented by phenols and phenolic meroterpenoids, many of them sulfated and/or halogenated. The content of these in the tissues may reach 20% by weight and they may play a role in the prevention of larval fixation by marine animals and for protection against bacteria. A major series is represented by the phlorotannins, which are radical-induced oligomers of phlorotannin containing C–C or C–O–C linkages. The genus *Cytoseira* has been much investigated and has yielded a large range of structurally diverse meroterpenoids.

Haptophyta and Ochrophyta: Bacillariophyceae (“Bacillariophyta”; Diatoms), Chrysophyceae (Golden Algae)

It was this grouping of unicellular organisms together with the phaeophyta that constituted the Stramenopiles. The term “algae” formerly applied to some of these groups is now considered in biochemical and sub-microstructural studies to be a misnomer (cf. phaeophyta). Although these organism types are linked together in the classification scheme used here, this is a tentative assignment. These organisms have been relatively little studied chemically by comparison with the phaeophyta. The diatoms and haptophytes secrete hard exoskeletons of aluminosilicates and calcium salts respectively, while the golden algae do not, though they may contain silica microspicules. There are ~500 known species of marine golden algae and ~500 haptophytes. The number of marine diatom species, recognized to be 5,000, may be as high as 50,000, constituting the bulk of the phytoplankton at certain times of the year, and therefore of crucial importance to marine ecosystems.

The storage polysaccharide of diatoms and golden algae is chrysolaminarin. Photosynthetic pigments resemble those of the brown algae, with no phycobilins but with chlorophylls *c* and the more recently discovered chlorophyll *c*₃. There have been extensive studies on their lipids on account of their biotechnological importance (cf. algae). The content of sulfur glycerides, especially 1,2-diacylglycerol 6-sulfoquinovosides [68] (also found in other classes of organism), is relatively high. The range of known steroids resembles that of the phaeophyta in being based on limited side-chain modification of the cholestane skeleton, with some sulfation. The prymnesins are toxic polyethers produced by a haptophyte [69]. The range of terpenoids isolated is very narrow and limited so far to simple phytanes. It is noteworthy that in two studied diatom species, the biosynthesis of these (in the chloroplasts) is by a non-mevalonate pathway while the steroids, produced in the cytoplasm, are mevalonate derived. Nitrogenous compounds are similarly few in number, but the toxic pyrrolidine *domoic acid* (see Fig. 1.6), also found in red algae, was isolated as a shellfish toxin resulting from *Nitzschia* infection [70].

1.3.2.5 Plantae

The algae, considered in their totality, can be described as lower, mostly multicellular plants of a simple body plan, lacking well-defined differentiation

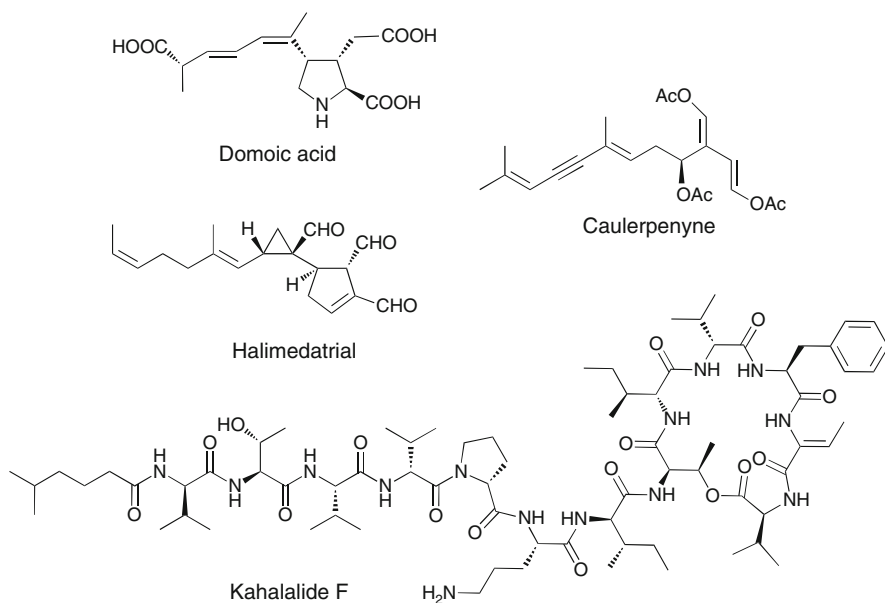


Fig. 1.6 Metabolites from “Bacillariophyta” and Chlorophyta

into roots, stems, and leaves. The higher plants, which show such differentiation, are virtually absent from the oceans, although some species (mangroves; several different spp. of higher plant) are important components of the estuarine saltmarsh environment and have currently become of considerable interest. The classification of algae has undergone a number of changes in recent decades and there is no definitive overall plan that takes care of every subgroup. The most fundamental division is between the brown algal branch, now better described as the phaeophyta as a grouping within the Chromista, and the green algal branch: two groupings which show large biochemical differences one from the other. The “green” branch comprises not only the green algae proper (Chlorophyta), but also the red algae (Rhodophyta), which are now considered more closely related to the green algae than either are to the phaeophyta and relatives.

Chlorophyta (Green Algae)

About 2,500 species are recognized inhabiting mostly surface waters of the calmer seas. Of these, about 20% have so far been investigated chemically, principally in the orders Bryopsidophyceae and Ulvophyceae. In their fundamental biochemistry (photosynthetic pigments, storage polysaccharides, etc.) the Chlorophyta resemble the higher plants. Some members are unicellular, sometimes as endophytes in other species of green algae. Green algae photosynthesize using the common carotenoids α - and β -carotenes, and contain a range of relatively common xanthophylls such as lutein. The most common storage polysaccharides are amylose and amylopectin, and the most common structural polysaccharide is cellulose, although

some groups also secrete β -1,3-xylan and β -1,4-mannan. The most widespread sterols are cholesterol, brassicasterol, sitosterol, and close relatives, although some rarer sterols have been characterized. Studies have not always distinguished between sterols involved in the algal membrane structure and those present in the cytoplasm.

The known secondary metabolites of the green algae are rather limited in structural range and are mostly confined to terpenoids of relatively common skeleton, and a range of aromatics including meroterpenoids. Halogenation is uncommon, and the terpenoids are so far limited to sesqui- and diterpenes and a few triterpenes. Many of the terpenoids contain enoloid functionality, for example, *caulerpenyne*, [71] and/or furan rings formed biogenetically by the cyclization of the related unsaturated aldehydes. Some of these metabolites have also been isolated from species that feed on green algae, such as molluscs. *Halimedatrial* is the only terpenoid so far isolated from green algae containing a carbon skeleton that has not been found elsewhere [72]. Nitrogenous compounds found in green algae tend to be low-molecular-weight amines related to aminoacids, or peptides and modified peptides such as the *kahalalides* [73].

Rhodophyta (Red Algae)

The red algae are characterized by a unique and complex reproductive cycle involving three alternating generations. The great majority of the 6,200 species known are marine, sometimes inhabiting deep water. They may be mono- or multicellular with a complete absence of flagellae. The chloroplasts have a double membrane similar to those of cyanobacteria and presumably arose by endosymbiosis with these organisms. There is no general agreement about the subclassification of red algae. An important biochemical similarity between the red algae and the cyanobacteria is the presence of the phycobilins, phycocyanobilin (blue-green), and phycoerythrobilin (red). It is the latter that is responsible for the red color of the tissues, but the color may be modified or masked by the presence of phycocyanobilin and/or chlorophylls. The red algae contain chlorophyll *a* and the characteristic pigment chlorophyll *d*.

The secondary metabolites of the red algae are characterized by a high proportion of halogenated terpenoids and aromatics, particularly in the intensively studied genus *Laurencia*. The terpene skeletons are strongly weighted toward the lower MW members of the series (especially sesquiterpenes), and there are many representatives of unique terpene skeletons not found in higher plants or elsewhere in the algae. The sesquiterpenes of *Laurencia* are based on more than 20 different carbon skeletons, some of them “traditional” and found also in terrestrial organisms, others novel. Many of these have also been isolated from molluscs and other animals that feed on red algae. There is also a wide range of halogenated (mostly brominated) diterpenes, many derived from the common (marine and terrestrial) skeleton labdane and other skeletons closely related to it. The parguerane skeleton, as found in *parguerene* (see Fig. 1.7) and related compounds, is however unique to marine organisms [74]. Certain *Laurencia* and *Chondria* species have also yielded a series of triterpenoid polyethers derived from squalene, for example, *thyransferol* [75]. The most characteristic class of natural product isolated from these genera,

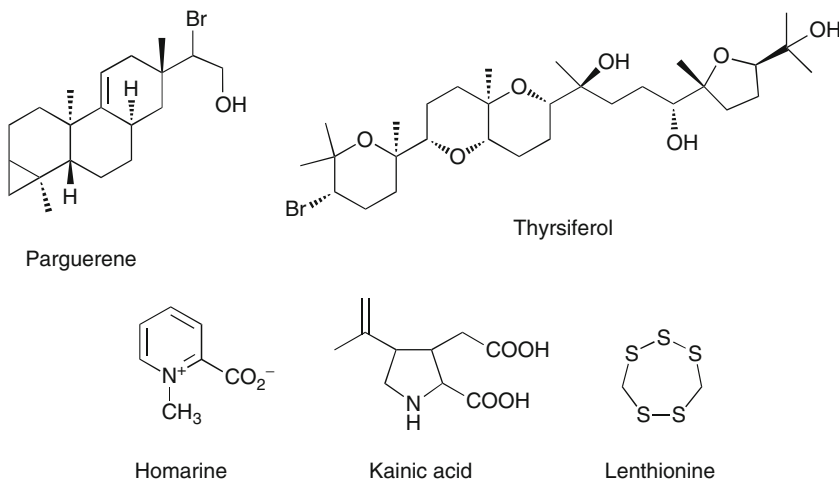


Fig. 1.7 Metabolites from Rhodophyta

however, is the extensive series of mostly halogenated compounds based on a linear C_{15} skeleton, the first of which to be discovered was laurencin in 1968 [76, 77]. A wide variety of structures based on ether formations are found on this basic skeleton (e.g., obtusenyne [78]), which probably arise by loss of a C_1 fragment from a C_{16} precursor. The Ceramiales also contain a range of halogenated phenolics. Nitrogenous natural products are relatively scarce in the majority of red algae, and mostly limited to widely distributed small molecules such as *homarine* [79, 80]. A range of simple halogenated indoles were isolated from *Rhodophyllis membranacea*. Once again, it is the Ceramiales that show a much greater range. A characteristic aminoacid is *kainic acid* [81] and other analogs. The chemotaxonomic unpredictability of this group of organisms is shown by studies of *Chondria californica*, which yielded a range of polysulfur compounds such as *lenthionine* [82]. These were unaccompanied by terpenes, and were not found in apparently closely related species.

1.3.2.6 Fungi

Fungi, part of the Eukaryota, are characterized by the lack of a photosynthetic mechanism and a mode of life which is saprophytic, parasitic, or symbiotic [83]. Another major biochemical difference from algae lies in their cell wall structure usually based on chitin rather than cellulose. Fungi are found throughout a wide range of terrestrial and marine environments and it is not possible to produce a meaningful definition of “marine fungi,” only to refer to a range of halotolerance among the various fungal species that are widely distributed. Thus marine sediments and marine invertebrate tissues yield fungal species from genera also found terrestrially, but which have developed a preference for growing in saline environments. Of the approximately 100,000 fungal species so far described, about

500 have been found in marine environments, but this figure is certain to increase in the light of further research. The majority of fungi fall into the category of higher fungi or Eumycetes having typical fungal biochemistry, and which can be subdivided into the four main classes of Zygomycetes, Ascomycetes, Basidiomycetes, and Deuteromycetes. These groups are distinguished by their method of spore formation (zygospores, asci, and basidia, respectively, for the first three groups). The Deuteromycetes are an ill-defined group roughly corresponding with the term fungi imperfecti (the terms Mycelia sterilia and Hyphomycetes are also found according to various schemes). These are fungi in which no reproduction is observable and which are therefore extremely difficult to identify. The Ascomycetes and the Deuteromycetes are the most represented in the marine environment and have been the most investigated chemically [84, 85].

The great majority of fungal secondary metabolites have been isolated from fungi associated with other organisms. Marine algae (green, red, and phaeophyta), like higher plants, harbor a wide variety of endophytic fungal species; for example, 116 different fungal strains were cultivated from a single specimen of *Fucus serratus* [86]. It is not in general known whether any particular relationship should be considered as symbiotic, benign, or pathogenic. There are usually strong structural similarities between the natural products from these epiphytic marine fungi and their terrestrial equivalents.

Fungal mycelia are also found in marine animal tissues. Evidence for their presence is based entirely on culturing experiments and as yet there is no evidence from direct microscopic examination or other techniques. Their role is unknown. In general, compounds produced by fungi associated with marine animals are structurally related to other fungal metabolites and are distinct from natural products produced by the organisms themselves. It does not appear that fungi are the biogenetic source of natural products isolated from marine invertebrates, unlike the situation found with bacteria. The most characteristic sterols of all fungi are ergosterol and related ergostanes. Reports of 5,7-dienic steroids from other marine species are suggestive of fungal contamination. There are very few reports of the incorporation of halogens. Most fungal secondary metabolites are based on a polyketide biogenesis, but some terpenoids are found, for example, the unusual nitrobenzoyl esters of 6,14-dihydroxy-7-drimen-12,11-olide (see Fig. 1.8) [87].

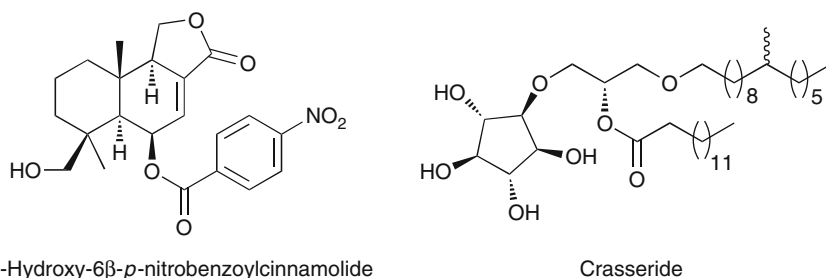


Fig. 1.8 Metabolites from fungi and Porifera

The alkaloids obtained from marine fungi are dominated by diketopiperazines/indoles, as is the case with terrestrial fungi. Very few biosynthetic studies have been reported for natural products specifically from marine fungi.

1.3.2.7 Animalia

All animals are members of the Animalia which range in size from no more than a few cells to organisms weighing many tons. Based on their body plans they are grouped into 30–33 different phyla of which the Arthropoda contains the greatest number of species (~1 million). All members of the Animalia are multicellular eukaryotes, a feature that separates them from bacteria and most protists, and they can be distinguished from plants, algae, and fungi by a lack of rigid cell walls. All members of the Animalia are heterotrophs and so rely directly or indirectly on other organisms for their nourishment. Most ingest food and digest it in an internal cavity with one or two entrances. The bodies of most animals, except the sponges (Phylum Porifera), are made up of cells organized into specialized tissues. Other distinguishing characteristics include a sexual mode of reproduction, at least at some point in the life cycle, and employ differentiated eggs and sperm.

Porifera

The sponges are considered as the most primitive of the multicellular organisms, providing an evolutionary bridge between the monocellular eukaryotes and the rest of the animal kingdom. They are multicellular organisms lacking all organ differentiation (including gonads) and some can uniquely reconstitute themselves after passing through a sieve. They are almost exclusively marine. Sponges are found at all marine depths but the proportion of calcareous sponges diminishes with depth owing to the physicochemical effect of pressure on the ability of the organisms to secrete calcium. The taxonomy of sponges is particularly difficult owing to the paucity of well-marked morphological feature by which they can be distinguished [88]. Many species have been synonymized and genera renamed (e.g., *Aplysina* = *Verongia*), and there are numerous views on their classification at higher levels; a recent multivolume treatise [89] proposes many changes. Three main subdivisions have been generally recognized, depending on the nature of the skeletons that they secrete; calcareous, siliceous, or askeletal. The largest group is the demosponges, about 95% of known species, in which the skeleton is of spongine, a proteinaceous polymer similar to keratin. The Hexactinellida sponges, characterized by silica spicules of sixfold symmetry, are found only at great depth and have been little studied chemically.

Sponges participate in a wide range of symbiotic/commensal relationships, and a large number of the isolations of natural products earlier reported from them are in fact owing to the presence of cyanophytes in particular. Given the extent of these associations, it is not surprising that the diversity of natural products reported from sponges and sponge aggregates covers the whole range of known types. Other natural products reported may be true metabolites of the symbionts [90]. A wide variety of cell membrane components have been isolated, not only extensive series

of both straight-chain, branched, and methylenic (cyclopropanoid) fatty acids but alkylglycerols and hopanoids as well as a vast range of steroids. There are also numerous brominated and α -hydroxyacids. Associated with the membrane structure is a wide variety of glycolipids, many of them of unique structural type [91]. The simpler *N*-containing parents are the sphingosines, the *N*-acyl derivatives collectively known as ceramides, and the glycosides, known as glycosphingolipids or cerebro-sides. The nitrogen-free glycolipid content also includes some structural types not found elsewhere, such as the *crasserides* [92], which as a class have been suggested to be uniquely diagnostic of the Porifera and found in all species examined.

Among calcareous sponges the most investigated genera are *Clathrina* and *Leucetta*. These genera have yielded in particular long-chain unsaturated aminoalcohols, a range of imidazole and other alkaloids, and cyclic peptides. By far the most studied have been the demosponges, reflecting their numerical preponderance and shallow-water accessibility. Demosponges contain a very wide range of steroids, which encompasses not only the conservatively modified structures biogenetically not far removed from cholesterol found in the algae, but also a large number showing more profound modification. These include 19-norsteroids and a range of A-ring abeosteroids (3-hydroxymethyl-A-norsteroids). The most common type of modification however is further side-chain methylation which leads to an extensive series of steroids having various branching patterns up to C₃₂. Side-chain cyclopropanolsterols occur in the range C₂₇–C₃₁, and there are also a large number of secosterols with fission at 5,6, 8,9, 8,14, and 9,11. There are also many polyhydroxylated and sulfated sterols of the type found in many other marine organisms, and many steroidal glycosides. Halogenated steroids and steroidal alkaloids are rare.

Demosponges of the genera *Plakortis* and *Plakinastrella* (order Homosclerophorida) contain a wide range of oxylipins, including many cyclic peroxides. Another group of unusual natural products found in sponges are the terpenic isocyanides together with their related isothiocyanates, isocyanates, and formamides. A wide range of alkaloids and terpenoids are found in demosponges. Indole alkaloids range from simple halogenated indoles such as the plakohypaphorines to polycyclics such as the pentacyclic pyridoacridines. Demosponges are the most prolific of all marine organisms in terms of the secondary metabolites that have been isolated from (but not necessarily produced by) them.

Cnidaria (Jellyfish, Sea Anemones, Gorgonians, and Corals)

This class of organisms represents the first major development in body plan over the undifferentiated sponges, showing cellular differentiation into cells with different functions, but in general no well-defined organs. The term Cnidarian replaces the older "Coelenterate." This is a class of organisms typified by a carnivorous lifestyle, the presence of specialized stinging cells (cnidocytes) used in the capture of prey and for defense, and a digestive system consisting of a sac with only one opening. They have a basically radial body plan, which may be modified either in the direction of a fixed polyp with a central gastric cavity (hydras) or a free-swimming medusa form (jellyfish) in which the gastric cavity is underneath. Reproduction is sexual, producing a free-swimming larval planula which develops into a free-swimming followed by a

polyp form, although in some species only one of these is formed. About 10,000 species are documented. The sea anemones, gorgonians, and corals have no free-floating phase and have a skeletal structure consisting either of secreted calcareous minerals or of proteinaceous material (gorgonine, analogous to the spongine found in the sponges). They are divided into two groups depending on their symmetry – eightfold in the octocorals (alcyonians or soft corals and gorgonians) and sixfold or a multiple of sixfold (hexacorals, including the sea-anemones and hard corals) [93] – and have been the most studied group of the cnidarians chemically.

In general, relatively few nitrogenous secondary metabolites have been isolated. The proportion of halogenated metabolites is also relatively low, except from *Briareum* spp. Octacorals are rich in prostanoids, steroids, terpenoids (but only sesqui- and diterpenes), and aromatics. The prostanoids include a number identical with those found in higher organisms of the prostaglandin series (A, B, E, and F), but also halogenated prostanoids containing Cl, Br, and I, especially from *Clavularia*. Further oxylipins are now being found in other cnidarians and it appears that their presence may be ubiquitous. The hexacorals also contain a range of polyunsaturated long-chain acids.

Like the sponges, cnidarians contain a wide range of sterols, both typical cholesterol related and those with modified side-chains. An important class are the side-chain cyclopropanoid steroids although it has been shown that these are produced by symbiotic dinoflagellates. There are many polyhydroxylated steroids, often showing side-chain epoxidation and a considerable number of secosteroids. Also encountered are pregnane glycosides, but in contrast to the sponges, *O*-sulfation is absent. The hexacorals produce polyhydroxylated ecdysteroids which are thought to protect the organism against crustacean larvae. The sesqui- and diterpenes found in the octacorals are diverse and include some skeletons unique to them that in most cases are unique to certain families. In contrast, terpenoids are almost absent from the hexacorals. The sesquiterpene hydrocarbon content of octacoral tissues may be exceptionally high and they are thought to play an ecological role as predator and larval implantation repellents. An important feature is the frequent occurrence of common terpenoids enantiomeric to those familiar from terrestrial plants. The hexacorals have yielded only a few sesquiterpenes; there is a complete absence of the isocyanides characteristic of the sponges and only a limited range of terpenoid alkaloids. The octacorals are very rich in diterpenoids, with over 1,900 belonging to 50 isolated skeletal types. As with the sesquiterpenes, some skeletons are widespread throughout the phylum, while others are restricted to a single family and can be considered as chemotaxonomic markers. Particularly widespread skeletons include cembranes, xenicanes, lobanes, briaranes, cladiellanes, dolabellanes, and amphilectanes. As with the sponges, many skeletons are prenylogues of widespread sesquiterpenoid skeletons. Some diterpene alkaloids have been found such as the *sarcodictyins* (see Fig. 1.9) [94]. The hexacorals produce a range of ceramides, often containing unusual sphingosines, and other acyclic amides. Their range of cyclic alkaloids is restricted, but includes the unique class of fluorescent pigments based on the cycloheptadiimidazole skeletons of parazoanthoxanthin A and *pseudozoanthoxanthin* A [95].

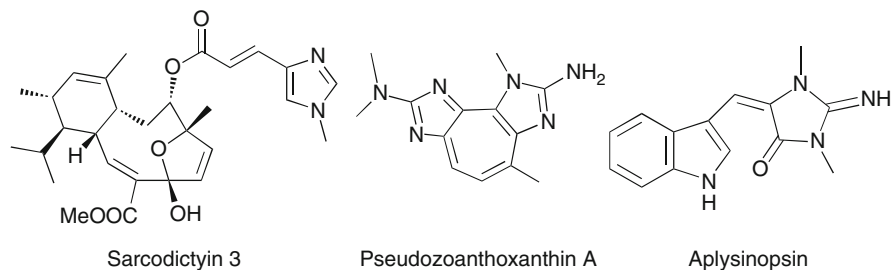


Fig. 1.9 Metabolites from Cnidaria

Hexacorals of the order Zoantharia (genus *Zoanthus*) have yielded a range of polyketide alkaloids. Chemically and pharmacologically, the most significant natural product isolated from cnidarians is probably palytoxin [35, 96]. Hexacorals inhabiting surface waters also contain a range of mycosporins which are closely related to analogs found in fungi and appear to perform a photoprotective function. They also contain a range of small nitrogenous betaines and other amines, some purines, and some simple indole-imidazole alkaloids centered on *aplysinopsin* [97].

Other classes of the cnidarians include the Cubozoa (box jellies), Hydrozoa (hydras), and Scyphozoa (true jellyfish). Chemical studies have been mostly confined to their venoms, which are peptides. One difficulty associated with studying their secondary metabolites is the large amount of water in the tissues, which can reach 98%. Some steroids have been identified, plus a small range of polyketides and simple alkaloids. There are also the nitrogenous compounds associated with the bioluminescence of some species such as *Cypridina*.

Platyhelminthes (Flukes, Tapeworms, and Free-Living Flatworms)

These are the flatworms, characterized by a bilateral body plan and the complete absence of a digestive cavity with about 15,000 species known. They may be terrestrial, freshwater, or marine and many belong to orders which are exclusively parasitic (e.g., flukes). The majority of marine species belong to the class of planarians (turbellarians). These are mobile, carnivorous animals having no physical means of defense and relying entirely on substances absorbed or modified from the diet, or produced by symbiotic organisms, as chemical antifeedants. The most studied genus is *Amphiscolops*. These worms are protected by amphidinolides produced by symbiotic dinoflagellates and other dinoflagellate metabolites [62, 63]. Other planarians feeding on ascidians have yielded alkaloids.

Annelida (True Worms)

These are the segmented worms, having an alimentary canal. They include the polychaetes, oligochaetes (earthworms; mostly terrestrial), hirudineans (leeches; mostly freshwater), echiurians, and Vestimentifera. They locomote by means of bristles which can be irritant or venomous. The best-known genus among the echiurians is the spoonworm *Bonellia viridis*, most studied on account

of its tetrapyrrole pigment bonellin which also plays a role in inducing sexual differentiation in the larva [98]. The Vestimentifera include the recently discovered giant hydrothermal vent dwellers *Riftia* which coexist with sulfur bacteria and store elemental sulfur in the tissues. So far there has been little study of lipid or steroid content. The carotenoid pigments appear to be mainstream components and are derived dietetically. Other annelid pigments are anthracene and anthraquinone based. Annelids also contain brominated phenols and derived aromatics which protect them against bacteria. Certain annelids exhibit bioluminescence and in *Odontosyllis* spp. this is based on pteridines such as 6-propionyllumazine. Nereistoxin is a simple aminodithiolane with powerful cytotoxic properties produced by *Lumbriconereis* sp. [99].

Nemertea and Phoronida

The ribbon-worms or nemerteans have yielded the powerful nicotinic receptor agonist anabaseine, used as a venom by the worm, together with several related oligopyridines. Toxins of the tetrodotoxin series are also found in the tissues, and also some peptide toxins. The unsegmented phoronidian worms *Phoronopsis* have yielded antibacterial bromophenols like those obtained from the annelids.

Bryozoa

These colonial organisms are entirely aquatic and mostly marine. They are distinguished by their unique form of gastric cavity, which is surrounded by tentacles forming an organ called the lophophore. The colonies are produced by budding and therefore consist of genetically identical individuals, each of which is surrounded by a bilayered exoskeleton, the inner layer calcareous (not always continuous) and the outer layer chitinous. They are suspension feeders, feeding on plankton and bacteria, and are found at all depths. Bryozoans have so far been less studied than the number of known species (5,700) would justify given the range of interesting natural products already isolated from them. This is probably a consequence of the difficulty of harvesting them.

Terpenoids and steroids have been little studied. The single diterpenoid murrayanolide isolated has a unique skeleton which implies that many more unusual terpenoids may exist in other bryozoans. The similarly limited studies of steroid content have yielded only relatively common types based on cholestane methylated in the side chain and/or hydroxylated. One or two anthraquinone pigments have been characterized, of which the most unusual is bryoanthrathiophene. The most numerous metabolites from bryozoans are defense chemicals, which comprise numerous alkaloids, and the *bryostatins* (see Fig. 1.10) [100], an important series of polyether polyketide toxins with anticancer properties, some of which have also been found in other marine organisms. The ultimate source of these may be a *Candidatus* bacterium [101]. The range of alkaloids is extensive taking into account the limited amount of work that has so far been done. There are simple halogenated phenethylamines, pyrroles, and pyrrolidines. The indoles found are mostly brominated simple indoles, but *Flustra foliacea* yielded a series of alkaloids of the physostigmine type unique in the marine environment [102]. The securamines, chartellines, and chartellamides

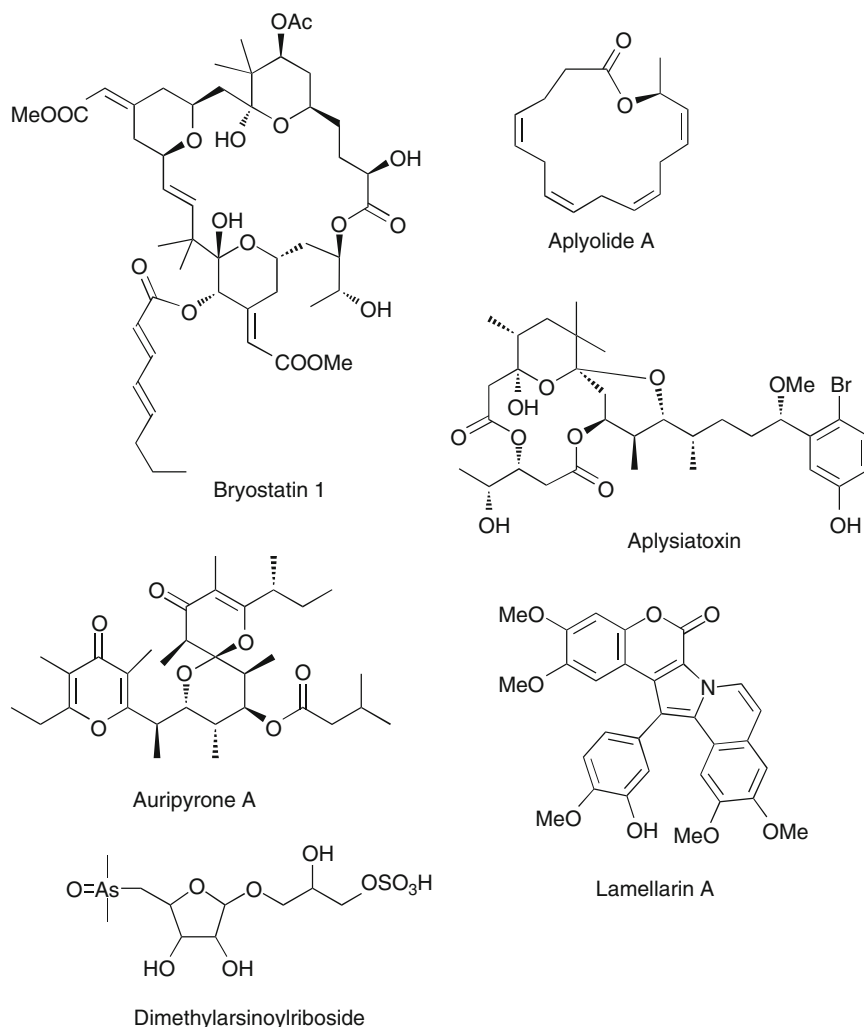


Fig. 1.10 Metabolites from Bryozoa and Mollusca

represent a further elaboration of this structural type up to a maximum of seven rings [103–105]. There are also a number of quinolinequinones, halogenated or bearing thioether substituents. The presence of nitro groups in a few alkaloids is notable.

Mollusca

This is a diverse and widely distributed phylum of organisms [106]. The body plan is basically non-segmented and bilateral, although in some molluscs (the gastropods) it is often modified by torsion into a spiral surrounded by a shell. There are well-developed organs inside a more or less thickened outer layer, the mantle,

which secretes a shell formed of calcareous matter and protein. This shell may be external, as in the gastropods, internal as in squids, or may be totally lacking (octopuses and nudibranchs). There is generally a muscular foot and a cephalic region which may be highly developed into tentacles and other organs, as in the cephalopods. The alimentary canal is well developed and furnished with a rasping radula used in feeding. Different classes of molluscs show variation in this general body plan, for example, the bivalves have a hinged shell, no cephalic region and no radula, and some of them also lack the foot. Many species of mollusc are known, present in marine, freshwater, and terrestrial environments, ranging in size from microscopic to very large. They show a wide range of dietary behavior (carnivores, herbivores, filter feeders, and detritus feeders) and undergo a wide range of symbiotic relationships. In particular, in some molluscs the mantle incorporates symbiotic algae providing toxic antipredator substances. The phylum is usually divided taxonomically into seven unequal classes, but of these four (including Chitons) are numerically limited and have been studied chemically little or not at all [107]. The most important classes both in terms of number of species, economic importance, and chemical studies are the gastropods, the bivalves, and the cephalopods. However, the bivalves, with their well-developed physical protective mechanism of the double shell, appear to have less need for chemical defense mechanisms and their secondary metabolites are less profuse. They have mostly been studied in terms of their economically important shellfish toxins, which are in fact microbial/dinoflagellate products. The cephalopods too have been rather little studied; their most characteristic metabolites are adenochromines [108]. The most studied organisms chemically have been various types of gastropod which have little or no physical defense and rely almost entirely on chemical defense against predators. The numerous gastropods are sometimes further divided into three subclasses: the Prosobranchia, the Opisthobranchia, and the Pulmonata. This division is not recognized by the *Catalogue of Life*, but since it is a convenient subdivision of a large group of natural product-producing organisms, it is followed here.

Terpenoids are numerous. The genus *Planaxis* (Gastropoda, Prosobranchia) has provided a series of cembranoids. Among the opisthobranchs, the sea hares or aplysians, which are herbivorous, feed on cyanobacteria and algae, and their digestive systems and mantles contain a wide variety of unchanged and metabolized secondary metabolites which perform an antifeedant function. These alimentary chains are complex and have been much studied. The two most studied genera are *Aplysia* and *Dolabella*; the former feed mostly on red algae and contain many halogenated and nonhalogenated terpenoids, cyclic halogenated ethers, lactones, and both peptide and nonpeptidal alkaloids. *Dolabella* spp. feed on brown algae, and in accordance with the terpenoid profile shown by these, contain mostly nonhalogenated diterpenoids as well as lactones, peptides (notably the extensive range of highly cytotoxic dolastatins, from cyanobacterial symbiosis), and alkaloids. A few *Aplysia* spp. feed on brown algae and also contain nonhalogenated diterpenes. Other products isolated from this type of mollusc appear to derive from symbiotic/commensal green algae, *aplyolidides* [109], and even fungi, *aplysiatoxin* [110, 111].

The shell-less nudibranchs can incorporate cnidocysts obtained from cnidarians into their mantle, and also rely heavily on compounds, especially terpenes, ingested in the diet as a means of defense. A wide range of skeletal types have been isolated, and include sponge-derived terpenoid isocyanides and compounds derived metabolically from them. However, nudibranchs also synthesize terpenoids *de novo* via the mevalonate pathway. Many terpenoids are present as glyceryl esters. In general it is possible to predict with a fair degree of accuracy what types of compounds (though not necessarily the exact compounds) will be isolable from nudibranch tissues by studying the prey of the different species. The sacoglossan gastropods also contain a range of terpenoids, but these animals are herbivorous and the terpenoids derive from commensal green algae entering into the tissues. Nudibranchs contain a narrow range of carotenoids and steroids. Other defense allomones include quinonoid and related meroterpenoids, and macrocyclic lactones. Also noteworthy is the isolation of prostanoid lactones from *Tethys fimbria*.

The distribution of polyketides in molluscs is patchy. They are found only in some classes of the gastropods, for example, the *auripyrones* (strictly, polypropionates) from *Dolabella* [112]. Pulmonarians have also afforded a number of polypropionates. Long chain aromatic and heteroaromatic metabolites, which do not appear to be derived from the diet, are found in *Navanax* spp., *Haminoea* spp., and other genera. Peptides, especially cyclic oligopeptides often containing unusual aminoacid residues, are probably widely distributed and show structural resemblances to similar compounds found further down the food chain, for example, the kahalalides [73]. Among other nitrogenous metabolites, the best-known from gastropods is the dye-stuff 6,6'-dibromoindigotin, known since ancient times. The genus *Lamellaria* (Gastropoda; Prosobranchia) yielded a wide range of the pyrrole alkaloids, the *lamellarins* [113].

Carnivorous gastropods of the genus *Conus* produce a vast series (there appear to be tens of thousands of chemically distinct compounds) of highly toxic peptides the conotoxins [114], which are delivered to the prey by means of a highly specialized injecting organ. The bivalve toxins (e.g., pinnatoxins [64, 65]) responsible for various kinds of shellfish poisoning are mostly produced by commensal dinoflagellates and have been mentioned above. There are differences in the distribution of different members of the saxitoxin series between the tissues of the bivalves and the originating dinoflagellates [115].

The kidneys of the giant clam *Tridacna maxima* concentrate up to 0.1% of arsenic, the function of which is unknown. It is stored as various *dimethylarsinoyl-ribosides* [116].

Echinodermata (Crinoids, Starfish, Sea Urchins, Sea Cucumbers, Brittle-Star, etc.)

These organisms are characterized by a radially symmetrical body plan (which is acquired in the adult stage, the larvae being bilaterally symmetrical) and a unique system of respiration through water-filled tube feet which also provide locomotion. There is a calcareous endoskeleton. This is the largest phylum of exclusively marine animals, with about 7,000 species known. They may be herbivores,

suspensivores, detritivores, carnivores, or necrophages, and the carnivorous species may prey, for example, on corals or other echinoderms. There are many examples of commensalism and parasitism between echinoderms and other organisms. Although various classification schemes for echinoderms differ in detail, five main groups are generally recognized. The most primitive, widely represented in the fossil record, are the Crinoids in which the mouth and anus are on the same surface. They have a planktonic larval form followed by an adult form that may be sessile (sea lilies) or mobile (feather stars). The other four groups, in which the mouth and anus are on opposing faces, are the starfish (Asterozoa), sea urchins (Echinozoa), sea cucumbers (Holourozoa) [117], and Ophiurozoa.

The presence of steroidal saponins of different types in the starfish and in the sea urchins is unique in the animal kingdom, and serves to delineate them from the other echinoderms and from each other. Other characteristic markers are the dominance of 3α -hydroxylated steroids in the ophiurians, and of quinonoid pigments of different types in the crinoids and in the sea urchins. The various types of echinoderm produce a variety of specialized polysaccharides, the study of which is still in its infancy. One that has been characterized is frondecside [118]. The lipid content of sea urchins and ophiurians is high in polyunsaturates. The starfish have been relatively little investigated but appear to follow the same pattern, with some prostanoid precursors. A high proportion of branched-chain acids have been isolated from sea cucumbers, but these are probably of bacterial origin. Phospholipids and glycosphingolipids appear to be universally present in echinoderms and a wide range of structural types of ceramides and cerebroside have been isolated from starfish and holothuroids. Throughout the echinoderms, halogenation is rare and found only in a few anthraquinone pigments such as the *gymnochromes* (see Fig. 1.11) (from crinoids) [119]. There are also few alkaloids of greater complexity than a range of aliphatic amines. The few exceptions to this generalization are most probably derived from organisms such as dinoflagellates present in the food chain.

The type and extent of steroid content is a major distinguishing feature of different types of echinoderm. The crinoids and echinoids have been little studied, but appear to contain exclusively “classical” steroid types closely related

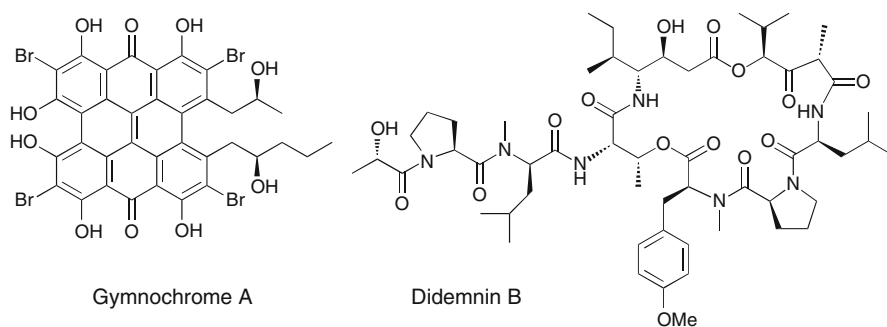


Fig. 1.11 Metabolites from Echinodermata and Ascidiaceae

structurally to cholesterol. The ophiurians, which in some respects are intermediate between the primitive crinoids and the more highly evolved echinoderms, contain many 3α -hydroxysteroids with only one or two glycosides. In the starfish, the range of glycosides and steroid sulfates is extensive, derived from a wide range of side-chain-modified parent steroids, which, however, are mostly 3β -hydroxylated. The side chain may be degraded or cyclopropanated. Polyhydroxylation/*O*-sulfation of the steroid nucleus, which is widespread in marine organisms, is at its most extensive here. The glycosides, such as the asterosaponins play a role in chemical defense through their surface-active properties. Both pentose and hexose residues are found. The holothurians contain many steroids, some biosynthesized *de novo* from acetate via lanostane triterpenes, others apparently derived from the diet. In *Holothuria*, it has been shown that two biosynthetic routes operate, one via lanosterol and the other via parkeol. The chief distinguishing feature of the holothurians, however, is the exclusive occurrence of specialized triterpenoid glycosides of the holostane type. Examples of the anthraquinonoid pigments are readily extracted from crinoids. Some of these are *O*-sulfates. The sea urchin pigments however are exclusively naphthoquinonoid. The number of alkaloid-like compounds isolated from echinoderms is extremely limited.

Arthropoda (Crustaceans)

The crustaceans, including the decapods, are the only type of animals in the vast arthropod phylum that occur to any extent in the sea. In the past the crustaceans have been considered a separate phylum, but it should be noted that the majority of taxonomists, including the *Catalogue of Life*, now assign the crustacea as a major subphylum of the arthropoda rather than as a separate phylum as they have in common the hard chitinous exoskeleton and the body divided into head, thorax, and abdomen. About 45,000 species are known, some of them (ostracods, e.g., *Cypridina*, and copepods, e.g., *Calanus*) very small planktonic organisms. The best known large species are the decapods (crabs and lobsters). Chitin, derived industrially from crab shells, is an important industrial material.

Chemical studies on crustaceans have been fragmentary and are mostly confined to their carotenoid pigments, some of which have also been obtained from other marine organisms but which were originally characterized as crustacean products. The molting hormones of crustaceans are terpenoid (methyl farnesate) and steroidal. Steroid studies have been fragmentary and have indicated a preponderance of cholesterol and closely related compounds.

Hemichordata

This is a numerically limited class of animal (about 100 species recorded), consisting of two surviving types of organisms; the acorn worms (Enteropneusts) inhabiting temperate and tropical waters, and the pterobranchs, colonial animals inhabiting chitinous tube galleries and found in polar waters. There is differentiation of the body into three well-defined zones, and they have some, but not all, of the morphological characters that define the chordates. Two types of natural products have been identified from them. The first is a range of toxic cyclohexanes,

halogenated phenols, and halogenated indoles isolated from *Ptychodera*, *Balanoglossus*, and *Glossobalanus* spp. These are used by the worms as defense chemicals and are of environmental significance. Of greater biochemical interest are the highly cytotoxic disteroidal metabolites the cephalostatins from *Cephalodiscus gilchristi* [120]. Owing to the difficulty of culturing hemichordate species, there is no information currently available concerning their possible distribution elsewhere in the phylum, or on their biosynthesis.

Chordata; Ascidiaceae (Ascidians, Tunicates)

These simplest chordate animals, also known as the protochordata, are generally divided into two unequal groups the urochordates (which include the ascidians or tunicates) and the cephalochordates which are free-swimming bilaterally symmetrical animals (*Branchiostoma*). Protochordates are the most developed of the invertebrates and have a notochord that is the evolutionary precursor of the spinal column characteristic of the vertebrates. They are exclusively marine. The larger group of urochordates is divided into three classes. Of these, two, including the free-floating salps, have been little investigated. Most chemical studies have been on the third group, the sessile ascidians [121]. These are filter feeders, often harboring commensal cyanobacteria and other organisms that may be the true source of some of the reported natural products. Their chemistry is dominated by the presence of an extraordinary range of mostly biologically potent nitrogen compounds. The ascidians also famously accumulate vanadium to a very high concentration in specialized cells, and some have highly acidic tissues (down to pH 1). The epidermis of ascidians contains a range of sulfated glycans, including some unusual residues such as L-iduronic acid, and the unusual polysulfated polymannose kakelokelose [122]. The membrane lipids have been little studied, and presumably are close to those of other higher organisms in structure. A few oxylipins have been isolated, along with ceramides and cerebrosides. These appear to be widespread as in the echinoderms, with some unusual types such as didemniserinolipids isolated [123]. Ascidians contain a range of carotenoids, both common ones and some rarer examples probably derived from metabolic alteration of more common carotenoids present in the filtered plankton. The steroids so far identified lack the wide structural range shown by the echinoderms and are mostly straightforward cholestanes and ergostanes, with some 5,8-epidioxysteroids and secosteroids. Nonnitrogenous secondary metabolites are few in number and terpenoids are rare. Several series of meroterpenoids have been isolated, especially from the Polyclinidae. The ritterazines from *Ritterella* have disteroid structures linked by a central pyrazine ring [124], showing close structural similarity to the cephalostatins from hemichordates [125].

Among the nitrogenous metabolites, many of which doubtless also spring from commensal organisms, there is a very wide range of structure including some with, and some without, analogies in other phyla. Firstly, there is an extensive range of modified peptides and depsipeptides. Several series of these are macrocyclic thiazoles and oxazoles, for example, the patellamides [125, 126]. Other cyclic depsipeptides are more strictly peptide related, although containing a range of unusual aminoacids.

The most studied have been the *didemnins* and their relatives [127, 128]. Heterocyclic alkaloids are numerous and include the extensive range of pyrroloisoquinolines, the lamellarins which were first isolated from molluscs (*vide supra*), but which are the products of ascidians on which they prey, or possibly of a symbiotic association involving sponges [113, 129]. Quinoline alkaloids are represented and the basic quinoline ring system is further elaborated into pyridoacridines. These too are also found in other marine organism classes. In the ascidians they fulfill the role of pigmentation and are also mostly cytotoxic. Indole alkaloids are also numerous, again known mostly as polycyclic condensed systems. Ascidians also contain a wide range of sulfur compounds, both sulfur-heterocycles and polysulfides.

Chordata; Actinopterygi (Fish)

The fish represent the most numerous of marine vertebrates. They are well studied taxonomically and extensively documented in the online database *Fishbase* (a contributor database to the *Catalogue of Life*). They can be divided into cartilaginous fishes (e.g., sharks), and the larger category of bony fishes, considered more highly evolved.

The cartilaginous fishes contain a wide range of polyhydroxylated nitrogenous and nonnitrogenous sterols based on 5 β -cholestane and include the important drug lead *squalamine* (see Fig. 1.12) [130]. The difference in the color of fish is due to the presence of various carotenoids and xanthophylls.

The fish products that have received the most chemical attention, apart from the lipids, are the toxins produced by various species. These may be steroidal, peptide, or alkaloid like, such as the much studied *tetrodotoxin* and its relatives from

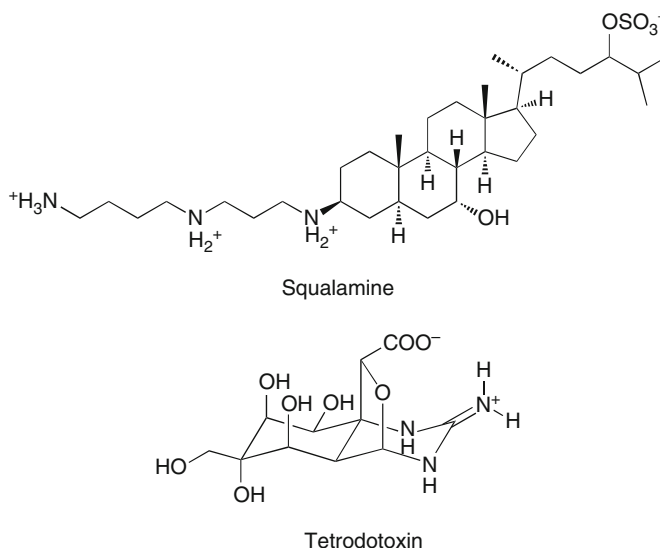


Fig. 1.12 Metabolites from Actinopterygi (fish)

fugu fish (various species of the Tetraodontidae) [131]. The latter, however, are metabolites of *Pseudomonas* bacteria or dinoflagellates in the fish, and are also found in other marine organisms and even terrestrial ones. Some fish secrete peptide venoms in specialized spines to deter prey.

1.4 Marine Taxonomy and Natural Products Chemistry

Biodiversity at the higher taxonomic levels (phyla and classes) is greater in the marine phyla. Of the 76+ phyla recognized by the *Catalogue of Life* across the Eukaryota, about 60 have marine representation compared with around 40 for terrestrial and freshwater environments. This comparison is even more extreme for the Animalia with all but one phylum out of the 30+ recognized having marine representatives (see Fig. 1.4). In contrast, species diversity is lower in the sea with just 250,000 species recognized against the >1.5 million terrestrial and freshwater species.

In looking back over the modern history of marine natural products, definite trends and preferences in the selection of phyla are discernible. To analyze these trends the database MarinLit [132] was used. This is a database of the marine natural products literature. In addition to the usual bibliographic data, the database contains an extensive collection of keywords, trivial names, compound information including structures, formulae, molecular mass, numbers of various functional groups, and UV data. All of these items can be searched for either individually or in various logical combinations. Taxonomic data are also included, permitting the exploration of relationships at various levels from genus up to phylum. The taxonomic descriptors used in MarinLit are aligned with the *Catalogue of Life*, thus avoiding the circumspection associated with alternative taxonomic schemes (cladification vs classification) and the use of pseudonyms. The data extracted from MarinLit were compared in the first instance against Bouchet's modified list of marine species [17] at the higher taxa level. The comparisons are shown in Tables 1.3 and 1.4. The criteria used were the total number of species studied in each taxon, the percentage this represented of that taxon, and the number of papers

Table 1.3 Comparative data for species studied from the higher-order taxonomic levels

Higher taxa	Number of marine species (Bouchet 17))	% of marine higher taxa	Species studied	% coverage of marine higher taxa	Number of papers by taxa	% of papers published
Archaea	>0	>0%	5	-	4	0.02%
Bacteria	5,800	2.5%	504	8.7%	1,622	8.0%
Fungi	500	0.2%	289	57.8%	612	3.0%
Protozoa	>14,800	~6.4%	192	~1.3%	929	4.6%
Chromista	7,600	3.3%	639	8.4%	1,3489	6.6%
Plantae	8,700	3.8%	1,062	12.2%	2,202	10.9%
Animalia	192,667	83.9%	4,071	2.1%	13,596	66.9%
	>230,117		6,762	~2.9%	20,314	

Table 1.4 Comparative data for marine natural products from the higher-order taxonomic levels

Higher taxa	Number of marine species (Bouchet [17])	% of marine taxa	Species producing new compounds (number, %)	Number (%) of compounds isolated	Number (%) of papers on new compounds
Archaea	>0	>0%	2 (?%) ^a	24 (0.1%) ^b	2 (0.03%) ^c
Bacteria	5,800	2.5%	201 (3.5%)	1,178 (5.9%)	545 (7.0%)
Fungi	500	0.2%	196 (39.2%)	969 (4.8%)	369 (4.7%)
Protozoa	>14,800	6.4%	60 (0.4%)	308 (1.5%)	193 (2.5%)
Chromista	7,600	3.3%	182 (2.4%)	1,231 (6.1%)	467 (6.0%)
Plantae	8,700	3.8%	282 (2.1%)	1,975 (9.9%)	798 (10.3%)
Animalia	192,667	83.9%	1,941 (1.0%)	14,372 (71.7%)	5421 (69.6%)
	>230,117		2,864 (~1.25%)	20,057	7,795

published along with the relative percentage contribution to the overall output of papers. Some 84% of all marine species belong to the Animalia. The observation that 4,071 of the 6,762 marine species studied belong to the Animalia is in keeping with this dominance of the Animalia among the marine species. The actual number of species studied is probably higher than this as many of the samples studied were identified to the genus level only. The 129 citations of *Laurencia* sp. or the 132 citations of *Streptomyces* sp. have each been counted as only one in the list of species studied, even though they might represent many different species. However, this will be offset as many will be identical to samples fully identified to the species level. The number of papers published by taxon is generally in step with the relative numbers of species/taxon with 13,596 of the 20,314 papers published up to early 2009 having an Animalia focus. Despite the focus on the phyla of the Animalia, the relative percentage coverage of this taxon (2.1%) is noticeably lower than for most of the other taxa, except the Archaea.

Many aspects of MNPs are covered in MarinLit. These include first syntheses of MNPs, assignment or correction of stereochemistry, environmental studies, as well as the isolation of new natural products, and these are the data covered in Table 1.3. The isolation of new natural products is the focus of Table 1.4. Studies on 2,864 species resulted in the isolation of 20,057 compounds reported in 7,795 papers. These are the data to early 2009. Again the actual number of species is not totally reliable as many samples were reported to the genus level only. Not surprisingly the major focus has once again been on the Animalia as the prime source of new compounds (14,372). There is a good correlation between the papers published and the numbers of compounds isolated. Despite the focus on Animalia the overall percentage of species in this taxon yielding new compounds is only 1%.

The data outlined in the Tables shows the output and general emphasis over the past 75 years in MNP chemistry, but to get to the detail it is necessary to examine the data at a phylum level. These data are portrayed in Tables 1.5 and 1.6. For some taxa, Bouchet's breakdown [17] was not detailed enough and the added phyla are shown in italics as, for example, in Table 1.5, Actinobacteria, etc.

Table 1.5 Comparative isolation and publication data for the Archaea, Bacteria, Fungi, Protozoa, Chromista, and Plantae taxa

Taxa	Marine species	Species with new compounds	Species studied	Compounds isolated	Papers with new compounds	Total papers
<i>Archaea</i>						
Euryarchaeota	–	2	3	24	2	4
	>0	2	3	24	2	4
<i>Bacteria</i>						
Bacteria	4,800	128	295	571	283	699
<i>Actinobacteria</i>		59	116	348	167	357
<i>Bacteroidetes</i>		8	15	16	8	25
<i>Firmicutes</i>		8	13	51	25	60
<i>Proteobacteria</i>		53	151	156	83	257
Cyanophyta	1,000	73	209	607	262	923
	5,800	201	504	1,178	545	1622
<i>Fungi</i>						
Fungi	500					
<i>Ascomycota</i>		195	278	968	368	605
<i>Basidiomycota</i>		1	5	1		4
<i>Zygomycota</i>			6		1	3
	500	196	289	969	369	612
<i>Protozoa</i>						
Ciliophora	?	7	11	27	10	18
Sporozoa						
Phylum not assigned	?					
Class Sporozoa						
Dinophyta (Dinomastigota)	4,000	52	177	278	182	905
Euglenozoa	250	1	3	2	1	5
Radiolaria		–	–	–	–	–
Phylum not assigned	550					
Class Sarcomastigophora						
Foraminifera						
Phylum not assigned	10,000					
Class Granuloreticulosea						
	>14,800	60	191	307	193	928
<i>Chromista</i>						
Ochrophyta	1,600	161	456	1166	437	1120
Class Phaeophyceae						

(continued)

Table 1.5 (continued)

Taxa	Marine species	Species with new compounds	Species studied	Compounds isolated	Papers with new compounds	Total papers
Ochrophyta	500	18	174	57	27	222
Class						
Chrysophyceae						
<i>Labyrinthista</i>		1	3	3	1	2
<i>Oomycota</i>		–	2	–	–	2
Haptophyta	500	1	1	3	1	1
“Bacillariophyta”	5,000	1	3	2	1	2
	7,600	182	639	1,231	467	1,349
<i>Plantae</i>						
Chlorophyta	2,500	60	305	275	113	541
Magnoliophyta	50	26	73	125	43	98
Rhodophyta	6,200	195	682	1,574	641	1,562
	8,750	281	1,060	1,974	798	2,201
Totals	37,450	922	2,683	5,683	2,371	6,712

For the taxa from Archaea through to Plantae, shown in Table 1.5, there are 37,450 species of which 2,683 have been studied at one level or another, some 5,683 compounds have been isolated, 2,371 compound structural papers published, and a total of 6,712 papers refer to these species in one way or another. These seven taxa represent just over 16% of the known/recognized marine species, but just over 7% of these recognized species have been examined with the bulk of this work having been accomplished over the past two decades.

The taxon Animalia, covered in Table 1.6, portrays a somewhat different picture.

This one higher taxon, the Animalia, represents 84% of the established marine species and comprises 30 phyla (Table 1.6), although the actual number of phyla is variable from 30 to 33 depending on the taxonomic authority consulted. Of the 29 phyla with recognized marine representatives, only 13 have been sampled over the years by natural product chemists (Table 1.6). In all 4,071 species out of a total of 192,667 (2.1%) of the Animalia have been examined. Of these 1,554, or 38%, have come from the Porifera alone, another 806 (20%) from Cnidaria, 587 (14%) from Mollusca, and 407 (10%) from Echinodermata. So, 82% of the Animalia species examined have come from just four phyla. Furthermore, about half of the compounds isolated from the Animalia have been of Porifera origin (7,024 out of 14,372) and the phylum accounts for one third of all publications across all branches of marine natural products chemistry. As only 5,683 compounds came from all the other higher taxa combined, this one phylum, the Porifera with an estimated 5,500 species, has been the origin of about 30% of all of the MNP chemistry. In keeping with the isolation and publication rate, the percentage

Table 1.6 Comparative isolation and publication data for the Animalia

<i>Taxa</i>	Marine species	Species with new compounds	Species studied	Compounds isolated	Papers on new compounds	Total papers
Animalia						
Acanthocephala	600	–	–	–	–	
Annelida	12,148	14	52	48	25	90
Arthropoda	47,217	9	77	11	10	88
Brachiopoda	550	–	2	–	–	2
Bryozoa	5,700	28	77	172	75	334
Cephalorhyncha	156	–	–	–	–	
Chaetognatha	121	–	–	–	–	
Chordata	21,517	184	475	957	396	1,513
Cnidaria	9,795	415	806	3,909	1,307	2,545
Ctenophora	166	–	–	–	–	
Cycliophora	1	–	–	–	–	
Echinodermata	7,000	205	407	1,172	446	852
Echiura	176	–	–	–	–	
Gastrotricha	395	–	–	–	–	
Gnathostomulida	97	–	–	–	–	
Hemichordata	106	3	18	29	12	68
Kamptozoa	170	–	–	–	–	
Mesozoa	106	–	–	–	–	
Mollusca	52,525	201	587	1,046	459	1,729
Nematoda	12,000	2	7	2	3	9
Nematomorpha	5	–	–	–	–	
Nemertea	1200	–	1	–	–	7
Onychophora	0	–	–	–	–	
Phoronida	10	–	–	–	–	
Placozoa	–	–	–	–	–	
Platyhelminthes	15,000	2	8	2	2	63
Porifera	5,500	878	1,554	7,024	2,686	6,296
Rotifera	50	–	–	–	–	
Sipuncula	144	–	–	–	–	
Tardigrada	212	–	–	–	–	
Totals	192,667	1,941	4,071	14,372	5,421	13,596

coverage of that phylum for chemistry has been very high with 878 out of the estimated 5,500 species having been examined for chemistry and a further 676 species implicated in environmental studies, reviews, and the like. This equates to a 28% overall coverage of that phylum.

When the outputs and the foci of MNP chemistry are examined, it is obvious that right from Bergman's first papers [21–27] MNP chemistry has been *Porifera-centric*. Is there an anthropomorphic bias to these results? Undoubtedly! There was no doubting the enormous academic and medicinal chemistry interest in

Bergman's discovery of the arabino-pentosyl nucleosides. It was from this discovery that the development of the nucleoside-based drugs ara-A, ara-C, and AZT could be traced, and this development has been well documented [133, 134]. The 1967 symposium held in Rhode Island with the ambitious title *Drugs from the Sea* [135] promoted greater interest in the field and raised the promise for other potential pharmaceuticals. Perhaps the mindset was that the Porifera must hold further secrets? Certainly the phylum Porifera has fascinated and held the interest of researchers from the 1950s onward. Every year 25–30% of all MNP publications refer to this phylum. This same Porifera-centric selection showed up in the marine component of the collections of the Natural Products Branch of the NCI's Developmental Therapeutics Program undertaken between 1986 and 2004. From the 9,945 individual organisms tested no less than 4,600 were sponges [136]. Again, this is a figure that is out of all proportion to the species-abundance of this phylum and strongly supportive of anthropomorphic bias in the collection process. This is not surprising as sponges are well represented in depths readily accessible by snorkeling or SCUBA diving, are often colorful and easily spotted underwater, quite varied in structure, and range in size from thin encrusting films (not usually collected) through a very convenient size range for collection in enormous vases and cups.

There have been different foci of interest at different points in time and this too was possibly a result of different collection techniques as well as advances in separation technologies. For example, during the 1960s and 1970s there was about as much interest in the red algae (Rhodophycota) as there was in the sponges. In the semi-decade 1974–1978, publications on red algae ran at about the 20% mark compared with 25% for sponges [132]. This then steadily dropped down over the years to the current level of about 5%. Interest in the brown algae (Ochrophyta) shows a similar pattern (10% decaying to about 4%). Both the red and the brown algae are easily accessible by shore-wading and not reliant on snorkeling or SCUBA diving, so early focus on red algae can probably in part be ascribed to ease of collection as chemists first started to explore the marine environment. Another readily collected phylum is the Mollusca which has featured in around 7% of all publications each year since the early 1960s [132].

The type of chemistry that has been published through the years also shows definite influences. The metabolites published in the early years tended to be nonpolar, lower molecular weight compounds, in keeping with the chromatographic practices of the 1960s and 1970s, for example, halogenated monoterpenes and sesquiterpenes from red algae. In Faulkner's first review of marine natural products chemistry covering the period 1974–1976 [137], >90% compounds covered were nonnitrogenous and nonpolar in character. This percentage rapidly decreased with the advent of new chromatographic techniques and chromatographic phases in the 1970s and 1980s that were better suited to dealing with polar compounds. Simultaneously, greater emphasis was being placed on biological activity. In keeping with Lipinski's rules [138] such compounds are polar molecules, so the range and type of metabolites sought, isolated, and characterized was changing from less polar to more polar metabolites.

Another advantage of shore-wading had been the ability to collect large samples relatively easily. Initially snorkeling and then SCUBA diving markedly expanded the range of species available, but necessarily limited the scale at which collections could be made. But, introduction of new techniques such as ESMS and progressive changes in NMR techniques and field strengths saw marked reductions in the amount of compound required and significant increases in the complexity of the molecules that could be successfully studied. This effectively allowed work on much smaller field samples, perhaps at the 10 g scale rather than a kg scale with a marked expansion of collection options as very small samples only needed to be collected. For example, effective sampling from the myriad of thin, encrusting invertebrates that compete for space on a cliff face. Other, more recent advances in NMR technologies has seen the introduction of capillary probes [139] and small diameter cryoprobes [140] leading to NMR spectroscopy on the nanomole scale [141]. This has effectively reduced the field sample requirement to 50 mg or less [142]. These sources of bias need to be borne in mind when considering how the field of MNP chemistry developed and why it evolved as it has.

1.5 The Results Achieved

Terrestrial natural products chemistry has traditionally been the source of the modern pharmacopeia: the expectations for the marine counterpart were not dissimilar. Despite that amazing start provided by Bergman, the realization of the potential of marine natural products has been a long time in coming. Through the years many other potently bioactive compounds have been identified. Few have been developed, but many are serving useful roles as biomolecular probes. The first marine natural product to be marketed as a drug was ω -conotoxin MVIIA, in 2004 under the trade name Prialt, for the treatment of intractable pain. ω -Conotoxin MVIIA had originally been isolated from the Pacific marine snail *Conus magus* [114]. This development was followed in 2007 by the approval of Yondelis for soft tissue sarcomas. Yondelis, or ET-743, is a fused tris-isoquinoline isolated from the Caribbean tunicate *Ecteinascidia turbinata* [143, 144]. Until about 12 years ago the bioactivity most sought after was anticancer. Since then a much wider range of selective bioassays have been deployed and more often than not the natural products chemists have been working in collaboration with pharmacologists to achieve these results. Recent reviews have highlighted marine natural products of biological relevance [145–148]. Of particular interest is the source organism for these compounds. The largest collection and screening effort on marine organisms has been that carried out by the NCI [136]. Approximately 12,000 marine samples were collected from the Caribbean and the Indo-Pacific, and extracts from 9,945 individual organisms were tested in the NCI human cancer one dose/60-cell-line prescreen. Close to 50% of these samples were from the phylum Porifera. From this assembly, 620 organisms across 12 phyla were considered active with 407 being of sponge origin. When the data were reduced to a percentage “hit-rate,” eliminating the Porifera-centric character of the collection strategy, other marine phyla with

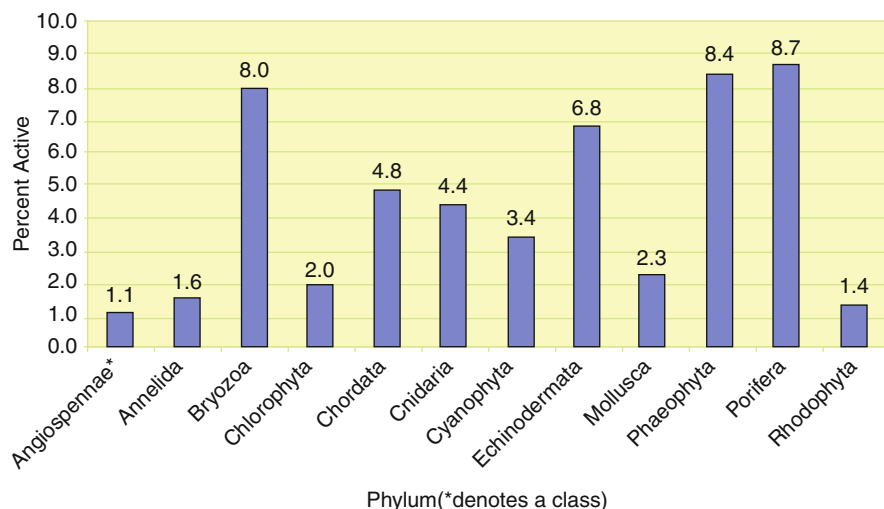


Fig. 1.13 Number of antileukemia “active” marine specimen extracts from marine phyla expressed as a percentage of the total number tested (Reproduced, with permission, from [136])

biological potential were revealed (see Fig. 1.13), suggesting that collection strategies in the future should be modified so as to be better balanced and include a wider range of marine phyla.

Over the past 30 years, many bioactive compounds have been isolated from marine organisms and a number have undergone extensive biological assessment and some are currently progressing through phase trials. These are potential candidates to join Prialt and Yondelis as drugs of marine origin. Others have been tested and for one reason or another were not suitable for advancement. A list of 40 bioactives and their biological origins has been compiled [73, 149–187] (Table 1.7 and Figs. 1.13 and 1.14) and serves to highlight the importance of marine phyla other than Porifera, if bioactivity is a consideration.

1.6 Macro or Micro: Which is the Producer?

Although isolated from macroorganisms such as sponges, bryozoans, or ascidians, it is by no means always certain that the parent organism is the producer of the (bioactive) compounds. Much progress has recently been made in assigning a definite microbial origin to many natural products. Take the case of swinholide A: originally isolated from the sponge *Theonella swinhoi*, centrifugation of macerated cell samples from the sponge showed that the macrolide was located within heterotrophic unicellular bacterial cells, but was absent from the sponge cells themselves and the co-occurring cyanobacterium *Aphanocapsa feldmanni* [188]. More recently, however, swinholide A has been found in field collections of

Table 1.7 A selection of bioactive marine compounds and their source phyla

Name	Phylum
Marinomycins [149]	Actinobacteria
Saliniketol A/B [150]	Actinobacteria
Salinosporamide A [151]	Actinobacteria
Thiocoraline [152]	Actinobacteria
Bryostatin 1 [100]	Bryozoa
Ascididemin [153]	Chordata
Aplidine [128]	Chordata
Diazonamide A [154]	Chordata
Didemnin B [127]	Chordata
<i>Yondelis</i> [143, 144]	Chordata
Meridianins [155]	Chordata
Vitilevuamide [156]	Chordata
Squalamine [157]	Chordata
Eleutherobin [158]	Cnidaria
Pseudopterosin [159]	Cnidaria
Apratoxin E [160]	Cyanophyta
Coibamide A [161]	Cyanophyta
Cryptophycins [162, 163]	Cyanophyta
Curacin A [164]	Cyanophyta
Largazole [165]	Cyanophyta
Symplostatin 1 [166]	Cyanophyta
Dolastatin 10 [167]	Mollusca
Indirubins [168]	Mollusca
Kahalalide F [73]	Mollusca
<i>Prialt</i> [114]	Mollusca
Spisulosine [169]	Mollusca
Bengamide [170, 171]	Porifera
Dictyodendrin [172]	Porifera
Dictyostatin [173]	Porifera
Discodermolide [174, 175]	Porifera
Dysidiolide [176]	Porifera
Halichondrin B [177]	Porifera
Hemiasterlin [178]	Porifera
Jaspamide [179, 180]	Porifera
Laulimalide [181]	Porifera
Nakijiquinone [182]	Porifera
Peloruside [183]	Porifera
Phorboxazole [184]	Porifera
Salicylhalamide A [185, 186]	Porifera
Variolin [187]	Porifera

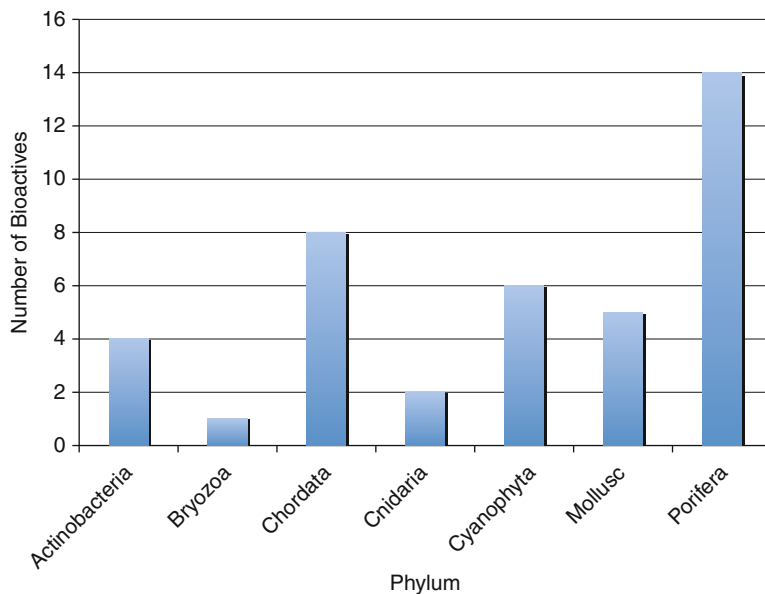


Fig. 1.14 The source phyla for a range of 40 bioactive marine metabolites

cyanobacteria [189], and it has been speculated that it may be produced by one component of this symbiont system, and stored by another [51, 189]. A comparable suggestion came from work on the phorbaxazoles and the phorbaxides with the comment that “they may actually be produced by cyanobacteria that either live within the host, or expressed from microbial genes that have been integrated into the host sponge.” [145]. Molecular genetics techniques were used to convincingly show that the patellamides A and C are biosynthesized by *Prochloron didemni*, the cyanobacterial symbiont that is hosted by the sponge *Lissoclinum patella* [190]. Molecular techniques also established that the bryostatins are likely produced by an unculturable endosymbiotic γ -proteobacterium “*Candidatus Endobugula sertula*” that is transmitted vertically between generations [101].

Natural products isolated from the higher marine organisms can also have a dietary origin. A good example would be dolastatin 10, isolated originally from an Indian Ocean sea hare (Mollusca) with a microbial origin suspected. The subsequent isolation of simplostatin, differing from dolastatin by a methyl group, from a cyanophyte suggested a possible Cyanophyta origin, which was subsequently confirmed by the isolation of dolastatin 10 from a *Symploca* species [166, 167, 191].

In some cases definite de novo biosynthesis of some natural products has been demonstrated, but it may also be true that although a particular metabolite isolated from a higher animal has not yet been found among the lower forms such as cyanophytes in the same ecosystem, this is merely an accident of the search process.

From a bioprospecting perspective the parent organism will remain the object of primary interest, but for development of a potential lead, the matter of supply is a vital question that must be answered right at the outset. It is at that point that questions on symbiont versus host-cell origin need to be answered, not during the search of the marine environment for new (bioactive) compounds.

1.7 Marine Biodiversity: Into the Future

The currently accepted number of marine species is of the order of 230,000–275,000 species and there are about 1,300–1,750 new species being added to that inventory each year, but these are mainly in the area of the Mollusca and Crustacea (Arthropoda). There is an enormous gulf between that accepted value and the estimated number of species which runs as high as 100 million depending on the authority consulted. Chapman has suggested a total of 11 million with dramatic rises in the invertebrates, most notably the arthropods, the fungi, bacteria, chromista, and protozoa with estimates in some of these taxa rising by several orders of magnitude [13]. Knowledge of the potential species remaining to be described is increasingly dependent on culture-independent molecular techniques. Although applied primarily to explore the diversity of Archaea and Bacteria assemblages, these techniques have not been restricted to prokaryote domains. The suggested 99,000 species of fungi [13] (described 45,000 [9]) is likely to rise to 1.5 million, an estimate considered “accurate” within a factor of 5 with the increase in described species likely to arise from ectoparasites and non-mycorrhizal endophytic species [192]. What proportion of these are marine is conjecture only, but Bouchet’s number of just 500 marine fungi seems very conservative.

Chromista and Protozoa diversities present uncertainties with only about 7,000 species in each taxon described (*Catalogue of Life*), but the numbers of projected species counts are listed in hundreds of thousands. Taking account of the large geographical areas still to be explored from a phycological perspective and the morphological similarities that mask genetic diversity, these suggested figures are not unreasonable. Culture-independent molecular techniques are also being widely used in studying protistan diversity [192].

Moving beyond the microbial world to the Animalia there are again important questions to ask on species biodiversity. A large part of the marine biodiversity is that of the symbionts – the commensals, associates, and parasites. How many copepods are there? How many marine helminthes? Reasoned answers suggest figures way beyond the currently accepted numbers. For example, the marine helminthes might number between 100 and 200,000 [17]. No comment has yet been made about the deep sea and what that area contributes to marine biodiversity. The deep sea was traditionally seen as a harsh environment inhabited only by those few and cosmopolitan species capable of living in the dark under enormous pressures and near freezing temperatures. But, following Grassle and Maciok’s 1992 seminal paper [193] on deep sea biodiversity, opinions have been markedly changed leading to comments such as “a riot of species in an environmental calm” [17] to describe the deep ocean and its accompanying biodiversity. Grassle and

Maciolok found 798 mainly new species of polychaetes and isopods in 233 box cores of 30×30 cm taken on a 176 km transect along a 2,100 m depth contour off the North Eastern coast of the USA. As there is 3×10^8 km² of ocean floor deeper than 1,000 m, it sparked a vigorous debate as to the actual numbers of species contributed by the deep sea ranging from 100 million downward. Until deepwater basins in the other oceans of the world are explored no consensus can be reached as to the contribution of the deep seas to overall marine biodiversity.

1.8 The “Neglected Phyla” and Marine Natural Products in the Future

Regardless of the actual numbers of marine species available, some conclusions can be reached based on the efforts over the past 75 years. Research on the phylum Porifera has dominated the effort and the subsequent chemistry. This focus has been productive and the chemistry novel and fascinating. It is not difficult to reach a conclusion for this fixation as succeeding generations of natural product chemists will naturally focus on areas that have proven successful in the past, and sponges are relatively easy to collect in good mass (>100 g), even for the inexperienced diver. This focus on sponges has led to a rather unequal coverage of the other major taxa and phyla. Some comparative data based on compounds isolated, papers published, and relative coverage of the major *macroorganisms*, which includes 12 of the phyla from Animalia, are presented in Table 1.8. The Cyanophyta have been included in this comparison as they too can be collected in bulk from the wild. Also included are the origins of 35 of the 40 compounds of interest listed in Table 1.7. Four of the remaining were of Bacteria origin and the fifth was isolated from a higher chordate (shark). Studies on the macrophyta have produced >90% of the marine natural products from just 1.4% of the accepted number of species in these phyla. These data, when coupled with the NCI’s study [136] (Fig. 1.13), suggest that studies that include Bryozoa, Cnidaria, Chordata (Ascidiaceae), Mollusca, Ochrophyta (Phaeophyceae), and Cyanophyta should be productive, particularly if the search for bioactivity is the objective. These phyla have been *neglected*. Furthermore, as no work has been reported on the other 18–21 phyla of the Animalia, one may be forgiven for coming to the conclusion that these are “forgotten” phyla.

Most of the biodiversity yet to be classified in the marine environment resides in the microscopic world of the Archaea, Bacteria, and the multicellular, but still microscopic members of the Eukaryota belonging to the Chromista and Protozoa taxa. The projected numbers of species still to be defined is estimated to be in the millions [13, 17, 52]. Despite the inherent difficulties of working with organisms from the Protozoa and Chromista, a significant body of work is evolving on the chemistry of the Ciliphora, Dinophyta, Euglenozoa, and from the Chrysophyceae (Ochrophyta), but as yet little or nothing has appeared on the chemistry of species in the Bacillariophyta, Radiolaria, and Foraminifera (Table 1.5). The chemistry of obligate marine, or at least marine-derived, fungi is of rapidly growing interest within the MNP community and already 289 species have been examined for new

Table 1.8 Comparative data for marine natural products from the macroorganisms

<i>Taxa</i>	Marine species	Species with new compounds	Coverage of phylum (%)	Compounds (% total)	Bioactive papers ^a (%)	Compounds of interest
Animalia						
Annelida	12,148	14	0.12	0.24	100	–
Arthropoda (Crustacea)	44,950	9	0.02	0.05	11	–
Brachiopoda	550	0	0.91	0	0	–
Bryozoa	5,700	28	0.49	0.86	14.1	1
Chordata (Ascidiaaceae)	4,900	184	3.76	4.77	65.4	7
Cnidaria	9,795	415	4.24	19.49	22.5	2
Echinodermata	7,000	205	2.9	5.84	18.8	–
Hemichordata	106	3	2.77	0.14	17.6	–
Mollusca	52,525	201	0.38	5.22	12.2	5
Nematoda	12,000	2	0.017	0.01	0	–
Platyhelminthes	15,000	2	0.013	0.01	0	–
Porifera	5,500	878	15.96	35.03	63.4	14
Chromista						
Ochrophyta (Phaeophyceae)	1,600	161	10.1	5.81%	13.1	–
Plantae						
Chlorophyta	2,500	60	2.4	1.37%	11.5	–
Magnoliophyta	50	26	52.0	0.62%	27.6	–
Rhodophyta	6,200	195	3.10	7.85%	11.0	–
Bacteria						
Cyanophyta	1,000	73	0.73	3.03%	64.9	6
	181,524	2,456		90.34%		35

^aNumber of papers reporting bioactive compounds as percentage of all papers reporting compounds for each phylum

chemistry (Table 1.5). This interest seems destined to continue, and with the predicted burgeoning of the fungal species to 1.5 million, [13] there will be enormous scope in this aspect of marine natural products. Soil bacteria, especially members of the *Streptomyces* and *Micromonospora* genera of the Actinobacteria, have been the source of over 50% of the clinically useful microbial antibiotics. The first marine actinomycete was discovered in 1984 [53]. Since then at least three marine genera have been described [54–56]. These include the genus *Salinispora* [56] which has an obligate requirement for sodium ions. This discovery by Fenical and Jensen of the first *Salinispora* sp. has been followed by the identification of at least six actinomycete families [52] including marine-derived species related to the genus *Streptomyces*. The chemistry associated with these obligate marine actinomycetes has also been remarkable with discoveries of compounds such as salinosporamide, which is currently in Phase 1 trials as a 20S-proteasome

inhibitor [194]. These metabolites being isolated from the obligate marine actinomycetes show a high degree of halogenation, a feature considered desirable for induction of biological activity [195], and in the case of salinosporamide an essential feature of the mechanism of action [196, 197].

Every milliliter of seawater contains 10^6 microorganisms with marine sediment being even richer (10^9) [52]. This is a resource beyond comprehension. The terrestrial actinomycetes have been chemically prolific. There is every reason to believe that the marine counterparts will be equally prolific. Using a combination of metagenomics, genome analysis, and selective culture techniques, the potential for discovering other genera and new chemical entities from the microscopic world is enormous. If this is coupled with a fuller exploration of the “neglected” macroorganism phyla, the future viability, stability, and promise of marine natural products chemistry is assured.

1.9 Study Questions

1. Taking a particular organism group (e.g., molluscs) make a brief study of the differing taxonomic classifications that have been proposed for this group by taxonomists.
2. Could the differing taxonomic views for such a group have had an impact on the statistics of natural product occurrence in the group?
3. For a particular organism, or a small group of organisms, ascertain what is known about the dietary regime and predation pattern and determine if that coincides with what is known about the characterized constituents.
4. (a) As an ambitious young starting academic in the field of marine natural products, what considerations should you give to the selection of organisms (phylum, class, order, family, or genus) to study that would optimize your chances of finding new compounds and thus gaining publications?
(b) Suggest the collecting resources that you would need to access to effectively pursue your organisms of choice.
(c) Besides collecting resources, list the other resources or collaborations you think would be necessary in order to be successful.

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The Chemistry of Marine Algae and Cyanobacteria

2

Hyukjae Choi, Alban R. Pereira, and William H. Gerwick

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H. Choi (✉) • A.R. Pereira • W.H. Gerwick
Scripps Institution of Oceanography, Skaggs School of Pharmacy and Pharmaceutical Sciences,
University of California, San Diego, CA, USA
e-mail: h5choi@ucsd.edu, alpereinabadilla@ucsd.edu, wgerwick@ucsd.edu

Abstract

This chapter reviews the major metabolic themes that are characteristic of the prominent groups of marine algae and cyanobacteria. The taxonomic organization of the chapter facilitates an appreciation of the uniqueness of each of these groups in their capacity to elaborate specific classes of secondary metabolites. For each compound discussed, which are chosen as representatives of chemical themes, a brief story is presented which describes the natural history of the organism, the isolation of the natural product, its structure elucidation, and as appropriate, the pharmacology, chemical ecology, and biosynthesis of the isolated metabolite. Many unanswered questions remain in understanding these diverse algal chemistries, and numerous areas for future exploration are suggested throughout the chapter.

2.1 Introduction

Some of the earliest efforts in exploring the organic chemistry of the marine environment involved study of the chemistry of marine algae, and thus this topic has a more mature and well-developed nature relative to other areas of marine natural products. Pioneering work in Japan and the United States first examined intertidal red algae for their unique constituents and quickly established that they had a spectacular capacity to produce halogenated organic compounds of unusual structure. Moreover, in Japan there was a developed ethnological use of some seaweeds for their medicinal qualities, and this was another focus of early work; for example, the red alga *Digenia simplex* had been used to eliminate intestinal parasites, and an early investigation of the chemical basis for this property revealed kainic acid. Kainic acid owes its anthelmintic properties to its activity at the kainate receptor and, as the naming would suggest, has become an important tool in neurobiology. Subsequently, over the period 1970–2000, various research groups explored one or another group of algae for their unique constituents, and over time, a picture has emerged of distinctive chemical trends in each of the various algal groups. Articulation and description of these trends are the goals of this chapter.

The groups of algae to be examined in this chapter include both the eukaryotic algae of macroscopic as well as microscopic size and the prokaryotic algae (blue-green algae = cyanobacteria), which also are of both an easily visible as well as microscopic character. In this regard, we hold to the definition of “algae” as aquatic photosynthetic organisms with plant-like qualities [1]. It should be noted that some controversy exists over this definition of “algae”; however, the main point of contention, the cyanobacteria, is currently classified using both the botanical and microbiological coding systems. From this perspective, as well as the ecological and environmental perspective of how these exist in nature, they are appropriately covered in this chapter.

Many review perspectives have been written on various specialized aspects of algal and cyanobacterial secondary metabolites, and a few of the most recent

ones are given here [2–4]. To the student of marine natural products chemistry, a extraordinarily wide range of natural product themes are present in the algae, and imbedded in these structures are diverse stories of organic chemistry, biosynthesis, chemical ecology, pharmacology, and drug development. It is the intention of this chapter to retell some of these accounts using the natural product structures as entry points.

2.2 Marine Cyanobacteria

2.2.1 Overview of the Biology of Cyanobacteria

The cyanobacteria, or blue-green algae, are photosynthetic chlorophyll *a*-containing bacteria which occur both as single cells, colonies of single cells, unbranched filaments, and even branched filaments [5]. Thus, they range in size from single cells of a micron in diameter (*Microcystis* species) to large mats and tufts that may be picked up by hand and weigh kilograms in mass. Several of the tuft-forming species of the genus *Lyngbya* are readily visible by snorkeling or SCUBA as finely divided filaments that wave back in forth in the currents and swell, looking much like human hair growing up off the seafloor; hence, the nickname “mermaid’s hair.” These wonderfully diverse groups of bacteria are ancient inhabitants of our planet, with specimens being identified in the geological record going back some 2.5 billion years. They have had many eons over which to diversify, occupy many specialized ecological niches, and evolve different routes of metabolism. As a result, they are among the most exciting groups of marine organisms for their production of structurally unique and biologically active secondary metabolites.

The taxonomy of the cyanobacteria is in a state of flux as the field is currently transitioning from using morphological and growth characteristics to assign taxonomy to a system of using 16S rRNA gene phylogeny. A major problem in our current taxonomic understanding results from the fact that many radiations of the cyanobacteria have separately evolved similar morphological features, such as filaments composed of short barrel-shaped cells, and thus, this traditional system has given an imprecise and oftentimes incorrect perception of their relationships. As we apply 16S rRNA gene sequences, or even more powerfully, a multitude of genes and gene types, as in multilocus sequence typing (MLST), we are finding that they are much more diverse than ever realized [6]. In the not-very-distant future, we will look back on our current efforts as quite primitive and lacking in power, as with new DNA sequencing approaches on the horizon that are estimated to provide 1-megabase of sequence for \$1.00, we will be soon performing genome-based phylogenies that more accurately and precisely delineate the relationships between these organisms. Nevertheless, the current understanding of the taxonomy of cyanobacteria derives in parallel from their consideration in both bacterial and botanical classifications, with a fair concordance between the two, which both divide these organisms into five

subcategories (bacteriological, five subsections groups I to V; botanical, five families Chroococcales, Pleurocapsales, Oscillatoriales, Nostocales, Stigonematales, respectively) [7].

Marine cyanobacteria occupy essentially all regions of the sea where there is sufficient light energy to drive photosynthesis, from pelagic to nearshore to benthic. In the tropics, they can become dominant members of shallow water environments, overgrowing many other organisms as thin veils or even dense mats (e.g., *Phormidium* and *Lyngbya* spp.); the latter are capable of smothering and killing subtending organisms such as corals. Cyanobacteria play a critical role in nitrogen cycling on coral reefs, habitats renowned for being limited in nitrogen and phosphorous, because of their capacity to fix atmospheric nitrogen into organic forms. Additionally, in areas of high nutrient input, such as from rivers and human activities, cyanobacteria abound and often form a dominant cover.

Cyanobacteria participate in numerous symbiotic relationships, growing in specialized tissue arrangements especially within tunicates (hemicordates) and sponges. Within these symbioses, the products of photosynthesis as well as secondary metabolism are exchanged between the cyanobacterium and the host [8]. Cyanobacteria are a favored food of some types of invertebrate mollusks, such as *Dolabella* and *Stylocheilus* sea slugs. These organisms are capable of chemolocation of cyanobacteria, often a *Lyngbya* or *Symploca* species, and consume it for both nutrition as well as assimilation of its natural products. It is generally regarded that these fleshy animals derive benefit from sequestration of the antipredatory natural products of their cyanobacterial diet. In summary of the above discussion, many marine natural products ascribed to sponges, tunicates, and sea hares have subsequently been shown, or are strongly implicated, to derive from the associated or consumed cyanobacteria.

As prokaryotes, cyanobacteria have distinctive metabolic and anatomical features [5]. The cells of different species range from spherical (e.g., unicells) 1–10 μm in diameter to flattened pancake-like shapes (e.g., in filaments) with cells only 1–2 μm long yet possessing a width of up to 60–80 μm . Cyanobacteria of filamentous construction are often covered with a sheath of extracellular material, and in some cases, this can become quite massive, resulting in individual filaments 10–20 cm in length and roughly the thickness of a human hair (overall width up to 100 μm). As prokaryotes, they lack cellular organelles; however, their photosynthetic apparatus is organized onto thylakoids, as in chloroplasts in plants and other algae (indeed, the latter represent ancient endosymbiotic incorporations of cyanobacteria!). Light is harvested by elaborate photoreceptor structures, known as phycobilisomes, which are arranged on the thylakoids and organize a complement of chlorophyll *a* and accessory pigments including phycoerythrin, phycocyanin, and allophycocyanin, as well as carotenoids. As a result, these “blue-green algae” can take on colors in nature ranging from brown to red to mossy green or blue green, depending on the organism and the available light quality and quantity.

2.2.2 Overview of the Trends in Secondary Metabolism in Marine Cyanobacteria

The major group contributing to the rich secondary metabolite chemistry of the cyanobacteria (773 metabolites reported as of 2011) is predominately the Oscillatoriales (58% of reported metabolites, group III), followed by the Nostocales (24%), Chroococcales (10%), and Stigonematales (8%) [9]. Metabolites from the fifth cyanobacterial group, the Pleurocapsales, have only rarely been reported, although the biosynthetic genes necessary for making nonribosomal peptides have been detected [10]. The most important marine group to contribute to this rich chemistry is the Oscillatoriales and is dominated by the genus *Lyngbya* (43% of all cyanobacterial metabolites, 336 compounds). However, as noted above, cyanobacterial taxonomy is both imprecise and in need of revision, and likely, a multitude of diverse organisms have been lumped into the *Lyngbya* group.

The molecular weights of cyanobacterial metabolites (excluding proteins and biopolymers) distribute into a skewed bell-shaped curve extending from as little as 100 to a maximum of 1801 Da. The majority of reported compounds are between 200 and 1100 molecular weight with an average of 645 Da and a mean of 604. Different classes of secondary metabolites predominate in these weight classes; for example, natural products greater than 700 Da are almost exclusively of a nonribosomal peptide synthetase (NRPS) origin, although oftentimes combined with some polyketide synthase (PKS)-derived sections. In fact, from an overview perspective, the dominant theme in the secondary metabolites of marine cyanobacterial natural products is the integration of these two biosynthetic classes, NRPSs and PKSs, to form ketopeptides (PKS to NRPS biosynthetic origin) and peptoketides (NRPS to PKS biosynthetic origin). However, pure peptides or polyketides are also common, as are alkaloids which are more distantly derived from peptides. Relatively few terpenoids, fatty acids, or other molecular classes have been described from these organisms to date [11].

The dominant amino acid classes used in cyanobacterial natural products are aliphatic and polar, dominated in the former by leucine, isoleucine, alanine, valine, phenylalanine, and proline and in the later by threonine, serine, cysteine, tyrosine, and glycine. Very often, these amino acids are modified by methylation (*N*-methyl or *O*-methyl), epimerization to the *D*-isomer, extended by a ketide section, heterocyclized to the carbonyl of an adjacent amino acid, or otherwise modified such as by halogenation. A number of reviews and perspectives have appeared over the past decade on the chemistry [11–13], biosynthesis [14], and biological properties [3] of marine cyanobacterial natural products.

2.2.3 Overview in Pharmacological Trends

With nearly 800 reported metabolites, the biological properties of the cyanobacterial natural products are highly diverse, and many or most are not described or known.

Nevertheless, a few trends can be discerned; many have potent cell toxicity by virtue of their ability to interfere with polymerization of either tubulin or actin, two well-validated targets of cytotoxins. Additionally, a number of fresh water cyanobacterial metabolites are known to exert neurotoxic activity, many through interactions at the voltage-gated sodium channel (VGSC) of neurons. Relatively recently, this pharmacological theme has also been observed in marine metabolites with a growing number of both VGSC blockers and activators being reported [15]. One way to advance the discovery of marine cyanobacterial metabolites into more meaningful scientific arenas is to develop a molecular level understanding of their pharmacology; this type of research should be given higher priority in the future.

2.2.4 Carbohydrate-based Metabolites

While a number of peptide and polyketide metabolites of marine cyanobacteria have been found as glycosides, usually with various methylated pentose or hexose sugars, pure sugar or oligosaccharide metabolites have only rarely been isolated (Fig. 2.1), and these have been exclusively reported from freshwater specimens. In part, this lack of reported pure carbohydrate-based metabolites may result from the bias of most natural product programs being away from water soluble materials. An example of a polyketide appended with a methylated pentose sugar is given by lyngbyalioside (**1**), isolated from *Lyngbya bouillonii* [16]. This 16-membered macrolide shows several interesting features which are typical of cyanobacterial polyketides, including a vinyl bromide, tetrahydropyran ring, and methyl groups attached to C-1 positions of the polyketide (e.g., so-called β -branches). The hexopyranose sugar (a trimethyldeoxymannose derivative) is α -linked, possesses methoxy groups at the 2-, 3-, and 4-positions, and is deoxygenated at the 6-position. Another example, a complex ketopeptolide with an attached methylated sugar, is given by malyngamide J (**2**), isolated from a Curaçao collection of *Lyngbya majuscula* [17]. In this case, the sugar is a dimethoxyxylose residue with an α -linkage to the polyketide cyclohexenone section. Malyngamide J shows modest toxicity to brine shrimp and fish, and thus may function as an antifeedant. Other highly bioactive polyketides with related methylated sugar residues have been reported from red algae, such as polycavernoside A (**3**), a metabolite which caused several fatal human poisonings in Guam [18]. However, structural precedents for both the aglycone and sugar portions strongly suggest a cyanobacterial source for polycavernoside A, and thus, it is likely that a fine turf of the producing cyanobacterium grows on the surface of this red alga.

2.2.5 Terpenoids

Cyanobacteria utilize the terpene biosynthetic pathway only to a limited extent, with the most common examples being to produce primary metabolites (essential to the basic life processes) rather than secondary metabolites (compounds with

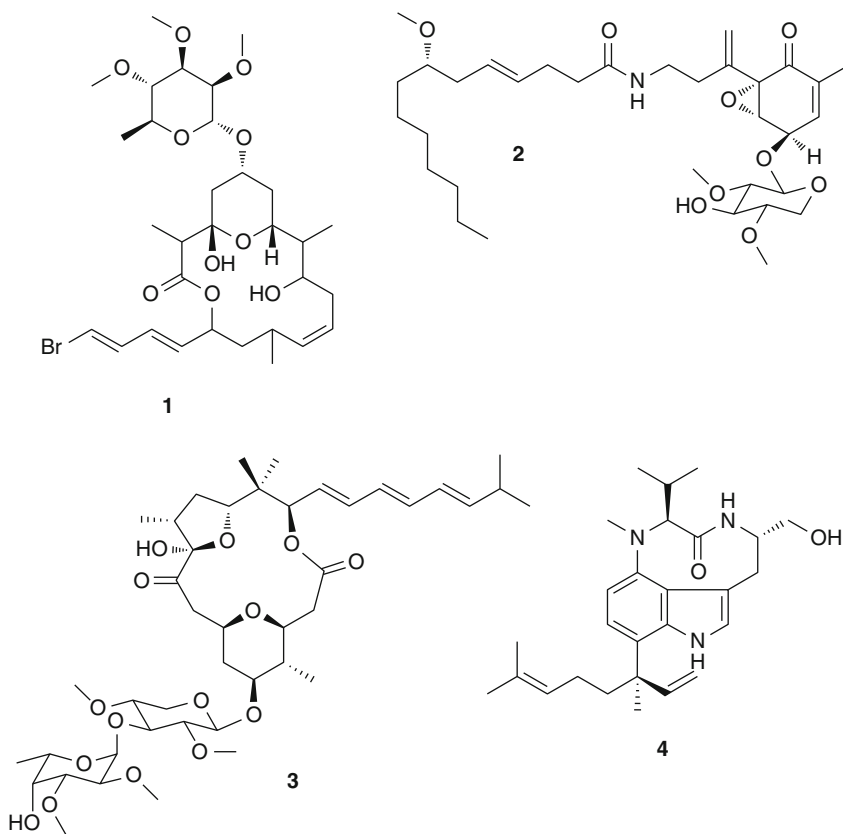


Fig. 2.1 Carbohydrate-based metabolites and terpenoids from marine cyanobacteria

adaptive functions). Examples of cyanobacterial terpenes falling into the primary metabolite class include carotenoid pigments (accessory pigments employed to harvest light and funnel its energy to photosynthesis) and steroid equivalents known as “hopanoids” which contribute to membrane structure [19].

An example of a cyanobacterial terpene-containing secondary metabolite is given by the lyngbyatoxins (e.g., lyngbyatoxin A, **4**) [20]. Following stormy periods around Waikiki, Hawaii, small tufts of the benthic cyanobacterium *Lyngbya majuscula* become dislodged from substrate and are frequently found floating in the nearshore surf zones. Swimmers coming in contact with these tufts, especially on areas of sensitive skin, develop rashes and occasionally ulcerations, giving rise to the common name for this occurrence as “swimmer’s itch.” The responsible secondary metabolite causing this irritation was investigated by the laboratory of the University of Hawaii pioneer of cyanobacterial natural products, Richard E. Moore, and resulted in characterization of a terpene section fused to a novel dipeptide derivative [20]. This metabolite, named lyngbyatoxin A (**4**), was shown to be a potent protein kinase C (PKC) activator, and thus has proinflammatory

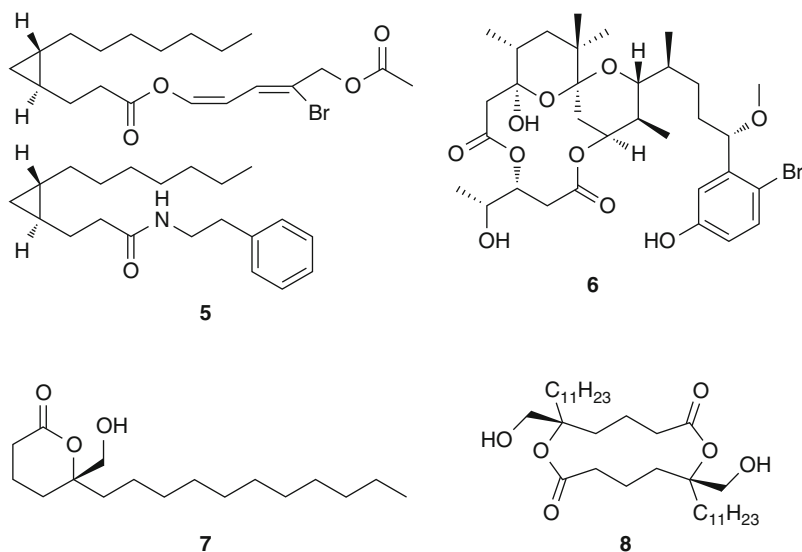


Fig. 2.2 Fatty acids and polyketides from marine cyanobacteria

activity. The biosynthesis of lyngbyatoxin A has been explored using a molecular genetics approach [21] and shown to possess several novel steps, including a reductive offloading of a dipeptide from a NRPS assembly system, a novel aromatic substitution reaction, and an interesting reverse prenylation of the core indole.

2.2.6 Fatty Acids

The common fatty acids of cyanobacteria, such as those present in membrane lipids, are typically of 16- and 18-carbon chain length, of variable degree of unsaturation, and remarkably, are present as complex lipid species quite similar to those found in higher plant chloroplast membranes (e.g., glycolipids) [22]. In the secondary metabolism of cyanobacteria, fatty acid metabolites have a number of interesting structural features, such as unusual pendant carbon atoms, isonitrile functionalities, and various patterns of oxidation to form oxylipins [11]. For example, collections of the cyanobacterium *Lyngbya majuscula* from Grenada in the Southeastern Caribbean Sea yielded a series of metabolites with cyclopropyl ring-containing fatty acids in amide or ester linkage with smaller functionalized moieties (e.g., 5) [23] (Fig. 2.2).

2.2.7 Polyketides

Predominately, the polyketide natural products found in marine cyanobacteria are present in combination with amino acid-derived sections, the latter almost certainly

incorporated by nonribosomal peptide synthetases. These mixed biosynthesis compounds, which constitute the dominant secondary metabolite biosynthetic theme of marine cyanobacteria, are considered in a separate section below. However, a few cyanobacterial metabolites are predicted to derive exclusively from the PKS pathway, and these show some interesting secondary modifications, including ring formation containing oxygen atoms, juncture of multiple PKS fragments by ester bonds, including dimerization, halogenations, and unique patterns of methylation. Two examples illustrating some of these biosynthetic themes are presented below.

As noted above, some strains of *L. majuscula* can cause skin irritation and ulceration in swimmers that come in contact with dislodged tufts of the cyanobacterium. This phenomenon of “swimmer’s itch” may be caused either by the presence of the lymngbytoxins discussed above [20] or pure polyketides of the aplysiatoxin family (e.g., **6**) [24]. The latter class of dermatotoxin was first described from the intestines of the cyanobacterial-feeding sea hare *Stylocheilus longicauda*, but was subsequently described as a metabolic product of the cyanobacterium *L. majuscula*, and is particularly abundant strains occurring in Hawaii, Australia, and Madagascar. Indeed, some bays of Australia are overgrown by aplysiatoxin-producing strains which render their waters unsuitable for human recreation [25]. In the authors’ experience, large accumulations of floating mats of *L. majuscula* were found in nearshore waters off the northwest coast of Madagascar, and upon collection by hand, rendered our skin tingling with a menthol-like coolness which lasted for several hours; subsequently, debromoaplysiatoxin was found as the major metabolite of this extract. Structure elucidation of the aplysiatoxins, and the related oscillatoxins, was initially accomplished by NMR and MS analysis to give planar structures with relative stereochemistry, and subsequently, CD analysis was used to assign absolute configurations [24]. Biosynthetically, it appears that a benzoic acid derivative may initiate assembly of the main PKS chain. Seven rounds of PKS extension are predicted along with several methylation events from *S*-adenosylmethionine (SAM) to introduce the five pendant methyl groups. The mechanism of formation of the two spiro-connected tetrahydropyran rings is currently unknown, but will certainly reveal new biochemical steps when studied. Similarly, the molecular logic by which the lower pentanoic acid chain is incorporated is unknown at present, but may involve a unique NRPS-like mechanism utilizing the β -hydroxy group of 3,4-dihydropentanoic acid. Due to the substitution pattern in those aplysiatoxins possessing an aromatic halogen atom, bromine incorporation likely involves a bromoperoxidase, an enzyme reported from other strains of cyanobacteria [26]. The potent biological effects of the aplysiatoxins have been studied in some detail [27], and these metabolites are also activators of protein kinase C (PKC), thereby possessing proinflammatory effects as well as promoting tumor formation. As such, they have become useful tool molecules in studying cell and animal physiology.

Another polyketide example is provided by the isolation of tanikolide (**7**) [28] and its dimeric form, tanikolide dimer (**8**) [29]. Collections of *L. majuscula* from near Tanikely Island, Madagascar first yielded the monomeric polyketide, and its

structure was elucidated by normal methods with absolute stereochemistry from a modified Mosher ester method. Tanikolide displayed both antifungal effects and brine shrimp toxicity at low microgram levels [28]. Subsequently, a dimeric form of tanikolide was isolated from this collection, and while the planar structure was readily apparent, determining the absolute configuration of both halves was significantly more involved. Initial data suggested that the metabolite was composed of one *R*-enantiomer and one *S*-enantiomer of tanikolide; however, subsequent chemical synthesis of all three possible tanikolide dimers and comparison by NMR and GCMS revealed tanikolide dimer to be formed from two monomeric *R*-enantiomers (8) [29]. Interestingly, all three of the synthetic tanikolide dimer pairs were equally active in inhibiting an enzyme involved in mammalian gene regulation, namely SIRT2, a member of the histone deacetylase (HDAC) family, with an $IC_{50} = 176$ nM in one assay format and 2.4 μ M in another. This was especially interesting because tanikolide dimer lacks a recognizable analog of the pharmacophore present in other known HDAC inhibitors (e.g., an alkyl chain with a zinc binding functional group at the terminus).

2.2.8 Polypeptides

As noted above, peptide-based metabolites are extremely common in marine cyanobacteria, although most contain sections of lipids, as described in the next section on lipopeptides. Nevertheless, pure peptides are well represented and, in general, are formed by amino acids with aliphatic and polar neutral amino acids. Alternately described, marine cyanobacterial peptides rarely contain charged amino acids (e.g., acidic residues such as glutamic or aspartic acid, or basic ones such as lysine or arginine); interestingly, this is a point of difference with the metabolites of freshwater cyanobacteria which tend to possess such charged amino acids more commonly.

In only the last few years, it has been revealed that peptide metabolites from marine cyanobacteria have two fundamentally different biosynthetic origins. On the one hand, they are synthesized by the nonribosomal peptide synthetase enzyme machinery which uses an assembly-line molecular logic and a discrete set of dedicated enzymes for the incorporation of each residue [30]. Alternatively, the ribosomal machinery of cyanobacteria has more recently been revealed to produce propeptides (small proteins), short sections of which are then modified, cleaved out, and usually cyclized to form a class of compound that has come to be known as the “cyanobactins” [31]. Examples of these two classes of peptide-based metabolites are described below (Fig. 2.3).

2.2.8.1 Nonribosomally Encoded Peptides and Their Biosynthesis

One of the more prevalent groups of pure peptides to be encoded by a cyanobacterial NRPS are the so-called cyanopeptolins, classified as such by their overall cyclic structure and presence of an aminohydroxypipicolinic (Ahp) acid unit. Characteristically, the overall cyclic structure is created by an ester

to a branching threonine residue, and this usually extends to an acyclic section with one or more modified amino acid residues. Cyanopeptolin metabolites have been isolated from diverse cyanobacteria, both freshwater and marine, and from taxonomic groups as varied as type I (Chroococcales) to type III (Oscillatoriales).

For example, from different marine collections of *Lyngbya* sp., somamide A (**9**) was isolated; its structure was determined by standard methods, including degradation to amino acid fragments and chiral analysis, and it was found to be a selective low nanomolar inhibitor of elastase [17, 32]. Thus, these cyanopeptolin metabolites are especially interesting for their biological properties in that they represent some of the most potent protease inhibitors known, with various showing selectivity for chymotrypsin, others for trypsin, and still others such as somamide A for elastase. Another example is given by investigations of a *Symploca* sp. from Papua New Guinea which led to the isolation of symplocamide A (**10**), an exceptionally potent cancer cell cytotoxin which also inhibits serine proteases with a 200-fold greater inhibition of chymotrypsin over trypsin [33]. The presence of several unusual structural features in symplocamide A provided new insights into the pharmacophore model for protease selectivity in this drug class, and its potent chymotrypsin inhibiting activity may underlie the exceptional cytotoxicity of this compound to H-460 human lung cancer cells ($IC_{50} = 40$ nM) as well as neuro-2a murine neuroblastoma cells ($IC_{50} = 29$ nM) [34].

The biosynthesis of members of this class has been studied at the molecular genetic level; however, these studies have employed freshwater strains such as *Anabaena*, *Planktothrix*, and *Microcystis* [35]. The beginning of each of these clusters is initiated in an interesting fashion, involving either the activation of a hydroxy acid (e.g., glyceric acid or phenylpyruvic acid) with its subsequent sulfation or phosphorylation, or activation of a polar amino acid (e.g., glutamine) and its *N*-formylation. Subsequent addition of amino acids occurs via regular NRPS mechanisms, and in each case, terminates with incorporation of a threonine residue that is involved in macrocyclization. One of the sequenced clusters was for a chlorinated metabolite (anabaenopeptilide 90B), and the cluster showed the presence a bacterial halogenase as expected. Symplocamide A (**10**), with its brominated tyrosine residue, would be expected to be produced by a highly analogous set of genes and enzymes. However, from analysis of the published gene clusters encoding for the biosynthesis of cyanopeptolin natural products, it is uncertain if these gene clusters are undergoing frequent exchange by horizontal gene transfer (HGT) events or if an ancient gene transfer event has been subject to parallel coevolutionary pressures in the various cyanobacterial strains.

2.2.8.2 Ribosomally Encoded Peptides (Cyanobactins) and Their Biosynthesis

The discovery that a large number of highly modified cyclic peptides, known as cyanobactins, are produced in cyanobacteria from ribosomally encoded peptide precursors was highly unexpected and only occurred quite recently (2005). Taking two complementary approaches, one by genome shotgun cloning and the other by genome sequencing, two groups simultaneously discovered this new pathway

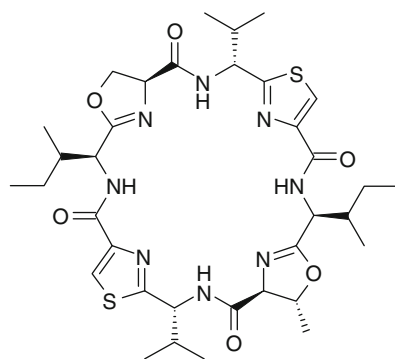
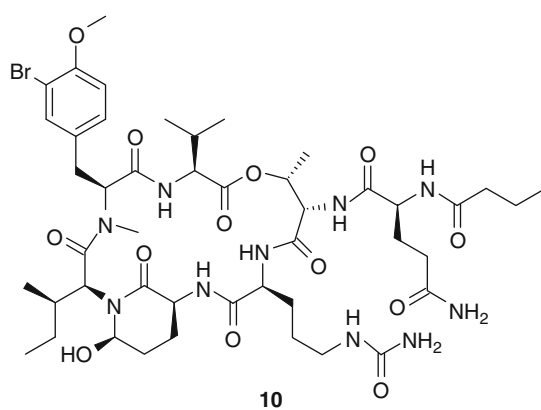
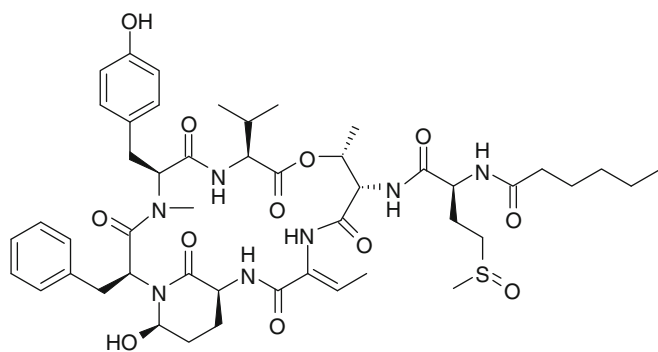


Fig. 2.3 Cyanobacterial polypeptides

to cyanobacterial peptides in the complex symbiotic relationship of a tropical South Pacific tunicate, *Lissoclinum patella*, and a cyanobacterium of the genus *Prochloron* [36, 37]. Indeed, emerald green veins identify channels within the translucent tunicate body where *Prochloron* cells are segregated and presumably, nurtured as a source of photosynthetic nutrients. The isolated metabolites from this symbiotic pair are a series of structurally distinctive cyclic peptides, the patellamides (e.g., **11**) and related substances, which, in general, have quite potent cancer cell toxicity properties [38].

Characteristic of these cyanobactin natural products is their overall cyclic structure, alternation of polar (cys, thr, or ser) and aliphatic residues (val, ala, ile, leu, phe), conversion of polar residues to oxazole/oxazoline or thiazole/thiazoline rings, or occasionally, prenylation of the polar residues. A growing understanding of the biosynthesis of the cyanobactins has revealed that the propeptides that give rise to the final structures are preceded by a short leader sequence which “programs” other enzymes encoded by nearby genes (thus forming a gene cluster) to proteolytically cleave out the final oligopeptide, convert the polar residues to their corresponding heterocycles (or engage in prenylation), and produce the macrocycle [39]. As such, this system is ideally suited for genetic manipulation and engineering to produce structurally diverse libraries that can be probed for their biological properties [14]. Subsequently, marine cyanobacteria have been identified by genetic and mass spectrometric methods to utilize ribosomal processes along with catalytically promiscuous enzymes to produce a vast array of intriguing molecular structures [40].

2.2.9 Lipopeptides

The dominant and distinctive theme in marine cyanobacterial metabolites is the production of lipopeptide-type natural products which merge sections deriving from polyketide or fatty acid origin with those coming from the NRPS pathway [11–13]. Some representatives of this complex class of natural products are among the most bioactive compounds known from cyanobacteria, and several have promising biomedical utility. The relative orientation of lipid and peptide sections varies, with the lipid section sometimes biosynthetically preceding the peptide section, other times following the peptide section, or quite often, both of these orientations are observed within a single metabolite. To distinguish them, the terms “keto-peptide,” “pepto-ketide,” and “complex keto-peptide” have been coined to refer to the above orientations, respectively, and are useful for discussing these various biosynthetic classes. Below are examples of each of these mixed biosynthetic classes of metabolites, and furthermore, these occur in both linear and cyclic forms.

2.2.9.1 Linear Lipopeptides

Linear keto-peptides are a familiar and common motif in cyanobacterial natural products (Fig. 2.4). While there are many examples, a notable example is given by

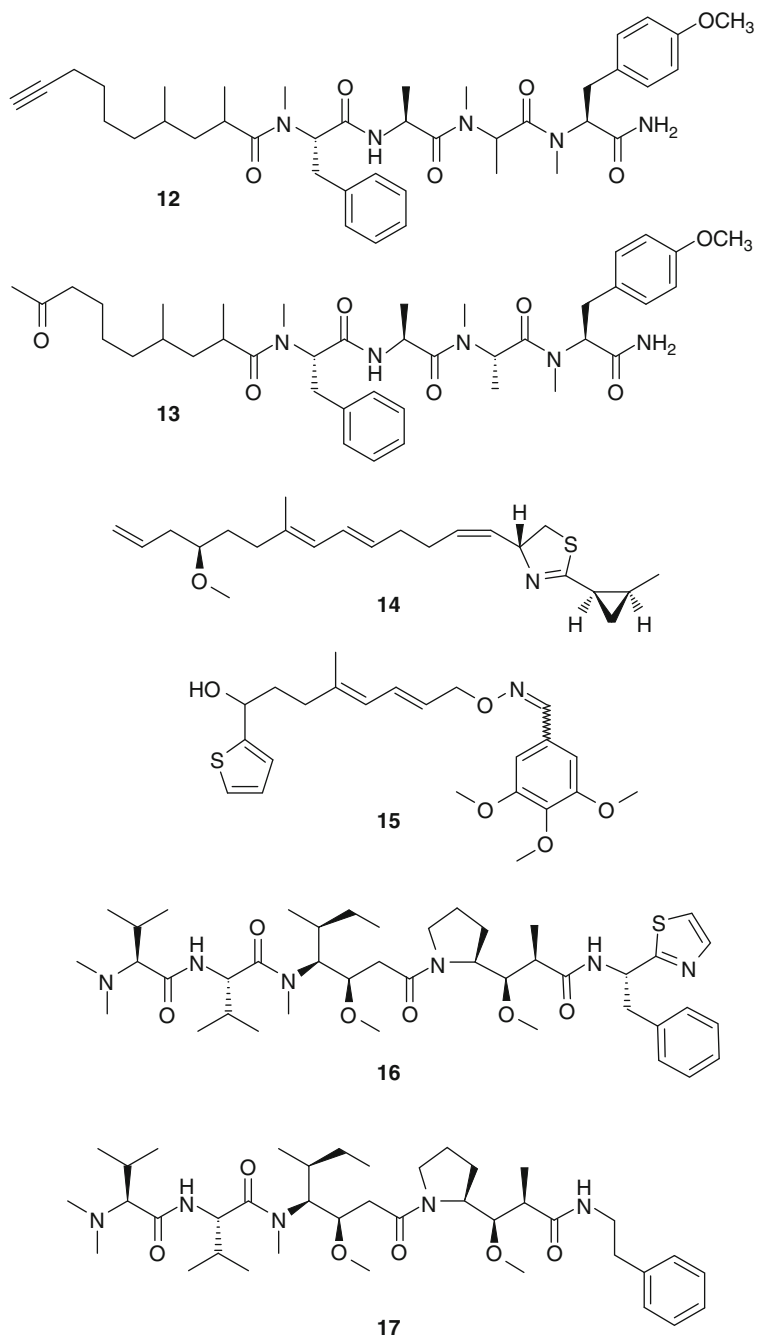


Fig. 2.4 Cyanobacterial linear lipopeptides

the carmabins (**12**, **13**) [41]. Carmabins A and B were reported from a Curaçao collection of the marine cyanobacterium *Lyngbya majuscula* and were isolated from relatively polar fractions in response to cancer cell cytotoxicity associated with this crude material. Unfortunately, the assays were no longer available by the time compound isolation was accomplished, and characterization of the carmabins in further cancer models has not occurred, although carmabin A has been reported to possess antimalarial-type properties [42]. Nevertheless, these are fascinating molecules with carmabin A possessing a 10-carbon chain with a terminal acetylene functionality and secondary methyl groups at the C-2 and C-4 position, whereas in carmabin B, the acetylene group is replaced by a methyl ketone. Attached to either of these acyl chains is a tetrapeptide composed of *N*-methyl Phe, Ala, *N*-methyl Ala, and *N,O*-dimethyl Tyr as its primary amide. Configurations at the six stereocenters have not yet been determined. A partial gene sequence encoding for the carmabins has been deduced and suggests that its biosynthesis is initiated by the incorporation of a hexanoic acid precursor, possibly 5-hexenoic acid. This is followed by a desaturase that presumably forms the acetylene bond, followed by two PKS modules with C-methylation domains (for incorporation of the two secondary methyl groups). A series of NRPS modules follow for incorporation of the four amino acids, three of which also have *N*-methyltransferase domains. The cluster terminates in an unexpected way with no clear type I thioesterase domain; it will be intriguing to study the biochemistry of this novel aspect of the pathway which is believed to be responsible for forming the unusual primary amide functionality.

A second linear and complex ketopeptide example is given by curacin A (**14**), a potent antiproliferative agent to cancer cells, also isolated from a *Lyngbya majuscula* collection from Curaçao [43]. Curacin A possesses a structure mainly composed of polyketide origin; however, a single cysteine unit intervenes and is cyclized and dehydrated to form the thiazoline ring. Curacin A was shown to possess low nanomolar to high picomolar antiproliferative activity in various cancer cell lines and to exert this powerful cytostatic activity via inhibition of tubulin polymerization through action at the colchicine binding site [44]. Because of these potentially useful biological properties as an anticancer agent, the National Cancer Institute performed advanced evaluations of this agent, and while it showed some slight activity in vivo, it was not nearly as efficacious as hoped. This result along with other clues helped to identify that the molecule was unstable in vivo and very difficult to formulate due to its high hydrophobicity. Hence, medicinal chemical efforts to synthesize analogs with improved pharmaceutical properties were undertaken, and an improved analog (**15**) with greater stability and water solubility was produced and showed equal in vitro potency to cancer cells [45]. However, for reasons unreported in the literature, this analog has also failed to advance into clinical trials.

Nevertheless, there has been intense interest into the biosynthesis of this deceptively simple marine cyanobacterial metabolite. These latter investigations were enabled by initial isotope-labeled precursor feeding experiments using cultures of the producing cyanobacterium [46]. This mapped out the fundamental units involved in creating curacin A, and revealed a very interesting initiation of the

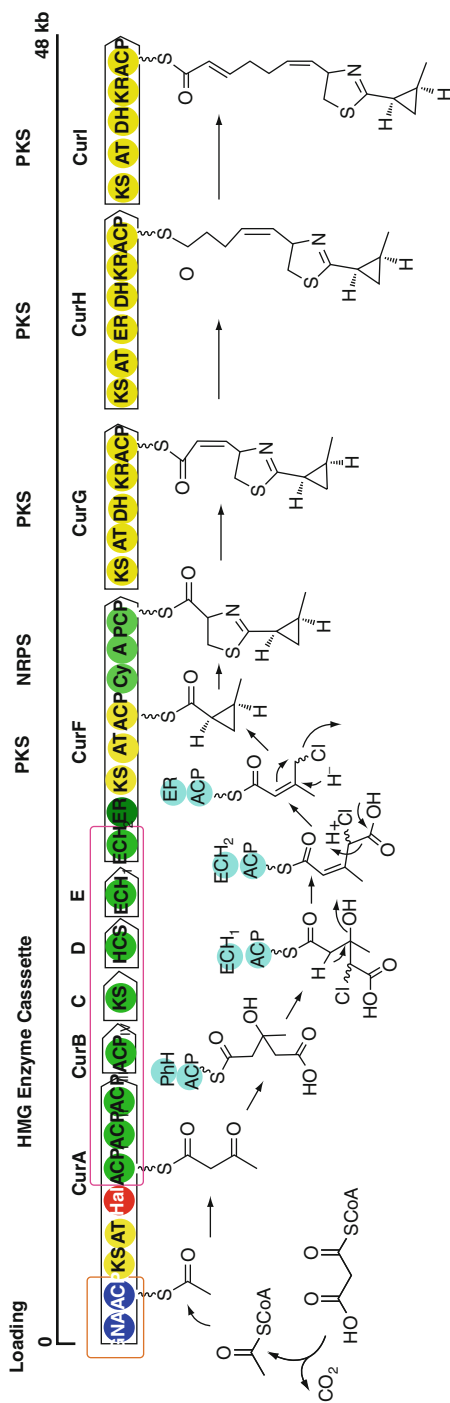


Fig. 2.5 (continued)

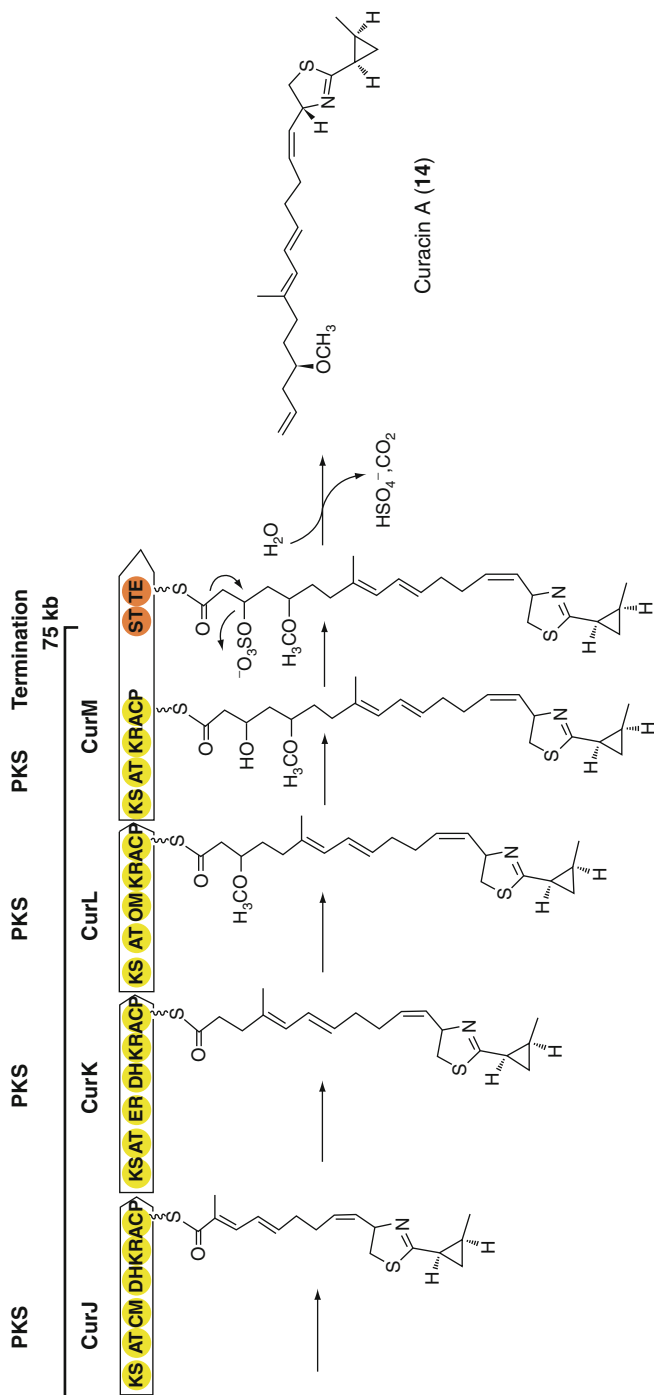


Fig. 2.5 Biosynthetic pathway and gene cluster of curacin A (14)

pathway to create the cyclopropyl ring, and an equally intriguing termination to produce the terminal olefinic bond. Ensuing, a gene cluster was identified for curacin A biosynthesis which gave powerful insight into the process of biosynthesis, especially these most unusual assembly steps [14] (Fig. 2.5). Expression of the biosynthetic enzymes and study of their catalytic properties *in vitro* have revealed that the cyclopropyl ring is formed by a variant of the terpene biosynthetic pathway and includes a cryptic chlorination reaction to activate a methyl group for cyclopropyl ring formation [47]. The chlorinating enzyme in this pathway, and many others of marine cyanobacterial metabolites, utilizes a novel mechanism involving very high energy chlorine radical species so as to halogenate at unactivated carbon centers [48]. The carbon branches that are produced in these terpene-like reactions, so-called β -branch reactions, are now realized to be of frequent occurrence in cyanobacterial metabolites, as well as other microbial natural products, and result in diverse functional groups such as secondary methyl groups, hydroxymethyl groups, exo-olefins with and without attached chlorine atoms, and cyclopropyl rings. At the other end of the curacin A molecule, an equally unusual set of reactions occur to activate the system for a terminal decarboxylation reaction as a novel mode of release from the biosynthetic enzyme manifold. Sulfation of the β -hydroxy group activates this group for departure coincident with decarboxylation, thus yielding a terminal olefin group as the enzyme-released product [49].

In 1972, the Pettit group in Arizona collected a large number of *Dolabella auricularia* sea hares from the Indian Ocean; biological evaluation at the National Cancer Institute showed their organic extract to increase life span in the P388 lymphocytic leukemia mouse model by 100%. Sea slugs are slow moving marine gastropods that lack obvious means of defense; however, in general, the extracts or secretions of the skin and organs of sea hares are highly toxic and have played a nefarious role in ancient history as poisons. The molecular basis for the more recently detected anticancer activity was not characterized until 1987 after some 15 years of intense effort because the active materials were present in vanishingly small quantities. This resulted in the identification of a group of potent toxins known as the “dolastatins” [50]. Dolastatin 10 (**16**) and its analogs generated much excitement due to their potent *in vivo* anticancer properties. Dolastatin 10 has been shown to act via disruption of cancer cell microtubule networks, thus disturbing normal cell division and the ordered separation of chromosomes. Although this natural product progressed into Phase II clinical trials, it was ultimately dropped as a single agent due to undesired peripheral toxicity. Chemical modification efforts to reduce toxicity resulted in the synthesis of TZT-1027 (**17**, Auristatin, Soblidotin), which more recently completed a Phase II clinical trial in patients with advanced or metastatic soft-tissue sarcomas [51]. The authors of this latter study indicated that “TZT-1027 was found to be safe and well tolerated.” Subsequently, dolastatin 10 (**16**) was isolated directly from the benthic cyanobacterium *Symploca* sp. [52], thus explaining the very low yield from the cyanobacterial-feeding sea hares.

2.2.9.2 Cyclic Lipopeptides

Throughout the Western and South Pacific, one may observe thin red veils covering small openings in the reef which are actually networks of the cyanobacterium *Lyngbya bouillonii*. However, laboratory cultures of this cyanobacterium do not grow with this morphology; rather, they grow as a flask of dispersed filaments. The key to this mystery is revealed when one collects this veil-like growth; suddenly, from behind the *L. bouillonii* comes a small shrimp with a massive single claw nearly the size of the animal's body. The claw is proportionately extremely powerful and makes an audible clicking noise underwater as it attempts to defend this covering to its home. Indeed, the shrimp is responsible for weaving the veil of cyanobacterial filaments and stitching this to the reef, deriving both visual and chemical protection against predation.

Initial efforts on the secondary metabolites of this cyanobacterium occurred from collections in Guam, but subsequently, efforts have involved samples obtained from Papua New Guinea and Palmyra Atoll as well. The initial work with Guam collections yielded a single major component with exquisitely potent cancer cell cytotoxicity, and was named apratoxin A (**18**) after these initial collections from Apra Harbor [53] (Fig. 2.6). The complete planar and stereostructure was deduced in these early efforts, but the molecule was inactive in an in vivo mouse model of cancer. The mechanism of action of apratoxin A has been studied by two laboratories, and while not completely defined yet, appears to involve inhibition of STAT phosphorylation, down-regulation of an IL-6 transducer and several cancer specific receptor tyrosine kinases, with subsequent prevention of the translocation of several proteins involved in the secretory pathway [54]. However, there is also a report that apratoxin A interacts with heat shock protein 90 (HSP90) [55]. A reinvestigation of the in vivo potential of apratoxin A, using synthetic materials [56], led to an understanding that the drug had to be administered as a daily injection rather than a single bolus, and under these conditions, in vivo anticancer effects were observed. Subsequently, apratoxins B, C, and E have been reported from Guam, D from Papua New Guinea, and F and G from Palmyra Atoll collections [57]. From these diverse molecular structures, some initial structure-activity relationships (SAR) have been deduced which begin to define the Eastern and Northern regions as being of critical importance, whereas the Western and Southern sections are more tolerant of modification [57].

The biosynthesis of apratoxin A (**18**) has been studied in some detail using an innovative gene cloning approach that depended on a partial genome sequence from DNA obtained from single cells [58]. This revealed a roughly 56 kB gene cluster with deduced proteins that exactly match the order and nature of the enzymes needed to construct apratoxin A by a combined NRPS and PKS logic. The pathway begins with the large Eastern PKS section of the molecule, and appears to involve an acetate moiety which is methylated three times to produce the tertiary butyl group. Following two additional rounds of PKS extension, a β -branch is produced, in this case with full reduction to a secondary methyl group. Additional PKS extensions are followed by an NRPS-incorporating cysteine and heterocyclization

to form a thiazoline ring. Fairly standard extensions with a PKS unit and then four NRPS-encoded amino acids follow, terminating with a proline unit. Interestingly, the final section of the gene cluster shows not the expected thioesterase (TE) which normally cleaves the growing lipopeptide from the enzyme assembly, but rather, the truncated condensation domain of yet another NRPS unit. While highly speculative at this point, it is attractive to propose that the condensation domain of this final module is responsible for catalyzing release of apratoxin A with coincident cyclization.

A Florida collection of the marine cyanobacterium *Symploca* sp. yielded a cytotoxic extract that was progressively fractionated to yield a novel cancer cell-selective cytotoxin named largazole (**19**) [59] (Fig. 2.6). The planar structure of largazole was determined by standard NMR and MS–MS methods, and its chirality was established by a reaction sequence involving ozonolysis, oxidative workup, acid hydrolysis, and chiral HPLC in comparison with chemical standards. Largazole possesses several highly unusual structural elements, including two polyketide sections connected through a thioester, a condensed cysteine-alanyl unit which forms a thiazole ring, and a 4-methyl thiazoline ring formed from a second cysteine residue. While this latter modification has been seen previously in cyanobacterial metabolites (e.g., in didehydromirabazole) [60], this was the first thioester linkage to be observed in a cyanobacterial natural product. Largazole (**19**) shows exceptional antiproliferative activity with GI₅₀ values to cancer cell lines in the low nanomolar range. Interestingly, non-transformed cells were much less sensitive to the effects of the drug, suggesting a drug target unique to cancerous cells. Recent work on the molecular mechanism of action of largazole has identified histone deacetylases, and it is tempting to suggest that the unusual thioester-containing side chain plays a role in this activity.

A final cyclic lipopeptide example is given by antillatoxin (**20**), another *Lyngbya majuscula* metabolite from the island country of Curaçao; however, this one shows remarkable neuromodulatory properties through interaction at VGSC [61] (Fig. 2.6). The extracts of collections of this cyanobacterium were highly toxic to goldfish in a matter of seconds, and this assay was then used to direct the isolation of two classes of fish toxic metabolites, the more potent of which was antillatoxin [62]. Antillatoxin is approximately as potent a fish toxin as brevetoxin B, a dinoflagellate polyether “red tide toxin” which annually kills thousands of fish along the Florida coastlines. The pharmacology of antillatoxin has been studied in some detail, and like brevetoxin, it activates VGSCs to increase passage of sodium into cells, an event which ultimately activates ligand gated calcium channels to increase calcium influx, a lethal event to neurons. However, antillatoxin promotes this channel activation at a novel pharmacological position on the channel, and thus defines a new drug binding site. The consequences of this are still under exploration; however, antillatoxin has already shown different pharmacological properties from other VGSC activators such as the brevetoxins and veratridine, and thus represents a new tool for pharmacological investigations [63]. Indeed, both marine and fresh water cyanobacteria, in general, have been a rich source of new tool compounds in the field of neuropharmacology [15]. Structurally, antillatoxin (**20**)

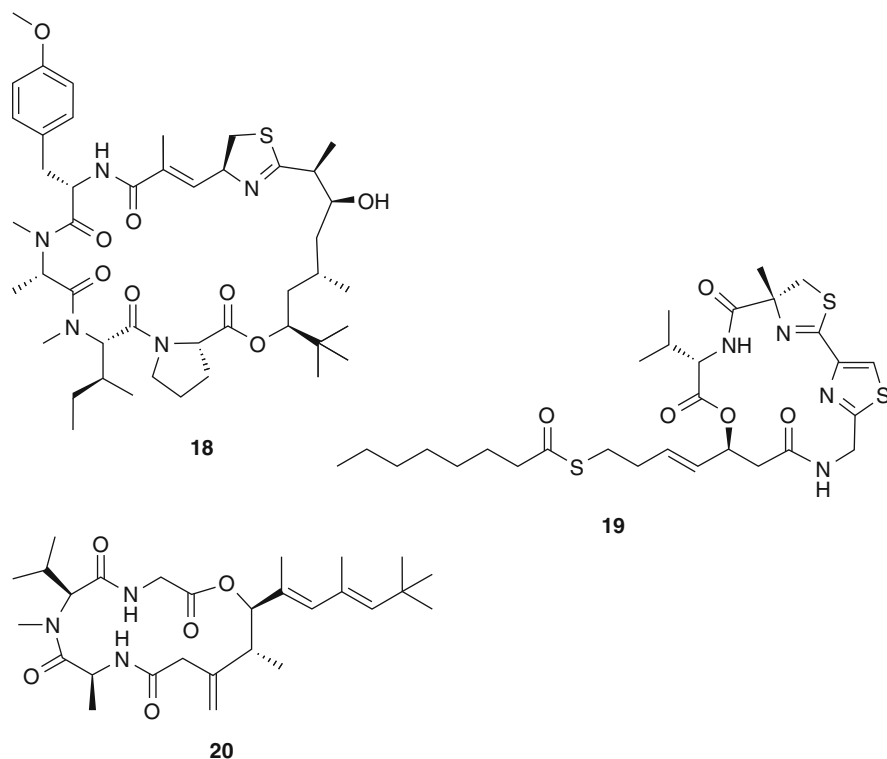


Fig. 2.6 Cyanobacterial cyclic lipopeptides

contains a tertiary butyl group at one end, a highly methyl-substituted polyketide chain, and a tripeptide section which also contains a high level of methylation (e.g., *N*-methylated aliphatic amino acids). The biosynthesis of antillatoxin has not been studied, but it seems reasonable that the pathway begins similarly to that of apratoxin (**18**), that almost all of the acetate units are *C*-methylated at *C*-2 positions of the acetate units from SAM, and that there is one β -branch at a *C*-1 position of acetate near the terminus of the polyketide (Fig. 2.6).

2.2.10 Conclusions on Cyanobacterial Natural Products

Summarizing on the natural products chemistry of marine cyanobacteria, they clearly constitute an extremely diverse source of nitrogen-rich lipids, largely constructed of segments introduced by NRPS and PKS biosynthetic assembly systems. Many of these are exquisitely bioactive in cellular systems, and in the few cases studied, they serve natural antipredatory roles for the producing cyanobacteria [64]. At the same time, these diverse and bioactive natural products represent a treasure trove of molecular scaffolds for drug discovery efforts. Indeed, marine cyanobacteria have

been identified as one of the most promising resources of bioactive compounds for pharmaceutical screening. As genomic and biosynthetic information has become more available in the past decade for these organisms, it appears that nearly every separate population has its own unique capacity to produce unique secondary metabolites, and thus, the opportunities for continued study are immense.

2.3 Marine Microalgae

2.3.1 General Introduction to Marine Microalgae

Marine microalgae are generally free-living eukaryotes and constitute the most important primary producers in the marine environment. Sometimes, populations of these microscopic algae increase rapidly and profoundly, and this causes algal blooms known as “red tides.” Marine microalgae are well-known producers of various natural products including polycyclic ethers, alkaloids, and polyhydroxylated compounds. Many of these marine microalgal metabolites are highly toxic to oceanic and terrestrial animals, including humans; thus, many marine microalgal toxic events have been reported. This section will describe selected secondary metabolites of the following groups of marine microalgae: dinoflagellates, diatoms, chrysophytes, and prymnesiophytes.

2.3.2 Dinoflagellates

2.3.2.1 General Introduction to Dinoflagellates

The dinoflagellates are unicellular microalgae which are mostly found in the marine environment, although some are also found in freshwater. While classified as eukaryotes, dinoflagellates are also considered as mesokaryotes due to their very low content of histones and nucleosomes as well as the presence of condensed chromosomes during mitosis. However, dinoflagellates do contain golgi, mitochondria, and chloroplasts which are typical organelles of eukaryotes.

Currently, nearly 2,000 species in 125 genera of dinoflagellates have been described. However, somewhat reminiscent of the cyanobacteria, dinoflagellates taxonomy is confusing as they were independently classified by both the zoological and botanical codes; only very recently have the disciplines converged to a single taxonomic system. Dinoflagellates characteristically have two flagella known as the longitudinal flagellum and the transverse flagellum. The longitudinal flagellum provides most of the motive force propelling the cell forward, whereas the transverse flagellum acts as a rudder. As a result, dinoflagellates have considerable motility as free-swimming organisms. However, some species of dinoflagellates are benthic or closely associated with other organisms (e.g., as the symbiotic zooxanthellae of corals).

Photosynthetic dinoflagellates, constituting about one half of all known dinoflagellates, have important roles in aquatic ecosystems as primary producers. They have chloroplasts containing chlorophyll *a* and *c* and either peridinin or fucoxanthin

as accessory pigments. The peridinin-containing plastid which is very abundant in photosynthetic dinoflagellates derives evolutionarily as a result of the endosymbiosis of a red alga. Nonpigmented dinoflagellates are general grazers of other protozoa. As noted above, many dinoflagellates live symbiotically with invertebrates and play critical roles in tropical reef ecosystems. For example, members of the genus *Symbiodinium* spp. live in association with corals and produce a number of interesting natural products. Members of another dinoflagellate genus, *Amphidinium*, live symbiotically in marine flat worms, and in isolated form as pure cultures, produce a series of macrolides with exceptionally potent cancer cell toxicities. Alternatively, some free-swimming dinoflagellates form blooms which discolor the ocean surface to produce “red tides”; many of these latter dinoflagellates produce potent toxins that are responsible for devastating toxic events. For further details on these toxins, the reader can see ► [Chap. 28](#).

2.3.2.2 Polyether Toxins

Okadaic Acid

A toxic event which occurred in Japan during 1976 was associated with the ingestion of contaminated shellfish. The typical symptom of intoxication was severe diarrhea, and thus, the event was termed as “diarrhetic shellfish poisoning” (DSP). Subsequently, the complex polyether metabolite, okadaic acid (**21**), was revealed as the toxin responsible for DSP [65] (Fig. 2.7). Interestingly, okadaic acid was named from the sponge *Halichondria okadai*, the original source from which the toxin was isolated. It was subsequently found to be produced by the dinoflagellates *Prorocentrum* spp. and *Dinophysis* spp. and then accumulates in filter feeders such as sponges and shellfish [66, 67]. Okadaic acid is a very potent cell toxin with an EC₅₀ value of 1.7 nM against the P388 cell line. It has also been shown to promote tumor formation as a result of its potent and specific inhibition of protein phosphatases 2A and 1 [68, 69].

Brevetoxins

The dinoflagellate *Karenia brevis* (formerly known as *Gymnodinium breve* or *Ptychodiscus brevis*) is common in the Gulf of Mexico, and it is responsible for red tides along the Florida coast [70]. Blooms of *K. brevis* cause massive fish kills, mollusk poisonings, and human food intoxications termed “neurotoxic shellfish poisoning” (NSP) [70]. The causative agents were first isolated from cultured *K. brevis* and thus named the “brevetoxins” [71]. Subsequently, they have also been found in other dinoflagellate species such as *Chattonella marina*, *Chattonella antiqua*, *Fibrocapsa japonica*, and *Heterosigma akashiwo* [72–74].

Structurally, the brevetoxins are ladder-like polycyclic ethers of fascinating molecular architecture. Brevetoxins A (**22**) and B (**23**) were first reported in 1975 as undefined compounds with the names GB-1 and GB-2 [75], but in 1981, the structure of brevetoxin B (= GB-2 and PbTx-2) was elucidated by X-ray crystallography [71]. The structure of brevetoxin A (= GB-1 and PbTx-1) was more challenging to determine, but following chemical modifications, Shimizu and coworkers were able to form a crystal that could also be analyzed by X-ray crystallography [76].

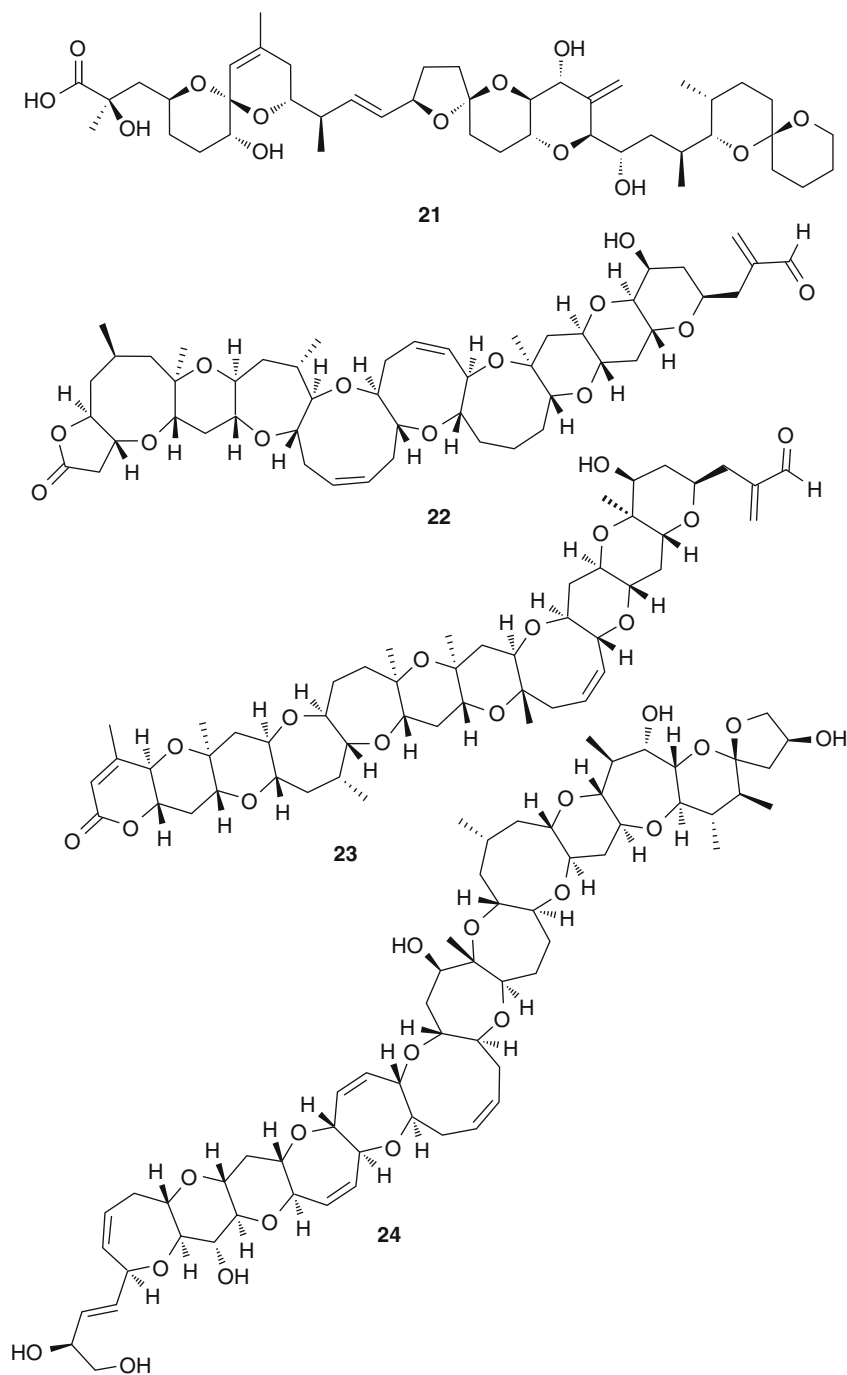


Fig. 2.7 Polyether toxins from dinoflagellates

Interestingly, brevetoxin A possesses 5-, 6-, 7-, 8-, and 9-membered rings, which have fascinated and challenged the synthetic organic chemistry community. However, due to the complexity of brevetoxin A, it was not until 1997 that the first total synthesis was accomplished by K. C. Nicolaou [77]. Although BTX A and B have two different carbon skeletons, they each consist of a single carbon chain (Fig. 2.8). This suggests that BTX A and B may derive from polyketide biosynthetic pathways. Further labeling experiments using sodium [1-¹³C]- and [2-¹³C]acetate and [methyl-¹³C] methionine have demonstrated that the citric acid cycle is involved in their biosynthesis. The brevetoxins bind to site 5 of VGSC, thus maintaining the channel in an open configuration and leading to uncontrolled sodium influx into cells [78]. As a result, the brevetoxins are extremely potent toxins to fish (lethal dose to guppies at 4 ng/mL) as well as mammals (lethal oral dose to mice of 520 µg/kg body weight) [76, 79]. The symptoms of sublethal NSP are gastroenteritis along with nausea, peripheral tingling and numbness, loss of motor control, and severe muscle pain [80, 81]. The brevetoxins can be transferred from contaminated water to air as aerosols, and inhalation of these has resulted in respiratory illnesses in coastal populations [82].

Ciguatoxin

Ciguatera fish poisoning (CFP) was first described by a surgeon's mate, John Anderson, on the crew of HMS Resolution in 1774 [83]. CFP is one of the most commonly reported seafood poisonings in the world. Annually, 25,000 people are intoxicated by the consumption of toxin-contaminated coral reef fish [84]. Ciguatoxin (CTX) (24), the causative toxin of CFP, was first isolated in 1980, and its structure was elucidated in 1989 [85, 86] (Fig. 2.7). To elucidate its structure, 0.35 mg of CTX was obtained from 4,000 kg of moray eel (*Gymnothorax javanicus*) collected in French Polynesian waters. This very limited quantity of CTX was insufficient to record a ¹³C NMR spectrum, and thus, its structure was elucidated entirely by ¹H NMR-based experiments. Absolute configuration of CTX was determined by Yasumoto and coworkers in 1997 via chemical degradation and chiral HPLC in combination with CD spectroscopy [87]. The dinoflagellate origin of CTX and its congeners was subsequently identified as *Gambierdiscus toxicus*, which is also the producer of maitotoxin, another exceedingly complex polyether toxin.

CTX-4B, a less oxygenated precursor of CTX, was reported from *G. toxicus* collected in the Gambier Islands [88]. It is first transferred to herbivorous fish by ingestion and subsequently to carnivorous fish via the food chain [89]. In fish, the precursor CTX-4B appears to be transformed into the more oxygenated form, CTX. Currently, more than twenty CTX congeners have been reported from *G. toxicus* or coral reef fish [90]. Similar to brevetoxins, CTX selectively binds to site 5 on α -subunits of the VGSC and permanently activates the channel at nanomolar to picomolar concentrations [91]. The binding affinity of CTX to site 5 is 30 times higher than brevetoxins. In mice, CTX is lethal when injected intraperitoneally at a dose of only 0.25 µg/kg [92]. CTX is very heat-resistant such that ciguatoxin-contaminated fish cannot be detoxified by conventional cooking [93]. The characteristic symptoms of CFP are severe neurologic disturbance and a reversal of thermal sensation (e.g., cold items are perceived as hot, and vice versa) [84, 91].

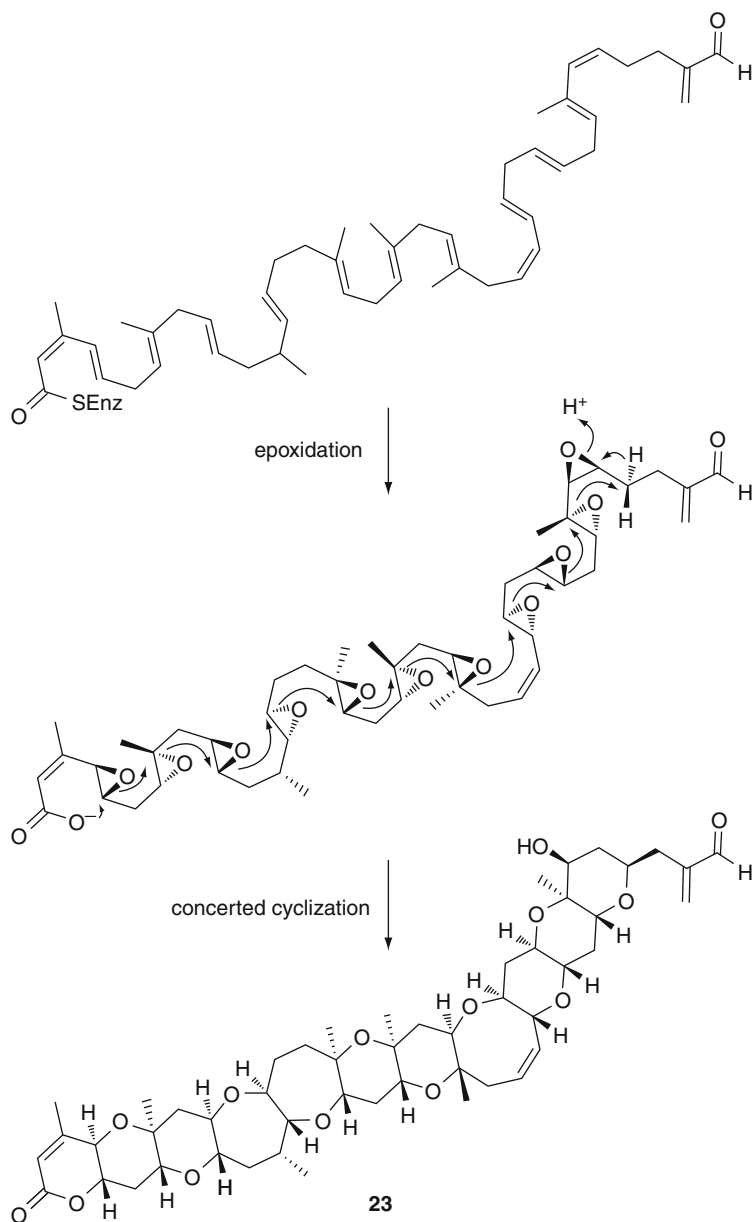


Fig. 2.8 Proposed biosynthesis of brevetoxin B (**23**) from a polyunsaturated fatty acid by epoxidation of double bonds and a concerted sequence of epoxide ring openings leading to the extended polyether structure of *trans*-fused rings

Palytoxin

In Hawaiian folklore, it was described that a poisonous reddish “moss” grown in a pond close to the ocean, in Muolea, in the district of Hana. The “moss” was coated on spear points to make them poisonous and was called “Limu make o hana” (Seaweed of Death from Hana). In 1971, its toxic component, palytoxin (PTX) (**25**), was first isolated from the seaweed-like soft coral *Palythoa toxica* [94]. The chemical structure of PTX was independently elucidated by two different groups in 1981 [95, 96] (Fig. 2.9). PTX is a very large and complex molecule with a long polyhydroxylated aliphatic chain containing 64 chiral centers. PTX has the longest chain of continuous carbon atoms of any known natural products. Remarkably, the total synthesis of PTX was accomplished by the Kishi laboratory in 1994 [97, 98]. PTX was originally isolated from colonial zoanthids; however, PTX and its analogs have since been isolated from a variety of marine organisms including the red alga *Chondria crispus* and the benthic dinoflagellate *Ostreopsis siamensis* [99, 100]. Symbiotic bacteria found in association with several of these organisms have been studied as a possible source of PTX production. PTX hemolytic activity has been observed in the extracts of several bacteria including *Pseudomonas*, *Brevibacterium*, and *Acinetobacter* [101, 102]. However, by enzyme-linked immunosorbent assay (ELISA), the Gram-negative bacteria *Vibrio* sp. and *Aeromonas* sp. were identified as potential producers of PTX or its congeners [103]. Indeed, the presence of PTX and its congeners in a variety of marine organisms suggests a bacterial origin for PTX production [102, 104].

PTX is regarded as one of the most potent toxins found in nature. Its pharmacological target has been identified as the extracellular portion of the Na^+/K^+ -ATPase with the result that Na^+ and K^+ transport is inhibited [105]. PTX shows an LD_{50} of 0.025 $\mu\text{g}/\text{kg}$ in rabbits and 0.45 $\mu\text{g}/\text{kg}$ in mice 24 h following intravenous injection [95]. Human fatalities by consumption of PTX-contaminated seafood have been reported in the Philippines (crabs), Brazil (sea urchins), and in Japan (fish) [106–110]. Recently, human intoxication in Germany and the USA occurred following dermal exposure to zoanthid corals being kept as home aquarium specimens [111, 112]. In Italy, a sea aerosol generated during an *Ostreopsis ovata* bloom caused human intoxications that involved respiratory illness [113]. Typical symptoms reported include bitter taste sensation, abdominal cramps, nausea, vomiting, diarrhea, cyanosis, and respiratory distress.

2.3.2.3 Alkaloids

Saxitoxin

Saxitoxin (STX) (**26**) is the most potent of the paralytic shellfish poisoning (PSP)-related toxins and is generally caused by the consumption of contaminated shellfish [114]. A toxic event occurring in 1927 in the San Francisco Bay is the earliest PSP-related report, the result of which sickened over 100 people and 6 died [115]. This toxic event was apparently caused by ingestion of sea mussels which had accumulated STX from the dinoflagellate *Alexandrium catenella*. STX was first isolated in pure form from the Alaskan butter clam *Saxidomus giganteus* in 1957

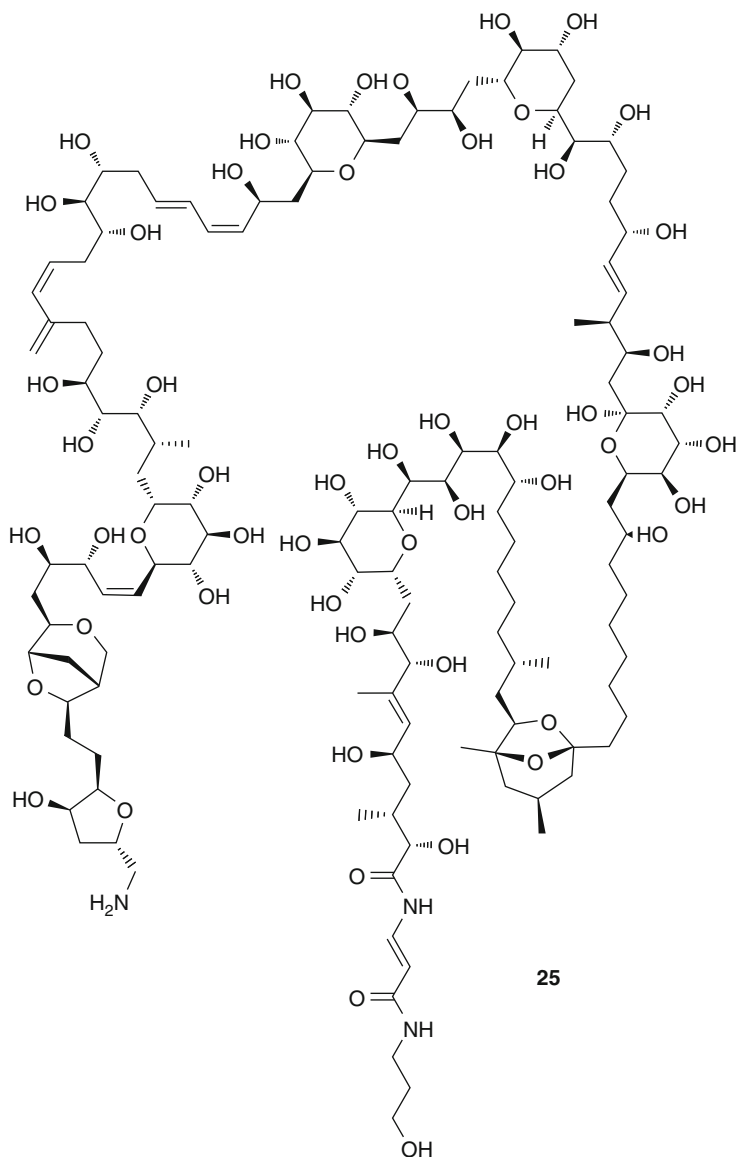


Fig. 2.9 Structure of palytoxin (25)

[116], and its structure subsequently elucidated by X-ray crystallography [117]. Notable features of the structure of STX are the presence of a carbamate and a 3,4-propinoperhydropurine tricyclic ring. The presence of two guanidine groups makes STX water soluble. Since the first total synthesis of racemic STX, accomplished in 1977 by the Kishi group [118], a number of syntheses have been developed by other groups [119, 120], and in 2006, the DuBois laboratory synthesized chiral

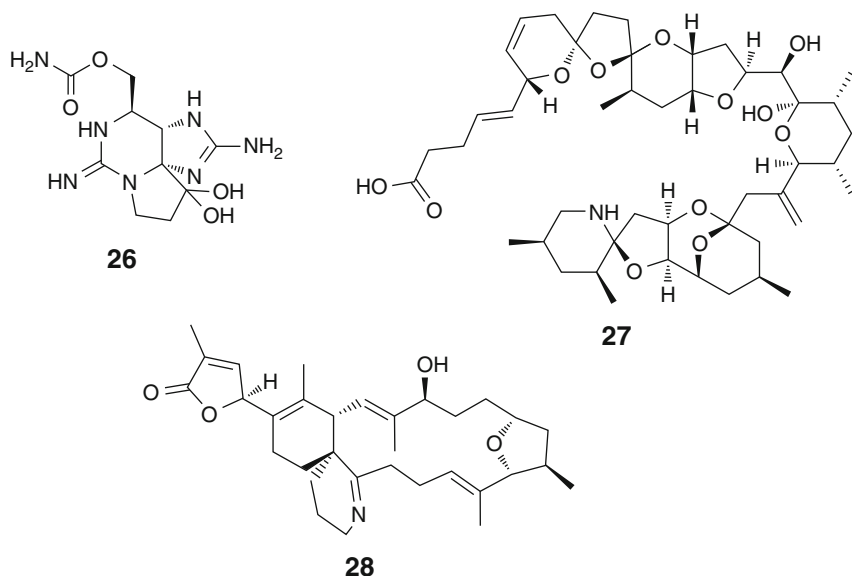


Fig. 2.10 Alkaloids from dinoflagellates

STX by selective oxidation of a nine-membered ring guanidine intermediate followed by dehydrative cyclization [120, 121]. Shimizu and coworkers performed an isotope-labeled precursor feeding study in 1984 and proposed the biosynthesis of STX analogs as produced in cyanobacteria [122]. In 2008, Kellmann revised the proposed biosynthetic pathway from *in silico* deduced functional inferences based on the STX biosynthetic gene cluster and complemented this with an LC–MS/MS analysis of biosynthetic intermediates [123].

Continued study has revealed that STX is present in diverse life forms, including dinoflagellates of the genera *Alexandrium*, *Gymnodinium*, and *Pyrodinium* [124], various cyanobacteria [125], marine pufferfish, and Brazilian freshwater tilapia [126]. Thus, it seems logical that STX is produced by symbiotic bacteria; however, the experimental evidence is not conclusive on this point. Pharmacologically, STX binds to neurotoxin site 1 of the VGSC, thereby blocking the ion channel pore and inhibiting sodium influx [127]. The LD₅₀ of orally administered STX was 3–10 µg/kg body weight in mice and 5.7 µg/kg for humans. The symptoms of intoxication include initially a tickling sensation of the mouth and tongue, followed by difficulty in breathing, respiratory arrest, and cardiovascular shock [128]. Because STX and its analogs are exceptionally toxic, their manufacture, use, transfer, and reuse are strictly regulated by the Organization for the Prohibition of Chemical Weapons (Fig. 2.10).

Azaspiracid

Azaspiracid (AZA) (27) is an alkaloidal polyether-type toxin that accumulates in shellfish and is associated with gastrointestinal intoxications. Since the first report

from the Netherlands in 1995, AZA has been found in shellfish from the coastal areas of Europe (Netherlands, Ireland, France, UK, and Norway) and Africa (Morocco) [129–136]. In 2004, the EU established a regulatory limit of AZA (160 μg AZA/kg shellfish in flesh) to protect public health [137]. The structure of AZA was elucidated in 1998 [129], and the name of AZA was based on its unusual structural features of a cyclic amine (aza group), a trispiro ring assembly and a carboxylic acid. However, the original structure reported in 1998 was found to be incorrect by total synthesis, and a structure revision was accomplished by extensive study of the NMR spectra in 2004 [138–141]. While originally isolated from shellfish, the polyether structure of AZA suggested a dinoflagellate origin, and subsequently, the heterotrophic dinoflagellate *Protoperidinium crassipes* has been identified as the likely producer of AZA [129, 142, 143]. A variety of analogs of AZA have been detected by LC–MS/MS from the extract of individually isolated *P. crassipes* [144, 145]; however, large scale culture or bulk sampling of this dinoflagellate for the presence of the toxin has been unsuccessful. The symptom of AZA intoxication is similar to that of okadaic acid in that it causes nausea, vomiting, severe diarrhea, and stomach cramps. Partially purified AZA was lethal to mice with an intraperitoneal injection of 150 $\mu\text{g}/\text{kg}$ [146] and induced organ damage in stomach, liver, thymus, and spleen tissues [147]. Little is known about the molecular pharmacology of AZA, and its molecular target has not yet been identified. However, the pathology of AZA is unique among other marine toxins.

Gymnodimine

Gymnodimine (**28**) was first isolated as a phycotoxin from New Zealand oysters and the dinoflagellate *Gymnodinium* sp. [148, 149]. Subsequent research has shown that this phycotoxin, found in such shellfish as the greenshell mussel, blue mussel, scallop, and abalone, is produced by the dinoflagellate *Karenia selliformis* (formerly named *Gymnodinium selliforme*) [150–152]. The structure of gymnodimine was elucidated by NMR spectroscopy and X-ray crystallography [148, 153]. Gymnodimine possesses several unusual structural features such as a 2,4-disubstituted butenolide, a spirocyclic imine ring, and a trisubstituted tetrahydrofuran embedded in a 16-membered macrocyclic ring. Gymnodimine was first suggested to act on VGSCs, but subsequently shown to target muscular and neuronal nicotinic acetylcholine receptors with high affinity [149, 154].

2.3.2.4 Macrolides

Marine dinoflagellates are rich producers of macrolides as well as polycyclic ethers (Figs. 2.11 and 2.12). A series of macrolides named the “amphidinolides” was obtained from the dinoflagellate *Amphidinium* sp., which lives symbiotically with Okinawan marine flatworms of the genus *Amphiscolops* sp. In turn, flatworms are typically found living on algae or seaweeds in coral reef environments [155]. Among the previously reported 42 analogs, amphidinolide N (**29**) is the most toxic compound with IC_{50} values of 0.00005 $\mu\text{g}/\text{mL}$ to murine lymphoma L1210 cells and 0.00006 $\mu\text{g}/\text{mL}$ to human epidermoid carcinoma KB cells [156]. The structure of amphidinolide N was elucidated as a 26-membered macrolide

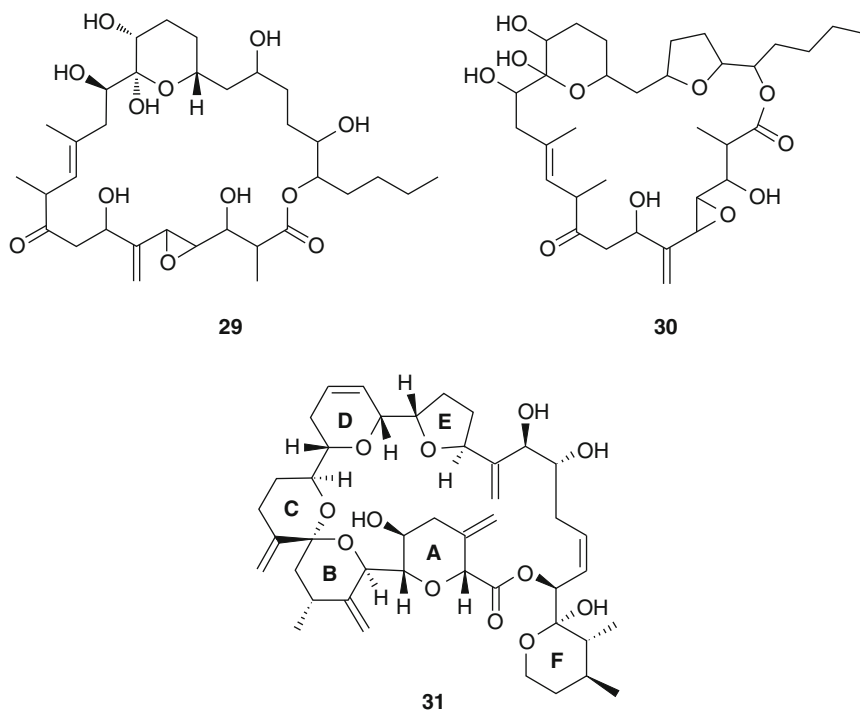


Fig. 2.11 Macrolides from dinoflagellates

containing a 6-membered hemiacetal ring, an epoxide, a ketone, four C1 branches, and seven hydroxy groups [156] (Fig. 2.11). The absolute stereochemistry at C-13 has not yet been determined.

Caribenolide I (**30**), having the same skeleton as amphidinolide N but with derivatization of the 1,4-diol to a furan ring, was isolated from a free-swimming dinoflagellate *Amphidinium operculatum* var nov *Gibbosum* by Shimizu and coworkers in 1995 [157] (Fig. 2.11). Caribenolide I was reported to show potent cytotoxicity with IC_{50} values of 0.001 $\mu\text{g/mL}$ against both drug sensitive and resistant HCT116 human colon tumor cell lines. In addition, caribenolide I showed in vivo activity against murine P388 tumors ($T/C = 150$ at 0.03 mg/kg).

In 1968, an antifungal agent named goniiodomin was isolated from the dinoflagellate *Goniiodoma* sp. by Sharma and coworkers; however, a structure was not reported in this initial report [158]. In 1988, Murakami and coworkers reported the structure of a goniiodomin-related compound, goniiodomin A (**31**), isolated from *Alexandrium hiranoi* (formerly known as *Goniiodoma pseudogoniaulax*) [159]. Goniiodomin A is a polyether macrolide with a spiroacetal ring (B/C-ring), four additional oxacycles (A, D, E, and F rings), and 17 stereogenic centers embedded within a 36-carbon chain (Fig. 2.11). Goniiodomin A showed inhibitory activity against *Mortierella ramannianus* and *Candida albicans* at a concentration of 0.5 $\mu\text{g/mL}$.

The dinoflagellate *Symbiodinium* sp., classified as a zooxanthella because of its common symbiotic relationship with corals and other marine invertebrates, is reported as a rich producer of “super carbon-chain compounds” (SCC) [160–162]. For example, in 1995, zooxanthellatoxin A (**32**) was isolated from *Symbiodinium* sp. collected from the flatworm *Amphiscolops* sp. [163]. Zooxanthellatoxin A is a polyol macrolide with 15 double bonds, 42 hydroxy groups, one sulfate, five tetrahydropyran rings, and a 62-membered ring, the largest lactone ring yet observed among natural products (Fig. 2.12). Zooxanthellatoxin A shows potent vasoconstrictive activity in rat blood vessels [164].

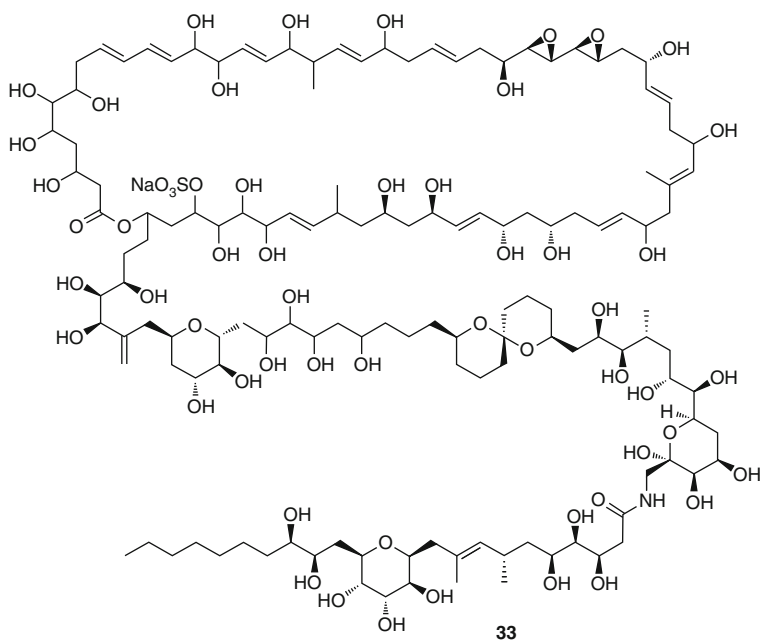
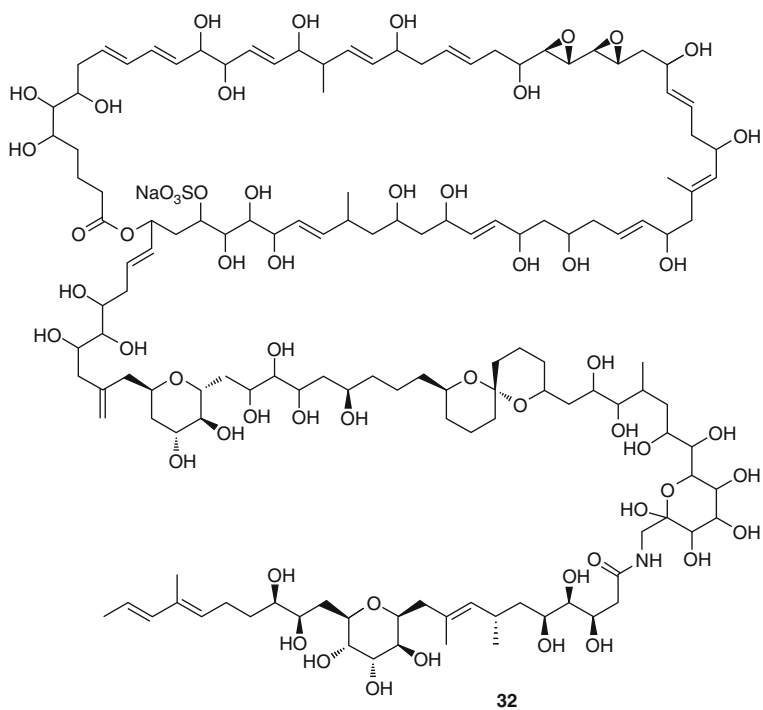
In 2007, symbiodinolide (**33**), a congener of zooxanthellatoxin A, was isolated from cultures of the symbiotic dinoflagellate *Symbiodinium* sp. collected from the Okinawan flatworm *Amphiscolops* sp. [165] (Fig. 2.12). Symbiodinolide showed a potent voltage-dependent *N*-type Ca^{2+} channel-opening activity and increased intracellular concentrations of free Ca^{2+} . In addition, symbiodinolide caused rapid rupturing of the tissue surface of host flatworm cells, and thus, this impressive natural product may constitute a defense against digestion by the host.

Dinoflagellates of the genus *Amphidinium* are rich producers of antifungal and hemolytic polyhydroxy secondary metabolites as well as cytotoxic macrolides. In 1991, amphidinol-1 (**34**) was described by Yasumoto and coworkers from cultures of field collected *A. klebsii* [166]. Amphidinol-1 is a polyhydroxypolyene compound with a conjugated triene, an exomethylene and two tetrahydropyran rings (Fig. 2.12). The bioactivities of amphidinol are associated with the membrane permeability of the molecule. It was proposed that the polyene region, two of the hydrophilic tetrahydropyran rings, and the polyhydroxy chain play key roles in binding to lipid bilayers, stabilizing the binding, and pore forming properties of these molecules in the cell membrane [167].

2.3.3 Diatoms

2.3.3.1 General Introduction to Diatoms

Diatoms are unicellular microalgae, also known as “golden-yellow algae,” due to their characteristic color resulting from chlorophyll *a* and *b* plus a number of carotenoids and are classified with the stramenopiles [5]. Some forms of diatoms can form pseudofilaments and aggregations which can give them a macroscopic appearance. They are ubiquitous in aquatic distribution, both in fresh and marine water, and comprise approximately 200 genera that are divided into two orders, the Pennales (pennate shaped) and the Centrales (centrosymmetric). Interestingly, pennate diatoms but not centric ones are capable of movement; the mechanism for this movement, which is sometimes coordinated between individuals, is not well understood; however, they do leave behind slime trails. The chloroplasts of diatoms derive from an ancient endosymbiosis of a red alga, and diatom cells are contained within a very characteristic frustule composed of two overlapping halves of silica, much like a petri dish for the centrate diatoms. This unique cell wall construction is accessed when trying to rid algal cultures of diatom contaminants. Addition

**Fig. 2.12** (continued)

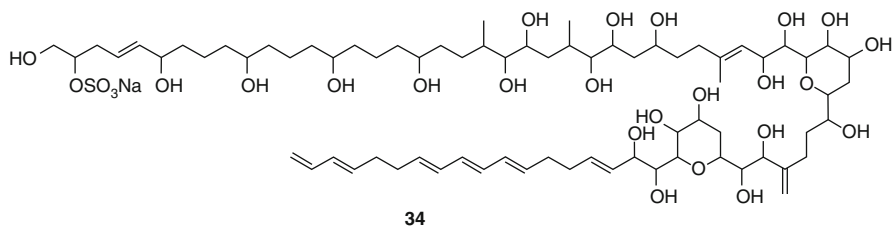


Fig. 2.12 Macrolides from dinoflagellates

of GeO_2 to contaminated cultures is selectively toxic to diatoms as it interferes with the biochemical machinery responsible for frustule formation. The accumulation of diatom outer cells walls over geological time scales has given rise to sedimentary deposits of diatomaceous earth. These deposits have been used as important components of water filters, paints, toothpastes, and many other common household products. Additionally, the frustules of diatoms are intricately created with many fine pores and other surface features, produced with great precision and fidelity by a set of enzymes known as silicases. The industrial value of silicases is being explored in various nanotechnology applications. Diatoms have the characteristic of storing oils rather than starches as a reserve energy source, and thus are leading candidates for algal biofuel production. In a couple of cases, draft genomes of diatoms have been deduced (e.g., *Thalassiosira pseudonana*), and they appear to be roughly of 32.4 MB [168, 169]. Finally, diatoms are capable of both sexual as well as vegetative reproduction. However, when reproducing vegetatively, the cell size becomes progressively smaller, ultimately terminating due to physical constraints of the solid silica cell wall.

2.3.3.2 The Natural Products of Diatoms

The natural products of diatoms have been studied to a fairly limited degree, and there is clearly much refinement and further exploration needed; this may well occur as a result of their being top candidates for algal biofuels. A first major trend in the secondary metabolism of diatoms is the capacity of some pennate diatoms to produce simple analogs of the amino acid glutamate, such as domoic acid (**35**), which function as powerful glutamate receptor agonists. When these build up in the food chain, they cause a well-described environmental toxicity to humans and marine mammals known as “amnesic shellfish poisoning.” A second very important natural product class is derived from polyunsaturated fatty acids that become oxidized and then undergo various ensuing reactions, such as carbocyclization, carbon-chain cleavage, and further oxidations; oxidized lipids of this type are known as “oxylipins.” A third major trend in diatom metabolism is a group of terpenoid hydrocarbons which are curious for their uniquely branched carbon framework.

Domoic Acid

In 1987, a cluster of symptoms emerged from individuals eating shellfish in Nova Scotia, Canada which were unlike any known shellfish intoxication, and involved

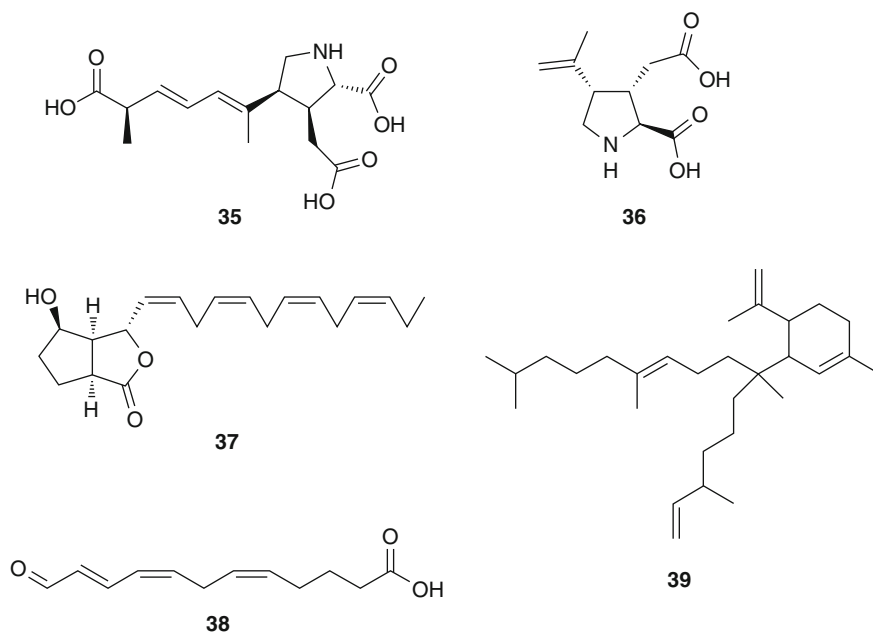


Fig. 2.13 Secondary metabolites of diatoms

gastrointestinal effects, extreme headache, and permanent short-term memory loss in strongly affected individuals, ultimately becoming known as “amnesic shellfish poisoning” [170]. A frantic effort to identify the responsible toxins and toxin sources ensued and ultimately traced this to the pennate diatom *Pseudo-nitzschia*. An investigation remarkable for its speed and efficiency identified the toxin as the known metabolite “domoic acid” (35), a natural product which had been earlier characterized as a product of the Japanese macrophytic red alga *Chondria armata* [171]. This and another red alga, *Digenia simplex*, were historically known in Japan for their ability to treat parasitic worm infections, and structural characterizations of the active compounds, named domoic acid after the Japanese name “doumoi” and kainic acid (36) after the name “Kainin-sou,” were two of the early discoveries in the field of marine natural products chemistry.

The structures of these two compounds are highly similar with the difference being an extra five-carbon “prenyl” group present in domoic acid (35) relative to kainic acid (36) (Fig. 2.13). It may be that the increased lipophilicity imparted by this modification enhances the neurotoxic effect of this agent when ingested. Imbedded in both structures is a “glutamate” residue, which for domoic acid is modified by the attachment of a ten-carbon terpenoid chain, presumably from geraniol. Investigations with isotope-labeled precursors provided evidence for the biosynthetic condensation of α -ketoglutarate with geraniol; however, because feeding studies to the diatom with [2- ^{13}C , $^2\text{H}_3$]acetate resulted in a complete absence of deuterium incorporation, it appears that the isoprenoid chain may be

synthesized by a novel pathway [172]. Pharmacologically, domoic acid activates AMPA, kainite, as well as NMDA neurochemical receptors by mimicking glutamate, thereby causing an influx of calcium and ensuing neurotoxicity [170]. The hippocampus and amygdaloid nucleus regions of the brain are especially prone to domoic acid-induced neurotoxicity which results in memory loss, seizures, and in extreme cases, death, both in humans and marine mammals.

Oxylipins

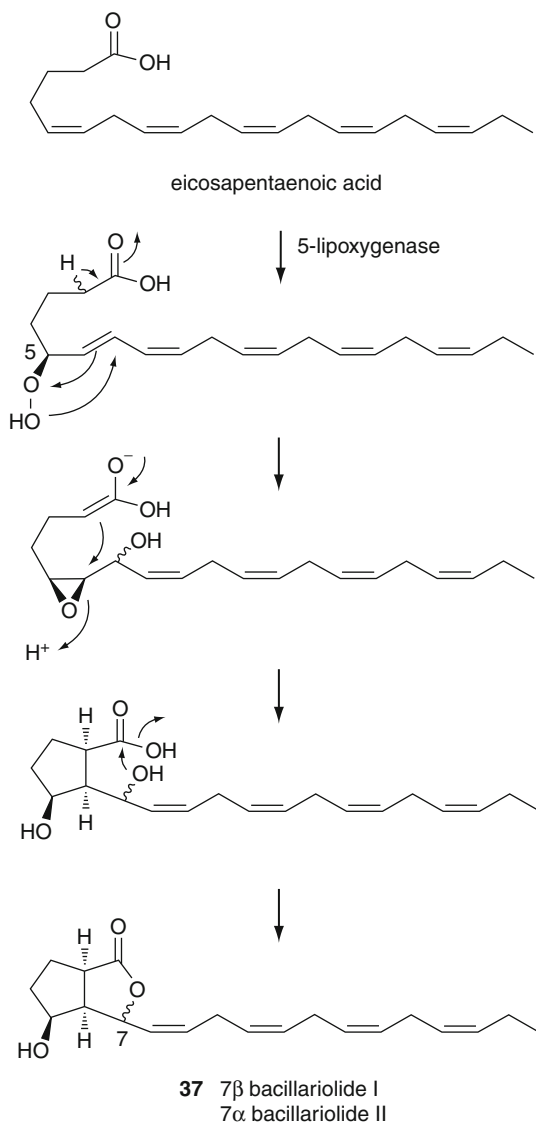
Oxylipins, defined as polyunsaturated fatty acids which are modified by molecular oxygen-dependent oxidations [173], are broadly present in various classes of marine photosynthetic organisms, including the diatoms. One of the earliest characterizations of an oxylipin from a diatom was by the Shimizu group during their independent investigations of the causative agent for amnesiac shellfish poisoning [174]. Their work, which focused on the pennate diatom *Nitzschia pungens*, led to the isolation and complete characterization of two epimeric oxylipins, named bacillariolide I (37) and II, which are unique for possessing a carbocycle involving C2 and C6 to form a five-membered ring. The presence of an adjacent C5 alcohol is tantalizing for the mechanistic suggestion that a 5-lipoxygenase initiates the biosynthetic pathway, followed by epoxide ring formation and then ring formation from a C2 anion equivalent [175]. Additionally, these metabolites contain a lactone ring which involves ester formation between the C1 carboxylic acid and a C7 carbocation, yielding a γ -lactone (see Fig. 2.14). The biological properties of the bacillariolides have not been reported, so it is uncertain to what extent they may contribute to some of the symptoms of amnesiac shellfish poisoning.

Since these earliest reports of diatom oxylipins, it has been found that natural blooms of these photosynthetic unicellular algae, as well as laboratory cultures, are very active in producing simple oxidized derivatives which decrease the reproductive success in planktonic micrograzers such as copepods [176]. Mechanistically, this appears to occur largely from the oxidative cleavage of polyunsaturated fatty acids to polyunsaturated aldehydes by action of a hydroperoxide lyase, and these induce apoptosis and teratogenesis in copepod nauplii [177]. In addition to aldehydes (e.g., 38), other classes of oxylipins are produced by diatoms which uniquely derive from eicosapentaenoic acid or variously unsaturated hexadecenoic acids, and possess hydroxy, ketone, or epoxyalcohol functional groups. In fact, various species of diatoms have unique “signatures” of oxylipin metabolites, and this can vary as a function of environmental parameters [178]. Characterization of the oxylipins of diatoms is an area of active investigation in several laboratories, notably the Ianora and Fontana laboratories in Italy and the Pohnert laboratory in Germany, and it is quite certain that new appreciation of the functional roles of oxylipin synthesis in diatoms will emerge from these continuing efforts.

Triterpenes

The final class of diatom natural products to be discussed is a series of curious C-30 triterpene hydrocarbons, unique for their irregular pattern of isoprene units (e.g., 39). Biosynthetic experiments utilizing [2-¹³C] acetate led to hydrocarbons labeled

Fig. 2.14 Proposed biogenesis of the bacillariolides (**37**) from eicosapentaenoic acid in the marine diatom *Nitzschia pungens*



at positions consistent with the mevalonate pathway and provided an overall perspective of the connection between separate diterpene and monoterpene components [179]. Related hydrocarbons have been detected in marine sediments and utilized as geochemical markers of planktonic diatoms of the genus *Pleurosigma* [180].

2.3.4 Chrysophytes

Chrysophytes or golden algae are common microscopic inhabitants of primarily freshwater bodies (e.g., *Ochromonas* and *Poterioochromonas*), although some species, particularly within the Sardinochrysidales and Chrysomeridales, occur in brackish, marine, or terrestrial environments. Some species are colorless, but the vast majority are photosynthetic. In addition to chlorophyll, they also contain the pigment fucoxanthin which gives them their characteristic yellow-brown color. There are more than a thousand described species of golden algae, and although the genera included within the chrysophytes are still in a state of flux, they are currently placed in the Heterokontophyta (Stramenopiles) within the Chromalveolates. Chrysophytes are morphologically diverse and occur as unicellular flagellates, colonial flagellates, filaments, and thalloids. Most chrysophytes are planktonic, but some are benthic, epibiotic, or neustonic.

Chlorosulfolipids, styrylchromones, and dimeric diarylbutene macrolides comprise the three natural product scaffolds reported thus far from chrysophytes, collected in both freshwater and marine habitats. Their intriguing structures and potent biological activities have made them the focus of multiple stereochemical studies and total syntheses, as well as novel target validation investigations.

2.3.4.1 Chlorosulfolipids

Chlorosulfolipids represent an unusual and fascinating class of natural product that was first reported in the late 1960s [181]. These compounds contain up to 11 chlorine atoms and 2 sulfate groups and have been isolated from the ubiquitous fresh water algae *Ochromonas danica* (40–46) [181–185] and *Poterioochromonas malhamensis* (47) [186–188], as well as from digestive glands of contaminated shellfish *Mytilus galloprovincialis* (48–50) along the Adriatic coast of Italy [189–193], and the Formosan octocoral *Dendronephthya griffini* (48) [194] (Fig. 2.15). The apparent localization of sulfolipids 40–46 in the cellular and flagellar membranes of *O. danica*, their substantial presence (91 mol% of the polar lipids in the flagellar membrane) [195], and the lack of significant quantities of phospholipids led to speculation that these unusual compounds might play a structural role within cell membranes. The planar structures of these lipids were initially elucidated by mass spectrometric analysis and chemical degradation studies [181–185], and just recently, assignments made for their relative and absolute configurations using a combination of *J*-based configuration, modified Mosher's analyses and chemical synthesis [196]. The extent of chlorination appears to be influenced by the concentration of chloride ion in the environment [181]. Chlorination likely occurs one halogen at a time at unactivated carbons, possibly via a radical mechanism, and the lipids are apparently formed as single stereoisomers [184]. Danicalipin A (46), which has been identified as the most abundant of all *O. danica* sulfolipids, displayed moderate toxicity to brine shrimp larvae (LC₅₀ 2.2 µg/mL) [196].

Malhamensilipin A (47) is the main component of extracts derived from laboratory cultured *P. malhamensis* [186–188]. Besides exhibiting antiviral and

antimicrobial activity, compound **47** displayed moderate inhibition of tyrosine kinase (IC_{50} 35 μ M); overactivated tyrosine kinases contribute to the initiation or progression of cancer [186]. The structure of **47** suggests that it might share a common biosynthetic origin with the lipids of *O. danica*, and this is further supported by the close taxonomic relationship of these two algal species.

Although their isolation and structural elucidation were first described from toxic mussels [189–193], based on their close structural relationship to the above chlorosulfolipids, compounds **48–50** are likely produced by microalgae. These compounds displayed modest cytotoxic activity and thus fueled a renewed interest by synthetic chemists into this class of natural products due to their possible involvement in Diarrhetic Shellfish Poisoning [190–193]. This aspect stimulated efforts toward their total synthesis and has resulted in the development of new stereoselective chlorination methodologies [197–200], a new procedure to produce (*E*)-chlorovinyl sulfate moieties [188], comprehensive configurational studies [201], and the total syntheses of **48** [200], **46** [202], and **47** [188].

2.3.4.2 Hormothamnione Styrylchromones

Hormothamnione (**51**) and 6-desmethoxyhormothamnione (**52**) constitute the two members of this unique class of chrysophyte-derived natural product, both isolated from *Chrysophaeum taylori* collected from the north coast of Puerto Rico [203, 204] (Fig. 2.16). These compounds constituted the first naturally occurring styrylchromones and were named after the marine cyanophyte *Hormothamnion enteromorphoides* which was the initially reported source organism for **51**, but later revised as *C. taylori* upon light microscopy experiments of fresh and preserved material, culture work, and comparison with original taxonomic descriptions [204, 205]. The structure of **51**, unprecedented in the natural products field at the time of its isolation, was solved using X-ray diffraction data obtained from the corresponding triacetylated derivative [203]. Classical heteronuclear long-range 2D NMR experiments were used to determine the substitution pattern of proton, hydroxy, and methoxy groups on the chromone ring of **52** [204]. Biosynthetically, it is equally plausible for hormothamnione to derive from acetate or shikimate pathways, although some of the sites of oxidation are inconsistent with the expected patterns resulting from either biogenetic sequence.

Hormothamnione (**51**) was found to be a potent cytotoxic agent to P388 lymphocytic leukemia (IC_{50} 11.5 nM) and HL-60 human promyelocytic leukemia (IC_{50} 250 pM) cell lines [203], whereas analog **52** showed significant toxicity to KB carcinoma cells (LD_{50} \sim 2.5 μ M) [204]. Further pharmacological characterization attributed antioxidant [206] and anti-inflammatory [207] activities to the semisynthetic diacetate **53** (Fig. 2.16). Both **51** and **52** have been the subject of multiple total syntheses [208–211], given the potent and diverse biological activities measured for these metabolites.

2.3.4.3 Chrysophaentins A–H

Chrysophaeum taylori, this time collected from Round Bay on the Island of St. John (US Virgin Islands), was found to produce a suite of eight symmetrical and

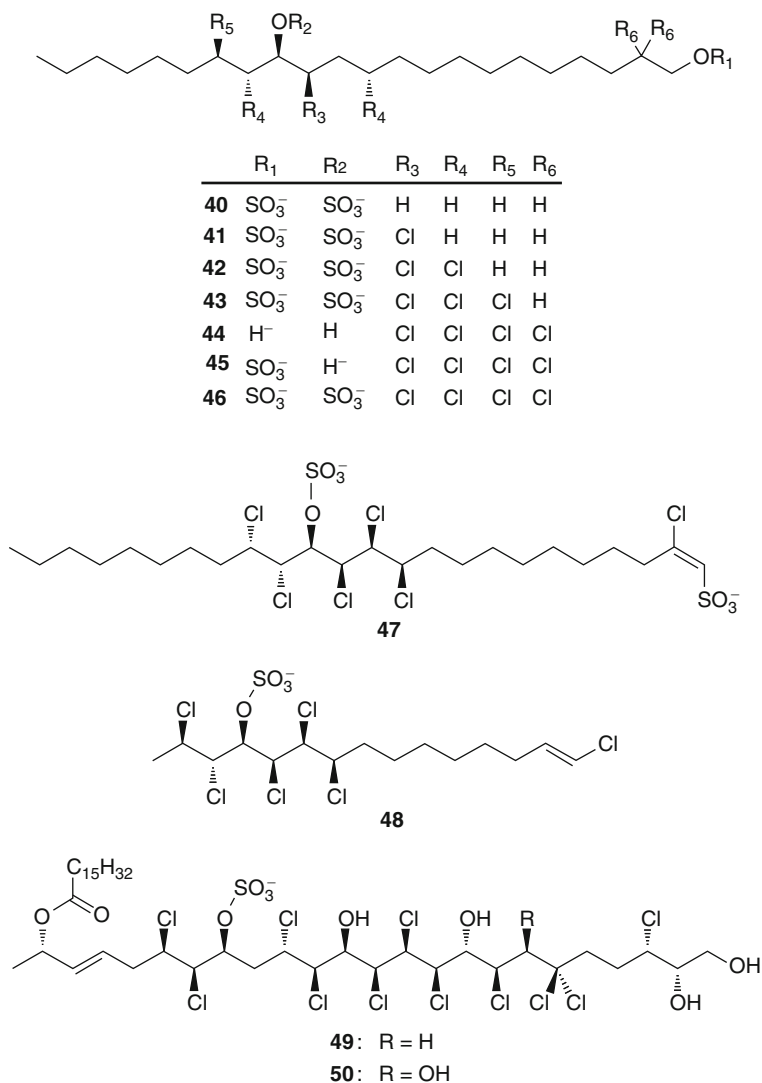


Fig. 2.15 Structures of chlorosulfolipids from chrysophytes

asymmetrical macrocycles comprised of two polyhydroxylated, polyhalogenated ω,ω' -diarylbutene units connected through two ether bonds [212]. Termed chrysosphaentins A–H (**54–61**) (Fig. 2.16), these compounds represented a new natural product scaffold in nature. Hormothamnione (**51**) was also found in these latter collections of *C. taylori* [212]. The most potent of these new antibiotics, chrysosphaentin A (**54**), inhibited the growth of clinically relevant Gram-positive

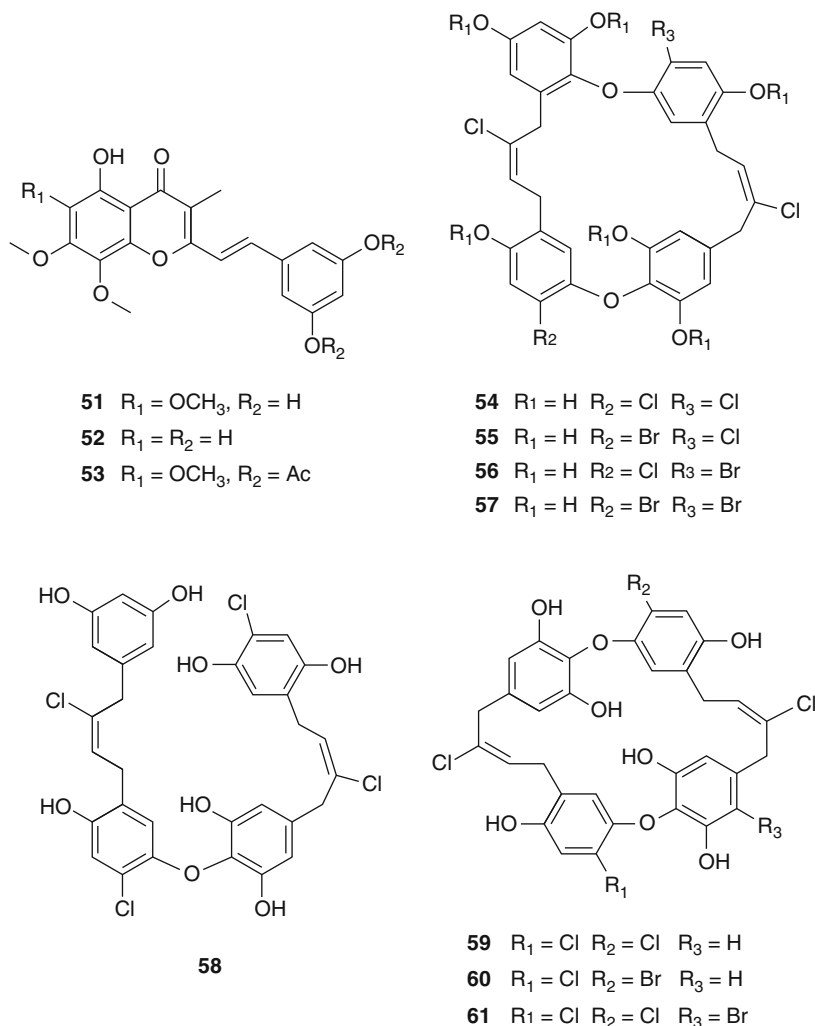


Fig. 2.16 Secondary metabolites of chrysophytes

bacteria including methicillin-resistant *Staphylococcus aureus* (MIC_{50} $1.5 \pm 0.7 \mu\text{g/mL}$), multidrug-resistant *S. aureus* ($1.3 \pm 0.4 \mu\text{g/mL}$), and vancomycin-resistant *Enterococcus faecium* ($2.9 \pm 0.8 \mu\text{g/mL}$). Additionally, in vitro enzyme assays, transmission electron microscopy, and saturation transfer difference (STD) NMR showed **54** to inhibit GTPase activity and polymerization of the bacterial cytoskeletal protein FtsZ (IC_{50} of $6.7 \pm 1.7 \mu\text{g/mL}$), a relatively new target in antimicrobial drug discovery due to its essential role in cell division and high degree of conservancy among almost all bacteria [213].

2.3.5 Prymnesiophytes

Over the past century, numerous toxic blooms of the red tide phytoflagellate *Prymnesium parvum* in low-salinity water have had devastating effects on coastal ecology by killing massive populations of fish, shellfish, mollusks, and virtually all benthic animals and algae [214–218]. This global phenomenon seems to have increased in both frequency and geographical distribution as a result of eutrophication of coastal waters, and these harmful algal blooms cause enormous economic damage to fish farming and the entire aquaculture industry [219, 220].

The toxicity of *P. parvum* was attributed for more than 30 years to a collection of compounds exhibiting potent cytotoxic, hemolytic, neurotoxic, and ichthyotoxic effects, known as the “prymnesins” [221–224]. However, the chemical nature of these toxins remained unknown until 1996, when the structure of the major component, prymnesin-2 (**63**), was elucidated via extensive 2D NMR and mass spectrometry analyses [219, 220, 225]. Both prymnesin-1 (**62**) and prymnesin-2 (**63**) have been shown to consist of a polycyclic ether moiety bearing polyhydroxy and polyenyne side chains, featuring a straight chain of 90 carbons with one branching methyl group, a fused polycyclic ether ring system (A–E), four distinct 1,6-dioxadecalin units (FG, HI, JK, and LM), multiple conjugated double and triple bonds, three chlorine atoms, and one amino group, as well as a variety of glycosidic residues. The relative stereochemistry of the fused A–E polycyclic ether ring domain and four 1,6-dioxadecalin units was determined by extensive NMR analysis and verified by NMR comparison with synthetic models [220, 226–228]. Degradation and derivatization studies established *S* absolute configuration for both the amino group-bearing C14 and the chlorinated C85 stereocenters in **63** [229]. The configuration of the C76–C85 acyclic portion remains undetermined (Fig. 2.17).

2.4 Marine Macroalgae

2.4.1 General Introduction to Marine Macroalgae

Marine macroalgae produce an impressive variety of secondary metabolites ranging from linear acyclic entities to complex polycyclic molecules. A significant portion of these natural products are halogenated, reflecting the availability of chloride and bromide ions in seawater. Interestingly, although chloride occurs in higher concentrations in seawater than any other halogen, bromide is more frequently integrated by algae for organohalogen compound production.

Thus, a major focus of macroalgae chemical research has been the discovery and characterization of new halogenated natural products, along with a remarkable effort toward the evaluation of their possible biomedical and biotechnological applications. Among all marine macroalgae, red algae are the main producers of chlorinated and brominated terpenes, with the genus *Laurencia* (Rhodophyceae)

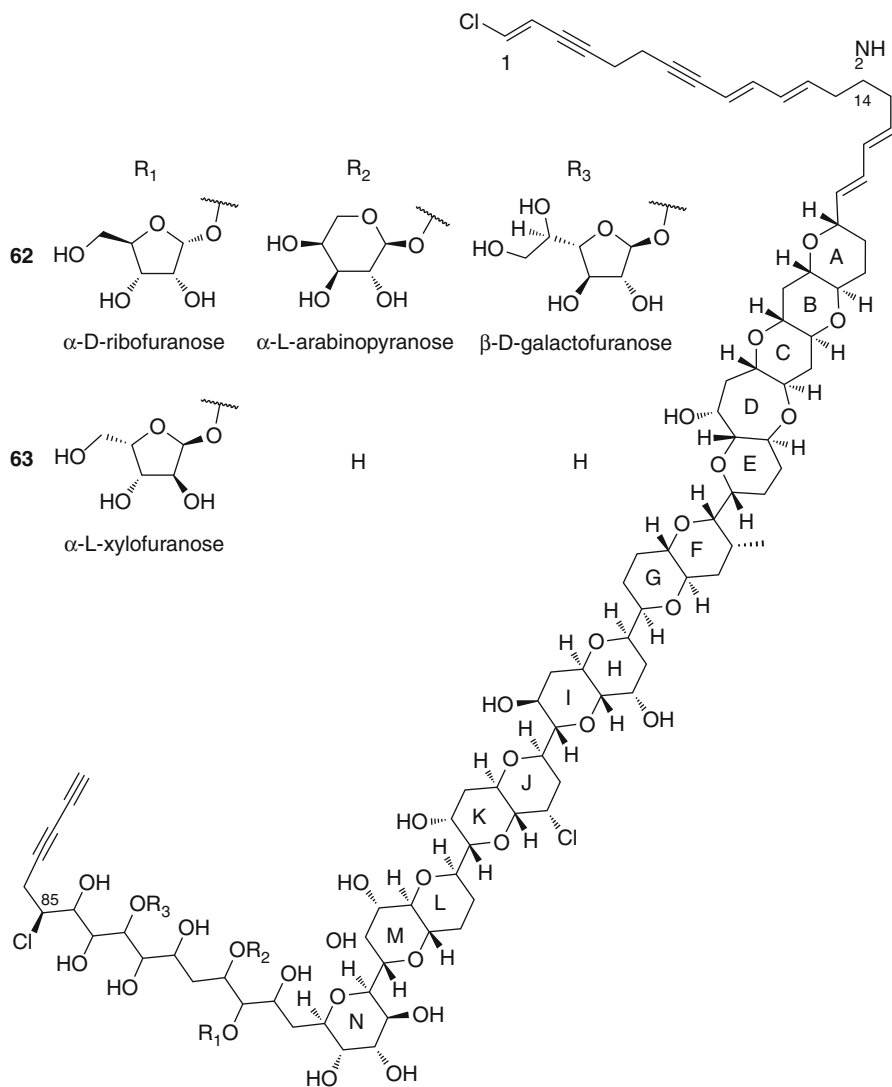


Fig. 2.17 Structures of prymnesins-1 (62) and -2 (63)

being the most prolific. Although incorporation of iodine and fluorine is quite unusual, some orders of brown algae, such as the Laminariales, accumulate and use iodine in halogenation processes. In fact, iodination is more frequent in brown algae than in red and green algae metabolites. The ecological role of most of these metabolites has not been experimentally investigated, although a few metabolites have been shown to have critical roles in reproduction and defense.

2.4.2 Chlorophyta

The Chlorophyta are major inhabitants of shallow marine, fresh, and brackish waters. Most of the known species are unicellular, benthic, or planktonic, and some are free-living while others are colonial or multicellular. One group, the Caulerpales are coenocytic in that cell walls are not created following nuclear division. The name “Chlorophyta” derives from the Greek words *chloros* and *phyton*, which mean “green plant.” Similar to terrestrial higher plants, members of the Chlorophyta contain chlorophyll *a* and *b*, carotenoids, and xanthophylls. They produce starch as a by-product of excess photosynthesis and store it in pyrenoids that are present in the chloroplasts. Most Chlorophyta undergo sexual reproduction, which is isogamous, anisogamous, or oogamous; however, asexual reproduction by fission, budding, fragmentation, or zoospores is also possible. The Chlorophyta have been classified into 15 orders, all within the class of Chlorophyceae. Marine representatives are found in the Cladophorales, Acrosiphonales, Ulvales, Dasycladales, Siphonocladales, and Caulerpales. Various classes of bioactive natural products reported from the Chlorophyta include terpenoids, halogenated meroterpenes, bisindoles, coumarin derivatives, bromophenols, and oxylipins, as described below.

2.4.2.1 Terpenoids

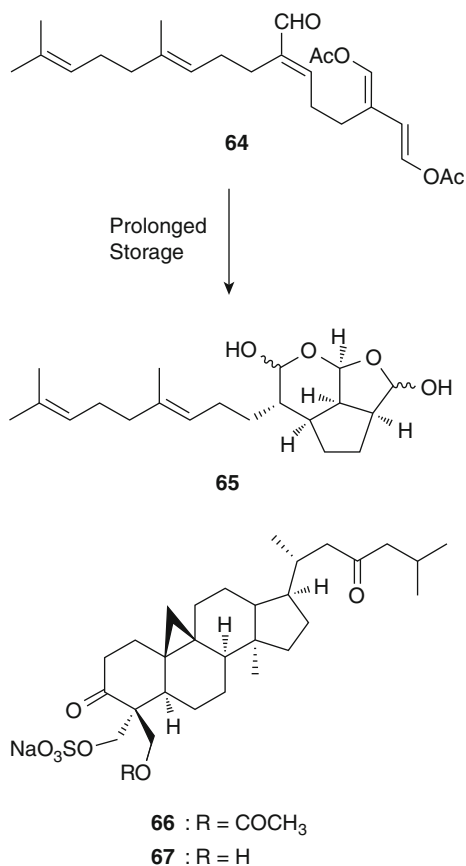
Udoteal

The calcareous green alga *Udotea flabellum* is very common in sandy environments of shallow tropical waters. *U. flabellum* produces several fish feeding-deterrent natural products, presumably aiding its survival in these intense herbivore environments. The major component of *U. flabellum* was found to be udoteal (**64**), a diterpenoid with 1,4-diacetoxybutadiene functionality. This protected 1,4-dialdehyde derivative is quite common among the chemical defense agents of other green algae, such as *Caulerpa*, *Chlorodesmus*, and *Rhizocephalus* [230]. Udoteal produces significant feeding avoidance by the herbivorous fish *Pomacentrus coeruleus*. Prolonged storage of udoteal (**64**) in ethanol promoted conversion into hydrates of udoteatrial (**65**) which, in turn, showed antimicrobial activity against *Staphylococcus aureus* and *Candida albicans* [231] (Fig. 2.18).

Capisterones

Marine benthic organisms are constantly exposed to the threats of water-borne marine pathogens. The green alga *Penicillus capitatus*, abundant in shallow water of the tropical Atlantic Ocean, was found to produce triterpene sulfate esters, capisterones A (**66**) and B (**67**), which are potent antifungal compounds against the marine algal pathogen *Lindra thallasiae*. Capisterones A and B inhibited the growth of *L. thallasiae* with LD₅₀ values equal to 0.03 and 0.94 µg/mL, respectively [232]. In biomedical testing, they enhanced the activity of the antifungal drug fluconazole against a strain of *Saccharomyces cerevisiae* which overexpresses a drug efflux pump of *Candida albicans*. However, they showed no inherent antifungal activity against several opportunistic pathogens and no cytotoxicity to

Fig. 2.18 Terpenoids from Chlorophyta



human cancer and noncancer cell lines [233]. Therefore, capisterones A and B may have potential in combination therapies of fungal infections caused by clinically relevant azole-resistant strains (Fig. 2.18).

2.4.2.2 Cymopols

Until the mid-1970s, halogenated natural products had been mostly reported from the Rhodophyta and Phaeophyta. However, two prenylated bromohydroquinones, cymopol (**68**) and cyclocymopol (**69**), were found from *Cymopolia barbata* in 1976, and since, a number of cymopol-related compounds have been reported from this alga [234]. Cymopol (**68**) exhibited potent antioxidant activity and inhibited bee venom-derived phospholipase A₂ function and cell adhesion of HL-60 cells to CHO-ICAM-1 cells [206, 207, 235]. A mixture of cyclocymopol diastereomers were isolated from the extract of *C. barbata* and found to inhibit sea urchin feeding [236, 237]. Subsequently, cymobarbatol (**70**) and 4-isocymobarbatol (**71**)

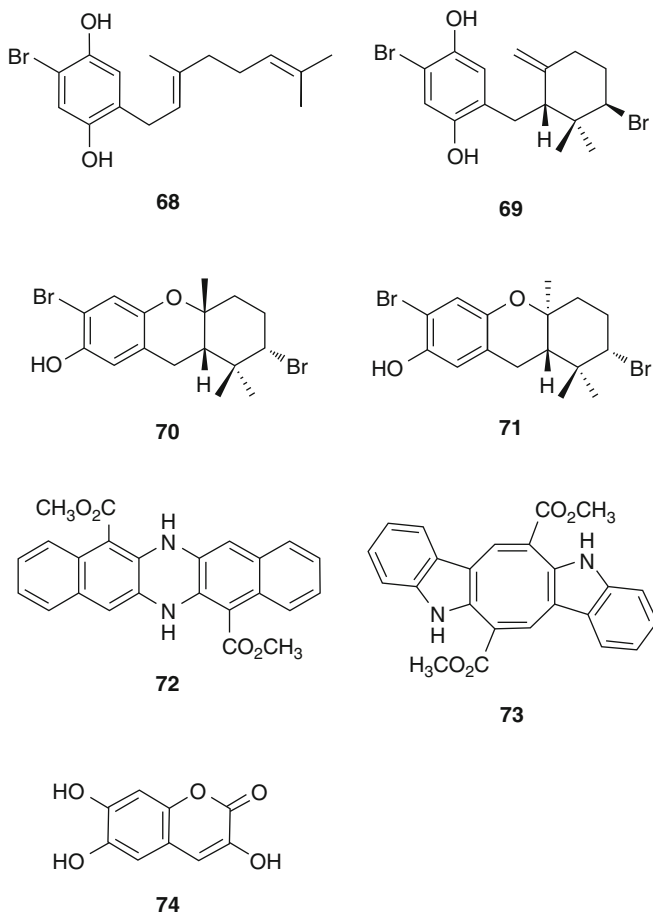


Fig. 2.19 Various secondary metabolites of Chlorophyta

were discovered and found to have antimutagenic properties [238]. The natural occurrence of the diastereomers of cyclocymopol and cymobarbatol support enzymatic conversion of cymopol to a *Z*-olefinic isomer followed by a bromonium ion-induced cyclization in their biosynthetic mechanism (Figs. 2.19, 2.20).

2.4.2.3 Bisindoles (Caulerpin)

Several species in the genus *Caulerpa* are edible and have been consumed for many years in the Philippines and other tropical Pacific regions. However, some of these consumed species are not eaten in the rainy season because they develop an extremely peppery taste. Aguilar-Santos and Doty investigated the toxic constituents of *Caulerpa* and found an orange-red pigment, designated as “caulerpin,” as one of the common components of this genus [239]. Caulerpin was first isolated from three species of *Caulerpa* in the Philippines: *C. racemosa* var. *clavifera*, *C. sertularioides*, and *C. serrulata*. The chemical structure of caulerpin was first

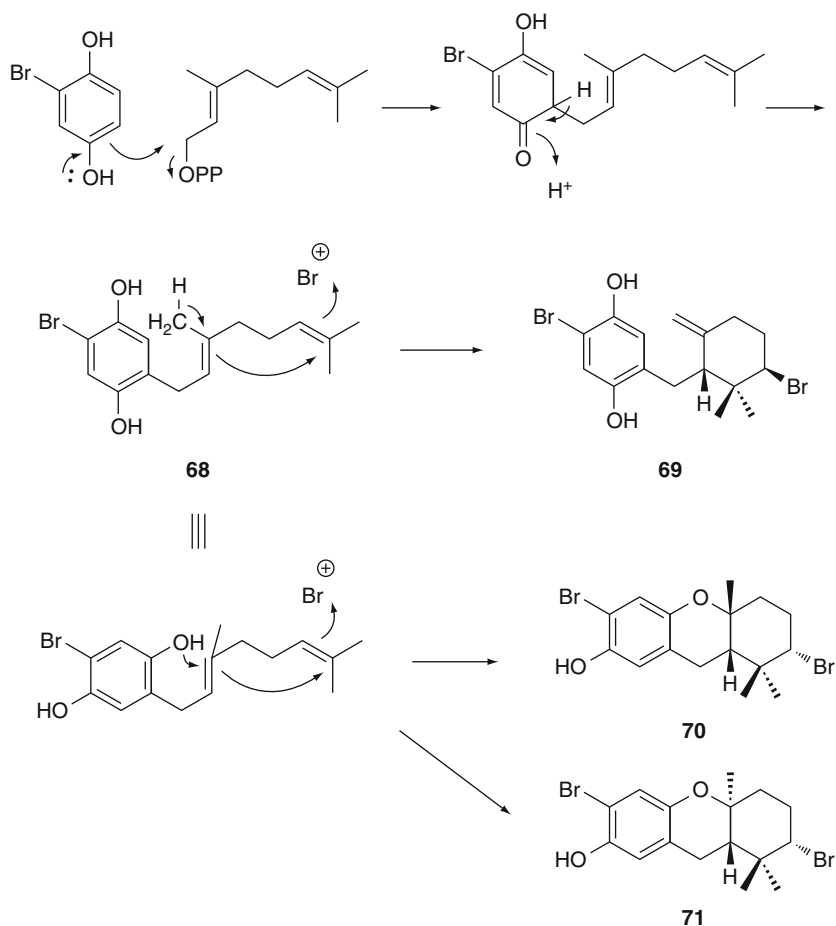


Fig. 2.20 Proposed biosynthesis of cymopol (**68**), cyclocymopol (**69**), cymobarbatol (**70**), and isocymobarbatol (**71**) by the green alga *Cymopolia barbata* involving bromonium ion-induced cyclization

reported as a dihydrodibenzo[b,i]phenazine (**72**) in 1970 [240]; however, this was later revised to the *bis*-indolyl structure **73** by Maiti and Thomson who used a combination of chemical degradation and synthesis techniques [241] (Fig. 2.19). Caulerpin, a dimer of indole-3-acrylic acid, promotes plant root growth similarly to its monomeric counterpart as well as indole-3-acetic acid (auxin) [242].

The diverse pharmacological activities of caulerpin have been studied over the intervening years. It has been shown to inhibit hypoxia-inducible factor-1 (HIF-1), an important molecular target for anticancer drug discovery, through inhibition of mitochondrial respiration [243]. It also has antinociceptive and anti-inflammatory activity in the mouse writhing and hot plate tests, the formalin-induced pain test,

the capsaicin-induced ear edema, and the carrageenan-induced peritonitis in mice [244]. Recently, it has been reported to possess insecticidal activity against the mosquito *Culex pipiens* [245].

2.4.2.4 3,6,7-Trihydroxycoumarin

Dasycladus vermicularis, a member of the siphonaceous green algae, is abundant in the North Atlantic and Mediterranean. In order to cope with a wide range of UV light intensities, *D. vermicularis* accumulates and excretes the UV-absorbing metabolite 3,6,7-trihydroxycoumarin (THC, **74**) [246, 247] (Fig. 2.19). Coumarins in the Dascladaceae, including THC, have been reported with diverse antimicrobial, antioxidant, and wound-healing properties [247–249]. Subsequently, the antioxidant role of THC under diverse environmental stressors was reported.

2.4.2.5 Brominated Phenols (Avrainvilleol)

Before avrainvilleol (**75**) was isolated from the green alga *Avrainvillea longicaulis* in 1983 [250], most bromophenolic natural products had been reported from marine annelids [251] and red algae [252, 253]. Avrainvilleol is a brominated diphenylmethane which appears to result from dimerization of a precursor bromo-*p*-hydroxybenzyl alcohol (Fig. 2.21). In 1987, another brominated diphenyl methane, 5'-hydroxyisovrainvilleol (**76**), was isolated from *A. nigricans* along with avrainvilleol and 3-bromo-4,5-dihydroxybenzyl alcohol (**77**), the presumed monomer of 5'-hydroxyavrainvilleol [254]. Subsequently, rawsonol (**78**) [255] and isorawsonol were described from *A. rawsonii* (**79**) [256]; these metabolites appear to form from condensation of two molecules of avrainvilleol (**75**) (Fig. 2.22). As revealed by this series of metabolites, these types of bromophenols have a chemical and biochemical propensity for condensation to form higher order oligomers [255].

Avrainvilleol was first reported for its antibacterial activity against *Vibrio anguillarum* as well as its fish toxicity and fish-feeding deterrence properties [250]. Subsequently, avrainvilleol was found to inhibit inosine 5'-monophosphate dehydrogenase (IMPDH) [256] and LFA-1/ICAM-1-mediated cell adhesion [207], as well as show potent antioxidant activities [206] (Figs. 2.21, 2.22).

2.4.2.6 Oxylipins Nigricanoside A

Monogalactosyldiacylglycerol derivatives are major constituents of membrane lipids in higher plants and cyanobacteria. In 2007, nigricanosides A (**80**) and B (**81**), unprecedented antimitotic glycoacylglycerolipids, were reported from *Avrainvillea nigricans* collected in Dominica [257]. The extract of *A. nigricans* showed extremely potent antimitotic activity. However, only trace quantities of the bioactive molecules were obtained, and this was insufficient for structure elucidation. As a result of an 8-year effort to collect enough material (28 kg wet wt of *A. nigricans*) for structural analysis of the bioactive compounds, the methyl esters of nigricanosides A (800 µg, 0.000003% wet wt) and B (400 µg, 0.0000015% wet wt) were obtained, and their planar structures elucidated (Fig. 2.23). Nigricanosides A and B contain a glycosidic linkage between galactose and C-1 of glycerol, a common structural feature

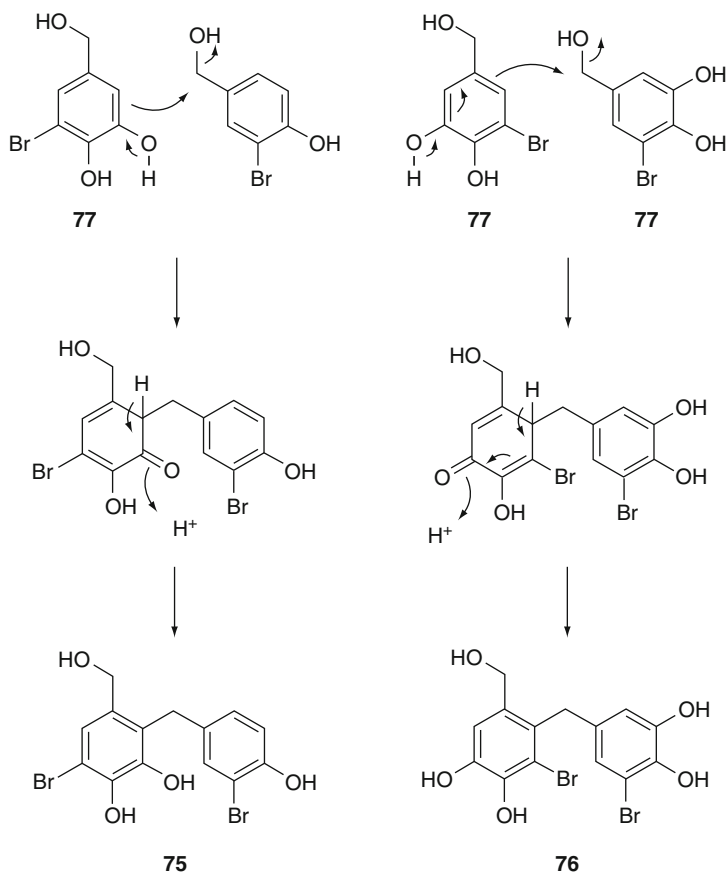


Fig. 2.21 Proposed biosynthesis of avrainvilleol (**75**) and 5'-hydroxyisoavrainvilleol (**76**) from 3-bromo-4,5-dihydroxybenzyl alcohol (**77**) by the green algae *Avrainvillea longicaulis* and *A. nigricans*

of glycolipids. However, two oxygen-containing fatty acid chains were linked together via an ether linkage, and one was further connected to the galactose residue; two other fatty acids were linked as normal esters to the glycerol backbone. Nigricanoside A dimethyl ester arrested cell mitosis in human breast cancer cells and promoted tubulin polymerization in human breast cancer and colon cancer cells. Methylation of the crude fractions, which was performed to facilitate the isolation process, diminished the potency of this material, and hence, the free dicarboxylic acids are thought to be the bioactive natural products.

Oxylipins from *Acrosiphonia coalita*

Although oxylipins are abundantly found in red algae [258] and other marine macroalgae [259], the first series of oxylipins to be isolated from a marine chlorophyte came from the Oregon coastal chlorophyte *Acrosiphonia coalita* [260]

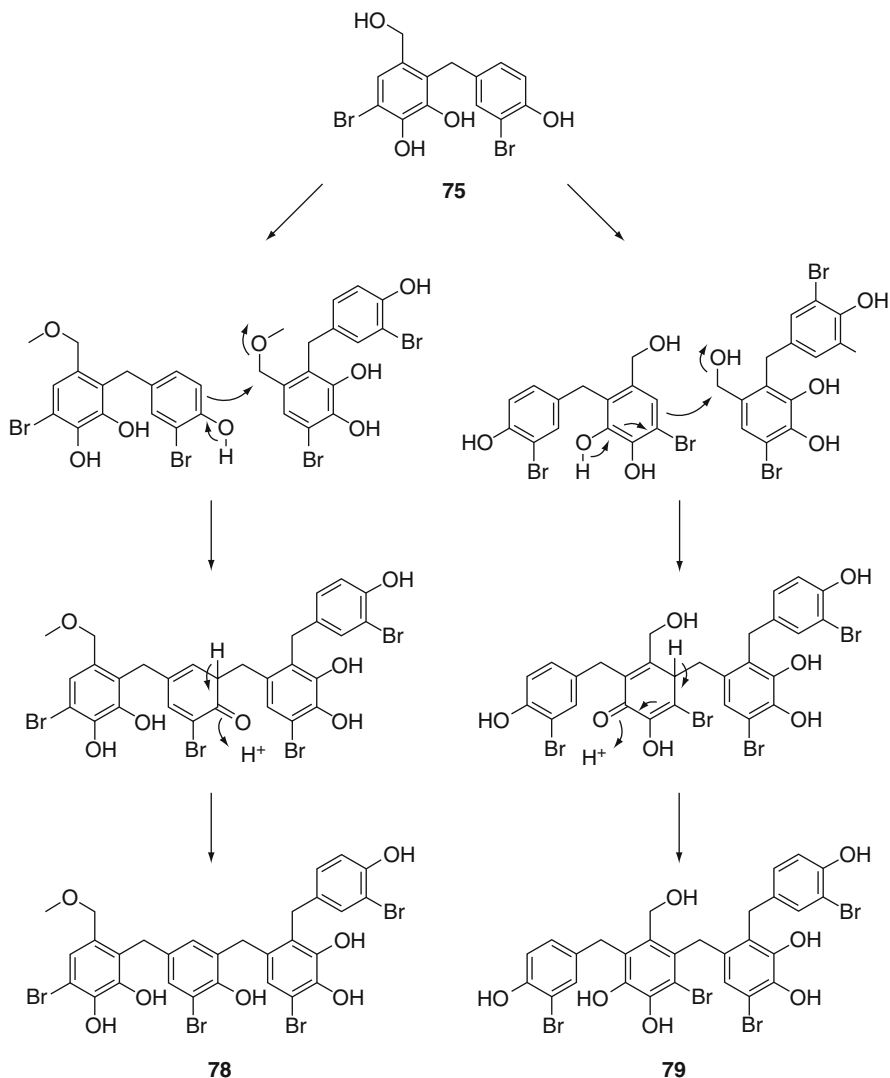


Fig. 2.22 Proposed biosynthesis of rawsonol (**78**) and isorawsonol (**79**) from avrainvilleol (**75**) by the green alga *A. rawsonii*

(Fig. 2.24). A ten-carbon conjugated trienal, named coalital (**82**), showed strong antimicrobial activity against *Candida albicans*. Related to coalital were three novel branched-chain conjugated trienal oxylipins (e.g., **83**, **84**) in which the aldehyde was present as a branching carbon on a 17-carbon fatty acid chain. Additionally, two novel conjugated unbranched trienone octadecanoids (**85**, **86**) were also isolated and characterized. It has been proposed that these trienals and trienones derive from α -linolenic acid or stearidonic acid by 9- and 16-lipoxygenase directed oxidation

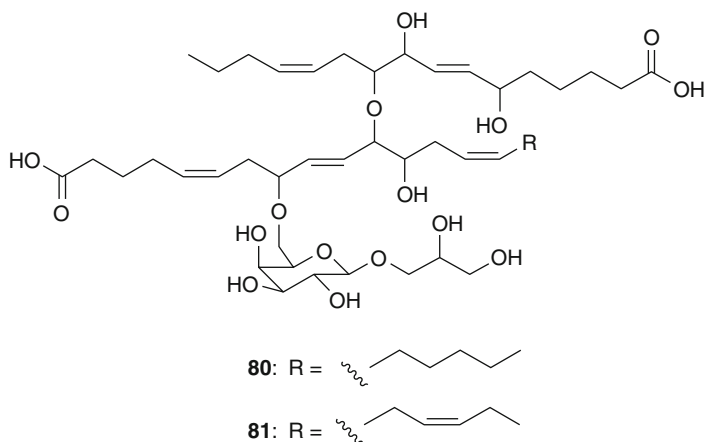


Fig. 2.23 Structures of nigricanosides A (**80**) and B (**81**)

reactions. A family of related epoxy-alcohols (**87–89**) was also obtained from *A. coalita*. As shown in the soybean lipoxygenase system, oxidation of linoleic or linolenic acids at either C-9 or C-13 by lipoxygenases is often followed by an oxygen-rebound reaction leading to the formation of epoxy-alcohols [261]. However, the mechanism of branched chain aldehyde formation in these green algae remains unknown at present.

2.4.3 Rhodophyta

2.4.3.1 General Biology of the Rhodophyta

The Rhodophyta, or red algae, are some of the more conspicuous inhabitants of the temperate intertidal environment, although there are many known from tropical, arctic, and subtidal locations as well. Overall, there are more than 5,000 species of red algae (possibly as many as 10,000), and they exist mainly as macroscopic plant-like algae, although a few unicellular or filamentous species do exist. In the larger multicellular species, their algal body is typically composed of holdfast, stipe and blade components which roughly accord to the root, stem, and leaf of higher plants [5].

The Rhodophyta are unique among all algae in that there is no flagellated stage in their life history. Also, they have unique accessory pigments, namely phycoerythrin, phycocyanin, allophycocyanin which are present as protein complexes known as phycobilisomes. The phycobilisomes are arranged on membranes within the chloroplasts known as thylakoids, and serve to harvest a broader range of light wavelengths than the normal complement of chlorophyll *a* and *d* present in these organisms. Floridean starch, which is similar to amylopectin, is used as a food reserve and is found with the cytoplasm. Reproduction and life histories are very complex in this group of algae, and much of the taxonomy of the Rhodophyta is based on reproductive appendages and processes. For example, they have quite

specialized cells and organs for reproduction, including carpogonia for female cells and spermatagia for male cells. Some species have both male and female individuals, whereas others have both within the same individual. Additionally, in some species, the 1n and 2n phases of the organism have the same morphology (isomorphic), whereas in others have different morphologies (heteromorphic).

The cell walls of Rhodophyte algae are composed of an amorphous matrix formed mainly by sulfated galactans, and resulting in extracted products known as agar and carrageenan. Calcium carbonate deposition occurs into the cell wall of many species, particularly in the Corallinaceae, either as calcite or aragonite, and contributes substantially to coral reef building in the tropics. Some multicellular red algae have specialized secretory or gland cells, particularly in the family Bonnemaisoniaceae, and this is the cellular site of halogenated natural product production and storage in these species.

As noted elsewhere in this chapter, the taxonomy of the algae is in a state flux as new insights into the relationships of organisms are generated from genome sequence data. However, the Rhodophyta are traditionally composed of two subclasses, although recent taxonomic treatments organize this group of algae differently. Natural products have been reported from the more advanced subclass, the Florideophycidae, and within this group, several notable families, such as the Bonnemaisoniaceae, Ceramiaceae, and Rhodomelaceae, are especially rich in secondary metabolites.

Perhaps because the Rhodophyta, as a group, are some of the more conspicuous members of the intertidal, and certainly as a result of the large number of species and their propensity to elaborate natural products, this taxonomic group was one of the first to be actively investigated for new and bioactive metabolites. Much of the early work occurred in Japan, with Toshi Irie being one of the true pioneers of this field [262], but soon afterward, numerous groups from the USA, Canada, Europe, and Australia focused their investigations on the red algae as well. Hence, several thousand natural products are now known from this group of algae, with the majority falling into the categories of metabolites discussed below. One of the dominant metabolic features, which is present in many of these natural product classes described below, is the covalent incorporation of halogen atoms (chlorine, bromine, and even iodine) [263–265], and it was this unique aspect that drew so many pioneering marine natural products chemists to first investigate this algal group.

2.4.3.2 Chemistry of the Rhodophyta

Simple and Complex Bromophenols

One of the first natural product classes described from red algae were simple bromophenols from such temperate and cold water species (e.g., Nova Scotia) of red algae as *Odonthalia dentata*, *Polysiphonia lanosa*, and *Rhodomela confervoides* [266]. A common and well-described member of this class is known as lanosol (**90**), a seven-carbon metabolite with two phenolic and one primary hydroxy group, and two bromine atoms. Often, one or more of the phenolic hydroxy groups are present as sulfate esters, and these are known to be quite hydrolytically unstable, ultimately

giving rise to a large number of presumed degradation products. Additionally, the benzylic alcohol is prone to oxidation (to the aldehyde or carboxylic acid) or ether formation with the extraction solvent (ethanol). Biologically, red algal bromophenols are believed to confer protection against microbial pathogens as well as epiphytes and herbivores [267], and their distribution within algal thalli is quite variable [268]. Surprisingly, the precise mechanism of bromine incorporation into lanosol has not been completely established, but is believed to involve an uncharacterized bromoperoxidase enzyme.

The essential bromophenolic unit of lanosol is a conceptual precursor to a wide number of other red algal metabolites. For example, a collection of *Polysiphonia ferulacea* from Senegal yielded an interesting dimeric metabolite (**91**) wherein two new carbon–carbon bonds link the subunits [269]. As a result of the new carbon linkages, and the large bromine substituent *ortho* to the direct biphenyl linkage, the molecule exists in a single conformation and thus exhibits atropisomerism. Its structure including absolute stereochemistry was established by a combination of spectroscopic methods complemented by molecular mechanic calculations.

Another interesting example of a likely product deriving from lanosol was obtained from the Rhodophyte *Vidalia obtusaloba* collected from Martinique in the Southeastern Caribbean [270]. Shipboard testing of its extract at the time of collection showed it potently inhibited PLA₂, a key enzyme involved in arachidonic acid release and ensuing inflammation in mammals. The major brominated metabolite, vidalol A (**92**), was found to be composed of one C₇ lanosol-type unit linked via a carbon–carbon bond to a second six-carbon bromophenol unit. Vidalol B was simply the next iteration of such an assembly with two lanosol units fused to a central C₆ core. These *ortho*-catechol metabolites were found to have antifungal and antibiotic properties, to inhibit feeding by herbivorous fish, and to inhibit inflammation and edema in the ears of mice topically stimulated with phorbol esters (PMA).

A final example in this class is given by a metabolite (**93**) found in another species of *Vidalia* from Australia, *V. spiralis* [271]. Unfortunately, while the CH₂Cl₂ extract possessed antihypertensive effects, the isolated bromophenol-type metabolite was inactive in this assay (the active antihypertensive agent remains unknown or unreported!). The relationship of vicinal bromine atoms and vicinol diol functionality is identical to that observed for lanosol, and thus, it appears that the aromaticity of the ring has been disrupted through an apparent ring contraction and carbon loss from a lanosol precursor. Intriguingly, the molecule was chiral ($[\alpha]_D +124^\circ$) with the two hydroxy groups oriented *trans* to one another; however, absolute configuration has not yet been assigned in this molecule (Fig. 2.25).

Halogenated Ketones and Quorum Sensing

Several species of the genus *Bonnemaisonia* have yielded halogenated alkanes and alkenes with a variety of oxygen functional groups, including ketones, alcohols, epoxides, and acids [272]. It appears that these derive from an initially formed methyl ketone which is polyhalogenated at the reactive alpha-positions (e.g., to produce 1,1,3,3-tetrabromoheptanone, **94**). The methyl ketone is believed to form

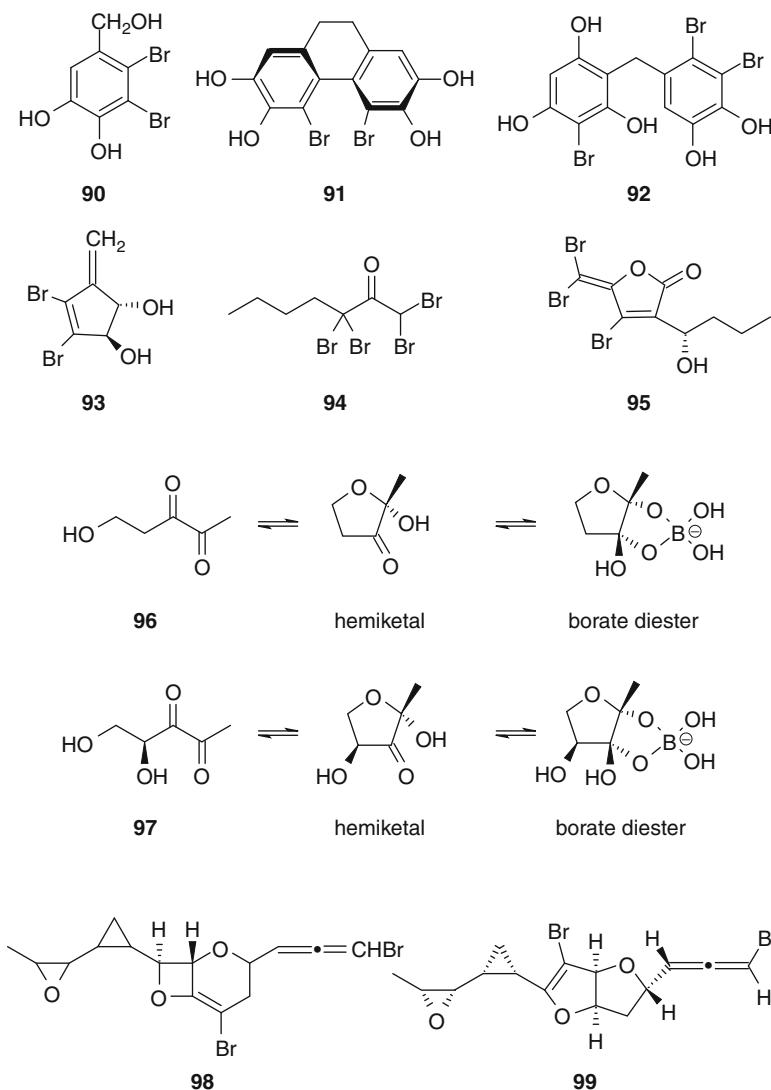


Fig. 2.25 Various secondary metabolites of Rhodophyta

from β -keto acids which undergo facile decarboxylation. The halogenated methyl ketones are then prone to various reactions, including Favorskii-type rearrangements, and this is believed to occur *in vivo* as even very gentle methods of extraction (e.g., a brief dipping in pentane or hexane) yield chain-rearranged alkanolic acids. These halogenated ketones are stored, and perhaps synthesized, in specialized gland cells that are characteristically present on the surface of the algal thalli in this genus. Early studies on these highly halogenated compounds found that some had powerful antibiotic activity, and more recent investigations have shown

that substances such as 1,1,3,3-tetrabromoheptanone exert potent antibiotic effects to bacteria occurring in these shallow water environments [273], and thus result in a reduced number of bacteria as well as an altered species composition on the surfaces of *Bonnemaisonia* [274].

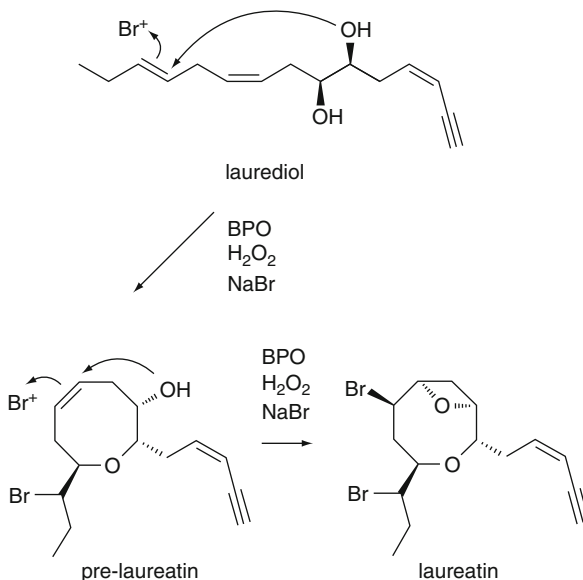
Similarly, on the south Australian coast, a subtidal species of red algae, *Delisea pulchra*, grows abundantly with a flat leaf-like morphology. Remarkably, this algal surface, continuously bathed in warm nutrient-laden seawater with high bacterial and spore counts, remains essentially free of bacterial biofilms or the downstream colonization by encrusting invertebrates or epiphytes. In this case, the answer to this mystery was found to be a small halogenated ketone, similar in biosynthetic origin to the above *Bonnemaisonia* compounds, and actually deriving from a carbon-chain-rearranged Favorskii reaction [275]. The natural products, known as “fimbrolides” (95), as well as various synthetic derivatives, have been actively pursued as potential additives to marine paints that could inhibit fouling in an environmentally benign fashion. Because organotin or organocopper-based paints have been or are in the process of removal from the market [276], there is a huge unmet need for antifouling marine paints, and this has motivated many in the marine natural product community to have antifouling screens in their portfolio of biological assays. In this case, several of the fimbrolides have been studied in considerable detail and shown to inhibit bacterial quorum sensing through antagonist activity at the luxR receptor, a component of the homoserine lactone quorum sensing system in Gram-negative bacteria [277].

When first isolated from the Oregon intertidal seaweed *Laurencia spectabilis*, laurencione (96) was more of a chemical curiosity with its simple five-carbon structure containing two carbonyls and one primary hydroxy group [278]. It was insightful at the time in revealing that this small metabolite was prone to oxidative dimerization or trimerization and hence, that several other reported “metabolites” were in fact isolation artifacts [279]. However, several years later, the crystal structure of a protein involved in bacterial signaling was found to have its cognate ligand bound, named autoinducer-2 (AI-2, 97), which was a borate diester of a metabolite very similar in structure to laurencione (the difference is that AI-2 has one more hydroxy group than laurencione) [280]. As a result, laurencione became a target of several chemical syntheses and bacterial quorum sensing programs, and its borate diester was characterized to have agonist activity as a quorum sensor, although less potent than AI-2 [281]. While it is tantalizing to envision that laurencione may function to maintain the algal surface free from biofilms and the resulting colonization by epiphytes, this interesting chemical ecological dimension remains unstudied to date.

C-15 Acetogenins

A large number of oxidized and halogenated C-15 polyketide or fatty acid-derived compounds have been isolated from various species of the genus *Laurencia*, and these represent one of the more intriguing biosynthetic classes from the Rhodophyta. Early on, it was envisioned that a simplified precursor, presumably arising by decarboxylation and oxidation of fatty acid precursors,

Fig. 2.26 Biosynthesis of laureatin from laurediol involving bromonium ion-induced oxycyclizations



was functionalized by a series of bromoperoxidases to result in several related metabolites that apparently arise from bromonium ion-induced oxycyclizations. Some of the ultimate precursors and intermediates to these diverse C-15 acetogenins have also been characterized, and a picture of the metabolic pathway is emerging. Embedded in these pathways are a range of interesting reactions, such as decarboxylations, halogenations, isomerizations, and carbon–carbon bond formations; the enzymological and mechanistic details of these remain unstudied. A proposed pathway involving some of these precursors and intermediates is shown in Fig. 2.26.

As an example of this metabolic class, the molecule known as okamurallene (originally **98**) provides a particularly fascinating illustration because of its dense functionalization and the complexities experienced in its structure elucidation [282]. Collected from the southwest coast of Hokkaido, Japan, the species *Laurencia okamurai* was found to contain a rich complement of natural products, both terpenoids and C-15 acetogenins. Okamurallene was isolated and analyzed by a number of 1D NMR techniques prevalent at the time of its isolation (1981), and a most unusual structure was proposed with sequential functional groups including an epoxide, cyclopropyl ring, four-membered oxetane fused to a vinyl bromide containing dihydropyrene ring, and an allene with terminal vinyl bromide (this may represent a record in terms of density of functional groups on a 15-carbon skeleton!). Ultimately however, continued study revealed an error in the structure elucidation, and this was revised first by 2D NMR and then confirmed with X-ray crystallographic information, the latter also providing absolute configuration [283]. The corrected structure (**99**) alters the relative bond connections of the central

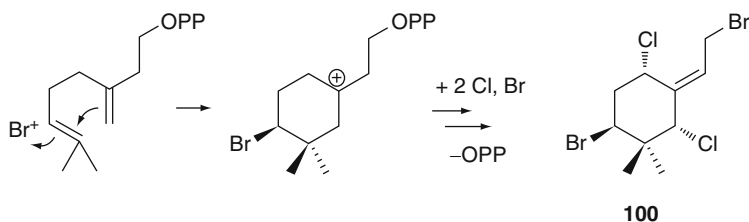


Fig. 2.27 Predicted early steps in the biosynthesis of ochtodene (**100**) involving bromonium ion-induced carbocyclization

bicyclo section, resulting in a fused dihydropyran–tetrahydropyran ring system with an embedded vinyl bromide. As is the case with so many natural products, structural characterization results in more questions than answers, and in this case, there are an abundance concerning the biosynthesis of such an amazing molecule.

Terpenoids

Another dominant theme in the secondary metabolism of red algae is the elaboration of various metabolites deriving from the terpene biosynthetic pathway. The size class of the terpene produced (e.g., C-10, C-15, or C-20) is relatively characteristic of the genus and species of organism, with some possessing exclusively monoterpenes, others sesquiterpenes, and still others di- or triterpenes. Many of the terpenes of the red algae are functionalized with either oxygen or halogen atoms, mostly bromine and chlorine, and logically derive from cyclization events involving halonium ion-induced events. The enzymology of electrophilic halogenations has been studied, and involves unique haloperoxidases that possess either vanadium or iron as the active site metal, and the intermediate production of a “Br⁺” species, possibly as HOBr, Br₂, Br₃, or Enz-Br [284].

The tropical red alga *Ochtodes osmundaceae* is a notable member of shallow wave swept environments in that it has a delicate appearance seemingly at odds with its preferred habitat, and further, it displays a colorful iridescence from its surface. Freshly collected specimens have a pungent “insecticidal” odor that reveals a rich suite of highly halogenated monoterpenes. Such a collection by the Fenical group and isolation by silica chromatography yielded a major component, named ochtodene (**100**), that possessed a cyclohexane-containing monoterpene skeleton with two bromine and two chlorine atoms [285]. A combination of chemical reactivity, mass spectrometry, and NMR spectroscopy was used to determine the planar structure and relative configuration of ochtodene (**100**). Biosynthetically, it is logical to again speculate on the involvement of a bromonium ion-induced cyclization in forming the skeleton of ochtodene and related halogenated monoterpenes (Fig. 2.27). Other red algal genera characteristically producing halogenated monoterpenes of a related nature are *Chondrococcus* and *Plocamium*, inhabitants of colder waters such as Southern Australia, South Africa, and Northern California/Oregon. The natural role of these monoterpenes has been characterized to some extent, and they generally

appear to deter potential predators from feeding upon their soft algal tissues. Interestingly, it seems that different terpenes have antifeedant activity against different classes of predators (e.g., octodene was effective against fish predation, whereas a mixture of other halogenated monoterpenes were selective in inhibiting copepod grazing) [286]. Nevertheless, specialist herbivores such as sea hares (e.g., *Stylocheilus longicauda* and *Dolabella auricularia*) selectively prey upon these and other natural product rich seaweeds, and while they sequester and store these algal natural products, this occurs only in the digestive gland, and thus, it is uncertain if this is involved in chemical defense [287]. Bioengineering efforts have used microplatelets of *Ochtodes* as a model organism for measuring the production of a natural product (e.g., octodene) as a function of bioreactor conditions and growth [288].

The genus *Laurencia* is extraordinarily rich in sesquiterpene-derived compounds, many of which also contain multiple bromine and chlorine atoms. An example of this structure class is given by the widespread bicyclic sesquiterpene elatol (**101**), originally isolated from *L. elata* in the Caribbean, but subsequently isolated from strains of this alga from many parts of the world. Its structure was developed from NMR features and ultimately solidified with absolute configuration from an X-ray diffraction study [289]. The bicyclic ring system, known as a “chamigrene,” is quite common among the sesquiterpenes of *Laurencia* and appears to form as a result of halonium-induced cyclization events as noted above (Fig. 2.28). Curiously, both enantiomers of elatol have been reported in the literature [290], suggesting that either (a) the biosynthetic events creating the stereocenters can occur from either face in the nascent terpene, or (b) these occur outside of a chiral environment (e.g., after release from the active site of the enzyme). The physical location of the rich suite of sesquiterpenes, such as elatol, in *Laurencia* tissues has been investigated by several techniques, including X-ray microanalysis and fluorescence microscopy, and these substances are generally found in distinctive intracellular compartments known by the French term *corps en cerise* (cherry bodies) due to their characteristic shape [291]. Elatol and other stored sesquiterpenoids are then released upon injury, or possibly through vesicle release, to prevent biofouling, inhibit bacterial infections, and deter predation [292]. However and as noted above, in some cases, specialist predators, such as *Aplysia dactylomela*, target these terpene-rich red algae for consumption and then sequester these substances both within the digestive gland and, in this case, the mantle as well; the presence of noxious halogenated terpenoids like elatol (**101**) in the latter tissues may protect against potential predators of these soft-bodied animals [293]. Purified elatol has been reported to possess cancer cell cytotoxicity, antimicrobial properties, and antileishmanial activities [294].

Diterpene-derived natural products are also abundant in red algae with more than 100 such metabolites reported from a few genera (e.g., *Laurencia*, *Sphaerococcus*, *Callophycus*) [295] and organisms which feed upon red algae (e.g., *Aplysia*). Because of their interesting structures and biological activities, and more recent discovery, a few of the metabolites of *Callophycus* will be used to illustrate the trends in this group. Actually, the *Callophycus* metabolites are all found attached

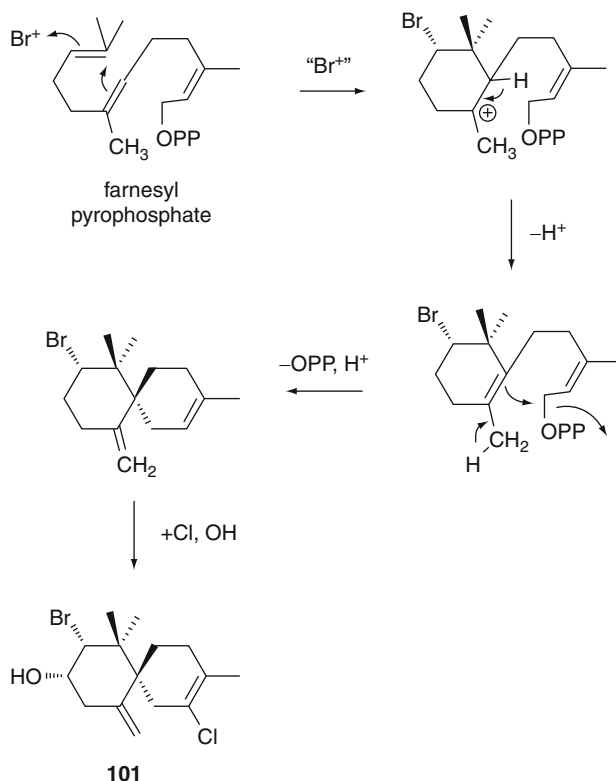


Fig. 2.28 Proposed bromonium ion-induced carbocyclization and ensuing reactions to form the sesquiterpene elatol (**101**)

by a carbon–carbon bond to a benzoic acid moiety, formally making these meroditerpenes (interestingly, meroditerpenes are also characteristic metabolites of the brown algal family Dictyotaceae). Another striking feature of these *Callophycus* metabolites is their abundance of covalent bromine atoms.

Callophycus serratus is a relatively abundant red alga in shallow waters around the Fijian Islands, appearing as finely divided bushy plants of pink to rose color. An investigation motivated by drug discovery efforts associated with the International Cooperative Biodiversity Group (ICBG) program in Fiji resulted in the initial characterization of a series of meroditerpenes, most of which contained several bromine atoms [296]. A combination of classical NMR-based approaches complemented by an X-ray diffraction analysis was used to define these as a series of macrolides formed by the closure of a benzoic acid residue to the terminal olefin of a tethered diterpene. As illustrated below (Fig. 2.29), the proposed biosynthesis of the major metabolite, bromophycolide A (**102**), involves three separate additions of electrophilic bromine to the carbon chain, two which produce bromohydrin-related structures and one apparently inducing cyclohexyl ring formation. Subsequently, a large series of related meroditerpenes were

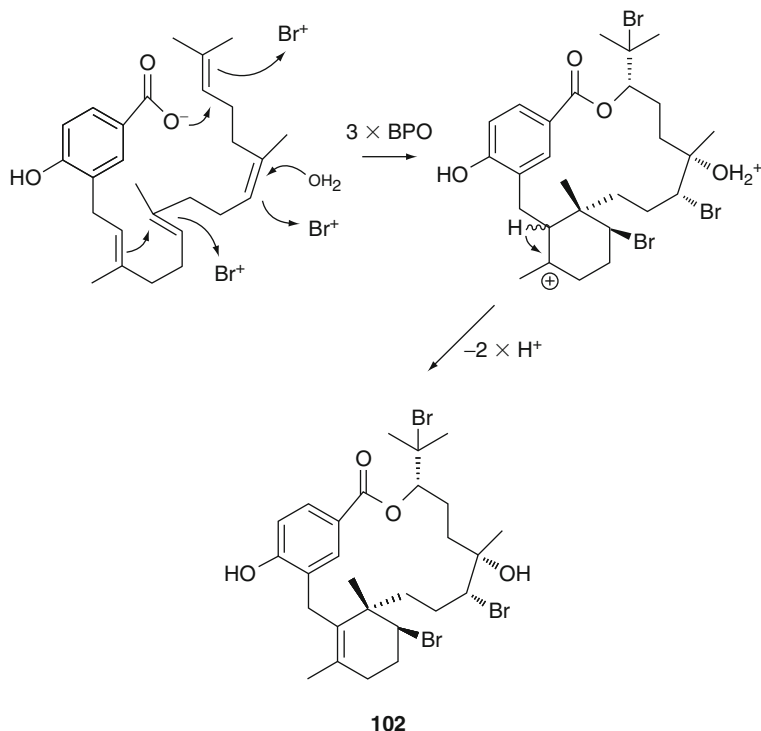
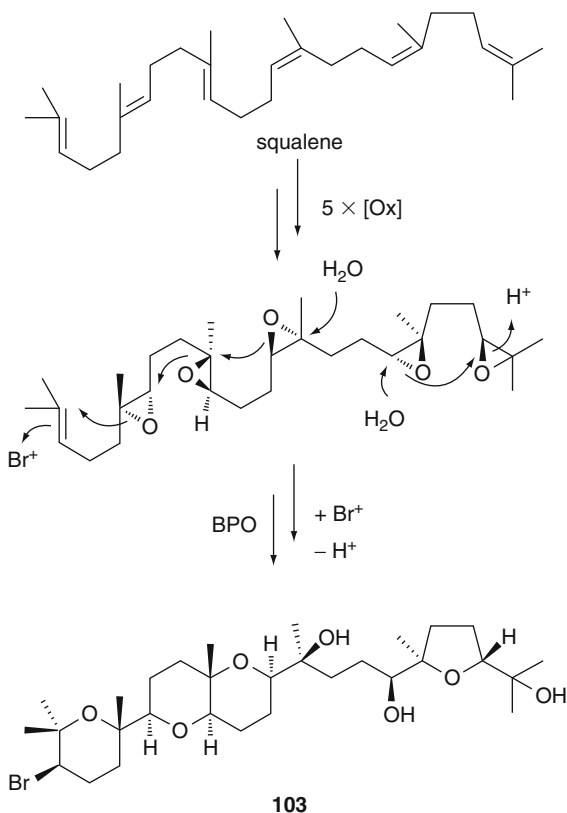


Fig. 2.29 Proposed biosynthesis of bromophycolide A (**102**) by the red alga *Callophycus serratus* involving multiple bromonium ion additions to a complex terpenoid precursor. BPO = bromoperoxidase

reported with alternate halogenations patterns, both on the diterpene skeleton and the aromatic ring. Again, the positions of bromine atoms, and in two cases chlorine, are consistent with their addition to positions of unsaturation in the terpenoid precursor, in some cases inducing further rearrangements of the terpene skeleton and forming diverse ring structures. All of these halogen additions suggest the involvement of a bromoperoxidase forming an electrophilic Br^+ like species. Indeed, a potential meroditerpene precursor containing only unsaturations and vicinal diol but no bromine atoms has recently been reported. Subsequent phylogenetic analysis suggests that there are two clades of *C. serratus* which alternately produce these different classes of meroditerpenoids [297]. While initial reports on these various structures revealed cancer cell toxicity and antimalarial properties (the latter submicromolar for some members) [298], a potential natural function for these substances was revealed when they were shown to possess potent antifungal activity to the pathogenic marine fungus, *Lindra thalassia*. An innovative use of DESI-mass spectrometry was able to localize these antifungal natural products to specific discolored patches on the algal thallus [299]. One suggestion given to explain this observation was that the alga secretes antifungal brominated meroditerpenoids into areas of the thallus that are injured by mechanical damage,

Fig. 2.30 Proposed biosynthesis of thyrseferol (**103**) from squalene by the red alga *Laurencia thyrseifera* involving a polyepoxide intermediate followed by two separate cascades of electrons and one bromonium ion addition. BPO = bromoperoxidase



and thus would be prone to pathogen attack. Overall, the emerging picture of the chemistry and pharmacology of this tropical red alga is a nice illustration of a number of principals in the biosynthesis and chemical ecology of red algal diterpene natural products.

The New Zealand red alga *Laurencia thyrseifera* was investigated for its antimicrobial products early on in the development of marine natural products chemistry by the group of Monroe and Blunt and found to contain a unique triterpene, named thyrseferol (**103**) [300] of which the relative configuration was assigned by X-ray crystallography. Subsequently, this and related compounds such as laurenmariannol have been isolated from other *Laurencia* species collected in diverse regions of the world, such as the Canary Islands and the South China Sea [301, 302]. Importantly, these later efforts revealed that compounds of this series have quite potent cancer cell toxicity, and thus combined with their intriguing polyether structure, they have been targets of multiple total synthesis investigations [303]. The relationship of ether rings and functional groups in thyrseferol has spawned considerable speculation on their biogenesis, which is envisioned as deriving from a polyepoxy precursor that undergoes a cascade of electron shifts to yield the final polyether system (Fig. 2.30).

Oxylipins

One of the more surprising yet pervasive chemical classes to be discovered in red algae is “oxylipins,” oxygenated fatty acid derivatives [304]. Some of the earliest work in this area occurred as a result of a poisoning syndrome known as “Ogonori poisoning” (nausea, vomiting, and hypotension, in some cases, lethal) observed in Japan after eating the red alga *Gracilaria verrucosa* [305]. An active compound was isolated and structurally defined as the known prostaglandin, PGE₂. Interestingly, coral prostaglandin derivatives of similar structure were studied as to their ecological role and appear to induce avoidance in potential consumers through an induced emesis [306]; indeed, prostaglandins taken orally by people have a similar effect. It may be that the *G. verrucosa* prostaglandins serve a similar avoidance role and when consumed by humans, produce such a toxic effect. The biosynthetic pathway to these *Gracilaria* prostaglandins has not been studied; however, because red algae have subsequently been found to be a very rich source of lipoxygenase products [304], their prostaglandins are speculated to involve lipoxygenase-mediated routes similar to those found in corals, rather than the cyclooxygenase pathways found in mammals.

As an example of a red algal metabolite clearly deriving from lipoxygenase metabolism, several red algae from the Oregon coast, including *Farlowia mollis* and *Gracilariopsis lemaneiformis*, were found to produce 12*R*,13*S*-dihydroxyecosapentaenoic acid (12*R*,13*S*-diHEPE, **104**) [307]. This metabolite, found both as a free acid and as a component of complex monogalactosyl diacylglycerol derivatives which are characteristic of chloroplast membranes, had the interesting property of interfering with luteal function in ewes (sheep), perhaps in part by altering luteal response to luteinizing hormone [308]. A study of its biosynthesis showed that it is initiated by a unique sodium-dependant lipoxygenase that stereospecifically incorporates dioxygen to the 12*S* position in an eicosapentaenoic acid (EPA) precursor. Subsequently, the distal oxygen is used to oxygenate the adjacent C-13 position in an oxygen-rebound mechanism [309].

Continued study of oxylipins from red algae has revealed many chemical structures with inherently interesting and partially characterized biosynthetic pathways; curiously however, their biological properties remain poorly characterized, and this represents an enormous opportunity in both the biomedical and ecological arenas! For example, *Laurencia hybrida* from Great Britain yielded hybridalactone (**105**), a fascinating polycyclic oxylipin [310]. A combination of synthetic studies and mechanistic proposals suggests that this metabolite also derives from a 12*S*-lipoxygenase-initiated metabolism and that a fascinating cascade of electron shifts occurs to ultimately lead to its complex structure (Fig. 2.31 and 2.32) [311]. A similar investigation of the wine glass-shaped red alga, *Constantinea simplex* from the Oregon coast, resulted in the constanolactones (e.g., **106**), and once again, a mixture of experiments and speculation strongly implicate a 12*S*-lipoxygenase-initiated metabolism with an ensuing series of electron rearrangements [312]. As a unifying biosynthetic theme, many of the unique carbocyclic oxylipins of red algae appear to involve an epoxy allylic carbocation as a strategic biosynthetic intermediate [313].

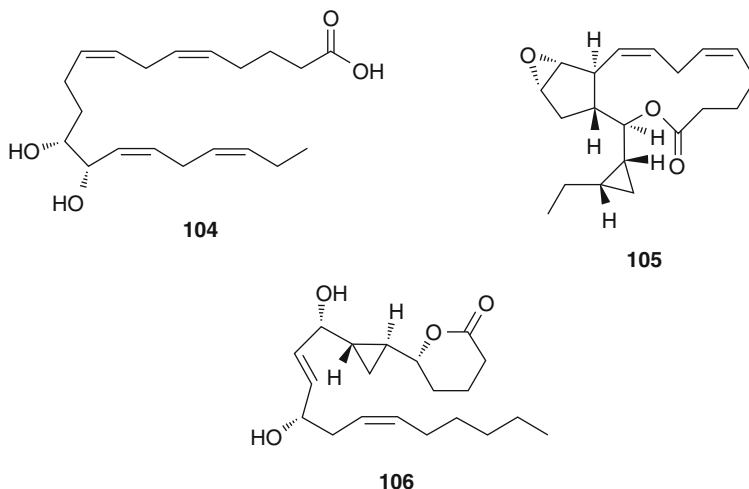


Fig. 2.31 Oxylipins from Rhodophyta

Future biosynthetic investigations of these oxylipin structures are certain to be rewarded with a wealth of enzymes possessing unique specificities and reactivities! (Fig. 2.32).

2.4.3.3 Conclusions on the Rhodophyta

In summary, the natural products of the Rhodophyta have been relatively well studied as a result of being the subject of continuing efforts since the beginning of marine natural products investigations in the 1960s. In general, red algae tend to produce non-nitrogenous metabolites (there are exceptions!) that derive from the shikimate, terpene, and fatty acid biosynthetic pathways. Secondary to these themes, they prolifically decorate carbon scaffolds with halogen atoms, primarily bromine and chlorine, which are incorporated via electrophilic halogenation mechanisms [284]. Many of these metabolites possess biological properties of utility in drug discovery, notably cytotoxicity with application to treating cancer, and antibiotic properties with applications in infectious and parasitic diseases. Remarkably, with new technologies in organic structure analysis, primarily soft ionization MS techniques and NMR able to investigate at the nanomole level [314], we are now able to reach more deeply into the secondary metabolomes of these organisms and find new metabolites with surprising structural features. Some of these recent discoveries, such as the bromophycolides described above (e.g., **102**), possess very interesting biological properties and thus could be useful in treating human diseases, such as malaria, that are currently untreated or poorly treated. Thus, there are still opportunities for fundamental discoveries in the natural products chemistry of red algae, and as presented in this section, natural product discoveries stimulate ensuing questions into biosynthesis, pharmacology, and chemical ecology, most of which remain poorly studied to date.

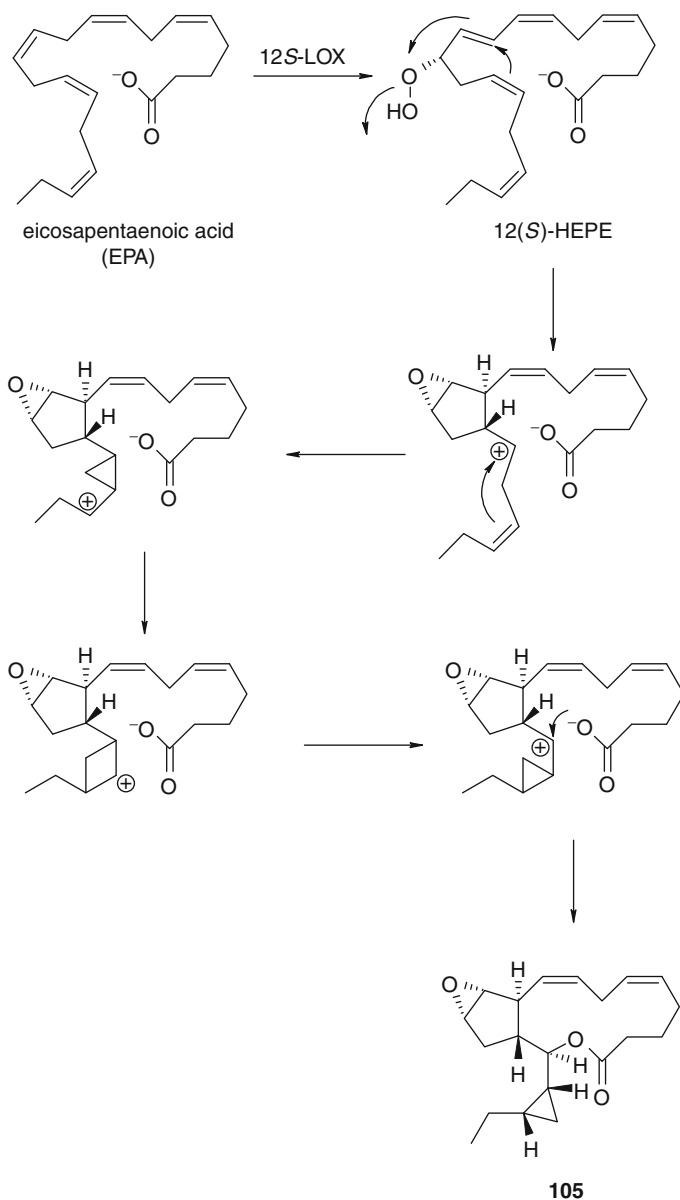


Fig. 2.32 Proposed biosynthesis of hybridalactone (**105**) from eicosapentaenoic acid by the red alga *Laurencia hybrida*, initiated by a 12S-lipoxygenase followed by multiple electron migrations including a cyclopropylcarbinyll-cyclobutyl-cyclopropylcarbinyll cation manifold, and ultimately quenched by the carboxylate anion

2.4.4 Phaeophyceae

Found almost exclusively in the marine environment, there are around 1,500–2,000 species of brown algae (Phaeophyceae) worldwide, varying in size from microscopic to the largest algae in the sea (e.g., the kelp *Macrocystis* grows up to 60 m in length) [315]. Some simple forms of brown seaweeds can be filamentous or have intertwined filaments, whereas more complex forms have differentiated cell types and complex morphologies, on par with higher plants [315–317]. Their cell wall is comprised of two layers, an inner one made of cellulose and an outer of alginic acid [315, 318–322]. The latter polysaccharide consists of a mixture of β -D-mannuronic and α -L-guluronic acids linked covalently in a 1–4 fashion. Alginic acid is used industrially as an additive in antacids, foods, microbiology encapsulation, and paper [318–322]. Brown algae employ another polysaccharide, the glucose-based laminaran, as their main food reserve [323, 324]. Their pigments include chlorophyll *a* and *c*, β -carotene, violaxanthin, and fucoxanthin; this latter one is responsible for their characteristic brown coloration [315, 325]. Sexual reproduction in the brown algae involves motile gametes [326, 327].

Brown algae produce a great variety of secondary metabolites possessing many different skeletal types and biological activities, including aliphatic hydrocarbons, resorcinols, and other polyphenolics, terpenes (sesquiterpenes, diterpenes, meroditerpenoids), and oxylipins. The biological properties of these diverse substances include antibacterial, antifungal, antiviral, anti-inflammatory, antiproliferative, antifouling, antifeedant, cytotoxic, ichthyotoxic, and insecticidal [328–331].

2.4.4.1 Aliphatic Pheromones

A variety of unsaturated but otherwise nonfunctionalized acyclic or cyclic C11 olefins are released as chemical signals by female gametes of marine brown algae in order to attract the corresponding motile male gametes [332]. These molecules constitute blends of pheromones containing various configurational isomers and enantiomeric mixtures which exhibit threshold concentrations for release and attraction generally in the range of 1–1000 picomoles using a water drop assay [332].

One representative example of a brown alga pheromone is the C8 hydrocarbon (3*E*,5*Z*)-octa-1,3,5-triene (fucoserratene, **107**), identified from *Fucus serratus* [333, 334]. Biosynthetically, **107** was found to derive from (5*Z*,8*Z*,11*Z*,14*Z*,17*Z*)-eicosapentaenoic acid (**108**) via oxidative cleavage of the corresponding 12-hydroperoxy intermediate **109** by a hydroperoxide lyase, to yield fucoserratene (**107**) and the polar fragment 12-oxododeca-5,8,10-trienoic acid (**110**) [335–338]. The involvement of a 12-lipoxygenase was supported by inhibition experiments in which the formation of **108** was suppressed under anaerobic conditions, and reactivated by addition of molecular oxygen [338]. A defensive role has also been suggested for compound **110** [336]. In turn, the biosynthesis of ectocarpene (**111**) in the cosmopolitan brown alga *Ectocarpus siliculosus* involves a presumed functionalization of **108** by a 9-lipoxygenase, yielding hydroperoxide **112** [339–341]. This intermediate is proposed to undergo rearrangement to the Hock-oxycarbenium ion **113** before cleavage into the labile C11

divinylcyclopropane **114** and the highly water soluble C9 by product **115**. Finally, spontaneous Cope rearrangement of **114** in principle yields the expected algal pheromone **111** [339–341] (Fig. 2.33).

Additional pheromone hydrocarbons isolated from *E. siliculosus* include dictyotene (**116**), multifidene (**117**), hormosirene (**118**), and finavarrene (**119**) [342] (Fig. 2.34). Biosynthetic studies using ²H-labeled natural eicosanoids and shortened unnatural fatty acids revealed that dictyotene (**116**) is derived from (5Z,8Z,11Z,14Z)-eicosatetraenoic acid (arachidonic acid), whereas the remaining metabolites are produced from eicosapentaenoic acid (EPA) (**108**) [343, 344].

2.4.4.2 Resorcinols

Resorcinols comprised of phloroglucinol with an attached C-20 acyl side chain are characteristic metabolites of the brown algae genus *Zonaria* [345] (Fig. 2.35). Compound **120** has been isolated from several *Zonaria* specimens [346–349], accompanied by numerous analogs displaying different methylation and acetylation patterns on the phloroglucinol substructure, as well as different degrees of unsaturation and oxidation on the acyl side chain. In general, they show antibacterial activity and toxicity against shrimp (*Artemia salina*, *Macrobrachium lanchesteri*), fish (*Poecilia reticulata*), and diatoms (*Chaetoceros gracilis*) [350]. Such effects suggest a possible role as chemical defenses against herbivores as well as reduction of biofouling by epiphytic algae and larvae.

2.4.4.3 Polyphenolics

Polyphenolic compounds have been reported from almost all brown algal orders and can be grouped into a single structural class known as the phlorotannins [351]. These metabolites are formed by the polymerization of 1,3,5-trihydroxybenzene (phloroglucinol, **121**) and biosynthesized via the acetate-malonate pathway [351, 352]. They present a wide range of molecular sizes (126–650 kDa) and can be considered counterparts to the terrestrial tannins produced by vascular plants [351, 353]. Brown algal cells store these phenolic secondary metabolites in vesicles called “physodes” [351, 354, 355], and they have been assigned a defensive role against natural enemies due to their function as herbivore deterrents, digestion inhibitors (e.g., reducing the nutritive value of the algal tissue), and antibacterial agents [351, 353, 356–359]. Additionally, phlorotannins protect algal cells from harmful UV radiation (280–320 nm) and may be involved in the chelation of metal ions [351, 360].

Based on the type of structural linkages that result from polymerization of phloroglucinol and also on the number of hydroxyl groups, phlorotannins are divided into six categories: fucols, phlorethols, fucophlorethols, fuhalols, isofuhalols, and eckols (compounds **122–127**) [351, 361, 362]. Eckol (**127**), a trimeric phlorotannin isolated from the cold water kelp *Eisenia arborea* collected near Vancouver Island, Canada, has been shown to be a potent and specific antiplasmin inhibitor as well as a possible lead compound for the development of antithrombotic agents [363–365]. The compound also inhibits α -2 macroglobulin, tyrosinase, human aldose reductase, hyaluronidases, HIV-1 reverse transcriptase

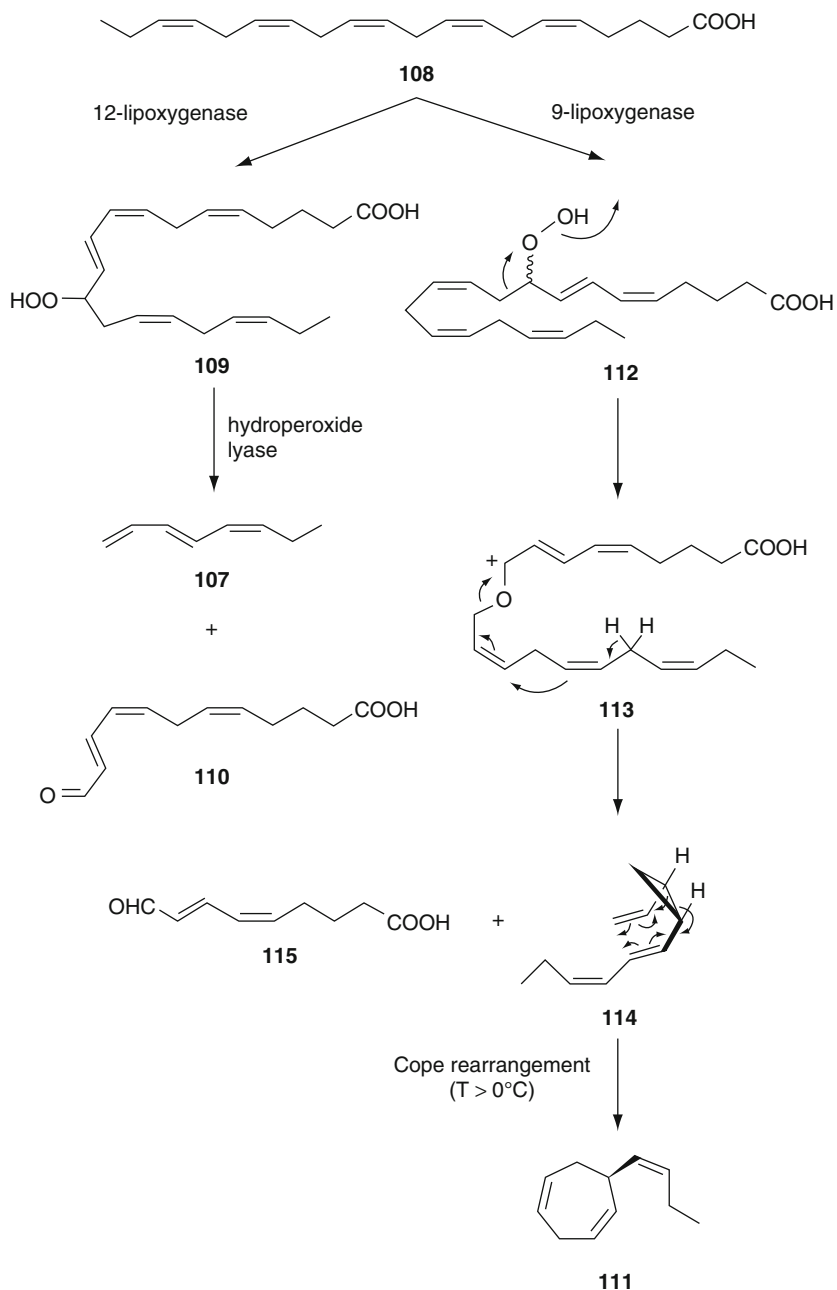
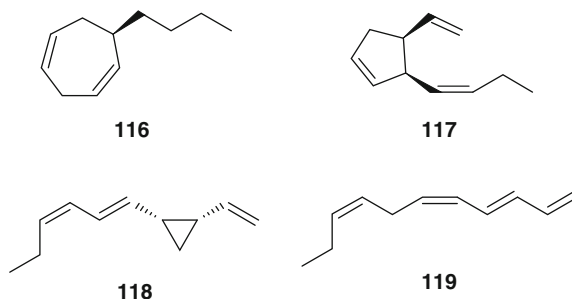


Fig. 2.33 Proposed biosynthesis of brown algal pheromone from (5Z,8Z,11Z,14Z,17Z)-eicosapentaenoic acid involving lipoxygenases

Fig. 2.34 Pheromone hydrocarbons isolated from *E. siliculosus*



and protease, among other therapeutically relevant enzymes [366–370], and exhibits potent antioxidant, bactericidal and algicidal activities [371–374].

2.4.4.4 Terpenes

Among the diterpenes produced by Phaeophyceae (Fig. 2.36, 2.37), pachydictyol A (**128**) was first reported from *Pachydictyon coriaceum*, found along the Pacific coast of California, from Santa Barbara to Baja California [375]. Its structure was determined by NMR and X-ray analyses. Later, specimens of *Dictyota dichotoma*, collected intertidally at Overton on the Bristol Channel (UK), afforded **128** accompanied by three closely related structural analogs [376]. Interestingly, *Dictyota* metabolites have been found to possess high inhibitory activity toward fish predation [377]. Pachydictyol A (**128**) is no exception, and inclusion of this metabolite as 1.0% of an algal dry mass diet led to a 48% reduction in the growth of commonly co-occurring fish (*Diplodus holbrooki*) [377]. After a few days, the fish came to “recognize” the presence of compound **128** and began avoiding algal diets containing pachydictyol A. Thus, fish predation on populations of *Dictyota* is reduced, and consequently, the seaweed becomes a “sanctuary” for smaller animals [378]. Although initially reported as a mild antibiotic, pachydictyol A and several of its analogs were subsequently shown to possess cytotoxic properties [379, 380]. Specifically, **128** has been shown to be cytotoxic against murine fibroblast KA3IT ($IC_{50} < 10 \mu\text{g/mL}$) [381], HeLa, SNU G4, and THP-1 cell lines ($IC_{50} < 100 \mu\text{M}$) [382].

Another representative terpenoid produced by a Phaeophyceae alga is dictyodial (**129**), a major diterpene isolated from the brown algae *Dictyota crenulata* and multiple *Dictyota* collections from other geographically diverse areas (e.g., Oahu, Hawaii; Sonora, Mexico; Aegean Sea, Greece; Oualidia lagoon, Morocco) [383–386]. The compound was initially isolated together with dictyodiol (**130**) and dictyolactone (**131**), and their structures were determined by a combination of NMR and X-ray diffraction experiments [383]. Dictyodial (**129**) and pachydictyol (**128**), among others, are components of an exceptional chemical defense strategy produced by the brown seaweeds *D. ciliata*, *D. menstrualis*, and *D. ciliolata* [387, 388]. These antifouling agents were found responsible for high levels of larval mortality, abnormal development, and reduced growth rates for 3 species of co-occurring invertebrates [388]. Dictyodial (**129**) showed good antibiotic activity against *Staphylococcus aureus* and *Bacillus subtilis*, as well as

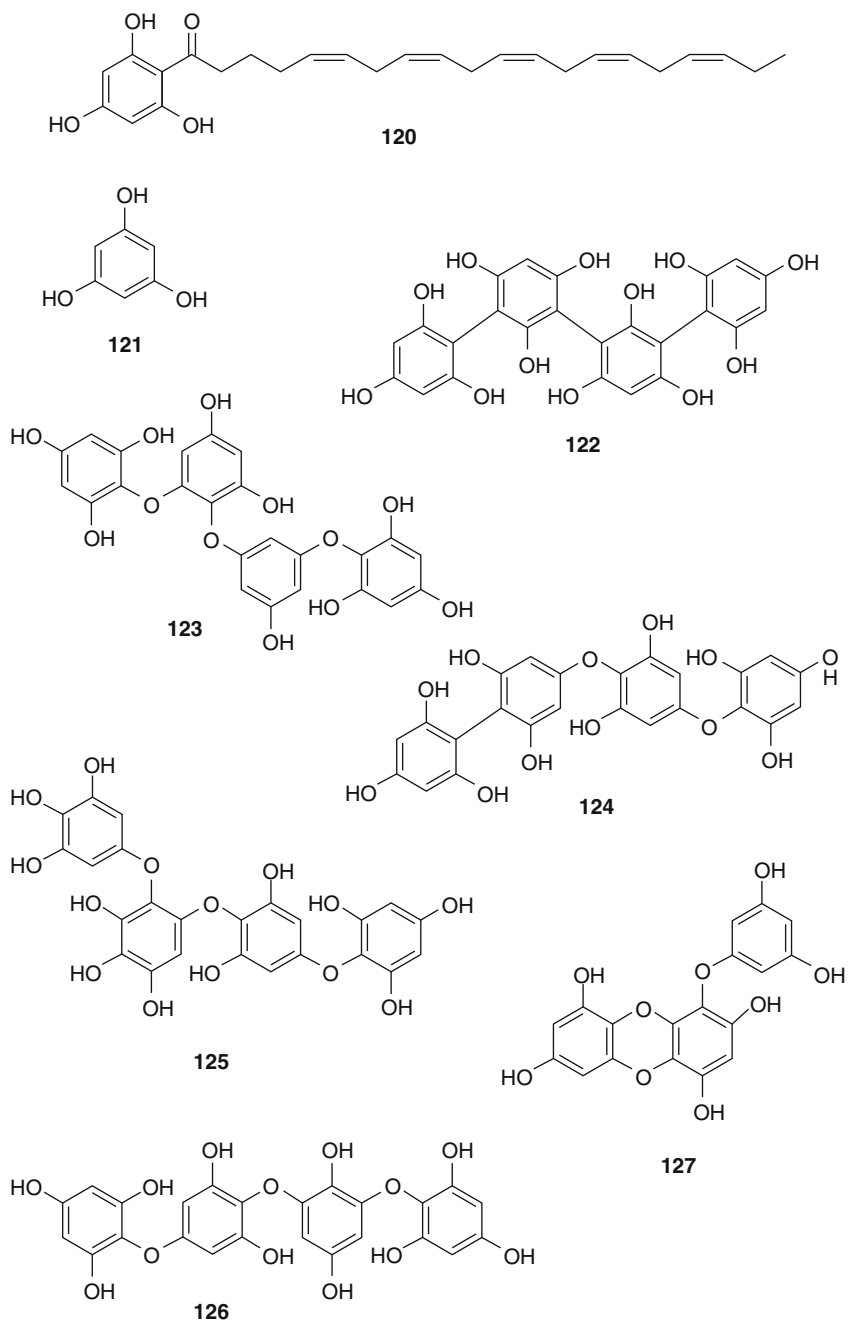


Fig. 2.35 Resorcinol and polyphenols from Phaeophyceae: resorcinol (**120**), phloroglucinol (**121**), tetrafulcol A (**122**), tetraphlorethol B (**123**), fucodiphlorethol A (**124**), tetrafulhalol (**125**), tetrafulhalol (**126**), and eckol (**127**)

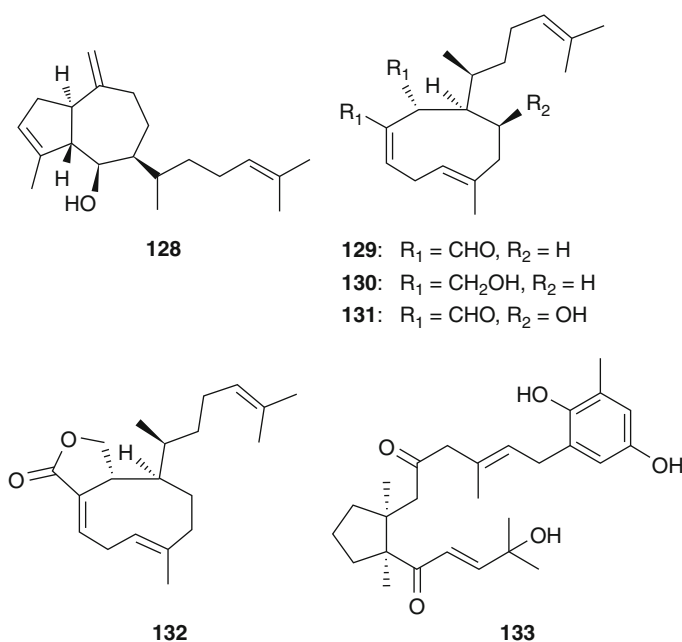


Fig. 2.36 Terpenes from Phaeophyceae

antifungal activity against *Candida albicans* [383]. Furthermore, compound **129** and the closely related 4-hydroxy analog (**132**) inhibited HIV-1 reverse transcriptase with IC₅₀ values of 9.2 and 4.3 μg/mL, respectively [389].

The meroterpenoid bifurcarenone (**133**), the major biologically active metabolite isolated from the brown seaweed *Bifurcaria galapagensis* (Cystoseiraceae) obtained from the Galapagos Islands, was the first marine natural product to exhibit a monocyclic diterpenoid moiety in combination with a hydroquinone unit [390]. Its planar structure was initially derived via chemical and NMR-based spectroscopic studies, and the compound displayed inhibition of mitotic cell division and moderate antibacterial activity [390]. Total synthesis of the natural product and its enantiomer led to a structural revision and allowed assignment of relative and absolute configurations [391, 392]. Subsequently, a number of bifurcarenone (**133**) structural analogs have been reported from diverse *Cystoseira* species collected around the globe [393].

The tropical brown algae genus *Styopodium* is also a well-known source of polycyclic meroditerpenoids [394–398]. Interestingly, the specific components within a given species vary depending on collection, location, and season [397, 399, 400]. Several of these meroditerpenoids display potent biological activities which may be of biomedical and pharmacological utility.

For example, stypolactone (**134**) [400] and atomaric acid (**135**) [395, 396] are cytotoxic to human lung and colon carcinoma cells, while stypoldione (**136**) and 14-keto stypodiol diacetate are inhibitors of microtubule assembly [401–403]. Stypoldione (**136**) [394], epistypodiol (**137**), stypodiol (**138**), stypotriol (**139**), and

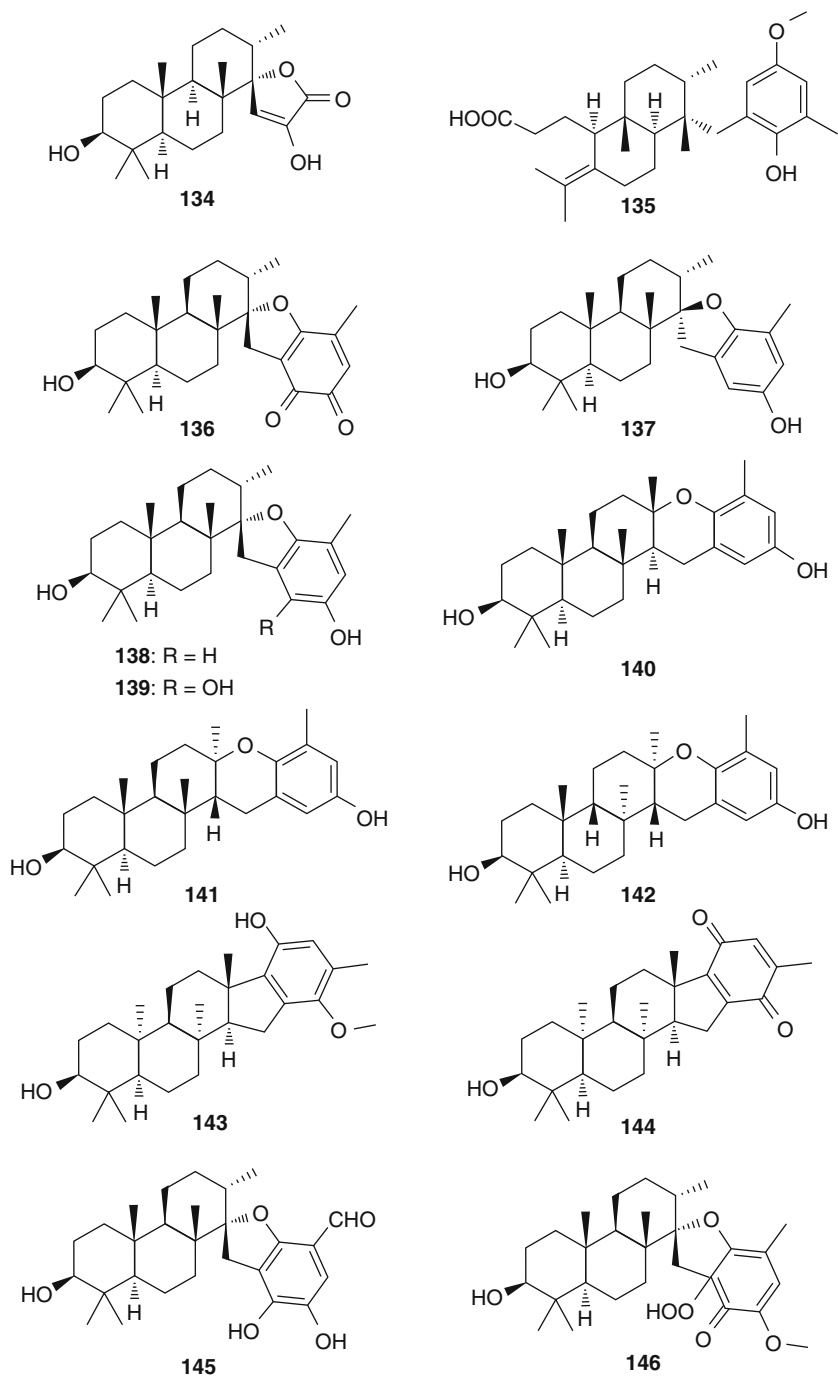
taondiol (**140**) are ichthyotoxic [395, 396]; diacetylepitaondiol has a negative inotropic effect on isolated rat atrium [404]; and stypoquinonic acid and atomaric acid inhibit tyrosine kinase [405]. Isoepitaondiol (**141**) is reported to have insecticidal activity [406]. In the case of 2 β ,3 α -epitaondiol (**142**), flabellinol (**143**), flabellinone (**144**), stypotriolaldehyde (**145**), and stypohydroperoxide (**146**), isolated from *Stypopodium flabelliforme* collected in Papua New Guinea, it has been suggested that their ichthyotoxic and cytotoxic activities are at least in part due to a blockade of the voltage-gated sodium channel (VGSC) [407] (Fig. 2.37).

The biosyntheses of these metabolites may occur via the cyclization of 2-(2,3-epoxygeranylgeranyl)-6-methylhydroquinone (**147**), in a manner reminiscent of sterol cyclizations [408]. For example, to produce 2 β ,3 α -epitaondiol (**142**), the terpene chain must be prefolded into a chair-boat-chair conformation with attack by the ortho-positioned phenolic hydroxy group occurring from the Re face (see Fig. 2.38). To produce flabellinol (**143**) and flabellinone (**144**), the terpene chain is predicted to be prefolded into a chair conformation for rings A and C and a twist boat for ring B. The five-membered carbocycle is proposed to be formed by electron shifts initiated from the *meta*-phenolic hydroxyl function, extending through the *ortho*-unsubstituted position and attacking the Si face of the C-2/C-3 double bond (see Fig. 2.38). Formation of the hydroperoxide in **146** would logically occur through the addition of singlet oxygen to stypotriol (**139**). In general, acyclic terpene folding patterns should be flexible during the biosynthesis so as to give metabolites in both the taondiol and epitaondiol stereochemical classes [407]. Additionally, quenching of the carbocations produced at the termini of terpene cyclizations can occur through direct interaction of the phenol functionality, producing benzofuran or benzopyran rings. Alternatively, quenching may occur through electron shifts emanating from the phenol function but involving formation of a five-membered carbocyclic ring. Finally, further oxidation of the aromatic ring leads to biologically reactive functionalities, such as aldehydes and hydroperoxides [407].

2.4.4.5 Oxylipins

Several members of the brown algae order Laminariaceae produce a suite of cyclopentane-containing oxylipins presumably via lipoxygenase-initiated biosynthetic routes (see below). The first reported family of such brown algal oxylipins, named the ecklonialactones, was isolated from *Ecklonia stolonifera* collected in Tsuruoka, Japan [409, 410]. Their structures were determined by spectral and chemical methods, as well as X-ray crystallography. Ecklonialactone A (**151**) showed weak feeding-deterrent activity against species of abalone of the genus *Haliotis* [409].

Subsequently, egregiachlorides A (**153**), B (**154**), and olefin analog **155** were identified via NMR and mass spectrometric methods from extracts of the Oregon kelp, *Egregia menziesii*, together with ecklonialactones A (**151**) and B (**152**), among others [411, 412]. The co-occurrence of these two families of oxylipins and their similar structural features suggest a common biogenetic origin, analogous to prostaglandin biosynthesis but presumably initiated by a lipoxygenase showing ω 6 specificity on stearidonic acid (**148**) [412] (Fig. 2.39). Subsequent formation of

**Fig. 2.37** Meroterpenes from Phaeophyceae

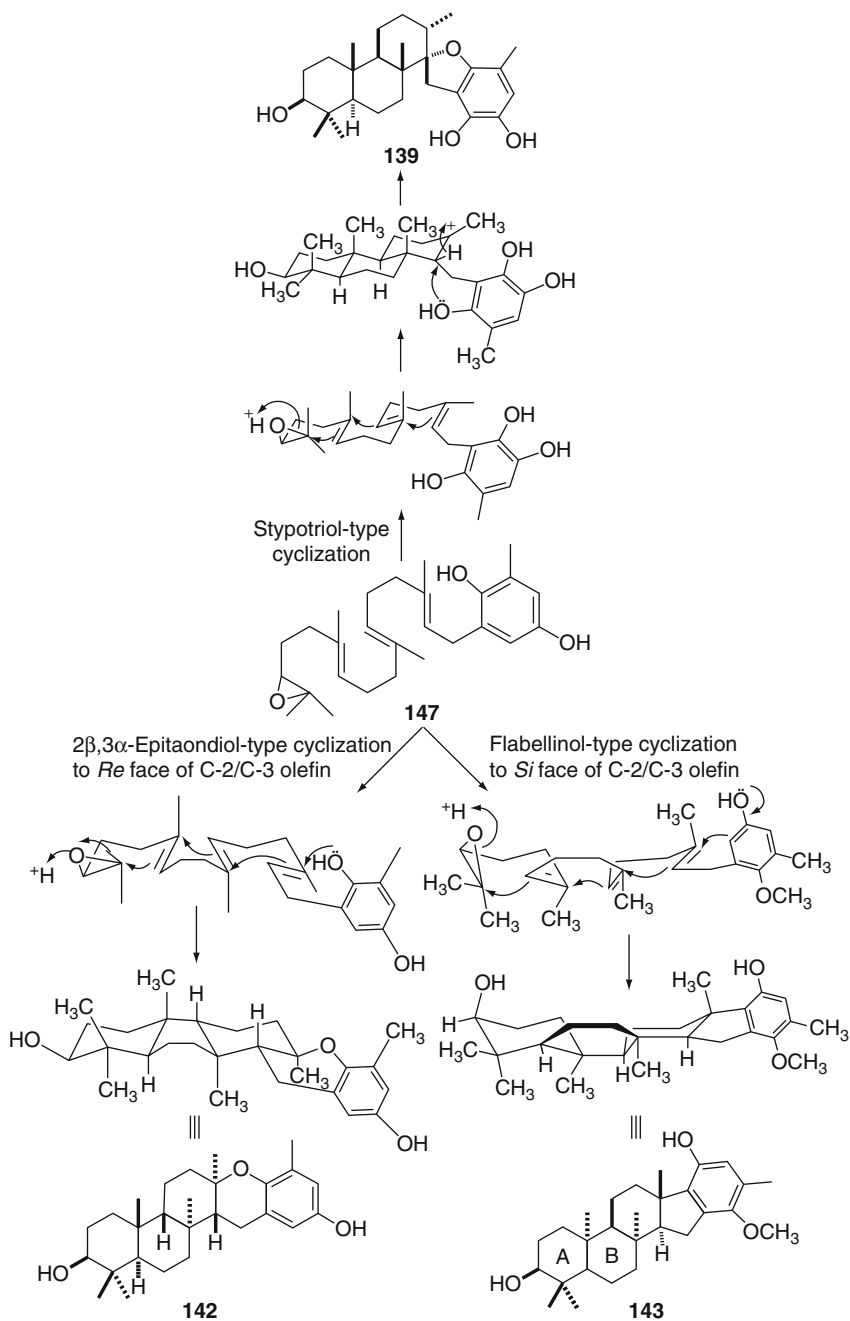


Fig. 2.38 Proposed biosynthesis of brown algal terpenes, styptotriol (**139**), 2β,3α-epitaondiol (**142**), and flabellinol (**143**) from 2-(2,3-epoxygeranylgeranyl)-6-methylhydroquinone (**147**) involving various cyclizations

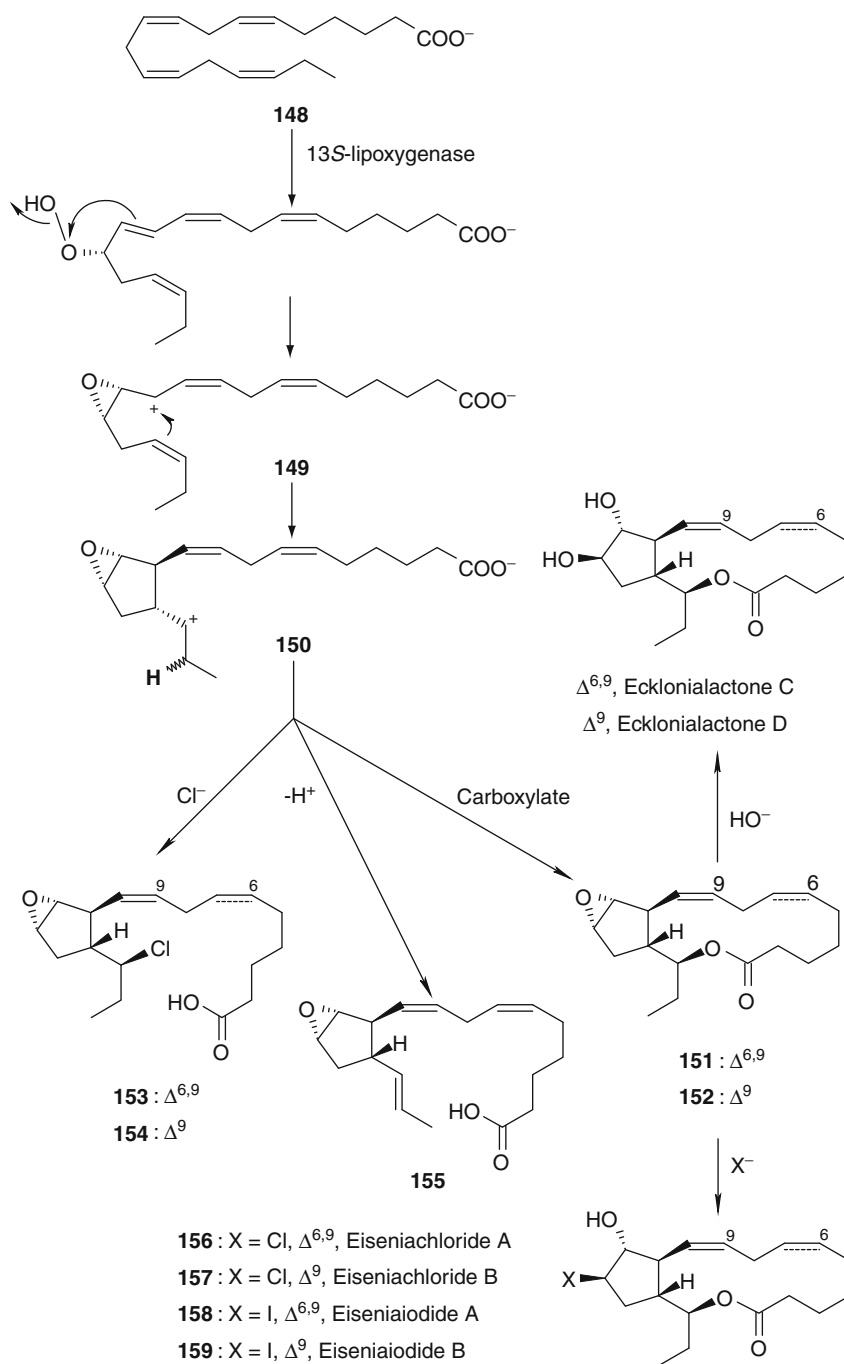


Fig. 2.39 Proposed biogenesis of various brown algal oxylipins from stearidonic acid (148)

Fig. 2.40 Structure of marine sediment-derived triterpene hydrocarbon

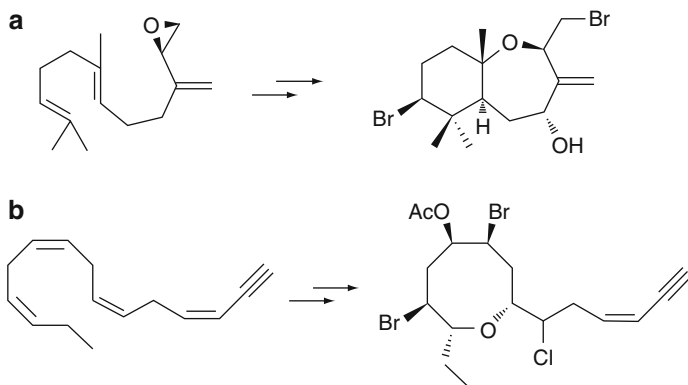
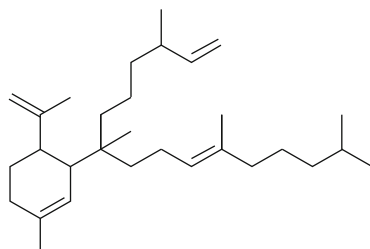


Fig. 2.41 Red algal metabolites and their biosynthetic precursors

a pivotal epoxy cation intermediate (**149**) could lead to a secondary cyclopentyl cation (**150**). Trapping of this latter intermediate could occur either with chloride or carboxylate addition, or by the loss of a proton. Further modification at the 3-membered epoxide ring leads to additional ecklonialactones and to a series of halogenated macrolactones, the most recent members of this oxylipin class. This latter family of oxylipins was reported from the brown seaweed *Eisenia bicyclis*, often visible around the coasts of Japan [413] (Fig. 2.39). In addition to the new eiseniachlorides and eiseniaioidides, the alga was found to contain two new olefin analogs as well as several ecklonialactones and egregiachloriades A–C, further supporting their common biogenesis. Compounds **156–159** showed weak antibacterial activity [413].

2.5 Conclusions

The natural products of marine algae and cyanobacteria are wonderfully diverse, essentially representing all molecular classes such as terpenes, fatty acids, alkaloids, peptides, polyketides, and polyphenolics. Moreover, many of these scaffolds are decorated by the producing organisms with unique functional groups, and most remarkably, many possess covalently attached halogen atoms such as bromine and

chlorine. A necessary consequence of this broad chemical diversity is that the biological properties of marine algal and cyanobacterial metabolites are in many different arenas, both in terms of their natural function as well as their potential biomedical application. For example, while many of the above discussed metabolites have been shown or are predicted to have antipredatory roles, a function that seems understandable in light of the benthic and non-motile life history of most of these organisms, other natural products have protective and defensive functions against microbial life forms, whereas others have been shown to have roles in intraspecies or interspecies communication phenomena. Thus, while much has been learned about the organic chemistry of marine algal and cyanobacterial natural products, and in some isolated cases, knowledge developed of their natural role, biomedical properties, and biosynthesis, many more questions have been raised in these studies, and there are many exciting frontiers in the areas of molecular pharmacology and ecology, marine biotechnology, and development of genomic level understanding of these organisms, their evolution and their interactions with one another.

2.6 Study Questions

1. *Cyanobacteria* Cyanobacteria, along with heterotrophic bacteria and fungi, are commonly associated with sponges. For example, the filamentous cyanobacterium *Oscillatoria spongellae* is abundant in tissues of the sponge *Dysidea herbacea*, and cyanobacterial-like compounds have been isolated from field collections of the sponge. Outline five (5) conceptual approaches you might use to demonstrate the biosynthesis of a natural product in a microbial subpopulation that is present in a complex community such as a sponge.
2. *Dinoflagellates* Propose a chemically rationale mechanism for the biosynthesis of brevetoxin A.
3. *Diatoms* Propose a chemically rationale mechanism for the biosynthesis of the marine sediment-derived triterpene hydrocarbon shown below (Fig. 2.40).
4. *Chrysophytes* The chrysophyte alga *Chrysosphaeum taylori* has been found to produce both the chrysosphaentins and hormothamnione. Are these metabolites biogenetically related? If so, propose a plausible biogenetic pathway for these compounds.
5. *Prymnesiophytes* Both prymnesin-1 and -2 possess structural motifs similar to those found in dinoflagellate natural products. What are the structural differences? Which biosynthetic pathways are behind those differences? Do they provide a sense of evolutionary divergence between prymnesiophytes and dinoflagellates?
6. *Chlorophyta* Udoteal, a fish feeding-deterrent terpenoid produced by *Udotea flabellum*, was chemically converted into udoteatrial under ethanol preservation. Propose a rationale mechanism for this chemical conversion.
7. *Rhodophyta* Propose a biogenetic pathway from the precursors shown in each case to the products formed. Show all electron and atom migrations as distinct

steps. Oxidations with molecular oxygen may be involved. In each case, outline a possible biosynthesis of the precursor as well (Fig. 2.41).

8. *Phaeophytes* Which class of brown algal metabolites is considered to be the counterpart to tannins produced by vascular plants? Why and for what purpose?

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Abstract

The world's oceans harbor extensive levels of bacterial diversity. Although much of this diversity remains uncharacterized, cultured representatives from a broad range of taxonomic groups are proving to be an important source of novel secondary metabolites. These metabolites include new carbon skeletons as well as compounds with a high degree of halogenation, a relatively common feature of marine-derived secondary metabolites. The bacteria being cultured from marine sources include new taxa, which are proving to be a particularly important source of new chemical entities. This chapter will provide the reader with a brief, though not comprehensive history of the secondary metabolites that

B.T. Murphy (✉) • P.R. Jensen • W. Fenical
Center for Marine Biotechnology and Biomedicine, Scripps Institution of Oceanography,
University of California, San Diego, CA, USA
e-mail: btmurphy@uic.edu, pjensen@ucsd.edu, wfenical@ucsd.edu

have been isolated from marine bacteria. The focus is on the taxonomic distribution of the producing strains and interesting structural features and biological activities of the compounds that are being discovered from marine bacteria.

3.1 Introduction

The marine environment is composed of a myriad of ecologically distinct habitats. Thus, it is not surprising that bacteria adapted to life in the marine environment are both diverse, phylogenetically distinct, and maintain survival adaptations that differ from bacteria that occur on land. One of the earliest physiological differences identified among marine-derived bacteria was the requirement of seawater, or more specifically sodium, for growth. Historically, bacteria demonstrating this physiological requirement were defined as obligate marine. However, there is no a priori reason to presume that bacteria lacking this specific marine adaptation should not be considered as part of the autochthonous marine bacterial community. It is common to culture bacteria from marine samples that grow equally well in media prepared with seawater or deionized water. Conversely, bacteria capable of growth on media prepared with salt concentrations equivalent to that of seawater can be readily cultured from nonmarine samples. These strains, it can be presumed, have the potential to grow in both environments. Studies of secondary metabolites from marine-derived bacteria have included strains that appear highly adapted to life in the ocean as well as more cosmopolitan taxa that occur both in the sea and on land. Both groups of bacteria are yielding interesting new secondary metabolites. The following sections highlight select secondary metabolites produced by various taxonomic groups of marine-derived bacteria.

After Alexander Fleming's discovery of penicillin in 1929, terrestrial microorganisms became the focal point for one of the most prolific drug discovery efforts in history. The discoveries of penicillin and later actinomycin (1940) led to the "Great Antibiotic Era" which yielded more than 120 drugs for the treatment of infectious diseases, cancer, elevated cholesterol, immunomodulation, and others. Some of the most important of these discoveries came from studies of the filamentous actinomycete bacteria, which because of their growth forms, were at one time considered to be fungi (hence the suffix "mycetes"). The actinomycetes are responsible for the majority of the antibiotics in clinical use today. From the period 1950 to 1990, most of the pharmaceutical companies invested heavily in microorganism-based drug discovery with financial commitments that reached in the vicinity of \$10 B per year. The intensity of these explorations led to discoveries of new microorganisms from virtually all accessible terrestrial environments, from arctic and cold temperate regions to tropical environments. Interestingly, although the world's oceans occupy more than 70% of the surface of the Earth, this massive resource remained unexplored.

It is now clear that bacteria use small organic molecules, or secondary metabolites, for many important adaptive functions including communication and antagonism. The unique environmental conditions experienced by marine bacteria afford

opportunities for the selective production of secondary metabolites that are not observed outside of the marine environment. One clear example of this is the high level of halogenation observed among the secondary metabolites of marine bacterial origin.

This chapter highlights some of the structurally interesting secondary metabolites that have been isolated from cultured marine bacteria. It is beyond its scope to provide a comprehensive review of all metabolites produced by marine bacteria or to report on cyanobacterial metabolites, which will be addressed in another chapter. Instead, an overview of the metabolites produced by various taxonomic groups of heterotrophic marine bacteria is offered, with a few compounds highlighted for each group. For further information on specific topics, the reader is referred to review articles cited in the Bibliography [1–16]. With a few exceptions, articles published after June 2010 are not included.

This chapter begins with unicellular Gram-negative bacteria and ends with filamentous Gram-positive actinomycetes. It is written with a focus on chemistry and includes details about compound biological activity and the environmental source of the producing strains. We chose to organize this chapter following the framework used in Bergey's Manual of Determinative Bacteriology and "The Prokaryotes – A Handbook on the Biology of Bacteria" [17].

3.2 Secondary Metabolites from Gram-Negative Marine Bacteria

Gram-negative bacteria are ubiquitous in marine environments. They are more abundant than their Gram-positive counterparts and are the best studied of the marine bacteria from a taxonomic, ecological, and phylogenetic perspective. In terms of secondary metabolite discovery, fewer compounds have been discovered from Gram-negative marine bacteria, possibly because these bacteria have not been studied as intensively with this goal in mind or that they do not maintain genes involved in secondary metabolism as commonly as Gram-positive forms.

3.2.1 Proteobacteria

The Proteobacteria, formerly known as purple bacteria, constitute the largest and most physiologically diverse bacterial phylum. Indicative of this diversity, the phylum was named after the Greek god Proteus, son of Poseidon, who had the ability to assume different shapes. This phylum comprises the majority of medically and agriculturally significant Gram-negative bacteria. Found within the β -, δ -, and γ -divisions of the Proteobacteria are bacteria that maintain gliding motility. These include a large group of chemically prolific gliding bacteria called the myxobacteria, many of which form fruiting bodies under low-nutrient conditions. In the following two sections, proteobacterial secondary metabolites are organized by class.

3.2.1.1 α - and δ -Proteobacteria

Categorized within the phylum Proteobacteria are the classes α - and δ -Proteobacteria. The mitochondria, found in the eukaryotic cell, are believed to have originated from α -Proteobacteria, a class that is crucial to the regulation of Earth's carbon, sulfur, and nitrogen cycles. The majority of the α -Proteobacteria are rod-shaped. This class includes prokaryotic predators (*Bdellovibrio*), strains that have the ability to glide (myxobacteria), and those that can reduce sulfur. To date, relatively few secondary metabolites have been identified from marine representatives within these classes.

From the cells of an undescribed species of the unicellular marine α -proteobacterium *Agrobacterium*, agrochelin A (**1**), a cytotoxic thiazole alkaloid was isolated [18, 19]. This strain was cultivated from a tunicate collected in the Mediterranean Sea off the east coast of Spain. It displayed inhibitory activity against a panel of tumor cell lines and was shown to form a complex with Zn^{2+} ions. In the search for endothelin-converting enzyme (ECE) inhibitors, B-90063 (**2**), a dimeric oxazole-pyridone analog was isolated from an undescribed species of the marine α -proteobacterium *Blastobacter* [20]. This strain was isolated from the water column on the coast of Ojika Peninsula, Japan, and required seawater for growth. It exhibited antagonistic activities toward endothelins, peptides responsible for the constriction of blood vessels. In addition to the two aforementioned metabolites from α -Proteobacteria, two polyketide-derived metabolites were discovered from two marine-derived myxobacterial strains. An ethylated polyene-substituted pyrone metabolite (phenylnannolone A, **3**) was isolated from the marine δ -proteobacterium *Nannocystis exedens* [21]. Although polyene pyrones have been reported from various terrestrial sources, the presence of an ethyl group on the polyene chain represented a novel deviation from this class of molecules. Biosynthetic studies suggested unprecedented biochemical reactions are employed to form phenylnannolone A. In a program designed to isolate marine myxobacteria, the δ -proteobacterium *Haliangium luteum* was isolated from a marine alga collected in Kanagawa, Japan. This myxobacterium required approximately 2–3% NaCl for growth and the production of the metabolite haliangicin (**4**) [22, 23]. Compound **4** was found to display antifungal activity toward a number of fungi, including the pathogenic strain *Phytophthora capsici* (Fig. 3.1).

3.2.1.2 γ -Proteobacteria

The γ -Proteobacteria consist of over 180 genera and more than 750 species (as of 2007) and are the largest class within the phylum Proteobacteria. This class contains several human and animal pathogens including *Escherichia coli*, *Salmonella typhi* (typhoid fever), *Yersinia pestis* (plague), *Vibrio cholerae* (cholera), *Pseudomonas aeruginosa*, and *Acinetobacter baumannii*. Of all Gram-negative marine bacteria, the γ -Proteobacteria harbor the greatest number of secondary metabolites published in the literature, and these metabolites subsequently exhibit the most structural and functional diversity. Four families within this class, namely, Vibrionaceae, Alteromonadaceae, Pseudoalteromonadaceae, and

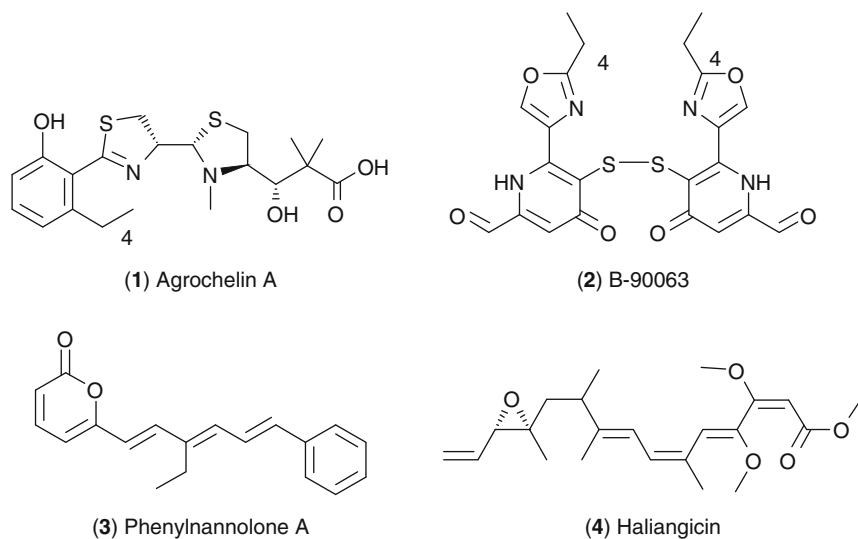


Fig. 3.1 Secondary metabolites from marine α - and δ - Proteobacteria

Pseudomonadaceae, contain genera responsible for the production of the majority of molecules from the Proteobacteria.

Members of the family Vibrionaceae are typically rod-shaped, facultative anaerobes and include several human pathogens such as *V. cholerae*. In the following few examples, indole natural products were isolated from two diverse marine environments. First, an undescribed species of *Vibrio* was isolated from an Okinawan sponge, *Hyrtios altum*. This bacterium produced an unusual indole trimer, trisindoline (**5**) [24]. Similarly, the toxic mucus of the boxfish *Ostracion cubicus* was found to harbor the microbial strain *V. parahaemolyticus*. This fish excretes mucus in response to stress. A structurally similar bis-indole (vibrindole A, **6**) was isolated from this strain and exhibited antibacterial activity against a number of pathogenic bacteria [25]. Also isolated from a *Vibrio* sp. colonizing the surface of the soft coral *Simularia polydactyla* in the Red Sea (Aquaba, Jordan) was aqabamycin E (**7**) [26].

In a program designed to discover bioactive metabolites from poorly studied taxa, the antibacterial cyclic depsipeptide unnarmicin A (**8**) was isolated from cultures of a bacterium of the genus *Photobacterium*, family Vibrionaceae [27]. The strain was isolated from the water column near Okinawa, Japan. Unnarmicin A exhibited inhibitory activity toward a few α -Proteobacterial strains of the genus *Pseudovibrio* that are common culturable strains from the marine environment. Antimicrobial activity against Gram-positive bacteria (*Bacillus subtilis*) and microalgae (*Prorocentrum micans*) was discovered in association with the unusual magnesium-containing metabolite magnesidin A (**9**) [28, 29]. Magnesidin A is produced by *Vibrio gazogenes*, a pink-colored bacterium isolated from the marine

alga *Caulerpa peltata*, though it originally appeared several years earlier as an impure mixture from a marine *Pseudomonas* sp.

One final example of a natural product isolated from the family Vibrionaceae is that of a rare boron-containing small molecule involved in cell-to-cell bacterial communication known as quorum sensing. AI-2 (**10**) is a fused, bicyclic boronic acid anion that acts as an autoinducer, or an extracellular signaling molecule. AI-2 was first identified in the marine bacterium *Vibrio harveyi*, but its structure eluded the scientific community until it was cocrystallized with its sensor protein target LuxP [30]. AI-2 was found to be one of two molecules that regulate bioluminescence in *V. harveyi* and is one of a growing number of signaling molecules isolated from marine microorganisms. It is now accepted that communication among microbes via secondary metabolites is essential to a variety of processes from bioluminescence to biofilm formation, and even secondary metabolite production (Fig. 3.2).

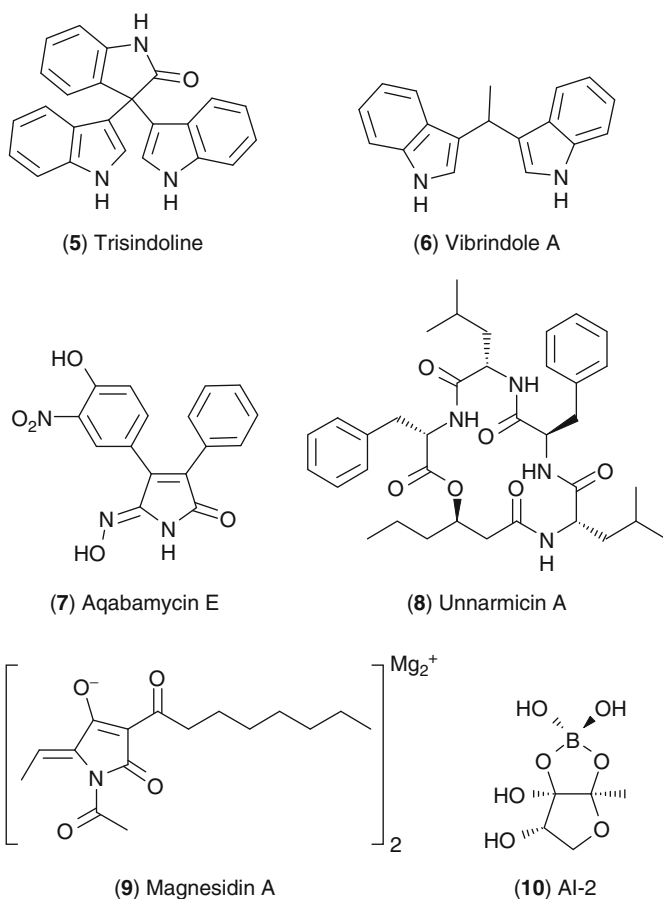


Fig. 3.2 Secondary metabolites from marine γ -Proteobacteria (Vibrionaceae)

As of 2007, the family Pseudomonadaceae contained approximately 15 genera characterized by straight or curved rods. It was from a marine strain of *Pseudomonas bromoutilis* that the first marine microbial natural product, pentabromopseudilin (**11**), was identified in 1966 [31]. This antibiotic contains an unusual framework, possessing a small carbon skeleton while the majority of its molecular mass is derived from bromine. Pentabromopseudilin was known to possess biological activity; however, it was not until 2009 that its specific mechanism of action was identified. It was shown to potently inhibit myosin, a motor protein that facilitates the transport of other important proteins such as tubulin [32]. The potential therapeutic applications of selective myosin inhibitors include the treatment of cancer, heart failure, and malaria.

Within the family Alteromonadaceae is the genus *Alteromonas*, which was originally described in 1972 in order to encompass a number of Gram-negative *Pseudomonas*-like strains isolated from the marine environment. A tripeptide-derived metabolite, **12**, with a novel β -aminopimelic acid component was isolated from a partly classified bacterium falling within the genera *Pseudomonas/Alteromonas* [33]. This bacterium was found associated with the common black sea sponge *Dysidea fragilis*. Another sponge associate, an undescribed species of *Alteromonas*, was shown to produce the macrocyclic lactam alteramide A (**13**) [34]. This bacterium was isolated from a sample of the sponge *Halichondria okadai* collected in Kanagawa, Japan, and the resulting metabolite displayed cytotoxicity toward a number of cancer cell lines. An additional *Alteromonas* species that has yet to undergo complete taxonomic identification is *Alteromonas* cf. *rava*. Isolated from seawater, this bacterium produced thiomarinol B (**14**), which displayed antibacterial activity against various Gram-negative and Gram-positive bacteria [35]. This metabolite is a hybrid structure of two previously known antibiotic classes: the pseudomonic acids and the pyrrothines. Finally, an undescribed species of *Alteromonas* was found to colonize the surface of shrimp embryos (*Palaemon macrodactylus*). This bacterium was found to produce a small molecule (isatin, **15**) that chemically defended the embryos from the common crustacean fungal pathogen *Lagenidium callinectes* [36]. This remains a rare example of the functional elucidation of a secondary metabolite within the ecological niche of its producing microorganism.

Within the family Pseudoalteromonadaceae is the genus *Pseudoalteromonas*, which is the source of a large number of marine natural products. Among them is a brominated korormicin derivative (**16**) isolated from a *Pseudoalteromonas* strain collected from the surface of an undescribed species of the macroalga *Halimeda* from the Palauan Sea [37]. The original metabolite korormicin inhibited Na^+ -translocating NADH-quinone reductase, a process of Na^+ ion translocation that is prevalent in Gram-negative bacteria [38]. This property suggested that korormicin may be useful as an antibiotic against any bacterial strain requiring a sodium pump for survival. The marine strain *Pseudoalteromonas maricaloris*, which was isolated as an epibiont of the Australian sponge *Fascaplysinopsis reticulata*, produced a brominated cyclic peptide (bromoalterochromide A', **17**) that possessed a unique peptidic chromophore [39]. This, and related peptides, exhibited cytotoxicity

toward developing eggs of the sea urchin *Strongylocentrotus intermedius*, thus suggesting a possible ecological role for the metabolites.

An unidentified species of *Halomonas* from the family Pseudomonadaceae, collected from a water sample in the East Frisian Wadden Sea, Germany, produces the metabolite HPPD-1 (**18**) [40]. It is a diarylpyrrole that exhibited chemopreventive properties. This study provided a nice example of the optimization of growth conditions to boost production of target metabolites. Since laboratory culture conditions do not perfectly represent the environment in which the bacterium previously existed, experimenting with different culture conditions may greatly alter the ability of a microorganism to produce secondary metabolites. One final example of a natural product from a *Halomonas* sp. is the amphiphilic siderophore loihichelin A (**19**) [41]. The producing strain was studied as part of an effort to explore reduced Fe-, Mn-, or S-requiring microorganisms from basaltic rocks. The strain was isolated at approximately 1,700 m from partially weathered surfaces of submarine basalts at the Loihi Seamount, an active Hawaiian volcano laden with Fe(II)-rich hydrothermal fluids. The loihichelins differ from other peptidic siderophores by an increased hydrophilicity due to their longer peptide and shorter fatty acid chains. Their role in nutrient acquisition and interactions with basaltic rock is the topic of ongoing studies (Fig. 3.3).

3.2.2 Bacteroidetes

The phylum Bacteroidetes contains some bacteria that are also considered gliding bacteria. They are typically chemoheterotrophs, found in a diversity of environments, and play important roles in the breakdown of high-molecular-weight dissolved organic matter. There are relatively few studies involving the isolation of natural products from genera within the phylum Bacteroidetes; a few examples are presented below.

Although some bacteria contain terpenoid biosynthetic pathways for the production of carotenoid pigments, bacteria only rarely produce terpenoid secondary metabolites. There are a couple of notable exceptions. From the gliding bacterium *Saprospira grandis* (Saprospiraceae), which captures and digests other bacteria, four diterpenoids of the neoverrucosane class, Fig. 3.4 (**20**), were isolated [42]. From an undescribed species of *Rapidithrix* (family Flammeovirgaceae), which also maintains gliding motility, a new linear hybrid NRPS–PKS peptide antibiotic called ariakemicin A (**21**) was isolated [43]. This compound exhibited selective antibiotic activity against Gram-positive bacteria and was especially potent against the pathogen *Staphylococcus aureus*.

The unusual metabolites **22–25** have also been isolated from two strains of *Cytophaga* (BIO137 and BIO138) within the family Flexibacteriaceae [44]. Strains BIO137 and BIO138 were isolated from biofilms in the North Sea. These new naturally occurring polysulfides were the result of an effort to identify volatile molecules that are typically overlooked in natural product studies. The investigators used gas chromatography coupled with mass

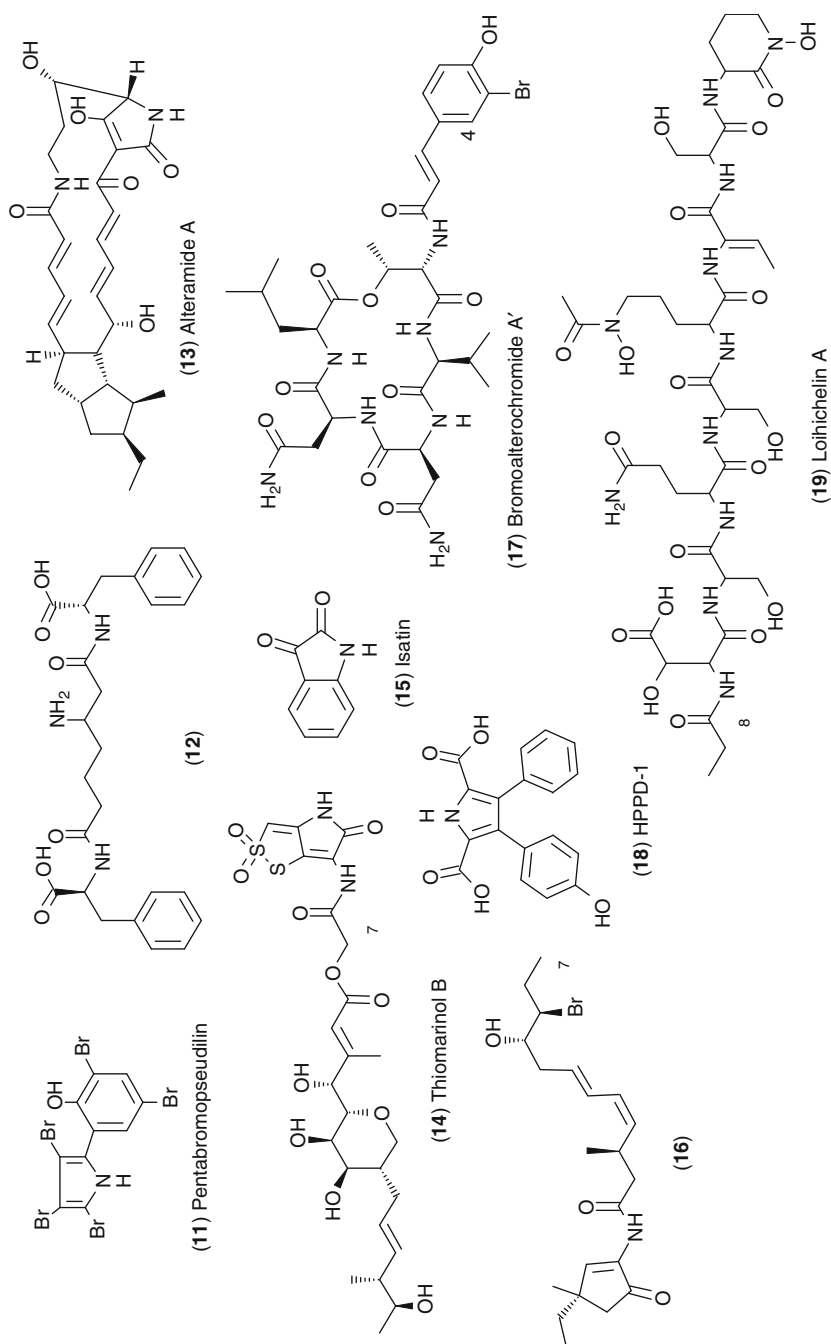


Fig. 3.3 Secondary metabolites from marine γ -Proteobacteria

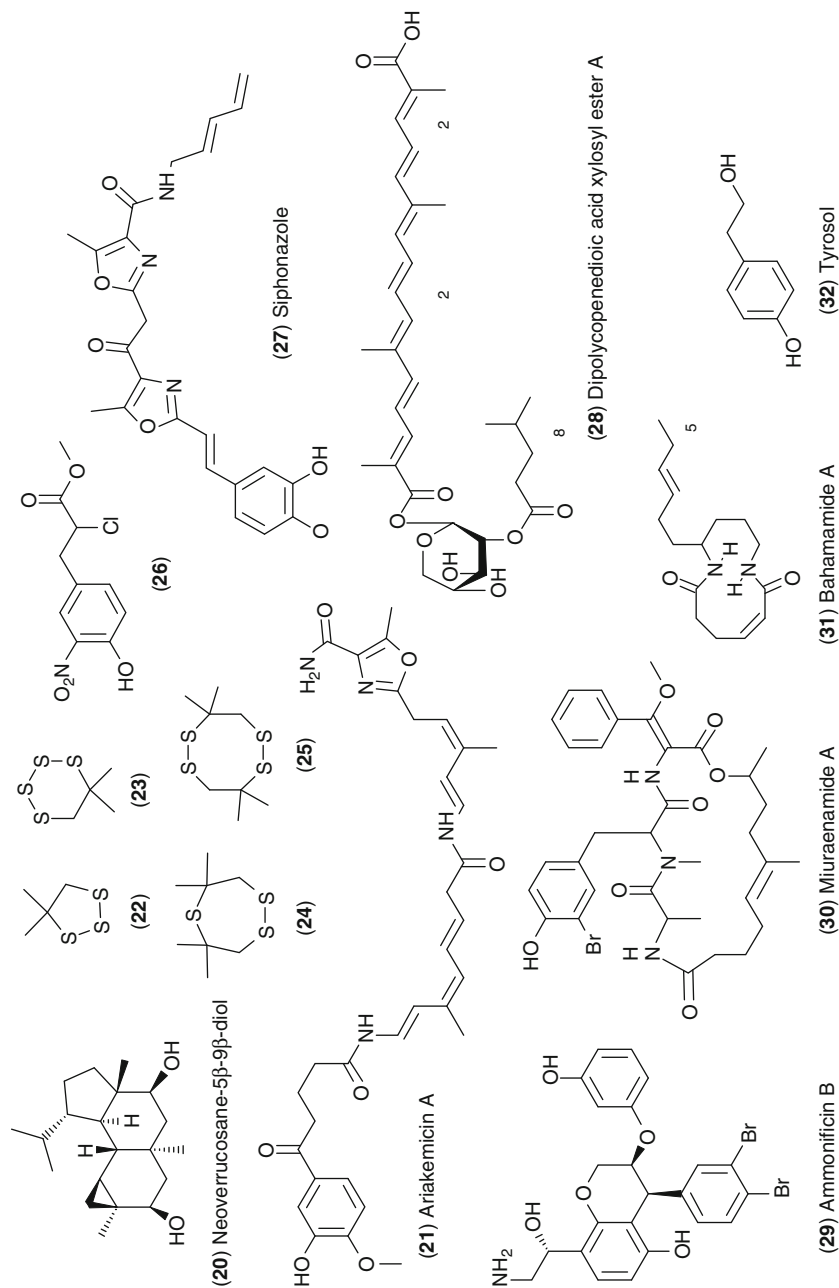


Fig. 3.4 Secondary metabolites from remaining marine Gram-negative bacteria

spectrometry to analyze the volatile components of these strains, and the result was the identification of seven unique thiacycloalkanes, four of which are presented here. Additional metabolites from this family include 25 aromatic nitro derivatives isolated in small yields from the psychrotolerant (ability to survive in cold temperatures) bacterium *Salegentibacter* sp., one of which is presented here (26) [45]. These were isolated as a result of efforts to explore secondary metabolite production by marine microorganisms in Arctic and Antarctic habitats.

3.2.3 Chloroflexi

The phylum Chloroflexi is highly diverse and can be divided into five major subdivisions. It is predominantly represented by Gram-negative, filamentous strains with unusual cell envelopes containing either no or little peptidoglycan in their cell walls. It is also the only phylum that consists entirely of bacteria that possess gliding motility. In an effort to expand upon what little is known about the capacity of strains from this phylum to produce secondary metabolites, siphonazole (27), a new class of natural products containing both oxazole and aromatic moieties, was isolated from a *Herpetosiphon* sp. [46].

3.2.4 Verrucomicrobia

The phylum Verrucomicrobia, which was established in 2001, is composed of strains that exhibit coccoid or rod-shaped morphologies. They have been observed in environments ranging from the cold sediment of the Arctic Ocean to the tissues of the giant tubeworm *Riftia pachyptila*, an organism found near deep-sea hydrothermal vents. A novel glycosylated polyene named dipolycopenedioic acid xylosyl ester A (28) was isolated from the strain *Rubritalea squalenifaciens* within the family Verrucomicrobiaceae [47]. This strain was isolated from the marine sponge *Halichondra okadai*. This molecule was isolated as part of a search for rare carotenoid-like molecules from pigmented marine bacteria.

3.2.5 Aquificae

Within the phylum Aquificae is the order *Aquificales*, members of which are chemolithoautotrophic thermophiles. The bacterium *Thermovibrio ammonificans*, within the family Desulfurobacteriaceae, was isolated from a deep-sea hydrothermal vent on the East Pacific Rise. *T. ammonificans* is a thermophilic, anaerobic strain that produced the dibrominated hydroxyethylamine chroman derivative ammonificin B (29) [48]. To date, this is the only known secondary metabolite isolated from this group of bacterial extremophiles.

3.2.6 Undescribed Gram-Negative Marine Bacteria

Taxonomic information has not always been provided from bacterial strains from which natural products have been reported, although there is a movement underway to at least require the deposition of a partial 16 S rRNA gene sequence in association with the report of a bacterial natural product. The following three examples are of metabolites isolated from undescribed Gram-negative marine bacteria. From a slightly halophilic myxobacterial strain (SMH-27-4) isolated from a shallow water sediment collected off the Miura Peninsula, Japan, the antibiotic depsipeptide miuraenamamide A (**30**) was isolated [49]. This was part of ongoing attempts to explore the secondary metabolite potential of slow-growing marine-derived strains. Compound **30** exhibited selective inhibition of the phytopathogenic fungus *Phytophthora* sp. and most likely targeted the electron transfer system of the mitochondrial respiratory chain. Bahamamide A (**31**), a 12-membered ring bis-amide that is not commonly observed in nature, was isolated from strain CNE-852 [50]. This strain was isolated from a sediment sample collected in the Bahamas. In an unusual example of symbiosis, embryo surfaces of the American lobster (*Homarus americanus*) were colonized almost entirely by a rod-shaped Gram-negative epibiotic bacterial strain, SGT-76. This strain produced the simple anti-fungal molecule tyrosol (**32**), which inhibited the growth of the common crustacean pathogenic fungus *Lagenidium callinectes*, thus suggesting a potential ecological function for the natural product and its producing bacterium [51] (Fig. 3.4).

3.3 Secondary Metabolites from Gram-Positive Marine Bacteria

Marine Gram-positive bacteria have been poorly studied by marine microbiologists relative to their Gram-negative counterparts. This may in part be due to the general observation that they are numerically less abundant in most marine habitats. Like terrestrial Gram-positive bacteria, however, marine strains have proven to be a rich source of secondary metabolites. In fact, the majority of natural products that have been characterized from marine bacteria are from Gram-positive strains. Representative compounds and producing organisms are described below.

3.3.1 Firmicutes

The name Firmicutes is derived from the Latin words “firmus” and “cutis,” which mean “strong” and “skin,” respectively. These bacteria are generally unicellular and contain a low G + C content. Within the phylum Firmicutes is the family Bacillaceae, which is typically comprised of rod-shaped cells capable of producing endospores. This family produces the majority of the secondary metabolites reported from the phylum, predominantly because of the chemical capacity of the

genus *Bacillus*. *Bacillus* is one of just under 40 genera in the family Bacillaceae and includes pathogenic strains such as *B. anthracis*, the causative agent of anthrax. Terrestrial bacilli are well-known producers of antibiotics as evidenced by bacitracin, polymyxin, tyrocidin, and gramicidin. As might be expected, marine-derived *Bacillus* strains are also proving to be a rich source of novel secondary metabolites.

From an undescribed deep-sea sediment bacterium (later isolated from a marine strain of *Bacillus amyloliquefaciens*), a novel 24-membered lactone (macrolactin A, **33**) representing a new class of macrolides was isolated [52, 53]. Macrolactin A exhibited considerable antibacterial activity and also antiviral activity against *Herpes simplex*. To date, there have been at least 18 macrolactins isolated, and nearly all have been produced by marine *Bacillus* strains (*B. marinus*, *B. subtilis*, *B. polyfermenticus*, *B. amyloliquefaciens*, and *Bacillus* spp.) [54].

A *Bacillus cereus* strain isolated from the Japanese sponge *Halichondria japonica* was found to produce a cyclic peptide (YM-266183, **34**) composed of a pyridine ring, six thiazole rings, and a number of unusual amino acids [55]. This peptide displayed antibacterial activity selective against a number of Gram-positive drug-resistant strains. Another *B. cereus* strain, isolated from the sea snail *Littorina* sp., was found to produce the potently cytotoxic cyclic peptide homocereulide (**35**) [56], while a strain of *B. silvestris* isolated from a crab collected off Chile was found to produce the antibacterial cyclic peptide bacillistatin 1 (**36**) [57]. Cyclic peptides were also isolated from two undescribed *Bacillus* strains, one sediment-derived strain produced the cyclic heptapeptide halobacillin (**37**), and one collected in Papua New Guinea produced the antibiotic cyclic decapeptide loloatin A (**38**) [58].

Another undescribed *Bacillus* species, isolated from the tissues of a tube worm collected in waters off Papua New Guinea, produced the unique nonribosomal peptide bogorol A (**39**) [59]. This linear, cationic peptide is thought to kill bacteria quickly by physically disrupting the cell membrane, and this structural class was proclaimed as a new template for cationic peptide antibiotics. Using the bogorol family of antibiotics, methods for determining the amino acid sequence of cationic peptides was subsequently described [60].

In a feeding study, an undescribed *Bacillus* sp. produced the antibiotic selenohomocysteine (**40**) when grown in a medium containing seleno-DL-methionine [61]. Compound **40** was antibacterial against the Gram-positive bacterial strain *Micrococcus luteus*. In another study, *B. subtilis* was isolated from the intestines of a sardine (*S. melanosticta*) collected off Japan and shown to produce the isocoumarin metabolite bacilosarcin A (**41**) [62]. Although no antibiotic activity was observed, it did contain an unprecedented bicyclic ring system combined with an otherwise common terrestrial metabolite.

In general, marine bacilli have been implicated in the production of cyclic peptides or polyketide-derived macrolides that possess antibacterial activity. The occurrence of macrolactins is, to this date, highly conserved among the genus *Bacillus*.

Of the non-*Bacillus* strains of the family Bacillaceae, a strain of *Halobacillus halophilus* produced the novel C₃₀ carotenoid (**42**) in a study aimed at isolating

carotenoids from pigmented bacteria [63]. *Halobacillus salinus* was shown to produce secondary metabolites that inhibit quorum-sensing-controlled phenotypes in Gram-negative bacteria [64]. This strain was isolated from a sea grass sample collected off the coast of Rhode Island. In cocultivation experiments, the bacterium was found to excrete a metabolite that inhibited bioluminescence in *Vibrio harveyi*. Subsequently, the phenethylamide derivative *N*-(2'-phenylethyl)-isobutyramide (**43**) was isolated and hypothesized to competitively inhibit typical Gram-negative bacterial signaling molecules (*N*-acyl homoserine lactones) and thereby act as bacterial quorum-sensing agonists.

An additional family within the phylum Firmicutes is the Thermoactinomycetaceae. All members of this taxon contain *meso*-diaminopimelic acid (*meso*-A_{2pm}) in their cell wall and are generally classified as aerobic, chemoorganotrophic microorganisms. From an undescribed species of the genus *Thermoactinomyces*, the potent antitumor thiopeptide mechercharmycin A (**44**) was discovered [65]. The producing strain was isolated from sea mud collected from Mercherchar in the Republic of Palau. In later studies, this molecule along with its analogs were shown to induce apoptosis in certain cancer cells [66] (Fig. 3.5a, b).

3.3.2 Actinobacteria (Actinomycetes)

In 1875, the first actinomycete genus *Streptothrix* was described, although because of its filamentous morphology, it was originally reported to be a fungus. To differentiate actinomycetes from fungi, the order Actinomycetales was proposed in 1917. Actinomycetes are high G + C content Gram-positive bacteria and are physiologically and morphologically quite diverse. A majority of these bacteria produce branching filaments and form mycelia. There are approximately 50 families containing 195 validated genera (as of 2007) within the phylum Actinobacteria, although only a few families account for more than half of microbial antibiotics discovered to this date, most of which are produced by the genus *Streptomyces*.

3.3.2.1 Streptomycetaceae

Within the family Streptomycetaceae, members of the genus *Streptomyces* are the source of the majority of secondary metabolites isolated from marine-derived bacteria. Although the genus *Streptomyces* is common in terrestrial soils, recent studies have revealed that phylogenetically distinct marine groups can be resolved within this highly diverse genus. The following section presents a compilation of unique structures that may be either of rare occurrence or completely unprecedented from terrestrial bacteria. Descriptions of their chemical and biological properties will be brief, as the focus is intended to be on the diversity of the structures isolated. Additional metabolites discovered from marine-derived *Streptomyces* sp. can be found in Table 3.1 and Figs. 3.6 and 3.7 [67–85].

An undescribed *Streptomyces* species (Merv8102) isolated from a sediment sample collected in the Mediterranean Sea along the Egyptian coastline produced

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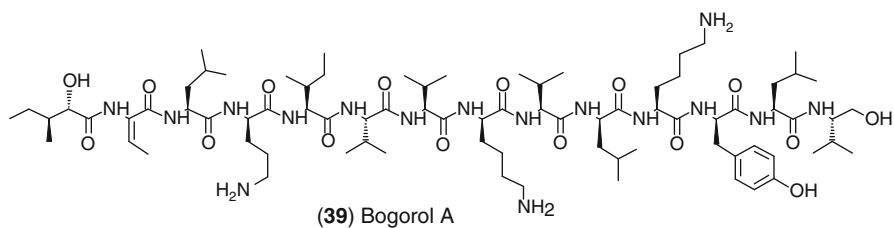
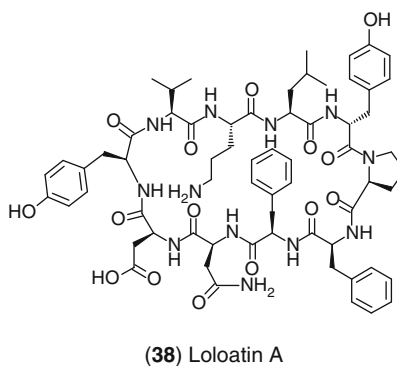
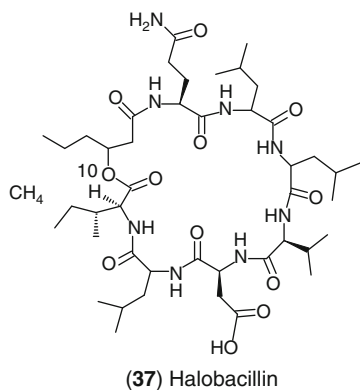
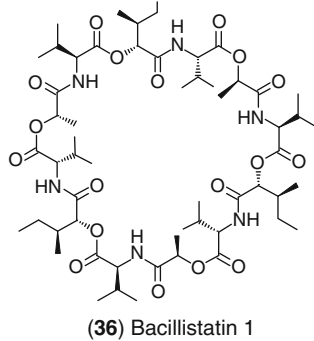
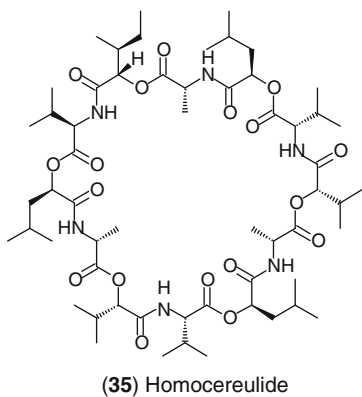
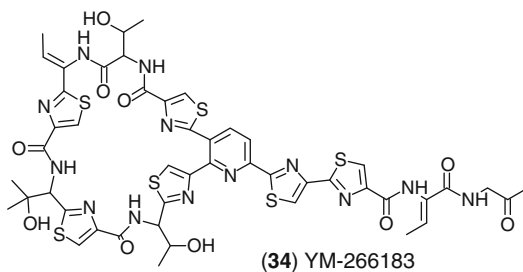
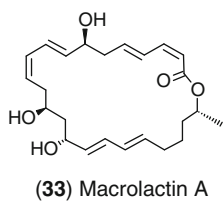


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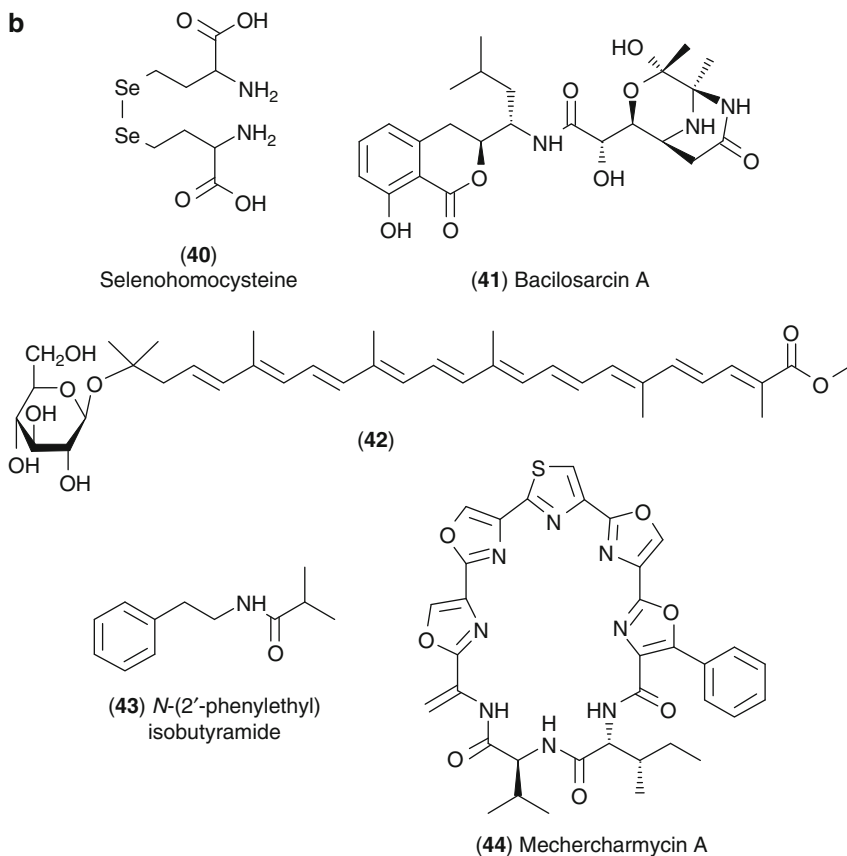


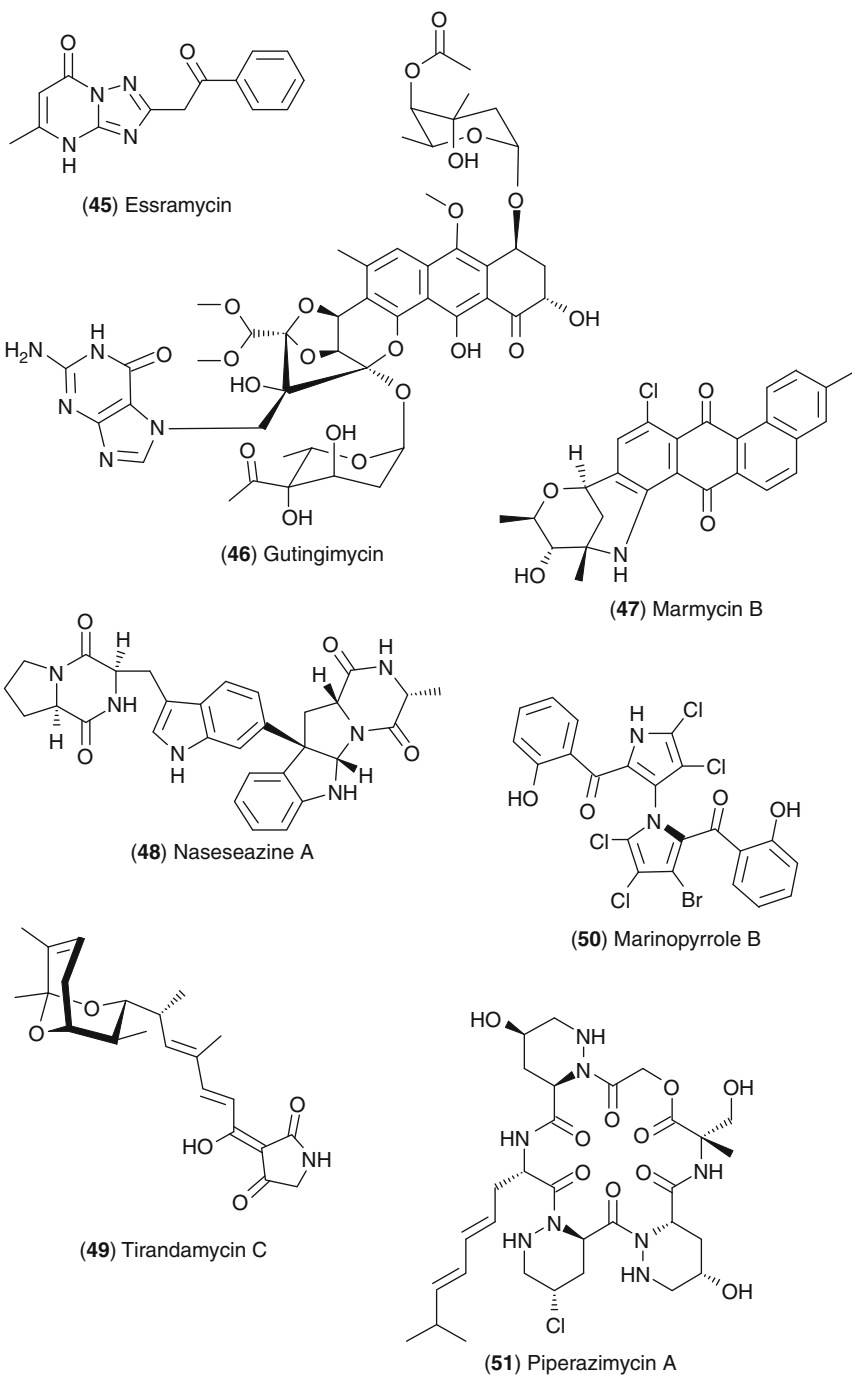
Fig. 3.5 Secondary metabolites from marine Bacillaceae

the first reported naturally occurring triazolopyrimidine antibiotic (essramycin, **45**) [86]. Gutingimycin (**46**), a complex guanine/trioxacarcin A conjugate, was also isolated from an undescribed *Streptomyces* species [87]. The compound was cytotoxic and showed antibacterial activity against a variety of Gram-positive and Gram-negative strains. The biological activity of this complex metabolite was hypothesized to be the result of nucleophilic attack on bacterial DNA resulting in strand cleavage thus offering a potential explanation for its potent cytotoxicity.

Another new structure was obtained from a *Streptomyces* strain cultured from a sediment sample collected in the Sea of Cortez, Baja California Sur, Mexico. Culture of this organism produced the angucycline-like cytotoxic quinone marmycin B (**47**) [88]. This was the first report of an angucycline with both C- and N-glycoside linkages, which resulted in a novel hexacyclic skeleton. From subunits of a common metabolite, new members of a novel chemical scaffold were

Table 3.1 Additional secondary metabolites produced by marine *Streptomyces* spp.

Compound	Source	Properties	Reference
(56) Aburatubolactam A	<i>Streptomyces</i> sp.	Polycyclic macrolactam exhibiting diverse bioactivity	Bae et al. [67]
(57) Altemicidin	<i>Streptomyces</i> sp.	Monoterpene alkaloid with rare azaindene skeleton	Takahashi et al. [68]
(58) Aureoverticillactam	<i>S. aureoverticillactus</i>	22-Membered cytotoxic macrocyclic lactam	Mitchell et al. [69]
(59) Bioxalomycin α 1	<i>Streptomyces</i> sp.	Complex aromatic, polycyclic alkaloid	Bernan et al. [70]
(60) Caboxamycin	<i>Streptomyces</i> sp.	A deep-sea benzoxazole antibiotic active against <i>B. Subtilis</i>	Hohmann et al. [71]
(61) Chinikomycin A	<i>Streptomyces</i> sp.	Chlorinated, aromatic manumycin derivatives; antitumor activity	Li et al. [72]
(62) Daryamide A	<i>Streptomyces</i> sp.	Cytotoxic and weak antifungal metabolite	Asolkar et al. [73]
(63) Glaciapyrrole A	<i>Streptomyces</i> sp.	Rare pyrrole-sesquiterpene metabolite	Macherla et al. [74]
(64) Halawanone A	<i>Streptomyces</i> sp.	Of the isochromane class of quinone antibiotics	Ford et al. [75]
(65) Halichomycin	<i>S. hygroscopicus</i>	16-Membered macrolactam isolated from fish; cytotoxic agent	Takahashi et al. [76]
(66) JBIR-34	<i>Streptomyces</i> sp.	Strain was selected on the basis of a screen for unique NRPS genes	Motohashi et al. [77]
(67) Lajollamycin	<i>S. nodosus</i>	Rare spiro- β -lactone- γ -lactam unit; antitumor and antibiotic activity	Manam et al. [78]
(68) Mansouramycin D	<i>Streptomyces</i> sp.	Compound class showed cytotoxicity toward a panel of tumor cells	Hawas et al. [79]
(69) Marineosin A	<i>Streptomyces</i> sp.	Cytotoxic; hypothesized to derive from novel prodigiosin pathway	Boonlarpradab et al. [80]
(70) Salinamide A	<i>Streptomyces</i> sp.	Complex bicyclic hexadepsipeptide; anti-inflammatory activity	Trischman et al. [81]
(71) Splenosin A	<i>Streptomyces</i> sp.	Inhibitor of pro-inflammatory cytokine production (antiasthma)	Strangman et al. [82]
(72) SS-228Y	<i>Chainia purpurogena</i> (e.g., <i>Streptomyces</i>)	Antibiotic; one of the earliest bioactive molecules isolated from a marine actinomycete	Okazaki et al. [83]
(73) Streptokordin	<i>Streptomyces</i> sp.	Cytotoxic metabolite of the methylpyridine class	Jeong et al. [84]
(74) Teleocidin A ₁	<i>Streptomyces</i> sp.	Isolated from marine-obligate <i>Streptomyces</i> , a sponge colonizer	Izumikawa et al. [85]

**Fig. 3.6** (continued)

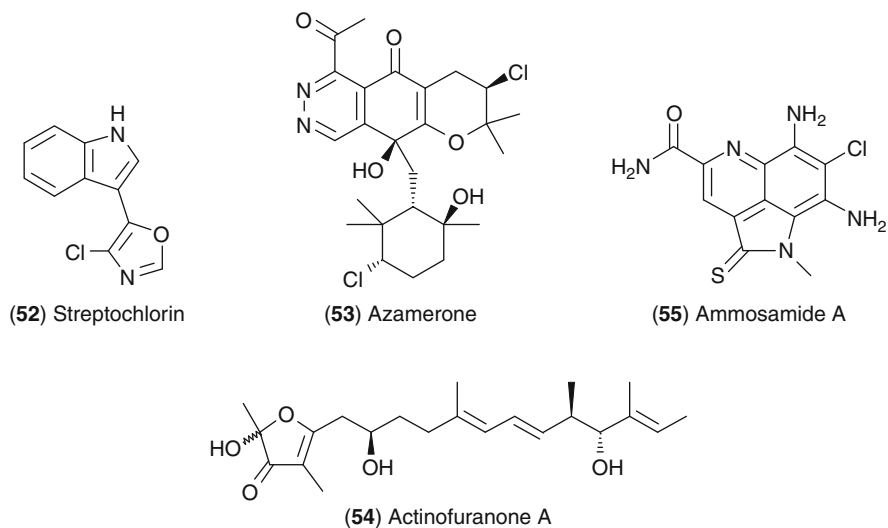
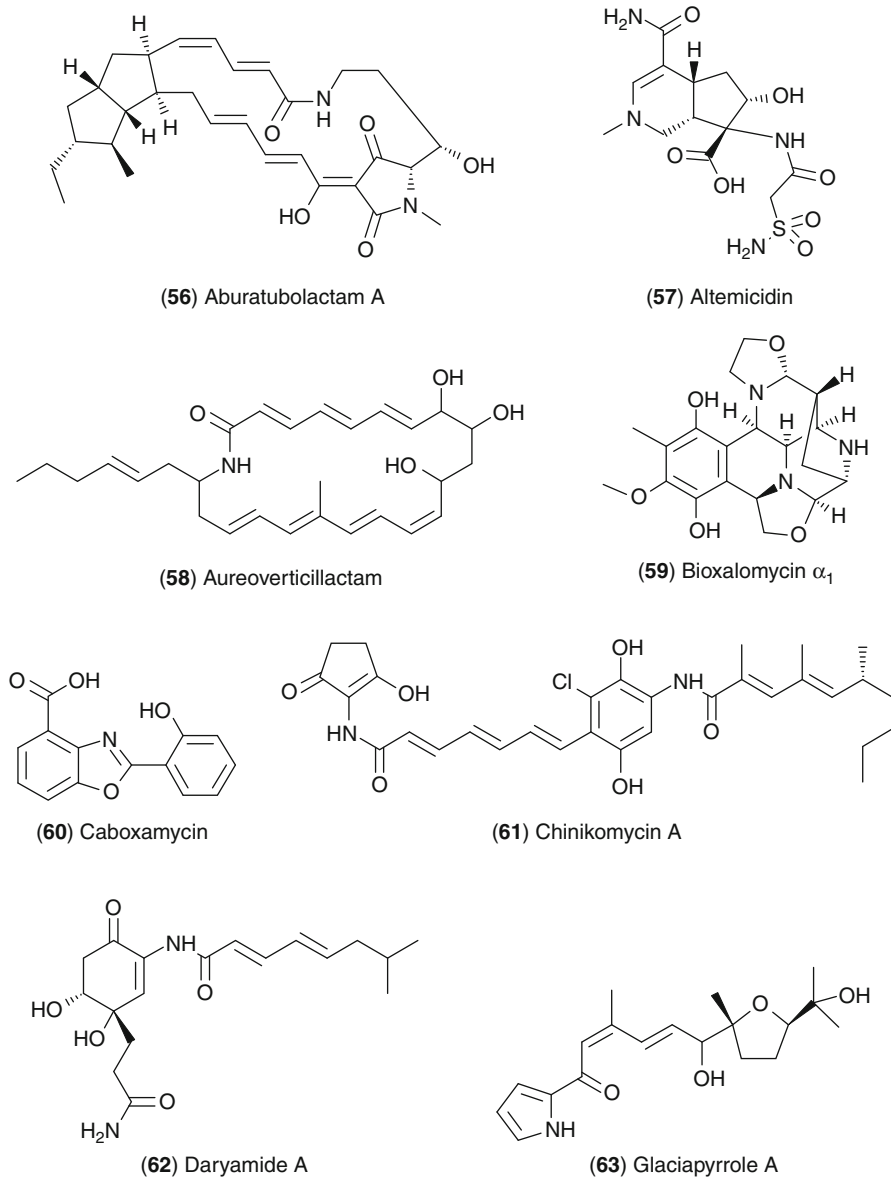


Fig. 3.6 Structures of secondary metabolites from marine *Streptomyces*

observed from a *Streptomyces* strain cultured from a Fijian marine sediment [89]. Nasesezine A (48) and two other classes of dimeric diketopiperazines (asperazines and pestalazines, produced by fungi; not shown here) were hypothesized to result from indole resonance from which nucleophilic attack yielded differing regioselective substitution patterns around the nucleophile's aromatic ring [89]. In a study that afforded the known antibiotic tirandamycin C (49), the authors employed a method commonly used to isolate unstable secondary metabolites [90]. Mesh bags of sterilized organic XAD resin were added directly to the microbial fermentation in order to capture metabolites as they were produced. This served to prevent compound degradation or enzymatic conversion within the broth and facilitate the extraction process. Tirandamycin C is a tetramic acid derivative with a 2,4-pyrrolidinedione and is predicted to be produced by hybrid polyketide-nonribosomal peptide biosynthetic machinery [91].

From a marine-derived *Streptomyces* strain that required seawater for growth, marinopyrrole B (50) was isolated [92]. This was the first report of a natural product bearing a *N*-, *C*-2-linked bispyrrole structure. In addition to cytotoxic activity, the marinopyrrole class of molecules displayed significant inhibition against MRSA and with further development may represent a novel pharmacophore for the treatment of this drug-resistant pathogen [93]. The marinopyrroles were also used to develop a streamlined approach toward cellular target elucidation of bioactive natural products [94]. Such an approach serves to increase the efficiency of drug discovery by elucidating the target of a potential drug candidate early in the discovery process; this is especially relevant for metabolites that interact with undesirable targets. In this study, an acyl dye transfer protocol enabled transfer of

**Fig. 3.7** (continued)

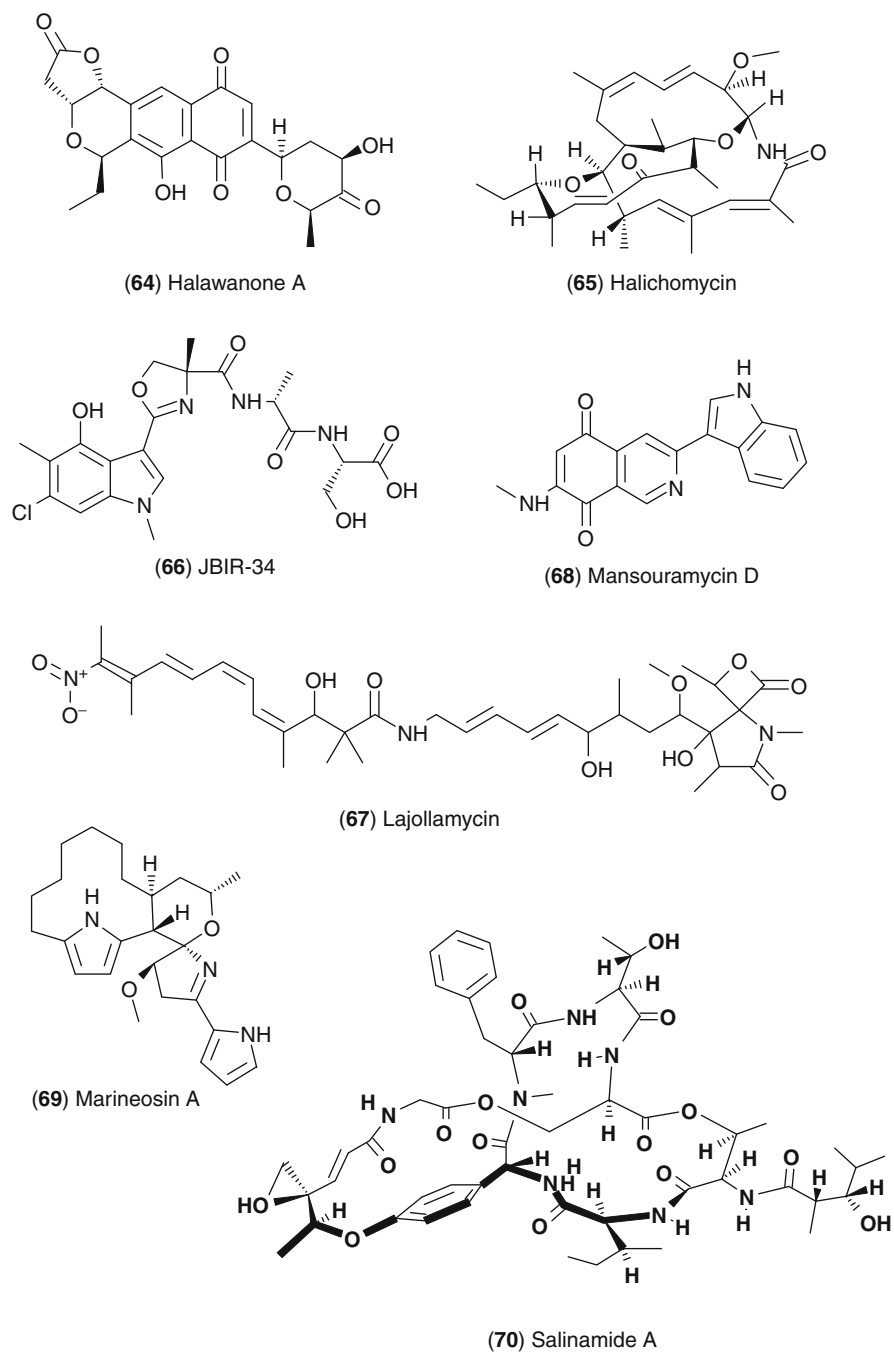


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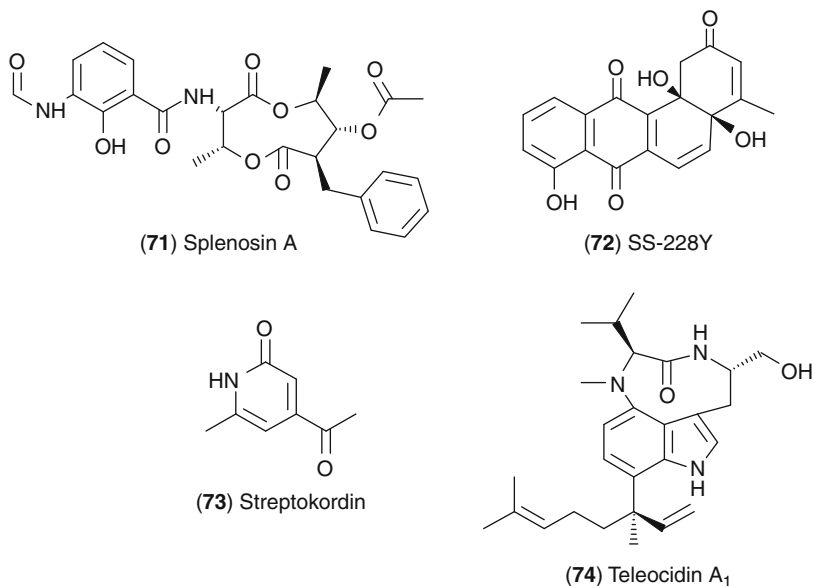


Fig. 3.7 Additional secondary metabolites from marine *Streptomyces*

an immunoaffinity fluorescent tag from the natural product to the protein target. After immunoprecipitation and mass spectral analyses, the protein target of the marinopyrrole class of natural products was determined to be actin.

A sediment-derived *Streptomyces* sp. collected in Guam produced the cyclic hexadepsipeptide piperazimycin A (**51**) [95]. The compound includes a number of rare amino acids. Screening of this molecule against the National Cancer Institute's (NCI) 60-cancer cell line panel revealed that it displayed broad, nanomolar-level cytotoxicity. Sediment from Ayajin Bay, East Sea, Korea, afforded an undescribed species of *Streptomyces*. This strain produced the small molecule streptochlorin (**52**), an indole-substituted chlorinated oxazole [96]. Streptochlorin was found to exhibit antiangiogenic properties through the inhibition of NFκB, a transcription factor implicated in the progression of certain cancers [97]. Azamerone (**53**) was isolated from a strain that is believed to belong to a new marine species within the genus *Streptomyces* [98]. Azamerone was found to have an unprecedented chloropyranophthalazinone core. This was the first report of a phthalazinone ring system in a natural product. Compound **53** is of mixed polyketide–terpene biosynthetic origin and belongs to the class of metabolites known as meroterpenoids. Thus far, the production of this class of compounds appears to be a trait that is a characteristic of a new group of marine-derived *Streptomyces*, which has tentatively been called MAR4. Also isolated from a related strain was actinofuranone A (**54**), a molecule of polyketide origin [99].

A final example of *Streptomyces* metabolites, the ammosamides, were produced by an undescribed *Streptomyces* species cultured from a deep-sea sediment (1,618 m)

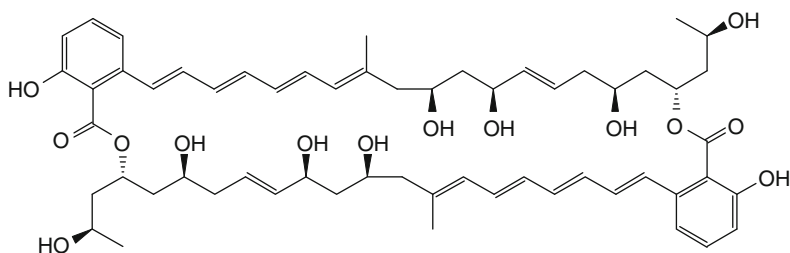
collected in the Bahamas [100]. The cytotoxic agent ammosamide A (**55**) resembled a few other microbial and sponge-derived metabolites, but it was the first natural product to contain a thio- γ -lactam moiety. Using fluorescent labeling techniques, it was determined that the ammosamides target the cytoskeletal protein myosin, an entity involved in cell cycle progression that is of particular interest in the treatment of cancer [101].

A number of new marine lineages have been observed closely related to the genus *Streptomyces* based on 16 S rRNA sequence analysis. Among these is a deeply rooted clade that was originally called MAR2 and subsequently given the informal genus name “*Marinispora*.” The first chemical study of a member of the genus “*Marinispora*” resulted in the isolation of the marinomycins, 44-membered ring macrolides with an unusual substitution pattern of polyol and polyene functionalities when compared to typical polyene macrolides such as amphotericin. Marinomycin A (**75**) showed selective cytotoxicity toward eight melanoma cell lines in the NCI 60 cell line panel and also displayed strong antibacterial activity toward a few drug-resistant bacterial pathogens [102]. Similarly, a study of a “*Marinispora*” strain collected from a sediment sample collected at a depth of 51 m off the coast of La Jolla, California, resulted in the isolation of several 34-membered ring macrolides called the marinisporolides [103]. Marinisporolide A (**76**) contains a bicyclic spiro-bis-tetrahydropyran ketal unit, the only examples of spiroketal-polyenol-polyol macrolides isolated from nature. Like the marinomycins, the marinisporolides are photoreactive and photoisomerize in sunlight to yield olefin isomers. From a sediment sample collected from Cocos Lagoon, Guam, three oxazolidinones were isolated (lipoxazolidinone A–C) from a member of the marine taxon “*Marinispora*” [104]. Lipoxazolidinone A (**77**) exhibited broad-spectrum antibiotic activity, and it was suggested that the oxazolidinone ring system was essential for their bioactivity. Also exhibiting broad-spectrum antibiotic activity were the lynamycins (lynamicin A, **78**), isolated from a “*Marinispora*” sp. cultured from a sediment sample collected from Mission Bay in San Diego, California [105]. These are novel, chlorinated *bis*-indole pyrroles that most importantly show activity against MRSA and vancomycin-resistant *Enterococcus faecium* (VREF) (Fig. 3.8).

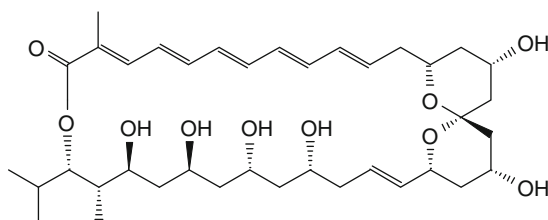
3.3.2.2 Micromonosporaceae

Described in 1938, the Micromonosporaceae is an actinomycete family comprised of more than 20 genera. Within this family are two genera, *Micromonospora* and *Salinispora*, which exemplify the capacity of marine bacteria to produce structurally intriguing secondary metabolites. The genus *Salinispora* is unique among the true marine actinomycete genera described to date in that strains fail to grow when seawater is replaced with deionized water in the culture medium. The genus is currently composed of three species: *S. arenicola*, *S. tropica*, and “*S. pacifica*” (proposed name).

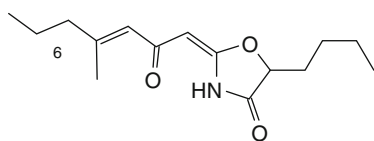
Salinosporamide A (**79**) is undoubtedly the most significant natural product to be isolated from a *Salinispora* species (*S. tropica*) [106]. The producing strain was isolated from a sediment sample collected in the Bahamas. The compound is



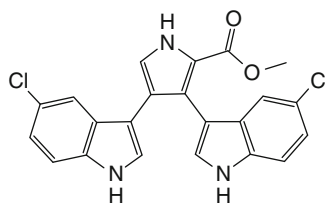
(75) Marinomycin A



(76) Marinisporolide A



(77) Lipoxazolidinone A



(78) Lynamycin A

Fig. 3.8 Secondary metabolites from “*Marinispora*”

structurally similar to the β -lactone omuralide. However, the conspicuous halogenation of the ethyl side chain provides an essential structural element that is required for the potent, irreversible binding to the 20 S proteasome, a validated target in cancer chemotherapy. This natural product is currently in Phase I clinical trials for the treatment of various cancers. Interestingly, it is the natural product itself, not any of the synthetic and semisynthetic analogs that were considered during preclinical development, that was taken into the clinic, further emphasizing “the beauty and power of a selection process offered only by nature [107].” In order to produce quantities sufficient for clinical development and commercialization, several steps of the bacterial fermentation process were optimized to increase production of **79** from a few mg/L (original laboratory conditions) to 450 mg/L [108–110]. This represented the first manufacture of a substance in clinical trials by saline fermentation and emphasized the advantages and flexibility of producing a drug candidate through microbial fermentation.

The discovery of salinosporamide A has also inspired molecular engineering of the pathway in an effort to produce new derivatives. One such example is the

engineered production of fluorosalinisporamide A (**80**) by *S. tropica* [111]. Though fluorinated natural products are rare, they account for 15% of pharmaceutical products on the market. To create the fluorinated version of the compound, a *S. tropica* mutant was generated in which the fluorination gene *flA*, taken from *Streptomyces cattleya*, was used to replace the *salL* chlorinase gene normally found in *S. tropica*. This mutant produced **80** in the presence of inorganic fluoride, thus emphasizing an avenue by which a host organism may be genetically engineered to produce novel analogs of a biomedically important secondary metabolite.

Other secondary metabolites from *S. tropica* include salinilactam (**81**) and the polycyclic macrolide sporelone A (**82**) [112, 113]. The biosynthetic pathway for salinilactam production was originally identified during the analysis of the *S. tropica* strain CNB-440 genome sequence. Bioinformatic analysis played a key role in assigning the final structure of this compound, thus illustrating the value of combining genomic analyses with natural product isolation and identification. Sporelone A is a remarkable polycyclic chlorinated macrolide that is composed of a highly oxidized carbon skeleton (23 out of its 24 carbons are oxygenated or sp² hybridized). The majority of this skeleton has never been reported in any chemical or biological study. The chlorinated cyclopenta[*a*]indene ring was shown to emerge from an unstable nine-membered enediyne precursor via the nucleophilic addition of chloride, a process that has been verified in laboratory experiments [114]. Sequence analysis of the *S. tropica* genome uncovered two biosynthetic loci that encoded for enediyne polyketide synthases (PKSEs), one of which strongly correlated with the formation of the proposed sporelone precursor. This biosynthetic study highlights the breadth of information available when genomic analyses are coupled with traditional drug discovery efforts.

Three cyclic heptapeptides (cyclomarins A-C) were found to be produced by *S. arenicola* (and earlier from a *Streptomyces* species) [115, 116]. Cyclomarin A (**83**), the major metabolite, was composed of four unusual amino acids and displayed in vitro and in vivo anti-inflammatory activity. An *S. arenicola* strain from a Fijian sediment collection was shown to produce the cyclohexadepsipeptide arenamide A (**84**) [117]. This metabolite displayed chemopreventive properties, inhibiting NFκB and nitric oxide production. From another *S. arenicola* strain, a 26-membered macrolide (arenicolide A, **85**) in addition to the unusual polyketide saliniketol (**86**) was isolated [118, 119]. Saliniketol contains a novel bicyclic ring system and was shown to inhibit ornithine decarboxylase induction, an important target for cancer chemoprevention. Both metabolites **85** and **86** were isolated from an *S. arenicola* strain cultured from sediment samples collected from the coastal waters off Guam. Arenimycin (**87**) was isolated from an *S. arenicola* strain found in association with the ascidian *Ecteinascidia turbinata*, collected from a mangrove channel at Sweetings Cay, Grand Bahama Island [120]. This program focused on the screening of actinomycetes against a rifampin-resistant strain of the pathogen MRSA. Arenimycin exhibited strong inhibition of this pathogen, although potent cytotoxicity prevented further exploration of its antibiotic activities.

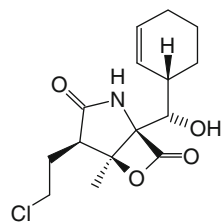
From a strain of "*S. pacifica*" isolated from a sediment sample collected in the waters off Palau, the simple polyketide salinipyronone A (**88**) was isolated [121].

This metabolite is thought to be derived from a mixed precursor polyketide biosynthesis involving acetate, propionate, and butyrate building blocks. Also produced by a "*S. pacifica*" strain isolated from a sediment sample collected at a depth of 500 m off Palau is cyanosporaside A (**89**) [122]. The cyano-containing halogenated aglycone was found to possess a novel 3-keto-pyranohexose sugar. Like sporolide A (**82**), cyanosporaside A is thought to be the cyclization product of an enediyne precursor (Fig. 3.9).

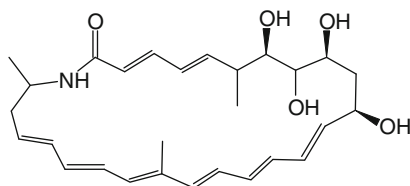
A *Micromonospora* strain cultured from the ascidian *Didemnum proliferum* produced diazepinomicin (**90**), whose unique dibenzodiazepine skeleton was the first to be reported in the peer-reviewed literature [123]. This metabolite was discovered as a result of a program designed to screen microbes for cytotoxic agents that can be linked to monoclonal antibodies targeting tumor-specific antigens. A halophilic strain of the same genus, *Micromonospora lomaivitiensis*, was isolated from the ascidian *Polysyncraton lithostrotum*. This bacterium produced two dimeric diazobenzofluorene glycosides (lomaiviticins A (**91**) and B) that exhibited potent cytotoxicity [124]. The structural architecture of the lomaiviticins is somewhat similar to the kinamycin antibiotics, although they are unique in the sense of their greater complexity. The antitumor agent thiocoraline (**92**) was isolated from a culture of *Micromonospora marina*, isolated from a soft coral from the Indian Ocean [125]. Thiocoraline A is a symmetric, octadepsipeptide that resembles the quinoxaline antibiotics echinomycin and triostin A, although thiocoraline contains a thioester in its backbone and two glycine residues in place of alanine residues. The latter trait has been proposed to afford improved DNA intercalation [126, 127]. A *Micromonospora* sp., isolated from an Indian Ocean coral, was found to produce the spiroketal-containing macrolide IB-96212 (**93**), which displayed cytotoxic properties [128].

The genus *Verrucosispora* within the family Micromonosporaceae has also proven to be chemically prolific. *Verrucosispora maris*, isolated from a sediment sample from the Sea of Japan (depth 289 m), produced the abyssomicins (abyssomicin C, **94**) and proximicins, the latter of which are characterized by 4-amino-furan-2-carboxylic acid cores [129, 130]. Abyssomicin C was the first natural product found to inhibit *p*-aminobenzoic acid biosynthesis (*p*ABA), a new target for antibiotic drug discovery. Its bioactivity, unique structure, and novel mechanism of action serve as an example of the potential for marine taxa to produce interesting, biomedically significant molecules. This discovery was the result of a program designed to screen microorganisms for inhibitors of the *p*ABA pathway. Proximicin A (**95**) was found to contain a previously unknown γ -amino acid and displayed cytotoxicity toward a few tumor cell lines.

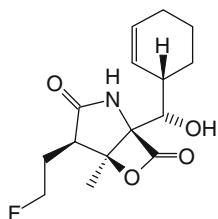
A strain of *Verrucosispora gifthornensis* cultured from an unidentified ascidian collected off Hiroshima, Japan, was found to produce the terpenoid gifthornelone A (**96**) [131]. This isopimaradiene derivative was the result of a program specifically designed to discover novel terpenoids from actinomycetes; its structural similarity to known steroidal androgen antagonists such as dihydrotestosterone led to the discovery of antagonistic activity against an androgen receptor.



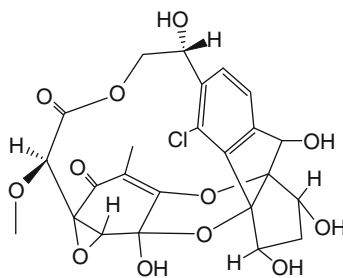
(79) Salinosporamide A



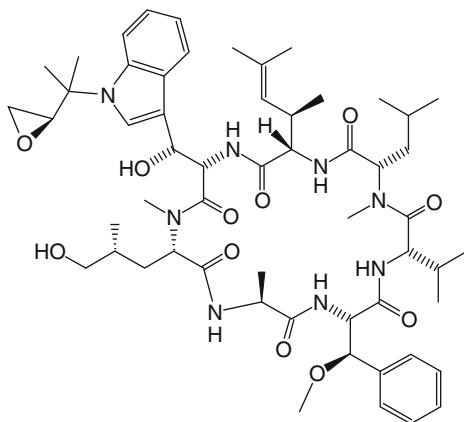
(81) Salinilactam



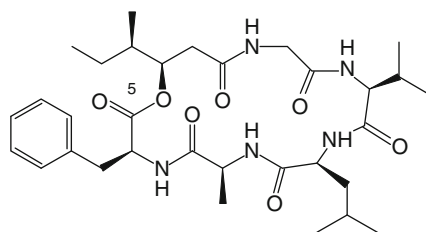
(80) Fluorosalinoporamide A



(82) Sporolide A



(83) Cyclomarins A



(84) Arenamide A

Fig. 3.9 (continued)

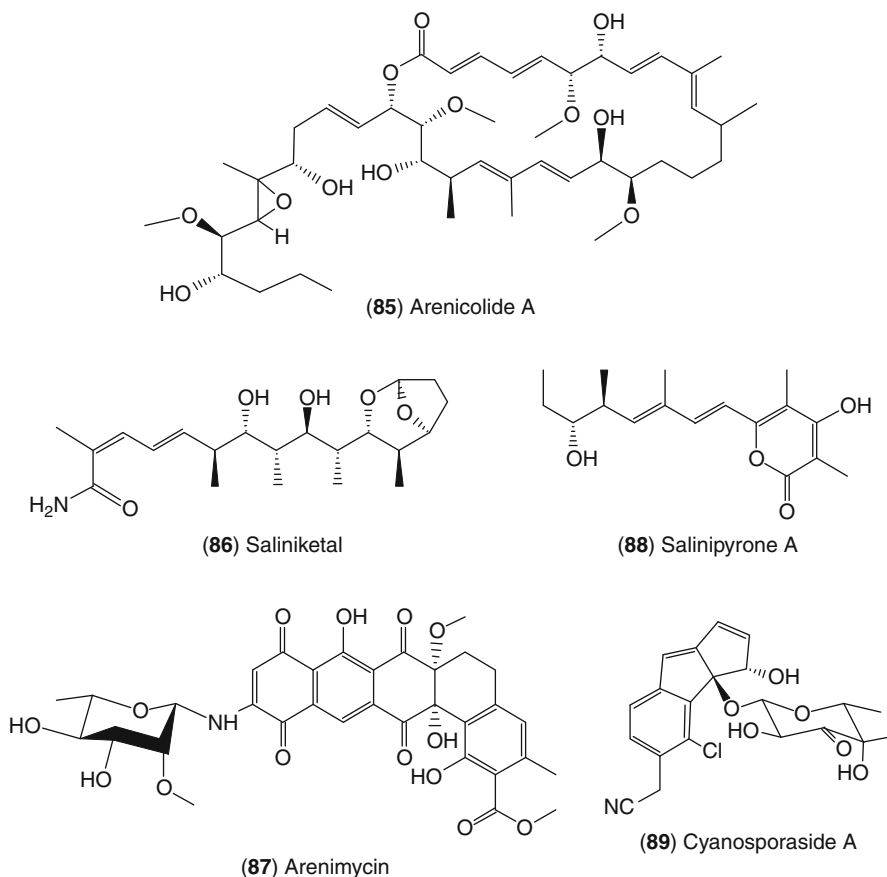


Fig. 3.9 Secondary metabolites from *Salinispora*

3.3.2.3 Additional Families of Actinobacteria

The family Nocardiopepsaceae was created in 1996 in order to accommodate a number of phylogenetically related strains of *Nocardiopepsis*. Two peptides, MKN-349A (97) and lucentamycin A (98), were reported from marine-derived strains of *Nocardiopepsis* [132, 133]. Lucentamycin A is a cytotoxic substance isolated from *Nocardiopepsis lucentensis*, cultured from a strain isolated from a shallow saline pond in the Bahamas. It was the first report of a ethylideneproline amino acid unit in nature. Kahakamide A (99) is a rare *N*-glycosyl indole antibiotic isolated from *N. dassonvillei* cultured from a marine sediment collected from Kauai, Hawaii [134]. It displayed antibacterial activity against *B. subtilis*.

The family Pseudonocardiopepsaceae is composed of fewer than 20 genera. Within this family is the genus *Saccharopolyspora*. A *Saccharopolyspora* strain was cultured from a sample of the sponge *Haliclona* sp. and found to produce

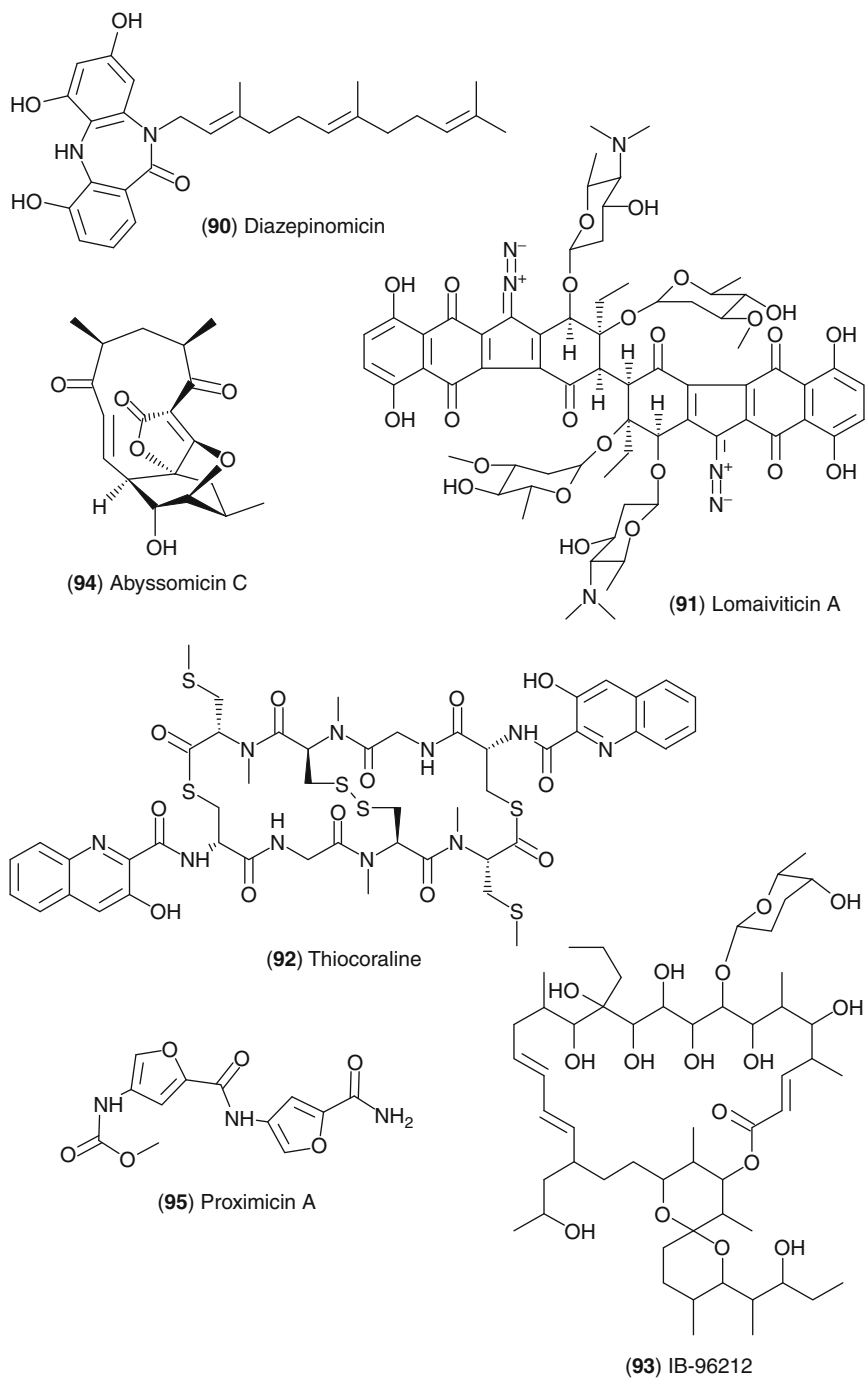


Fig. 3.10 (continued)

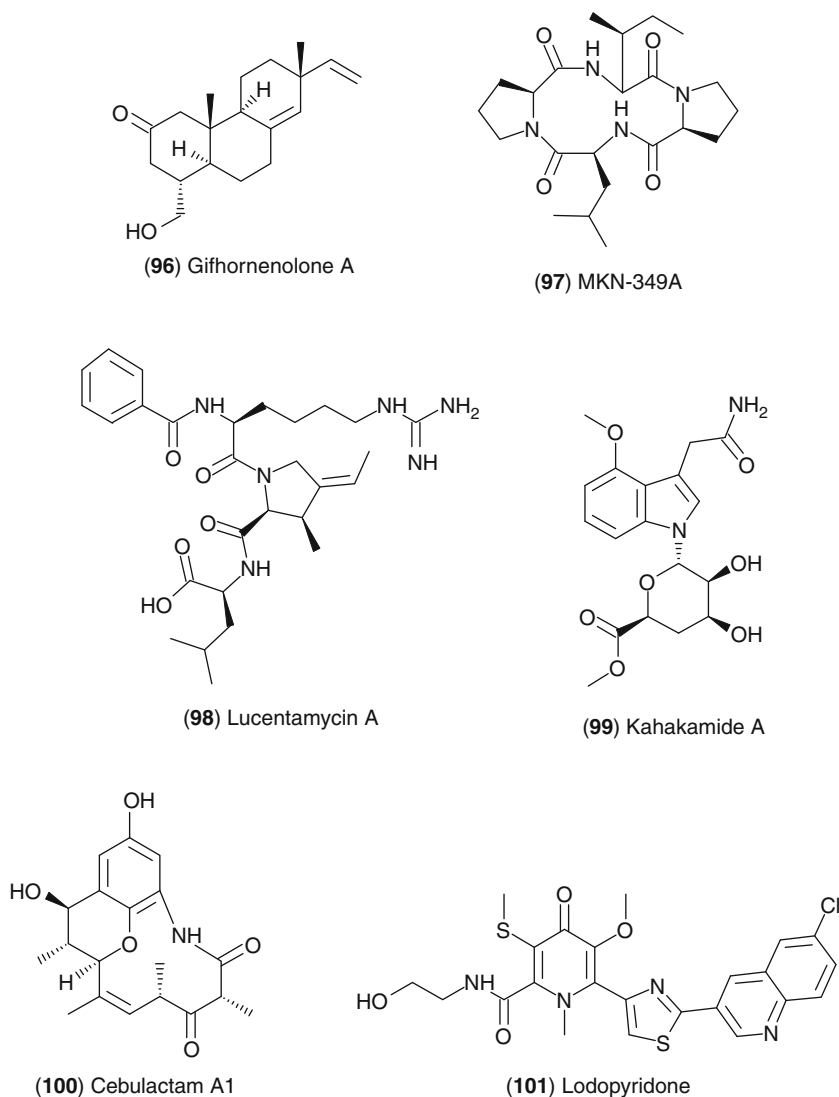


Fig. 3.10 Secondary metabolites from marine *Micromonosporaceae*

cebulactam A1 (**100**) [135]. This study included the first report of an obligate marine *Saccharopolyspora*. Another actinomycete that was reported to have an obligate requirement of seawater for growth was the *Saccharomonospora* strain CNQ-490. This strain was isolated at a depth of 45 m from a sediment sample collected in the La Jolla Canyon off San Diego, CA. In culture, this strain produced lodopyridone (**101**), a quinoline alkaloid of an unprecedented carbon skeleton

whose combination of heterocyclic units (oxygenated 4-pyridone, thiazole, and chlorinated quinoline) is unlike any secondary metabolite observed to this date [136] (Fig. 3.10).

3.4 Conclusions

Bacteria produce small molecules that are not essential for survival but that may enhance fitness or provide survival advantage. These secondary metabolites not only serve as both initiators and regulators of diverse ecological processes, but they can also be used to treat or probe the causes of human disease. Modern medicine has long relied on microbial natural products to treat infectious disease, cancer, and other recalcitrant ailments. However, the arsenal of small molecule drug candidates has shrunk in part due to a paradigm shift by the pharmaceutical industry away from microbial natural products in favor of other drug discovery platforms. There is now however an ongoing resurgence of interest in natural product drug discovery. This interest is fueled by the availability of new and more precise techniques in analytical chemistry and the recognition that nature remains the best resource for the types of new small molecule organic scaffolds around which pharmaceutical agents have historically been developed. Included among current natural product discovery efforts are studies of new populations of bacteria, including those that reside in the marine environment. Marine-derived bacteria include new taxonomy groups as well as species that also occur on land. Collectively, these bacteria are yielding a wealth of new structures including agents that are advancing through various stages of clinical development, solidifying the importance of exploring new habitats and resources in the search for novel bacterial secondary metabolites.

3.5 Study Questions

1. Although often similar in appearance, how are bacteria different from fungi?
2. What family of bacteria is recognized as the most prolific producers of bioactive compounds? What is the most important genus?
3. What is the fundamental difference between Gram-positive and Gram-negative bacteria?
4. What was the first truly marine genus of bacteria to be described?
5. When and by whom was penicillin discovered?
6. The ocean comprises what percentage of the Earth's surface?
7. Which bacterial group, Gram-positive or Gram-negative, produces the most antibiotics?

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Abstract

Marine sponges continue to attract wide attention from marine natural product chemists and pharmacologists alike due to their remarkable diversity of bioactive compounds. Since the early days of marine natural products research in

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S.S. Ebada (✉)

Institute of Pharmaceutical Biology and Biotechnology, Heinrich-Heine University,
Universitätsstrasse 1, Duesseldorf, Germany

and

Department of Pharmacognosy and Phytochemistry, Faculty of Pharmacy, Ain-Shams University,
Organization of African Unity, Street 1, Cairo, Egypt

e-mail: sherif.Elsayed@uni-duesseldorf.de, sherif_elsayed@pharm.asu.edu.eg

P. Proksch

Institute of Pharmaceutical Biology and Biotechnology, Heinrich-Heine University,
Universitätsstrasse 1, Duesseldorf, Germany

e-mail: proksch@uni-duesseldorf.de

the 1960s, sponges have notoriously yielded the largest number of new metabolites reported per year compared to any other plant or animal phylum known from the marine environment. This not only reflects the remarkable productivity of sponges with regard to biosynthesis and accumulation of structurally diverse compounds but also highlights the continued interest of marine natural product researchers in this fascinating group of marine invertebrates.

Among the numerous classes of natural products reported from marine sponges over the years, alkaloids, peptides, and terpenoids have attracted particularly wide attention due to their unprecedented structural features as well as their pronounced pharmacological activities which make several of these metabolites interesting candidates for drug discovery. This chapter consequently highlights several important groups of sponge-derived alkaloids, peptides, and terpenoids and describes their biological and/or pharmacological properties.

4.1 Introduction

The true chemical and biological diversity of the marine environment is far from being understood today, and the oceans continue to be unique resources for bioprospecting providing a diverse array of natural products that are encountered in each group of marine organisms from prokaryotic bacteria and cyanobacteria to the top predators of the food chain such as sharks [1]. Nevertheless, the largest numbers of natural products reported since the early days of marine natural product research in the 1960s until today originate from marine invertebrates, with sponges being clearly at the top [2]. More than 5,300 different natural products are known from sponges, and more than 200 additional new metabolites from sponges are reported each year [3]. It is widely accepted today that the rich chemical diversity of sponges provides an effective chemical defense to these sedentary and soft-bodied organisms against environmental threats such as predation, overgrowth by fouling organisms, or microbial infections [4].

Numerous sponge-derived natural products such as the halichondrins, discodermolide, hemiasterlins, and arenastatin A exhibit also pronounced activities in pharmacologically driven screening programs and have been identified as lead compounds for the treatment of tumors, inflammation, and other diseases [5]. On the other hand, evidence is mounting that not all sponge-derived natural products are necessarily biosynthesized by sponges but may rather trace back to bacteria and other microorganisms that either reside within sponges or are inhaled by filter feeding [6, 7]. Examples of metabolites originally isolated from sponges that are in fact biosynthetic products of microorganisms include okadaic acid, a phosphatase inhibitor obtained from *Halichondria* sponges [8] that was shown later to be produced by dinoflagellates of the genus *Prorocentrum* [9]. Other examples include manzamine A and its 8-hydroxy derivative, antimalarial compounds first obtained from marine sponge of the genus *Haliclona*, that were isolated from a *Micromonospora* strain from the sponge *Acanthostrongylophora* sp. [7]. For many other compounds originally reported from sponges, a microbial origin is

likewise suspected even though clear evidence apart from obvious structural analogies with known microbial compounds is still lacking.

In this chapter, we will survey prominent groups of secondary metabolites derived from marine sponges and will focus on alkaloids, peptides, and terpenes which continue to attract wide attention of marine natural product researchers around the globe.

4.2 Alkaloids

Alkaloids are one of the most important classes of natural products providing drugs since ancient times. During the last decades, marine-derived alkaloids proved to be particularly important for drug discovery as exemplified by the new antitumor drug Yondelis[®] (ET-743). Marine alkaloids represent about one quarter of the more than 25,000 marine natural products reported to date, and a little more than half of them were obtained from sponges [2]. The present review will focus on three typical and major classes of sponge-derived alkaloids which include manzamine alkaloids, bromopyrrole alkaloids, and bromotyrosine-derived compounds.

4.2.1 Manzamine Alkaloids

The manzamines are polycyclic β -carboline-derived alkaloids. Manzamine A (**1**) (Fig. 4.1), the prototype of this group of compounds, was first isolated (as hydrochloride salt) in 1986 from an Okinawan sponge of the genus *Haliclona* and exhibited significant in vitro cytotoxicity against P388 murine leukemia cells with an IC_{50} of 0.07 $\mu\text{g}/\text{mL}$ (0.13 μM) [10].

Since the first report of **1**, more than 50 further manzamine-type alkaloids have been identified from nine other different sponge genera belonging to four different taxonomic orders [11–14]. These compounds are characterized by featuring a fused and bridged tetra- or pentacyclic ring system, which is linked to a β -carboline moiety through an apparent Pictet-Splenger reaction involving an aldehyde known as ircinal A (**2**) as shown in Scheme 4.1 [15]. This proposed biogenetic pathway was supported

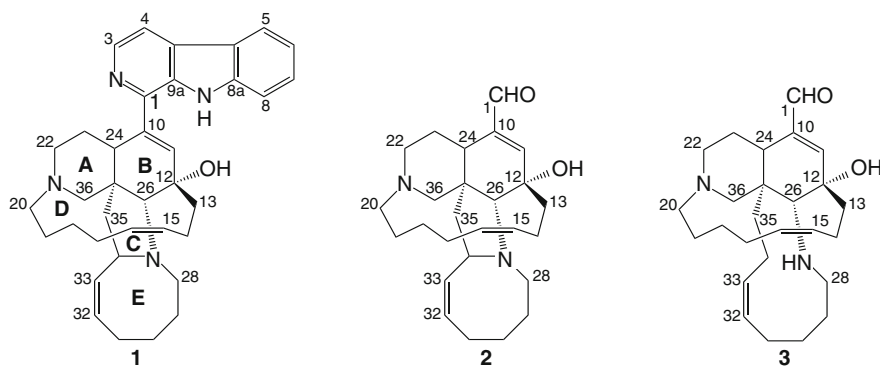
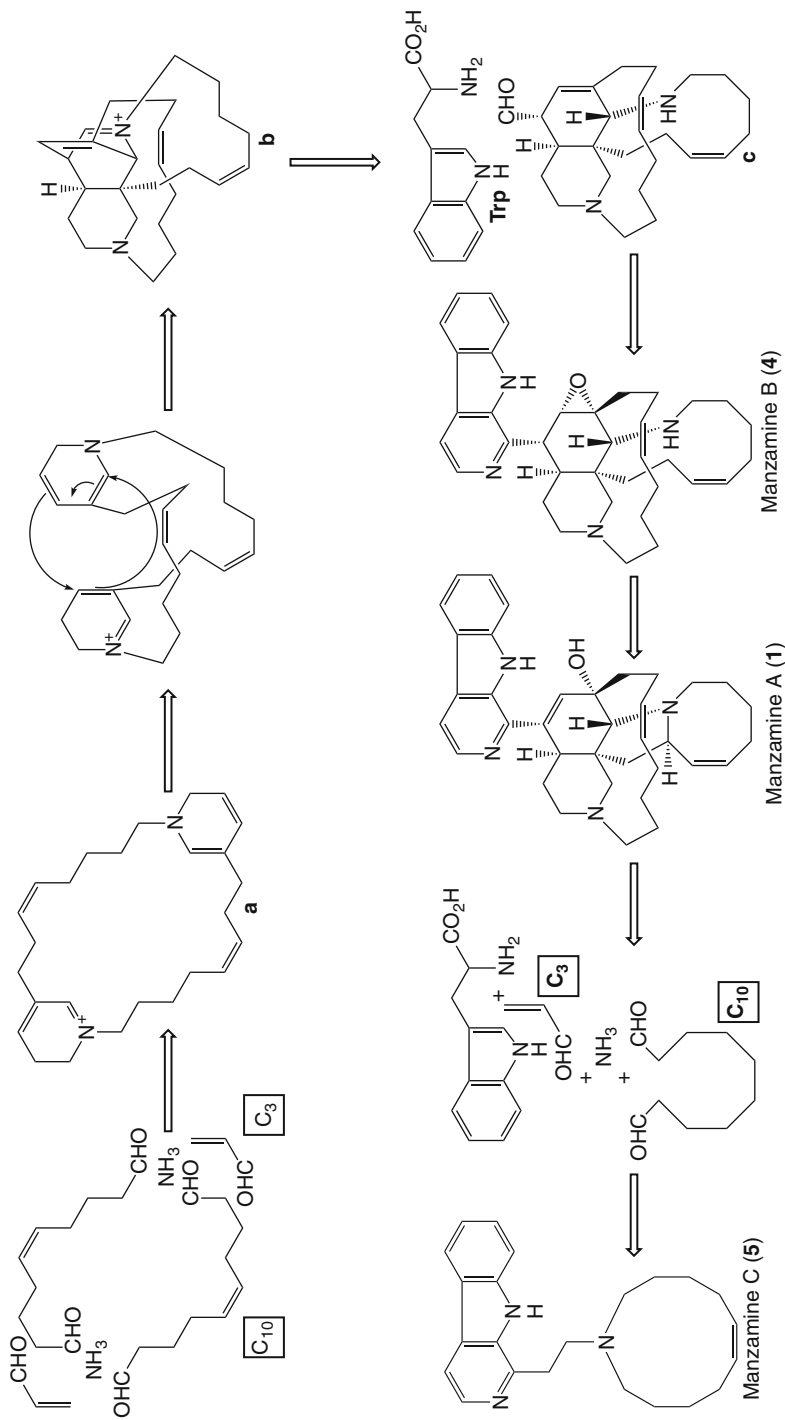


Fig. 4.1 Structures of manzamine A (**1**), ircinal A (**2**), and B (**3**)



Scheme 4.1 Plausible biogenetic pathway of manzamines A–C proposed by Baldwin and Whitehead [15]

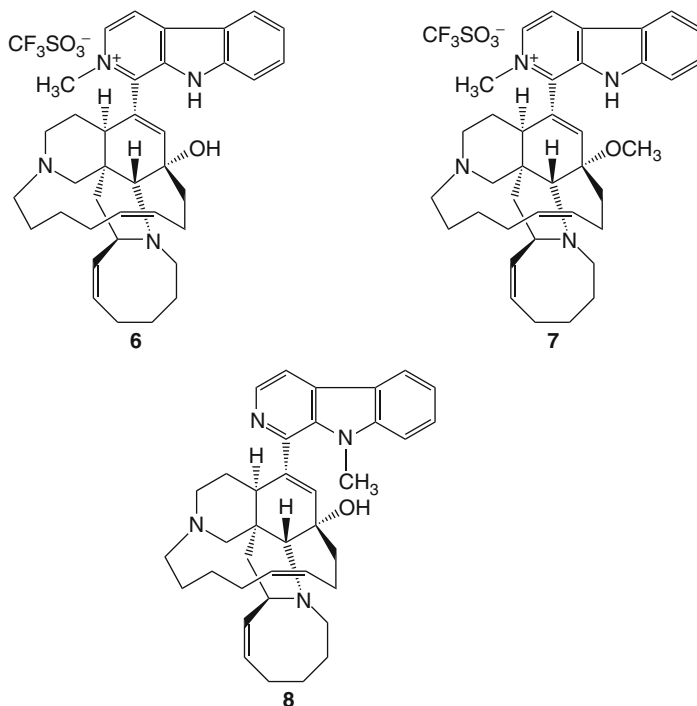


Fig. 4.2 Structures of synthetic mono- and dimethylated quaternary carbonilium cations (6–8) of manzamine A

by isolation of ircinal A (**2**) and B (**3**) (Fig. 4.1) from the Okinawan marine sponge *Ircinia* sp. [16]. Two further alkaloids isolated from a sponge of the genus *Amphimedon* which were designated as ircinols A and B were depicted to have opposite absolute configurations compared to **2** and **3**, respectively [17] (Fig. 4.1).

In addition to ircinols A and B, Kobayashi et al. in 1994 isolated a further β -carboline alkaloid, keramaphidin B, that was considered as a plausible biogenetic precursor of ircinal A (**2**) and B (**3**) and manzamine alkaloids as well [18, 19] (Scheme 4.1).

The broad range of bioactivities exhibited by manzamine alkaloids includes cytotoxicity [10], insecticidal [20], and antibacterial [21] as well as the interesting in vivo curative activity against malaria in animal models [22, 23]. These findings increasingly stimulated research efforts to synthesize manzamine alkaloids and their derivatives as well to conduct structure-activity relationship (SAR) studies [24–26].

In 2008, Ibrahim et al. performed a SAR study on the 2-*N*-methyl modifications of manzamine A [27]. In this study, mono- and dimethylated quaternary carbonilium cations of manzamine A (**1**) were synthesized (6–8) (Fig. 4.2) and evaluated for their in vitro antiplasmodial and antimicrobial activities, cytotoxicity, and also for their potential as inhibitors of glycogen synthase kinase (GSK-3 β) activity using molecular docking studies. Among the synthesized analogues,

2-*N*-methylmanzamine A (6) exhibited in vitro antiplasmodial activity (IC_{50} 0.7–1.0 μ M) but was less potent than manzamine A (1) (IC_{50} 0.017–0.02 μ M). However, 6 was less cytotoxic to mammalian kidney fibroblasts (Vero cells), and hence, the selectivity index was in the same range as for manzamine A (Fig. 4.2).

A new group of manzamine-related compounds includes nakadomarin A (9) [28], ma'eganedin A (10) [29], manadomanzamines A (11) and B (12) [30], and zamamidines A–C (13–15) [31, 32] which were isolated from different specimens of the sponge *Amphimedon* collected from Kerawa and Seragaki Islands, Okinawa, along with the unprecedented manzamine dimer, *neo*-kauluamine (16), from the common Indo-Pacific sponge genus *Acanthostrongylophora* [33, 34].

Zamamidines A–C (13–15) as well as manzamine A revealed inhibitory activities against *Trypanosoma brucei brucei*, the parasite causing sleeping sickness, (IC_{50} values: 1.4, 1.4, 0.4, and 0.07 μ M) and against *Plasmodium falciparum* (IC_{50} : 9.6, 16.3, 0.8, and 1.8 μ M, respectively) [32]. In vitro analysis of several manzamine analogues against *Toxoplasma gondii* indicated significant activity. Manzamine A (1) displayed 70% inhibition of the parasite at 0.1 μ M concentrations without displaying host cell toxicity. The activity significantly increased at concentrations of 1 and 10 μ M even though it was accompanied by an increase in host-cell toxicity. As a result, manzamine A was selected for in vivo analysis. A daily intraperitoneal (i.p.) dose of 8 mg/kg of manzamine A, given for 8 consecutive days, beginning on day 1 following the infection, prolonged the survival of SW mice to 20 days, as compared to 16 days for untreated controls [35]. Additional information on the antiprotozoan activity of manzamines can be found in ► Chap. 21 (Fig. 4.3).

SAR studies and optimized dosing will probably further improve the in vivo efficacy of the manzamines against *T. gondii*. All new and known manzamines, with the exception of *neo*-kauluamine (16), induced 98–99% inhibition of *Mycobacterium tuberculosis* (H37Rv) with an MIC < 12.5 μ g/mL. Manzamine A, E, and 8-hydroxymanzamine A exhibited MIC endpoints of 2.8, 5.5, and 5.5 μ M, respectively [35].

In conclusion, manzamine alkaloids are valuable candidates for further investigation and possibly even development as promising leads against malaria and other serious infectious diseases. The need for developing antimalarials derived from novel structural classes and with unique mechanisms of action is important for the long-term and sustainable control of drug resistant *Plasmodium* strains.

The occurrence of manzamine alkaloids in seemingly unrelated sponge genera has raised speculations about a possible microbial origin of these compounds [36].

4.2.2 Bromopyrrole Alkaloids

Bromopyrrole alkaloids constitute a class of marine compounds found exclusively in marine sponges. Oroidin (17) (Fig. 4.4) was the prototype of this group and was first isolated from the marine sponge *Agelas oroides* in 1971 [37]. Oroidin (17) is considered as the key precursor for this group of compounds since many

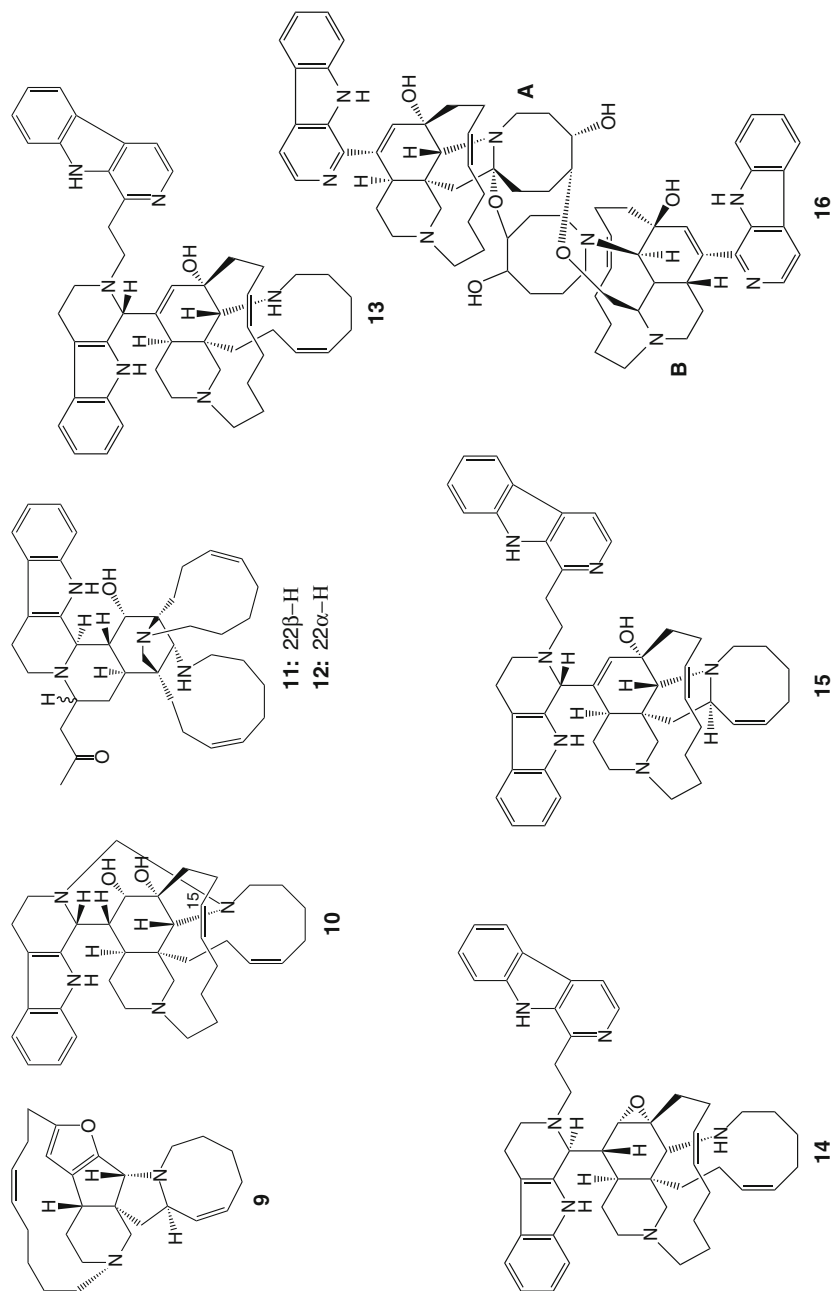
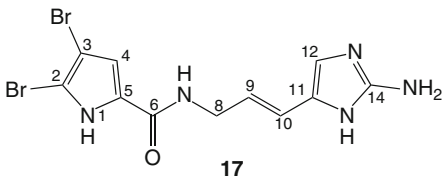
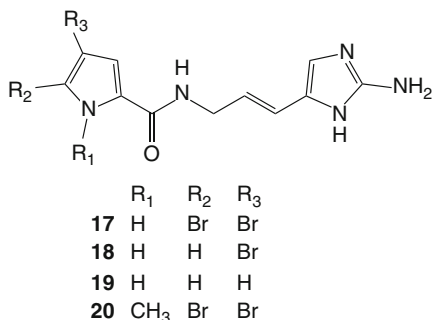
**Fig. 4.3** Structures of manzamine-related alkaloids (9–16)

Fig. 4.4 Oroidin, the prototype precursor of bromopyrrole alkaloids

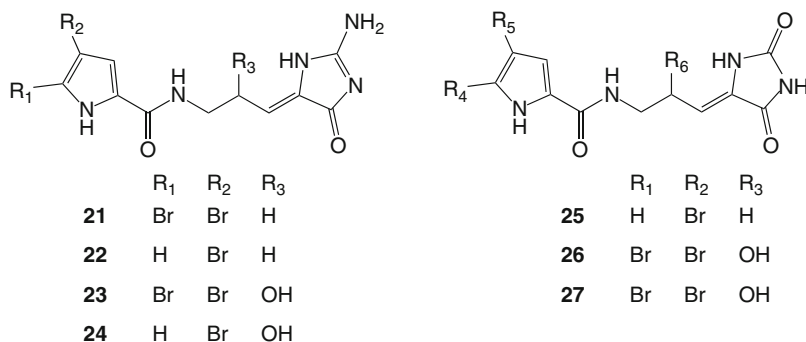


bromopyrrole alkaloids constituting a pyrrole-imidazole unit can be considered as metabolic derivatives of the C₁₁N₅ skeleton of oroidin.

Since the discovery of oroidin, more than 150 derivatives, with a wide variety of structures and interesting bioactivities, have been isolated from more than 20 different sponge taxa from different genera belonging mainly to the families Agelasidae, Axinellidae, and Halichondridae [38]. Their deterrent activity against predators is of ecological significance as shown for Caribbean reef sponges of the genus *Agelas* [39, 40]. Bromopyrrole alkaloids are also of interest due to their pronounced pharmacological activities including cytotoxicity, antimicrobial, and immunosuppressive activities which have driven the research interest of natural product chemists toward their total syntheses primarily during the last decade. These synthetic efforts lead to successful total syntheses of many bromopyrrole alkaloids such as dimeric pyrrole-imidazole alkaloids including sceptrin, oxysceptrin, and ageliferin [41]; nagelamides D [42] and E [41]; and hymenialdisine analogues [72].

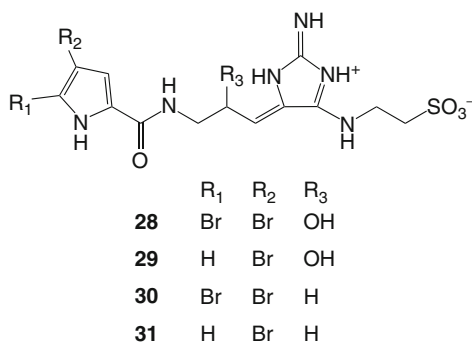


Hymenidin (2-debromooroidin) (18), clathrocin (2,3-debromooroidin) (19), and sventrin (pyrrole *N*-methyloroidin) (20) were isolated from an unspecified Okinawan marine sponge of the genus *Hymeniacidon* [43] and from the Caribbean sponges *Agelas clathrodes* [44], and *A. sventres* [45], respectively. The biological activities of these compounds were found to be linked to the bromination pattern of the pyrrole moiety. For example, in a feeding assay, hymenidin exhibited lower deterrence against fishes as compared to oroidin [46]. *N*-methylation of pyrrole moiety in sventrin (20) likewise reduced fish feeding deterency [45]. The reduction of voltage-dependent calcium elevation in PC12 cells was found to be directly proportional to the number of bromine atoms associated with the pyrrole ring in oroidin and hymenidin [47]. Oroidin, hymenidin, and clathrocin furthermore revealed pronounced anticholinergic and antiserotonergic activities [43, 45].

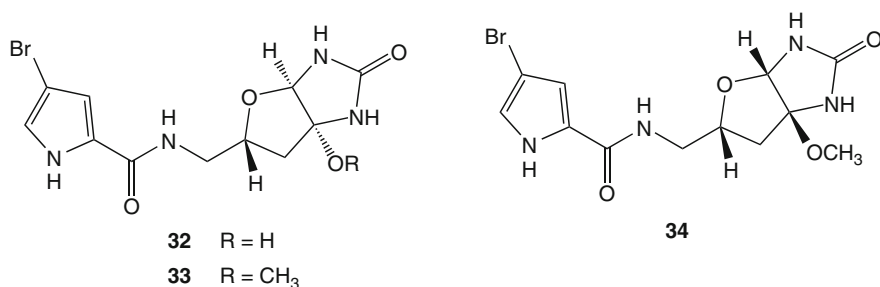


Dispacamides A–D (21–24) were isolated from four different species of the genus *Agelas* namely, *A. conifer*, *A. longissima*, *A. clathrodes*, and *A. dispar* [48, 49], in which the 2-aminoimidazole moiety was oxidized to an alkylidene glycoyamidine. Dispacamide A (21) and B (22) differ from oroidin (17) and hymenidin (18), respectively, both with regard to the position of the double bond in the amine side chain and with regard to the presence of an aminoimidazolone moiety. Compounds (21) and (22) were found inactive with regard to anticholinergic and antiserotonergic activities. On the contrary, all dispacamides exhibited a remarkable antihistaminic activity on the guinea pig ileum through a reversible noncompetitive binding to histamine receptors, with dispacamide A (21) being the most active derivative [48]. Dispacamide C (23) and D (24) showed only mild activity in comparison which indicated the importance of the hydroxyl group in the side chain and also implicated that its orientation resulted in a notable reduction of antihistaminic activity [49]. Recently, debromodispacamides B and D were reported from *Agelas mauritiana* collected off the Solomon Islands [50].

Mukanadin A (= dispacamide D) (24) and B (25) have been isolated from the Okinawan sponge *Agelas nakamura* [51]. Mukanadin D (26) was obtained from the Jamaican sponge *Didiscus oleata* [52]. In mukanadin B (25), D (26), and compound (27), isolated from *Axinella verrucosa* [53], the 2-aminoimidazole unit of dispacamides is replaced by a hydantoin moiety.



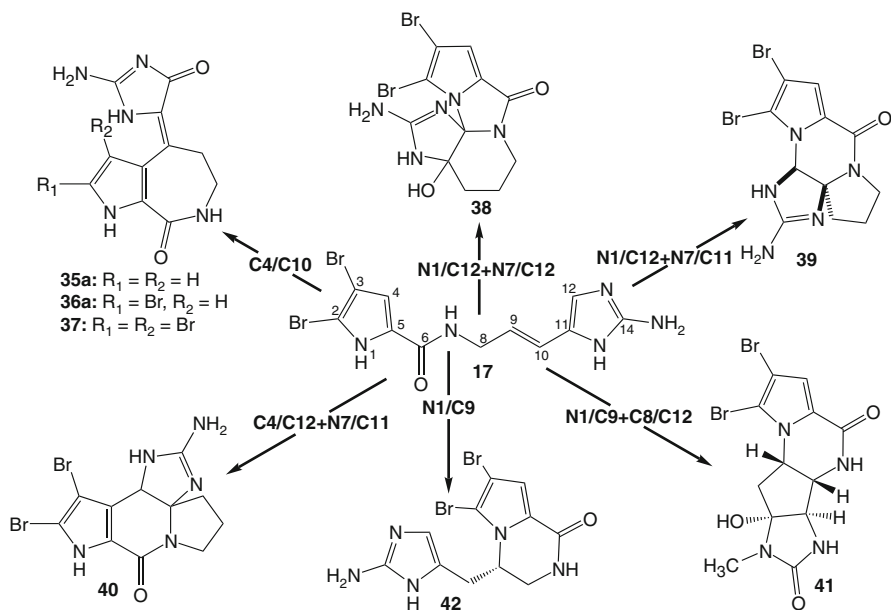
Mauritamide A, isolated from the Fijian sponge *Agelas mauritiana*, was the first bromopyrrole alkaloid featuring a rare taurine moiety [54]. Taurine moieties are also present in tauroacidin A (28) and B (29), isolated from an Okinawan *Hymeniacidon* sp. [55]; in taurodispacamide (30), isolated from the Mediterranean sponge *Agelas oroides* [56]; and in its debromo derivative (31), isolated from *Axinella verrucosa* [53]. Interestingly, various pharmacological activities have been reported for these four compounds (28–31). Tauroacidins A (28) and B (29) inhibited EGF receptor kinase and *c-erbB-2* kinase activities ($IC_{50} = 20 \mu\text{g/mL}$) [55]. Taurodispacamide (30) showed significant antihistaminic activity [56], while its debromo derivative (31) showed potent neuroprotection through acting as glutamate and serotonin antagonist [53].



Slagenins A–C (32–34) were isolated from the Okinawan marine sponge *Agelas nakamura* [57]. They are characterized by an additional cyclization step in comparison to oroidin (17), the key precursor for this class. Both slagenins B (33) and C (34) were proven to be cytotoxic against murine leukemia L1210 cells in vitro with IC_{50} values of 21 and 19.5 μM , respectively, although slagenin A (32) proved to be inactive [57].

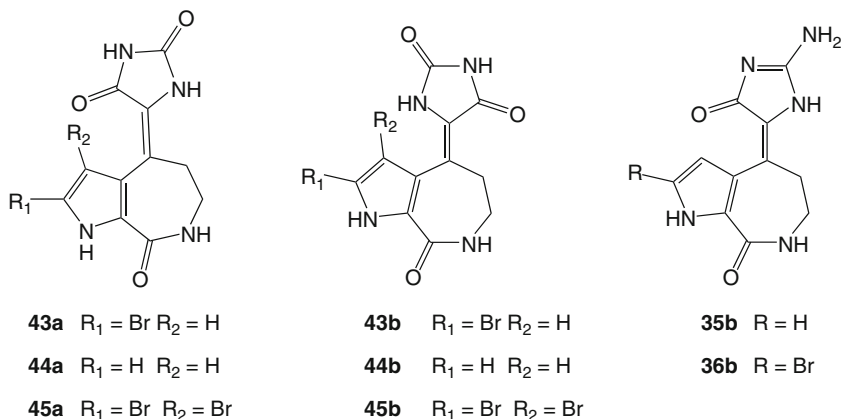
Polycyclic bromopyrrole alkaloids are thought to be derived from oroidin, the parent compound, through formation of one (or more) C–C or C–N bonds. Polycyclic bromopyrrole alkaloids can be divided into five major classes based on the oroidin atoms involved in the cyclization (Scheme 4.2) [56].

Debromohymenialdisine (35a), hymenialdisine (36a), and 3-bromohymenialdisine (37) (Scheme 4.2) represent the first cyclization mode of oroidin which occurs between C4 and C10. Debromohymenialdisine (35a) was first isolated from the Great Barrier Reef sponge *Phakellia* sp. in 1980 [58], while hymenialdisine (36a) was reported 2 years later from different sponge genera including *Acanthella*, *Axinella*, and *Hymeniacidon* [59–61]. 3-Bromohymenialdisine (37) was first isolated from the tropical marine sponge *Axinella carteri* [62]. All compounds (35a, 36a, and 37) were tested for cytotoxicity and insecticidal activity. In a cytotoxicity assay, debromohymenialdisine (35a) was the most active compound against mouse lymphoma L5178Y cells with IC_{50} value of 1.8 $\mu\text{g/mL}$ (4.1 μM) [62], while hymenialdisine (36a) and 3-bromohymenialdisine (37) were essentially



Scheme 4.2 An overview of cyclization modes of the oroidin skeleton [56]

equitoxic with $IC_{50} = 3.9 \mu g/mL$ for both. Both **35a** and **36a** exhibited insecticidal activity toward larvae of the pest insect *Spodoptera littoralis* (LD_{50} values of 88 and 125 ppm, respectively), whereas **37** proved to be inactive in this assay [62].

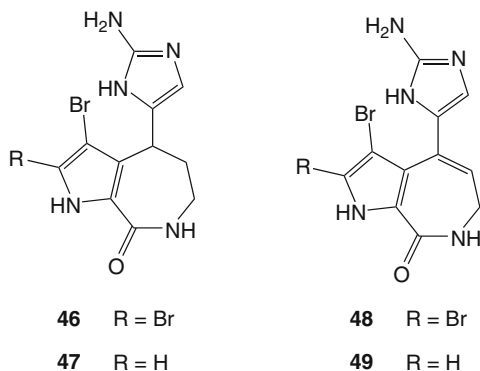


Axinohydantoin (43–45) feature the same fused pyrroloazepine ring as present in hymenialdisine (**36a**). However, instead of a glycohydantoin ring, a pyrroloazepine ring is linked to a hydantoin ring via either (*E*) or (*Z*) double bond. (*E*)-axinohydantoin (**43a**) was isolated in 1990 from the sponge *Axinella* sp., and its structure was proven

by X-ray crystallography [63]. (*Z*)-Axinohydantoin (**43b**) as well as the bromine derivatives (**44b**, **45b**) were reported in 1997 [64] and 1998 [65], respectively. As for the axinohydantoin, the (*E*) isomers of debromohymenialdisine (**35b**) and hymenialdisine (**36b**) have also been isolated [66].

Hymenin (46) is an α -adrenoceptor antagonist isolated from *Hymeniacidon* sp. and furthermore exhibits antibacterial activity against *Bacillus subtilis* and *Escherichia coli* [67]. Another hymenin analogue differing in the presence of a double bond between C9 and C10 was isolated from *Pseudaxynissa cantharella* [68], and it was named stevensine (= odiline) (48). 2-Debrominated derivatives of both hymenin (47) and stevensine (49) were isolated from the Indo-Pacific sponge *Stylissa carteri* [69]. Stevensine (48) has been demonstrated to play a major role in the chemical defense of the reef sponge *Axinella corrugata* against predators [70].

Hymenialdisine and its analogues are of interest due to their strong inhibitory activity against several protein kinases, such as CDKs, GSK-3 β , CK1, and Chk1, which are involved in regulating vital cellular functions such as gene expression, cellular proliferation, membrane transport, and apoptosis [71, 74]. Targeting these kinases has been appealing for the treatment of diseases like Alzheimer's disease, type II diabetes, and cancer [72, 73] thereby providing a rationale for medication. In addition, hymenialdisines inhibited formation of several proinflammatory cytokines (IL-1, IL-2, IL-6, and NO) through inhibition of the NF- κ B signaling pathway [71] which is potentially valuable for treatment of serious inflammatory diseases such as rheumatoid arthritis and osteoarthritis or for treatment of cancer.



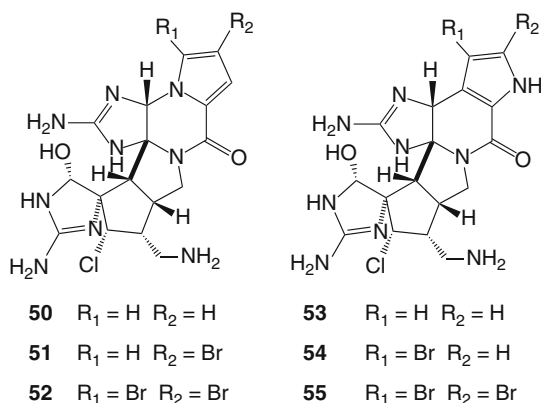
In 2009, an elegant review summarized all known hymenialdisines and provided a summary of their protein kinase inhibitory activities [75]. It came to the conclusion that (1) halogenation at R₁ and R₂ of the pyrrole ring does not significantly increase or decrease the activity of these compounds, (2) pyrrole derivatives appear to be more potent inhibitors than indole analogues which resulted in up to a fourfold reduction in activity, (3) a change in the geometry of the double bond (either (*E*) or (*Z*)) does not influence the activity, and (4) the existence of an aminoimidazolone ring, in particular the guanidine moiety, is crucial for the activity. Modifying the amino group dramatically decreased

activity possibly due to steric hindrance and loss of hydrogen bonding and hymenine (46), which features an aminoimidazole ring, proved to have much lower kinase inhibitory activity than hymenialdisine analogues [75].

The second cyclization mode, occurring between both N1 and N7 with C12, is exemplified, to the best of our knowledge, only in dibromoagelospongine (38) - (Scheme 4.2) which was isolated from the marine sponge *Agelas* sp. collected off the Tanzanian coasts [76]. Dibromoagelospongine (38) is closely related to dibromophakellin (39) (Scheme 4.2) in which N7 is bonded to C11 instead. The latter was first isolated in 1971 by Sharma et al. [77]. Later, several other phakellins have been reported from *Pseudaxynissa cantharella* [68] and *Agelas* sp. [78]. In 1997, a further derivative, phakellistatin, which differs from 39 in having a urea-type carbonyl instead of amino group present in the guanidine moiety, was isolated from the Indian Ocean sponge *Phakellia mauritiana* [79]. Phakellistatin exhibited potent antiproliferative activity against a variety of human cancer cell lines (IC₅₀ values from 0.3 to 0.4 μM) [79].

The next cyclization mode of oroidin involving N7/C11 and C4/C12 affords a class of compounds called isophakellins, from which dibromoisophakellin (40) was the first derivative reported [80]. The compounds of this class are isomeric compared to the phakellins with the only difference in the linkage of imidazole C12 with C4 instead of N1.

The group of phakellins and isophakellins includes structurally complex metabolites known as palau'amines (50–52) or styloguanidines (53–55), respectively. In each of these compounds, the corresponding basic skeleton of phakellin or isophakellin is conjugated with an aminoimidazolyl propene unit.



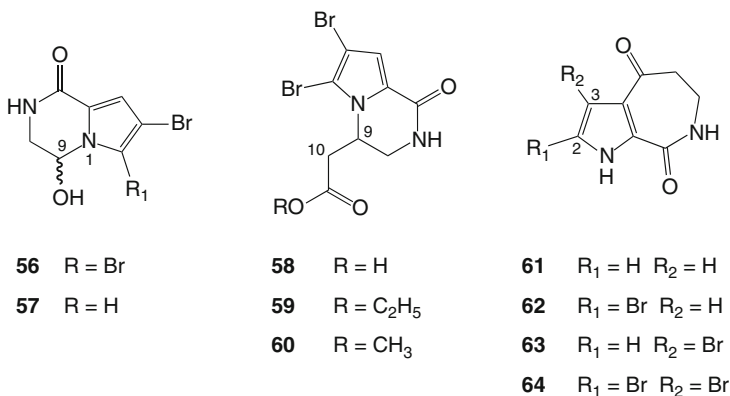
Palau'amines (50–52) were reported from *Stylotella agminata* [81] and from *Stylotella aurantium* [82]. They revealed potent cytotoxicity against several cancer cell lines with IC₅₀ values from 0.1 to 10 μg/mL along with antibacterial, antifungal, and immunosuppressive activities [81, 82]. Styloguanidines (53–55) were obtained together with palau'amines from the sponge *Stylotella aurantium* collected in the Yap Sea and exhibited potent inhibition of chitinase, a key enzyme involved, e.g., in the ecdysis of insects and crustaceans. The inhibition of this

enzyme affects the settlement of barnacles and hence could be a potential target for antifouling agents [83].

Agelastatin A (**41**) (Scheme 4.2) was the first reported member of the N1/C9 and C8/C12 cyclization series and was isolated from *Agelas dendromorpha* [84]. Other derivatives were later reported from the same sponge [85] as well as from *Cymbastela* sp. [86]. Agelastatins are potent antiproliferative agents against several cancer cell lines [85]. Moreover, agelastatin A (**41**) inhibited glycogen synthase kinase (GSK-3 β), which could be useful for treatment of serious diseases including Alzheimer's disease, cancer, and type II diabetes [71].

The last proposed cyclization mode of oroidin (**17**) occurring between N1 and C9, as shown in Scheme 4.2, affords cyclooroidin (**42**), first reported in the year 2000 from the Mediterranean sponge *Agelas oroides* [56]. Other members of this class of compounds include agesamides, isolated from an Okinawan sponge *Agelas* sp. [87], which differ from **42** in featuring a hydantoin ring instead of a glycoxyamidine ring. Oxycyclostylidol, another compound of this class was the first pyrrole-imidazole alkaloid, reported containing an oxidized pyrrole moiety [88].

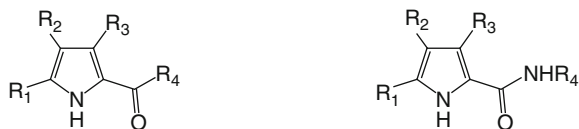
Cyclooroidin (**42**) can be considered as a biosynthetic precursor of the nonimidazole bromopyrrole alkaloids including longamides (**56–60**) and aldisines (**61–64**).



Longamide A (**56**) was identified as a novel unusual pyrrolo-piperazine alkaloid and was isolated as (9*S*) isomer from the Caribbean sponge *Agelas longissima* [89]. The 2-debromo derivative (= mukanadin A) (**57**) was obtained from the sponge *Axinella carteri* [90] together with 2-bromoaldisine (**62**), while aldisine (**61**) was reported from the sponge *Hymeniacidon aldis* [91]. 3-Bromoaldisine (**63**) and 2,3-dibromoaldisine (**64**) were isolated from *Axinella damicornis* and *Stylissa flabelliformis* [92]. Longamide B (**58**) has been isolated as a racemate from the Caribbean sponge *Agelas dispar* [93]. Hanishin, longamide B ethyl ester (**59**) was named after the Hanish Islands (Red Sea) where the sponge *Acanthella carteri* was collected [94].

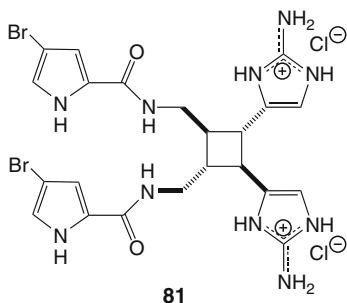
Other smaller bromopyrrole alkaloids (**65–73**), which are considered as building blocks leading to oroidin (**17**), have been isolated from *Agelas oroides* (**65**) [36], *Agelas flabelliformis* (**66**) [96], *Acanthella carteri* (**67**, **68**) [94], *Axinella damicornis* (**69**, **70**) [92], *Agelas nakamurai* (**71**, **74**) [97], *Acanthostylotella* sp.

(**72**, **73**) [98], *Homaxinella* sp. (**75**) [95], and *Axinella verrucosa* (**76**) [53]. Acanthamides A–D (**77–80**) were isolated from an Indonesian marine sponge *Acanthostylotella* sp. [98]. Antipredatory activity seems to be the main ecological function for these small bromopyrroles [36, 92, 94].



	R ₁	R ₂	R ₃	R ₄		R ₁	R ₂	R ₃	R ₄
65	Br	Br	H	OH	74	Br	H	H	CH ₂ OCH ₃
66	Br	Br	H	OCH ₃	75	Br	Br	H	CH ₂ OCH ₃
67	Br	Br	H	NH ₂	76	H	Br	H	CH ₂ OCH ₃
68	Br	H	H	NH ₂	77	H	Br	Br	(CH ₂) ₃ OCH ₃
69	H	Br	Br	NH ₂	78	H	Br	Br	(CH ₂) ₃ OC ₂ H ₅
70	H	Br	Br	OH	79	H	Br	Br	(CH ₂) ₂ OCH ₃
71	Br	H	H	NH ₂	80	H	Br	Br	(CH ₂) ₂ OC ₂ H ₅
72	H	Br	Br	OCH ₃					
73	Br	H	Br	OH					

In 1981, dimeric bromopyrrole alkaloids have been reported for the first time from the Caribbean sponge *Agelas sceptrum* which gave the name *sceptrin* to one of the metabolites isolated (**81**) [99]. Historically, **81** is considered as the parent compound of this group and represents a symmetrical dimer of 2-debromooidin. *Sceptrin* (**81**) displayed a broad spectrum of bioactivities such as antimicrobial activity against different bacterial and fungal pathogens [99]. In addition, it exhibited antiviral [100], antimuscarinic [45], and antihistaminic properties [49].

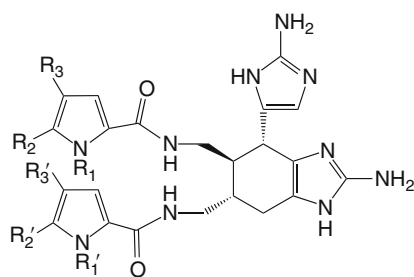


Later, dimeric bromopyrrole alkaloids were also reported from other genera of marine sponges including *Stylissa* [101, 102], *Axinella* [103], *Hymeniacidon* [104], and most frequently from *Agelas*. Among this group of

dimeric alkaloids, two series can be identified which include agelifferins and nagelamides.

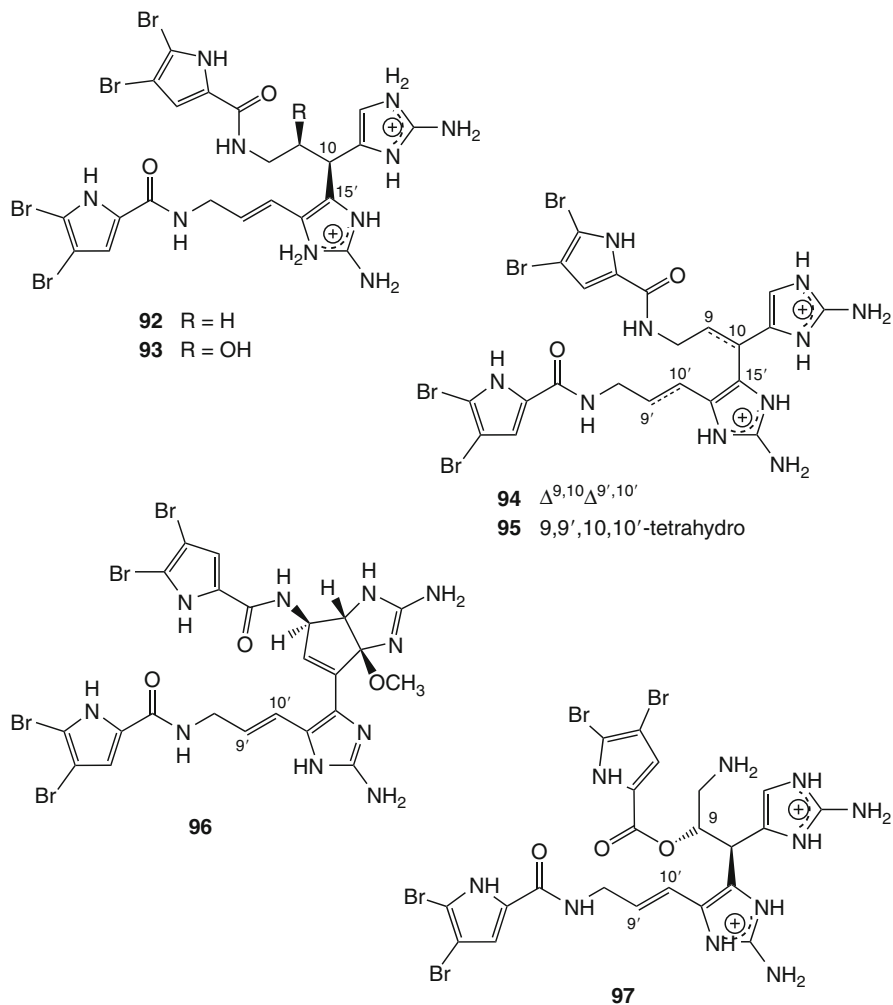
Agelifferin (**82**), bromoagelifferin (**83**), and dibromoagelifferin (**84**) were first isolated from *Agelas conifera* and *A. cf. mauritiana* in 1989 by Rinehart [105]. Afterward, their detailed structural elucidation and stereochemistry were reported in 1990 by Kobayashi et al. [106]. Both **83** and **84** reduced voltage-dependent calcium entry in PC12 cells which leads to vasorelaxation [107].

Seven further agelifferin derivatives (**85–91**), methylated at one or at several of the pyrrole nitrogens, together with the formerly isolated bromo- (**83**) and dibromoagelifferin (**84**) were obtained from the calcareous sponge *Astrosclera willeyana* collected off Ant Atoll, Pohnpei, Micronesia [108].

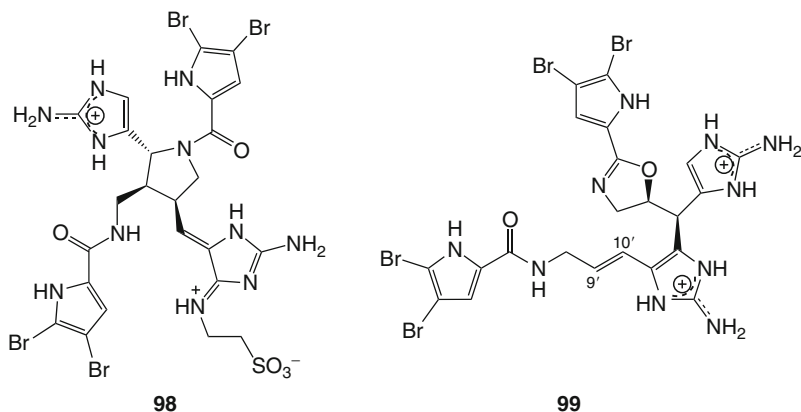


	R ₁	R ₂	R ₃	R ₁ '	R ₂ '	R ₃ '
82	H	H	Br	H	H	Br
83	H	Br	Br	H	H	Br
84	H	Br	Br	H	Br	Br
85	H	H	Br	CH ₃	H	Br
86	CH ₃	H	Br	CH ₃	H	Br
87	H	H	Br	CH ₃	Br	H
88	CH ₃	H	Br	CH ₃	Br	H
89	H	Br	Br	CH ₃	H	Br
90	H	H	Br	CH ₃	Br	Br
91	H	Br	Br	CH ₃	Br	Br

Nagelamides comprise 15 dimeric bromopyrrole derivatives including nagelamides A–H [109], J–L [110, 111], and O–R [112, 113]. All of them were reported by Kobayashi et al. from different collections of an unspecified Okinawan sponge of the genus *Agelas* collected off Seragaki beach.



Nagelamides A–D (**92–95**) are connected via a C–C bond between C10 and C15'. Nagelamides E–G were proven to be diastereomers of ageliferin (**82**), bromoageliferin (**83**), and dibromoageliferin (**84**), respectively. Nagelamide J (**96**) is the first bromopyrrole alkaloid possessing a cyclopentane ring fused to an aminoimidazole ring [110]. In addition, nagelamide L (**97**) was identified as a unique dimeric bromopyrrole alkaloid containing an ester linkage [111].

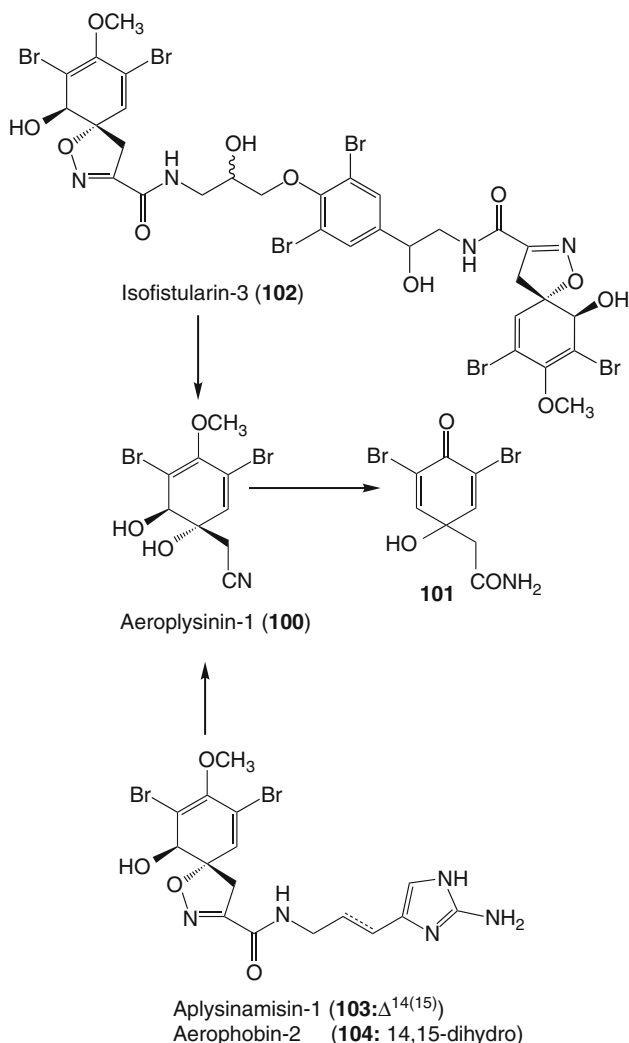


Nagelamide Q (**98**) is a rare dimeric bromopyrrole alkaloid possessing a pyrrolidine ring, while nagelamide R (**99**) was the first bromopyrrole alkaloid featuring an oxazoline ring [113]. Nagelamides have been tested for antimicrobial activity against a vast array of bacterial and fungal pathogens including *Bacillus subtilis*, *Escherichia coli*, *Micrococcus luteus*, *Staphylococcus aureus*, *Trichophyton mentagrophytes*, *Cryptococcus neoformans*, *Candida albicans*, and *Aspergillus niger*. Most of the nagelamides showed antimicrobial activity with MIC values between 7.7 and 38.4 μM [109–113]. Nagelamides A, G, and H showed also inhibitory activity against protein phosphatase 2A, a major serine/threonine protein phosphatase involved in cellular growth and potentially in cancer development, with IC_{50} values of 48, 13, and 46 μM , respectively [109].

4.2.3 Bromotyrosine Derivatives

(+)-Aeropylsinin-1 (**100**, Scheme 4.3) was the first reported member of this group of alkaloids. It was obtained from marine sponges belonging to the order Verongida. In 1970, Fattorusso et al. isolated **100** from *Verongia aerophoba* collected off the Bay of Naples (Italy) [114]. Later, it was also reported from other marine sponges from different geographic locations including *Psammoposilla purpurea* (Marshall Islands) [115], *Aplysina laevis* (Australia) [116], and *Aplysia caissara* (Brazil) [117]. Its (–)-isomer was first isolated from *Ianthella ardis* [118].

Aeropylsinin-1 (**100**) proved to be antiproliferative in small micromolar doses against various cancer cell lines such as Hela (human cervical carcinoma) and L5178Y (mouse lymphoma) in addition to human mammary and colon carcinoma cell lines [119–121]. In 2002, Rodríguez-Nieto et al. reported that **100** inhibited the growth of BAECs (bovine aortic endothelial cells) and induced apoptotic cell death [122]. Aeropylsinin-1 inhibits the endothelial cell migration and capillary tube formation in matrigel through inhibition of matrix-metalloproteinase 2 and urokinase in endothelial cell conditioned medium [119]. The same study reported in vivo inhibition of



Scheme 4.3 Enzymatic transformation of isoxazoline alkaloids in *Aplysina* sponges into aeroplysinin-1 (**100**) and a dienone analogue (**101**) [120, 123–127]

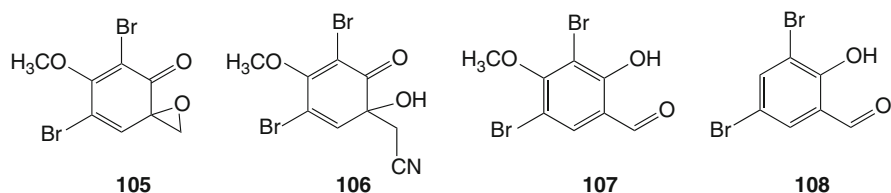
angiogenesis as demonstrated in the CAM (chick chorioallantoic membrane) assay and matrigel plug assay. Aeroplysinin-1 exhibited preferential cytotoxicity against L5178Y cells compared to murine spleen lymphocytes through reducing the incorporation rates of ^3H -thymidine [119]. In vivo experiments by the same group revealed an antileukemic activity of **100** in L5178Y cell/NMRI mouse system. In conclusion, aeroplysinin-1 proved to be an inhibitor of both angiogenesis and tumor proliferation.

Various ecological and biochemical studies of *Aplysina* sponges suggested that aeroplysinin-1 arises through enzymatic biotransformation of more complex brominated isoxazoline alkaloids as a response to sponge tissue damage yielding

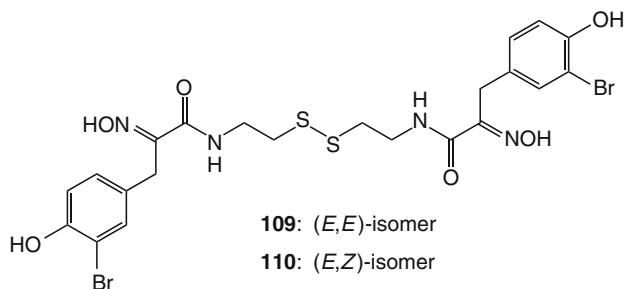
aerplysinin-1 (**100**) and a dienone analogue (**101**) (Scheme 4.3) [120, 123–127] (Scheme 4.3).

Receptor tyrosine kinases (RTKs), such as the epidermal growth factor receptor (EGFR) and the platelet-derived growth factor receptor (PDGFR), are critically involved in the transduction of mitogenic signals across the plasma membrane and therefore in the regulation of cell growth and proliferation. Enhanced RTK activity is associated with proliferative diseases such as cancer, psoriasis, and atherosclerosis, while decreased function may be associated, for instance, with diabetes [128]. Aeroplysinin-1 inhibited tyrosine kinase activity of EGFR in vitro and blocked ligand-induced endocytosis of the EGF receptor and PDGF receptor in vitro [129]. Hence, a proposed EGFR-dependent mechanism of action was depicted; however, the compound showed no activity when tested in a whole-cell assay system [129].

Therefore, a series of aeroplysinin-1 analogues was synthesized and evaluated as RTK inhibitors to enhance membrane permeability in cell-based assays with retained tendency for nucleophilic covalent binding to the enzyme-binding site [128]. Four synthetic analogues (**105–108**) exhibited promising inhibitory activity against EGFR and PDGFR tyrosine kinases in cellular assays with IC_{50} values in the low micromolar range, but none of them have yet been assessed for antiangiogenesis.



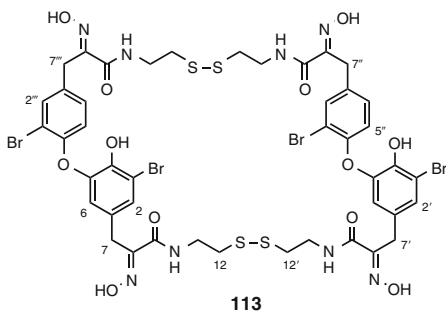
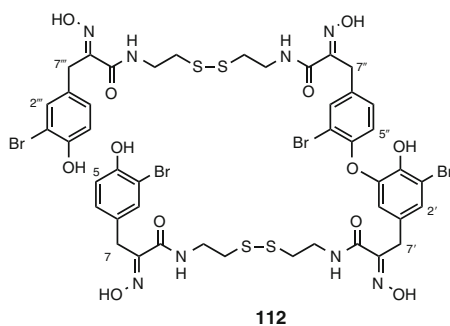
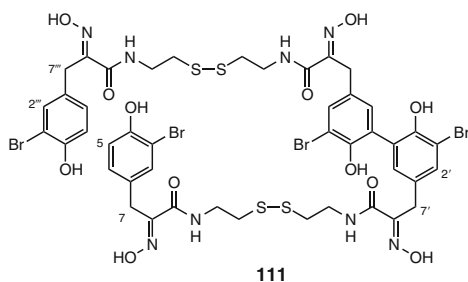
Psammaplin A is a symmetrical brominated tyrosine metabolite containing a disulfide linkage and is usually obtained as a mixture of isomers, [(*E,E*)-isomer (**109**) and (*E,Z*)-isomer (**110**)] which differ in the configuration of their oxime groups.



In 1987, psammaplin A was reported simultaneously by Quiñoà and Crews [130] and Rodríguez et al. [131] from *Psammaplysilla purpurea* and *Thorectopsamma xana* sponges, both belonging to the order Verongida. Psammaplin A was also obtained from *Aplysinella rhax* [132] and *Pseudoceratina purpurea* [133] in addition to two Korean non-Verongid sponges of the genera *Jaspis* and *Poecillastra*

[134, 135]. Later, a vast diversity of psammaplins have been reported, including 13 monomeric psammaplins (A–M) isolated from the Indo-Pacific sponge *Pseudoceratina purpurea* [133], the Fijian sponge *Aplysinella rhax* (thought to be synonymous with *Pseudoceratina purpurea*) [136] and from two-sponge associations of *Jaspis* sp. and *Poecillastra* sp. collected from Korean waters [135].

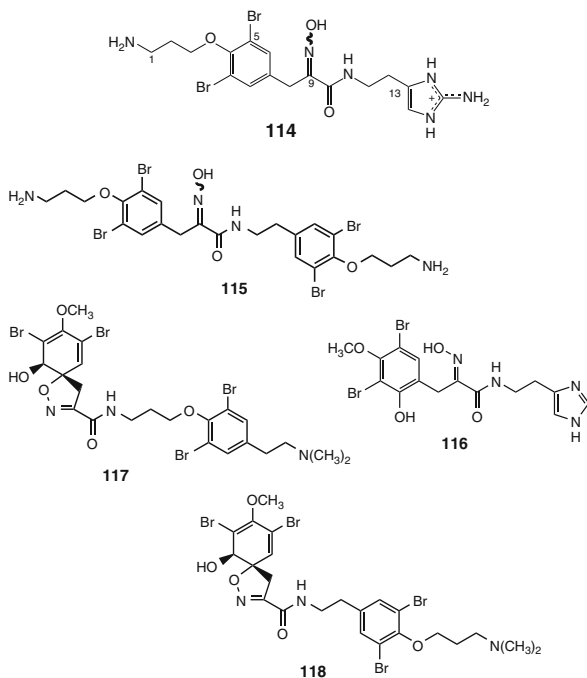
In addition, dimeric psammaplins were obtained which occur either in an opened form such as bisaprasin A (**111**) and bispsammaplins A (**112**) or in a cyclized form represented by cyclobispsammaplins A (**113**). All of these compounds were reported from different Korean collections of sponges of the genera *Jaspis* and *Poecillastra* [134, 135]. Moreover, 11'-sulfate derivatives of **109** and **111** were isolated from the sponge *Aplysinella rhax* collected from Queensland (Australia) [132].



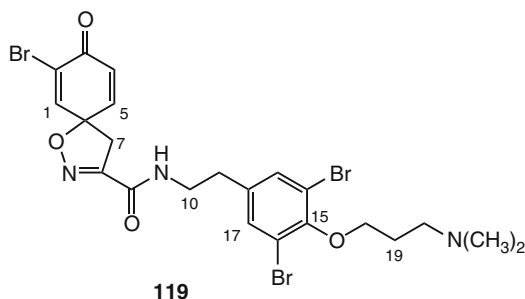
The cytotoxicity of psammaplins A (PsA, **109**) toward a vast array of human cancer cells was studied by numerous groups [134, 135, 137–139]. PsA inhibits the

proliferation of BAECs [139]. It furthermore inhibits DNA synthesis and DNA gyrase [140], farnesyl protein transferase and leucine aminopeptidase [137], chitinase B from *Serratia mercerscens* [136], in vitro replication of SV40 DNA through α -primase targeting [138], activation of peroxisome proliferator-activated receptor gamma [141], and histone deacetylases (HDACs) in cell-based assays, the latter having been highlighted as one of the key enzymes involved in both oncogenesis and angiogenesis, inducing cell cycle arrest and apoptosis [143–145]. PsA also inhibited DNA methyltransferase activity in vitro [142]. However, the lack of in vivo inhibition of DNA methylation suggests that this enzyme is not a major cellular target. Furthermore, it inhibited aminopeptidase N (APN), a Zn-dependent metalloproteinase that has been implicated in tumor invasion and angiogenesis [139]. Both homodimers and heterodimers were further assayed for antibacterial activity against methicillin-resistant *Staphylococcus aureus* and structure refinement of promising lead compounds through parallel synthesis afforded a series of antibacterial agents significantly more active than the natural product [140, 146].

Purealidin A (**114**) represents the prototype of a group of bromotyrosine-derived alkaloids that includes 17 additional purealidins (B–H and J–S) [147–153]. All compounds were isolated from different collections of the Okinawan sponge *Psammaphysilla porea* except for purealidins J and S that were obtained from the Fijian sponge *Druinella* sp. [153].

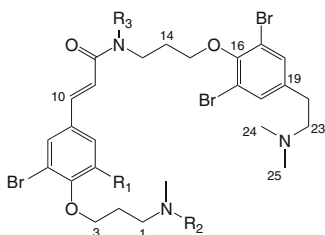


Purealidin A (**114**) exhibited cytotoxic activity against murine leukemia L1210 cells in vitro with IC_{50} value of $2.1 \mu\text{M}$ [147], while purealidins C (**115**), N (**116**), P (**117**), and Q (**118**) showed cytotoxicity against human epidermoid carcinoma KB cells (IC_{50} : 4.3, 0.16, 10.2, and $1.6 \mu\text{M}$, respectively) and murine lymphoma L1210 cells (IC_{50} : 3.2, 0.15, 3.8, and $1.3 \mu\text{M}$, respectively) [148, 152]. In both cell lines, purealidin N (**116**) was found to be the most potent analogue followed by purealidin Q (**118**). Furthermore, purealidin C (**115**) proved antifungal and antibacterial [148] while purealidins P (**117**) and Q (**118**) revealed inhibitory activity against EGF receptor kinase with IC_{50} values of 24.2 and $14.8 \mu\text{M}$, respectively [152]. Eight purpurealidins (A–H) were isolated from the Indian sponge *Psammaplysilla purpurea* [154].



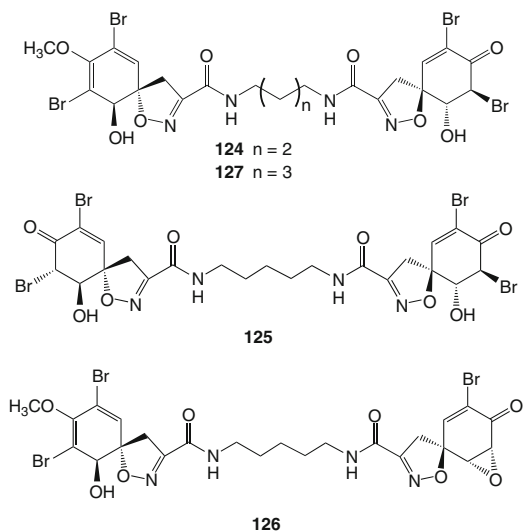
All purpurealidins were screened for antibacterial and antifungal activities. Only purpurealidin B (**119**) showed moderate activity against *Staphylococcus aureus*, *Escherichia coli*, and *Vibrio cholerae* and weak activity against *Shigella flexineri* with MIC values of 10, >12, 25, and $100 \mu\text{g/mL}$, respectively [154]. Suggested ecological roles for these bromotyrosine compounds are mainly feeding deterrents [121].

Psammaplysenes A–D (**120–123**) represent a group of bromotyrosine-derived alkaloids which have been obtained from *Psammaplysilla* sp. collected in the Indian Ocean [155] and from the Australian sponge *Psammoclema* sp. [156]. Psammaplysene A (**120**) compensated for the loss of PTEN tumor suppressor by relocating the transcription factor FOXO1a to the nucleus ($IC_{50} = 5 \mu\text{M}$) compared to psammaplysene B (**121**) ($IC_{50} = 20 \mu\text{M}$) [155]. The growth-inhibiting PTEN phosphatase proved important for regulation of the growth-promoting PI3-kinase signal. Hence, loss of functional mutations in PTEN can result in an inappropriate increase in stimulatory signals, and such mutations have been linked with Cowden's disease, a hereditary disease with a predisposition to breast, thyroid, and other cancers [155]. Both psammaplysene C (**122**) and D (**123**) showed cytotoxicity ($IC_{50} = 7 \mu\text{M}$). Hence, their bioactivity in both P2X₇ and hemolysin specificity assays was attributed to cytotoxicity against the premonocytic cell line THP-1, which expresses the P2X₇ receptor [156]. In 2005, Georgiades and Clardy synthesized **120** and **121** by a flexible efficient route using 4-iodophenol as a common starting substrate [157].

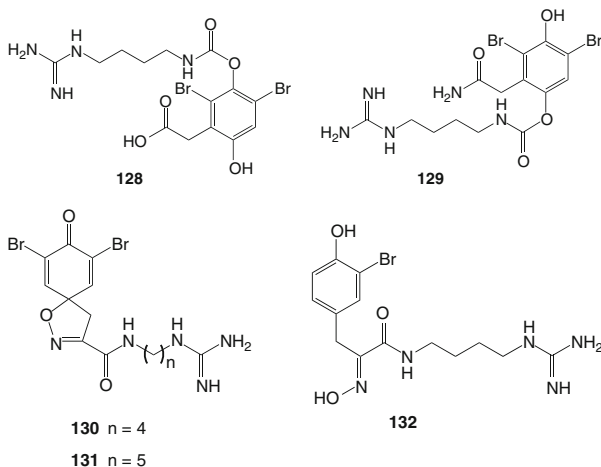


- 120** R₁ = Br R₂ = CH₃ R₃ = H
121 R₁ = Br R₂ = H R₃ = H
122 R₁ = H R₂ = CH₃ R₃ = CH₃
123 R₁ = Br R₂ = CH₃ R₃ = CH₃

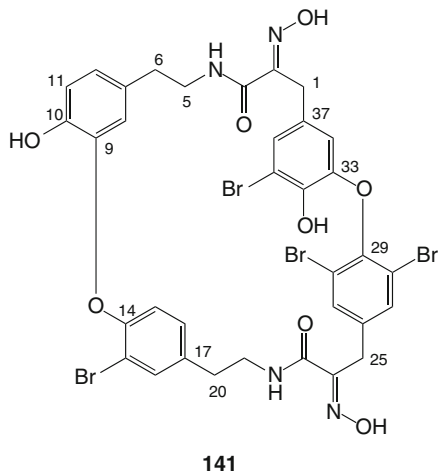
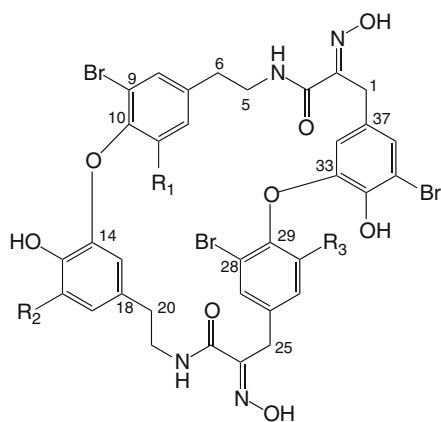
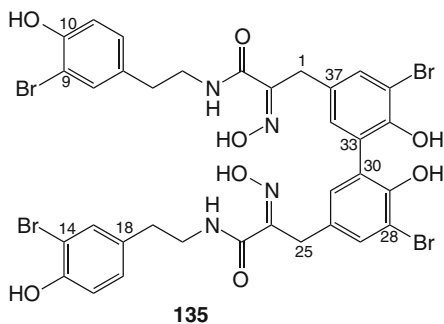
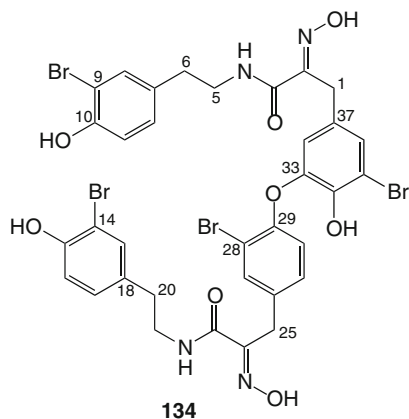
The sponge *Aplysina gerardogreeni* collected at the Gulf of California yielded four cytotoxic dibromotyrosine-derived metabolites, aplysinones A–D (**124**–**127**) [158]. Cytotoxicity of aplysinones (A–D) was evaluated against three human tumor cell lines MDA-MB-231 (breast adenocarcinoma), A-549 (lung carcinoma), and HT-29 (colon adenocarcinoma) [158]. Against MDA-MB-231 cells, all aplysinones showed cytotoxicity with IC₅₀ values between 3.0 and 7.6 μM, whereas only aplysinone B (**125**) showed cytotoxicity against lung carcinoma A-549 cells with an IC₅₀ value of 4.1 μM. Furthermore, aplysinones A (**124**), B (**125**), and D (**127**) proved cytotoxic against colon adenocarcinoma HT-29 cells with IC₅₀ values of 9.1, 3.0, and 11.3 μM, respectively [158].



Antithrombotics (= anticoagulants) are crucial therapeutic agents for a number of thrombotic disorders such as myocardial infarction, angina, pulmonary embolism, and cerebrovascular incidences. The conventional antithrombotic therapy is performed by intravenous administration of heparin followed by oral treatment with warfarin. Besides being indirect and nonspecific inhibitors of coagulation serine proteases, both heparin and warfarin require very careful and costly monitoring to ensure safe therapeutic drug levels over treatment duration due to the high risk of bleeding. Therefore, enormous efforts focused on new plausible drug candidates with an improved efficacy-to-safety index compared to heparin and warfarin. Factor XIa (FXIa) is a trypsin-like serine protease that plays a major role in the amplification phase of the coagulation cascade and in maintaining clot integrity. FXIa is a unique target as its specific inhibitors might inhibit thrombosis without intimate interruption of normal hemostasis and thus might prevent or minimize the risks of hemostatic complications. In an attempt to achieve this target, Buchanan et al. isolated a series of bromotyrosine-derived alkaloids from two different collections of the Australian Verongid sponge *Suberea clavata*, trivially named as clavatadine A–E (**128**–**132**) [159, 160]. All clavatadines were tested for their inhibitory activities against factor XIa. Only clavatadines A (**128**) and B (**129**) inhibited selectively FXIa with IC₅₀ values of 1.3 and 27 μM, respectively [159], while other clavatadines showed only weak inhibitory activity (17–37%) against FXIa at concentrations up to 222 μM [160]. The crystal structure and molecular docking of **128** enabled understanding of SARs. Conclusively, they revealed that clavatadine A (**128**) can approach/bind in the S1–S1' pocket of FXIa by favorable interactions with Asp189 at its guanidine group on one end and the free carboxylate to either Arg37D or Lys192 of the other. This would result in a close contact between the side chain of Ser195 and the carbamate group of **128**, which eventually leads to the covalent binding with FXIa. Clavatadine B (**129**) is more than one order of magnitude less potent than **128**, presumably due to weaker interactions between its amide group and either Arg37D or Lys192, compared to the carboxylate moiety in **128** [159].



Bastadins are heterodimers biogenetically derived from oxidative coupling of two brominated tyrosine-tyramine amides. To date, a total of 24 bastadin analogues have been isolated from the Indo-Pacific Verongid sponges *Ianthella basta* [161–171], *Ianthella quadrangulata* [172, 173], *Ianthella* sp. [174], and *Psammaplysilla purpurea* [175, 176] in addition to the Dendroceratid sponge *Dendrilla cactos* [177].



	R ₁	R ₂	R ₃
136	H	Br, EA ^{5,6}	H
137	Br	Br	H
138	H	H	H
139	Br	H	H
140	Br	Br	Br

Bastadins are structurally classified into three groups, according to the proposed biosynthetic pathway by Jaspars et al. [166] (Scheme 4.4), depending upon the degree and position of the phenolic couplings linking the monomeric units such as hemibastadin (**133**) (Scheme 4.4) [165, 178]. The linear (= acyclic) bastadins contain a single ether or biaryl linkage like in bastadin 1 (**134**) and bastadin 3 (**135**), while the macrocyclic members of the series possess either the bastarane skeleton (Scheme 4.4) including bastadin 4 (**136**), 6 (**137**), 9 (**138**), 16 (**139**), and 24 (**140**) in which the hemibastadin units are linked by phenolic ethers from C10 to C14 and from C29 to C33, or the isobastarane skeleton (Scheme 4.4) such as bastadin 13 (**141**), in which ethers link C9 to C14 and C29 to C33 (Scheme 4.4).

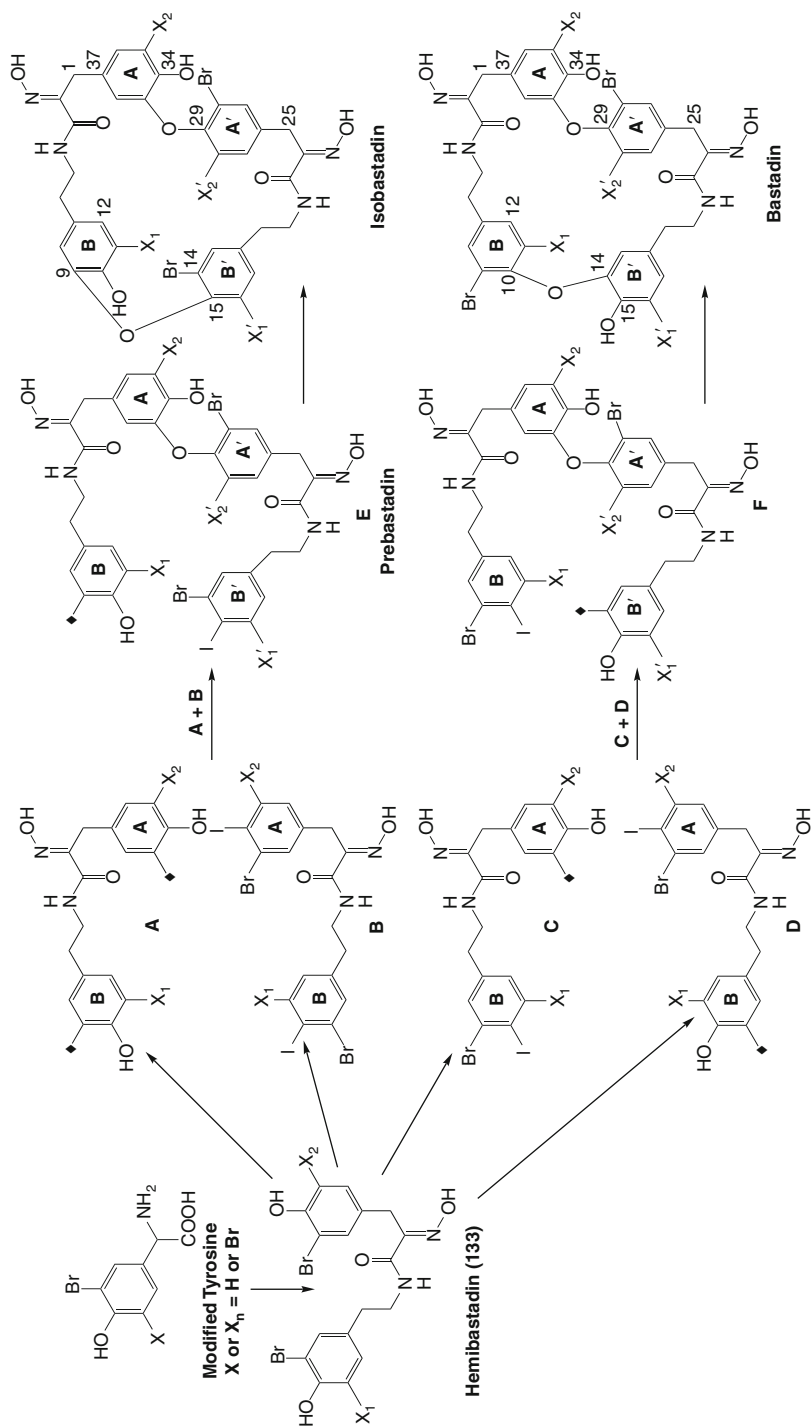
Bastadins were first isolated from the Australian sponge *Ianthella basta* and revealed potent in vitro antimicrobial activity against Gram-positive bacteria [161, 162]. Since then, bastadins have demonstrated a vast array of biological activities including cytotoxicity [163, 164, 173, 175, 177, 179], anti-inflammatory activity [163], inhibitory activity of topoisomerase II, dehydrofolate reductase, inosine 5'-phosphate dehydrogenase, 12- and 15-human lipoxygenases [166, 175, 180], and agonistic activity toward the sarcoplasmic reticulum Ca^{2+} channel through modulation of the Ry_1R FKBP12 receptor complex [168, 181, 182]. In addition, the antiangiogenic activity of the bastadins has been reported by Kobayashi et al. [169, 170]. Furthermore, Proksch et al. investigated the antifouling activity of selected sponge metabolites on settling of barnacle larvae, or cyprids, of *Balanus improvisus* [171].

The study included selected sponge-derived natural products displaying pronounced activity in other bioassays such as ageliferin (**82**), isofistularin-3 (**102**) (Scheme 4.3), and sceptrin (**81**) which are known to be fish deterrents [183, 184] and hymenidin (**18**) and **81** inhibit serotonin being involved in cyprid settling behavior [106] in addition to psammaplin A (**109**), hemibastadin (**133**), bastadins 3 (**135**), 4 (**136**), 9 (**138**), and 16 (**139**). In this study, only bastadins and psammaplin A inhibited the settlement of the cyprids in a dose-dependent manner in a range of 0.1–10 μM [171].

However, hemibastadin (**133**) and psammaplin A (**109**) proved to be toxic to *B. improvisus* when tested at a dose of 10 μM . The antifouling activity of the active compounds is linked to the oxime moiety as a uniting structural feature. In order to justify this hypothesis, two synthetic products including debromohemibastadin-1 and L-tyrosinyltyramine, differing only in the presence of an oxime vs. amino function, were investigated. Although L-tyrosinyltyramine proved to be completely inactive even at a concentration of 100 μM , the oxime-bearing debromohemibastadin inhibited barnacle settlement at almost similar concentrations as the brominated derivatives thus corroborating the importance of the oxime function [171].

4.3 Peptides

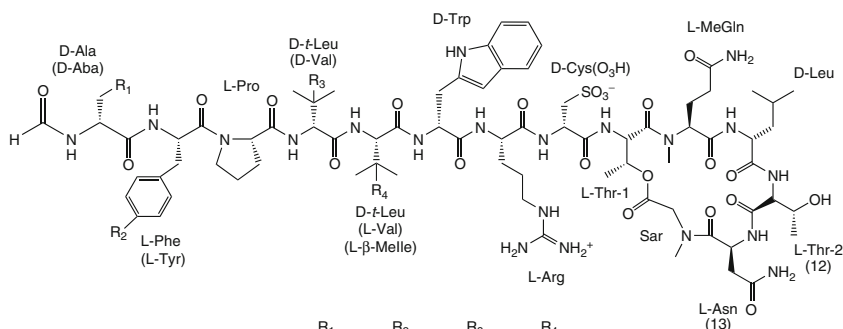
Bioactive peptides from marine sponges are receiving considerable interest by natural product chemists and pharmacologists alike and represent



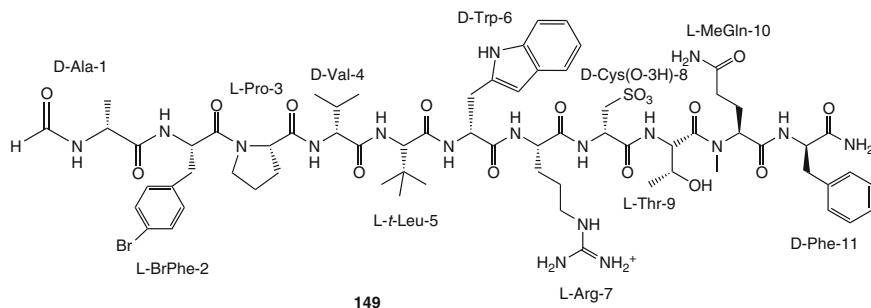
Scheme 4.4 Biosynthetic pathway of bastadins as proposed by Jaspars et al. [166]. Donor site = ● (phenolic oxygen) Acceptor site = ◆ (aryl bromine)

a well-established sector of marine natural products research. Most bioactive peptides from marine sponges comprise unique structures in comparison with those from other sources. For example, marine peptides are often cyclic or linear peptides containing unusual amino acids which are either rare or even absent in terrestrial and microbial peptides. In addition they frequently contain uncommon linkages between amino acids such as kapakahines isolated from a Pohnpei sponge *Cribrochalina olemda* [185–187].

Discodermin A (**142**) was the first bioactive peptide isolated from the marine sponge *Discodermia kiiensis* collected at Shikine Island (Japan) [188, 189]. Further chemical investigation of the extract of the same sponge resulted in the isolation of three additional discodermins B–D (**143–145**) [190], whereas bioassay-guided fractionation of the extract of *D. kiiensis* collected off Atami in the Gulf of Sagami (Japan) led to the isolation of discodermin E [191]. Structural study of discodermin E revealed the presence of a D-kynurenine residue replacing a D-Trp residue and a reversed sequence of the 12th and 13th residues from the *N*-terminus compared to discodermin A (**142**) [191]. In addition to discodermin E, three further congeners including discodermins F–H (**146–148**) were obtained from the latter sponge [192]. Discodermins A–H and the structurally related discobahamins A and B [193], polydiscamides A–D [194, 195], and halicylindramides A–E [196, 197] have been obtained from marine sponges of the genera *Discodermia*, *Iricina* and *Halichondria*, respectively. They represent a group of bioactive peptides containing 13 to 14 known as well as rare amino acid residues with a macrocyclic ring formed by lactonization of a threonine moiety with the carboxy terminal of the peptide chain. Halicylindramide E (**149**) is an exception as it is a linear peptide composed of 11 amino acids.



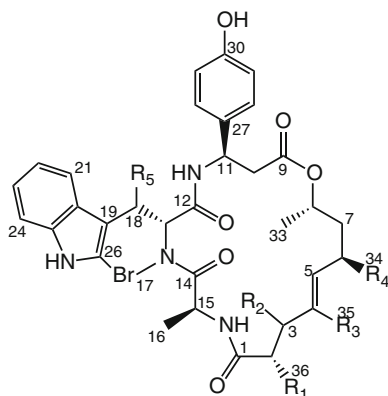
	R ₁	R ₂	R ₃	R ₄
142	H	H	CH ₃	CH ₃
143	H	H	H	CH ₃
144	H	H	CH ₃	H
145	H	H	H	H
146	H	H	CH ₃	C ₂ H ₅
147	CH ₃	H	CH ₃	CH ₃
148	H	OH	CH ₃	CH ₃



Discodermins A–D (**142–145**) revealed *in vitro* antibacterial activity [188–191]. They were later found to be potent inhibitors of phospholipase A₂ (PLA₂) and **142** inhibited the tumor promotion activity of okadaic acid [191]. In addition, discodermins F–H (**146–148**) were cytotoxic against P388 murine leukemia cells with IC₅₀ values of 0.6, 0.23, and 0.6 μM, respectively [192]. Discobahamins A and B exhibited weak antifungal activity against *Candida albicans* [193]. Polydiscamide A inhibited the proliferation of human lung cancer A549 cell line (IC₅₀ = 0.4 μM) *in vitro* and the growth of *Bacillus subtilis* (MIC of 1.8 μM) [194]. Interestingly, polydiscamides B–D acted as pain modulators by activating the sensory neuron-specific G protein coupled receptors (SNSRs), which are expressed solely in dorsal root ganglia [198]. Previous studies showed that SNSRs are key players in both acute and persistent pain [199]. Due to the highly restricted distribution of SNSRs in the body, ligands that interact with these receptors may potentially modulate pain with very few side effects [195]. Polydiscamides B–D showed potent agonist activity against human SNSR with EC₅₀ values of 1.26, 3.57, and 2.80 μM [195], and they were the first examples of nonendogenous compounds with human SNSR agonist activity. Therefore, they could potentially be modified for therapeutic use as pain modulators.

Halicylindramides A–D, featuring D-Phe and L-BrPhe instead of D-Leu and L-Phe (or L-Tyr) in discodermins, respectively, exhibited antifungal activity against *Mortierella ramanniana* at 7.5 μg/disk as well as cytotoxic activity against P388 murine leukemia cells with IC₅₀ values of 0.3, 0.1, 0.01, and 1.2 μM, respectively [196, 197].

Two families of closely related cyclic depsipeptides, the jaspamides and the geodiamolides, have been isolated from a variety of tropical marine sponges. Jaspamide (jasplakinolide) (**150**), obtained independently from *Jaspis* sp. collected off Palau [200] and Fiji [201] in 1986, was the first member of this group of depsipeptides to be reported. Thereafter, several reports on the presence of jaspamide in other sponge genera, including *Auletta* cf. *constricta* [202] and *Hemiamsterella minor* [203] were published. Geodiamolides A (**154**) and B (**155**) were isolated from the Caribbean sponge *Geodia* sp. [204].



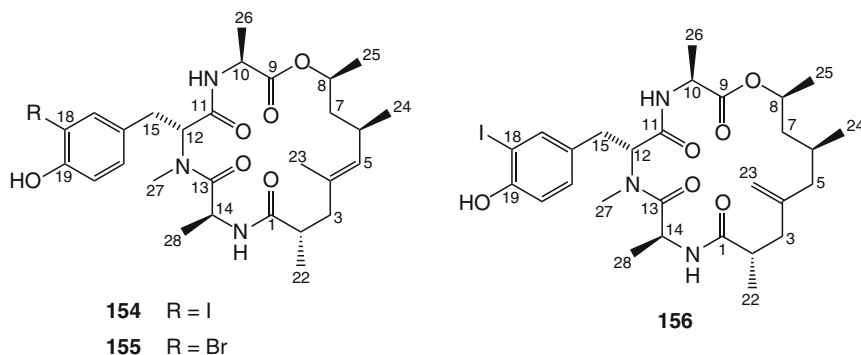
	R ₁	R ₂	R ₃	R ₄	R ₅
150	CH ₃	H	CH ₃	CH ₃	H
151	H	H	CH ₃	CH ₃	H
152	CH ₃	H	CH ₃	H	H
153	CH ₃	H	CH ₃	CH ₃	OH

After the discovery of jaspamide (**150**) and its pronounced biological activities which include antifungal [205], anthelmintic, insecticidal [200, 201], and cytotoxic activity [206], sponges of the genus *Jaspis* have received considerable attention. Sixteen additional jaspamide derivatives (B–H and J–R) have been isolated from different collections of the marine sponge *Jaspis splendens* [207–211]. All jaspamide derivatives exhibited a consistent antiproliferative activity with IC₅₀ values ranging from 0.01 to 10 μM [210, 211] when tested against MCF-7 human breast adenocarcinoma, HT-29 colon carcinoma, or L5178Y mouse lymphoma cell lines.

The antimicrofilament activity was measured and paralleled the observed in vitro cytotoxicity. A thorough structural analysis indicated that the sole invariable residue in all jaspamides is β-tyrosine whereas a wide variability of the alkylation and oxidation pattern of the polypropionate subunit as well as of the identity of the first two amino acids, namely, alanine and abrine (*N*-methyltryptophan), of the tripeptide portion was observed. Therefore, the β-tyrosine residue appeared to be the only strict common feature essential for biological activity in the tested tumor cell lines, mainly assuring a β-turn motif for the folding of the entire molecule [210]. Moreover, the modifications of the abrine residue, claimed as essential for the observed biological activity [212], appeared to have little influence on the observed antiproliferative effect with the exception of jaspamide N (**153**), where the β-hydroxylation of tryptophan unit causes a diminution of the biological activity. As suggested by Maier [213], the 1,3 methyl groups of the polypropionate subunit, imposing to the macrocycle conformational constraints through *syn* pentane

interactions, play a significant role in assuring a correct folding of the entire molecule as suggested by the drop of activity for jaspamides F (**151**) and H (**152**).

Geodiamolides A (**154**) and B (**155**) were first isolated from the Caribbean sponge *Geodia* sp. [204]. Geodiamolides C–F [214] and geodiamolide G (**156**) [215] have been reported from a *Cymbastela* sp. collected in Papua New Guinea. Geodiamolides H and I have been reported from the marine sponge *Geodia* sp. collected off Macqueripe Bay (Trinidad) [216]. Geodiamolide TA was isolated from the South African sponge *Hemiasterella minor* [203], while the structurally related neosiphoniamolide A has been obtained from the New Caledonian sponge *Neosiphonia superstes* [217]. In addition, geodiamolides J–P and R were isolated from the marine sponge *Cymbastela* sp. collected in Papua New Guinea [218].

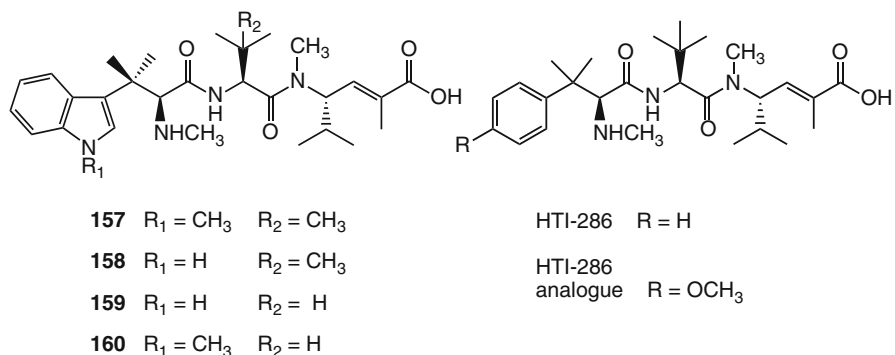


There are now, to the best of our knowledge, 19 known members of the geodiamolide family of cyclodepsipeptides. Variations have been observed in all three amino acid positions and also in the polyketide portion of the molecule. However, comparison of their cytotoxicities showed that significant variation in the three amino acid residues causes only minor changes in the levels of cytotoxicity exhibited by this class of compounds. In contrast, geodiamolide G (**156**) (in vitro human glioblastoma/astrocytoma U373, IC_{50} 12 μ M; in vitro inhibition of human ovarian carcinoma HEY, IC_{50} 13.4 μ M) [215], with its modified polyketide fragment, is significantly less toxic than the analogous geodiamolide A (**154**) (in vitro inhibition of human glioblastoma/astrocytoma U373, IC_{50} 0.02 μ M; in vitro inhibition of human ovarian carcinoma HEY, IC_{50} 0.07 μ M) [218].

The jaspamide/geodiamolide family of metabolites occurs across taxonomically distant groups of sponge species [200–218]. It has been suggested that microorganisms associated with the respective sponges may be responsible for the production of these metabolites [203]. The isolation of chondramides, which are jaspamide analogues, from cultures of various strains of *Chondromyces crocatus* [219] strongly supported the hypothesis of a microbial origin for the jaspamides/geodiamolides.

Hemiasterlin (**157**) is a prototype of a group of antimitotic tripeptides which was first isolated together with geodiamolide TA in 1994 from the marine sponge *Hemiasterella minor* [203]. It revealed significant cytotoxicity against P388 leukemia cell line with IC_{50} value of \sim 0.02 μ M [203]. The related isomers hemiasterlins

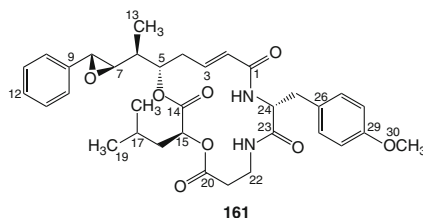
A (**158**) and B (**159**) were obtained from sponges of the genus *Auletta* and *Cymbastella* in 1995 [215], whereas a fourth analogue, hemiasterlin C (**160**) was isolated from the marine sponge *Siphonochalina* sp. collected off the coast of Papua New Guinea in 1999 [220]. In 1996, an X-ray crystal structure analysis of the hemiasterlin methyl ester confirmed its linear structure and unusual amino acids existence [221]. All hemiasterlins (**157–160**) exhibited pronounced *in vitro* cytotoxicity against a variety of human and murine cell lines with IC_{50} values in the nanomolar range [215]. The potent antiproliferative activity of hemiasterlins was found to be due to the induction of mitotic arrest in metaphase with cellular dynamics similar to those of known tubulin binders, such as the chemotherapeutics paclitaxel or vinblastine, at ED_{50} values ranged from 0.5 nM (hemiasterlin) to 28 nM (hemiasterlin B) [222].



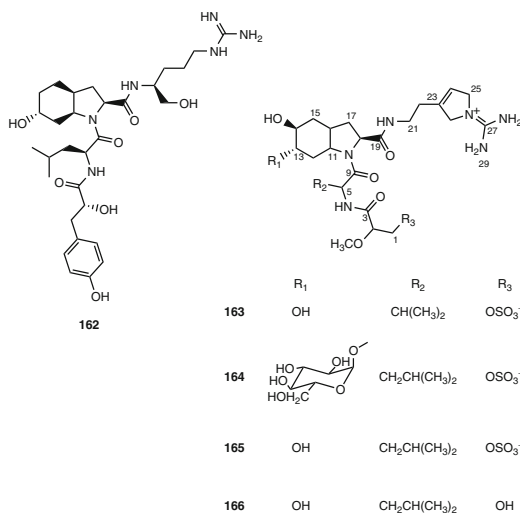
Extensive SAR studies demonstrated that HTI-286, a simpler synthetic analogue of hemiasterlin (**157**) with a phenyl substituent replacing the *N*-methyltryptophan, is more potent than **157** [221], whereas an analogue of HTI-286 with a *para*-methoxyl substituent on the benzene ring was even more potent [220]. Other structural elements, including the geminal β,β -dimethyl group and the *N*-methyl on the first amino acid residue (N terminus), the isopropyl and an olefin in the homologated γ -amino acid (C terminus) including a terminal carboxylic acid or methyl ester, were essential for activity. The aryl side chain on the N terminus could be replaced synthetically by alkyl groups (e.g., *tert*-butyl) while still retaining potent activity [223–226]. Preclinical studies showed that HTI-286 causes tumor regression and growth inhibition of human xenografts in mice [227]. An open-label phase I clinical trial of HTI-286 was completed in patients with advanced solid tumors; however, there were no objective responses and common toxicities observed including neutropenia, nausea, alopecia and pain [228]. Therefore, phase II trials have been halted. Nevertheless, there is still interest in HTI-286 according to recent results including high antitumor activity in androgen-dependent and androgen-independent mouse models of refractory prostate cancer and in a newly established *in vitro* taxane-resistant prostate PC-3 cell line [229].

Arenastatin A (**161**) is another example of cytotoxic cyclic depsipeptides that was isolated from the Okinawan marine sponge *Dysidea arenaria* [230]. Arenastatin A exhibited potent cytotoxicity against KB human epidermoid

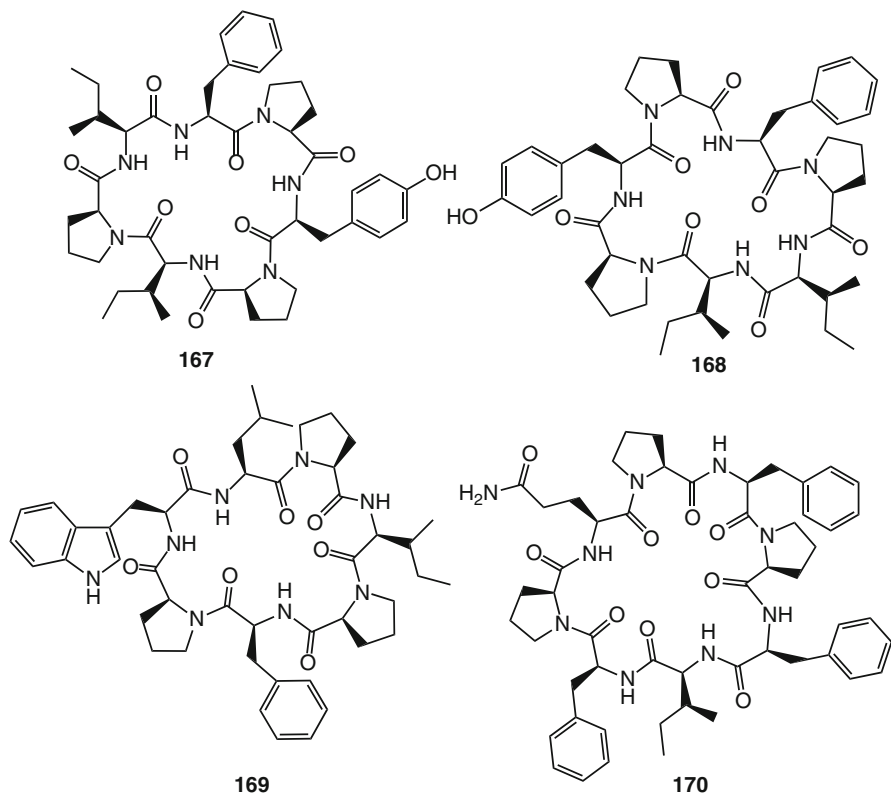
carcinoma cells with IC_{50} value of 8.3 μM [230]. Its absolute configuration [231] and its total synthesis [232] were reported.



From the family Dysideidae, dysinosins A–D (**163–166**) have been reported [233, 234]. Dysinosin A (**163**) was isolated from a new genus of sponges found near Lizard Island (Australia) [233]. Afterward, it was reisolated together with the other three dysinosins B–D from the Australian marine sponge *Lamellodysidea chlorea* [234]. Dysinosins are structurally related to the cyanobacterial metabolites aeruginosins [235–237]. Aeruginosin 98-A (**162**) was reported in 1994 as a thrombin and trypsin inhibitor from the cyanobacterium *Microcystis aeruginosa* [235]. Not surprisingly, dysinosins A–D also exhibited inhibitory activity against thrombin (IC_{50} values of 0.17– > 5.1 μM) and factor VIIa (IC_{50} values of 0.09–1.32 μM) [233, 234]. Dysinosins A–D (**163–166**) were further investigated to assess their SARs. The X-ray structural analysis of dysinosin A (**163**) revealed a hydrogen bonding network forming the dysinosin-A-thrombin complex [233]. The introduction of a sugar unit at C-13 in dysinosin B (**164**) gave a slight increase in inhibition of factor VIIa compared to both dysinosins A (**163**) and C (**165**) (0.09 μM compared to 0.108 and 0.124 μM , respectively), while selectivity relative to thrombin decreased to 1.9 compared to 4.2 and 4.4, respectively [234]. Desulfated dysinosin D (**166**) was found to be ten times less potent against both factor VIIa and thrombin compared to other sulfated dysinosins, indicating the importance of the sulfate group [234].



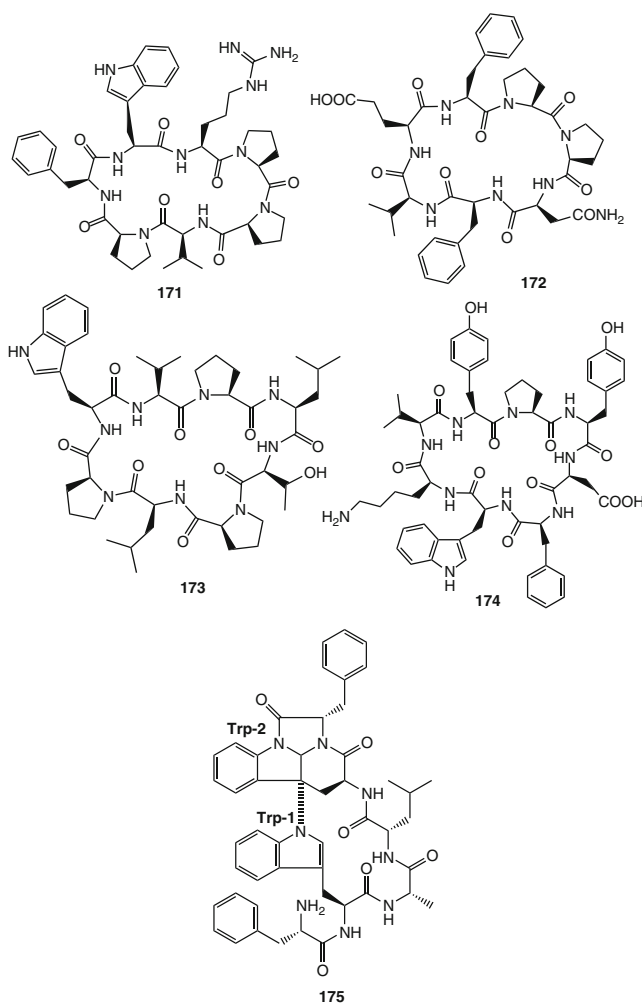
Phakellistatins and hymenamides are two groups of proline-rich cyclopeptides. They were isolated mainly from different species of the marine sponge genera *Phakellia* and *Hymeniacidon*, respectively. However, phakellistatins 1–14 and isophakellin 3 were isolated from different species of the genus *Phakellia* [238–247], and two conformers of phakellistatin 2 have been reported from the Fijian marine sponge *Stylotella aurantium* [248]. Phakellistatin 1 (**167**) was the first reported congener from the Indo-Pacific (Truk Archipelago) marine sponge *Phakellia costata* [238]. Phakellistatin 1 revealed moderate cytotoxicity against P388 cells ($IC_{50} = 9.0 \mu M$) [238]. Amongst the reported phakellistatins to date, phakellistatins 2 (**168**) [239], 6 (**169**) [242], and 11 (**170**) [244] exhibited the most potent antiproliferative activity against P388 murine leukemia cell line with IC_{50} values of 0.4, 0.2, and 0.2 μM , respectively. Moreover, phakellistatin 6 (**169**) was more active than phakellistatin 2 (**168**) against a panel of six human cancer cell lines, namely, ovarian (OVCAR-3), brain (SF-295), renal (A498), lung (NCI-H460), colon (KM20L2), and melanoma (SK-MEL-5) cell lines, with GI_{50} ranges of 0.02–0.09 μM [242] and 1.2–3.6 μM [239], respectively.



Hymenamides (A–K) have been isolated from the Okinawan marine sponge *Hymeniacidon* sp. [249–252]. Hymenamides A (**171**) and B (**172**) were reported in 1994, and only the latter exhibited cytotoxicity against L1210 and KB tumor cell lines

with IC_{50} values of 3.8 and 7.2 μM , respectively [249]. In addition to hymenamides B, only hymenamide J (**174**) showed cytotoxicity against L1210 and KB tumor cell lines (IC_{50} values of 2.4 and 0.7 μM , respectively), while hymenamide H (**173**) exhibited cytotoxicity only against L1210 cells ($IC_{50} = 7.0 \mu M$) [252].

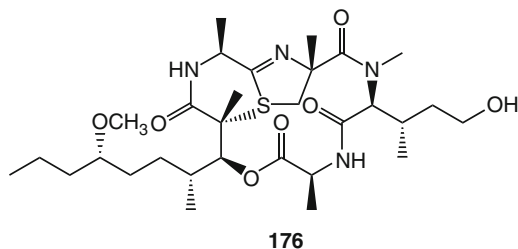
Beside hymenamides, hymenistatin 1, a proline-rich cyclo-octapeptide, was also purified from the marine sponge *Hymeniacidon* sp. collected in Palau [253]. Hymenistatin 1 was active against the P388 murine leukemia cell line (IC_{50} 3.9 μM) [253]. In addition, it was found to exert an immunosuppressive effect (both in the humoral and cellular immune responses) comparable to that of the well-known immunosuppressive agent cyclosporin [254].



From other sponges of the same order Halichondrida, axinastatins [255, 256], axinellins A–C [257, 258], and stylissamides A–D [259] have been reported

from different species of the marine sponge genus *Axinella*, the Fijian marine sponge *Stylotella aurantium* and *Stylissa caribica*, respectively. They all exhibited mild to moderate antiproliferative activity. However, from a Jamaican collection of *Stylissa caribica*, two proline-rich cyclic heptapeptides, stylisins 1 and 2, have been isolated. In contrast to other peptides, stylisins 1 and 2 proved inactive in antimicrobial, antimalarial, anticancer, anti-HIV-1, anti-Mtb, and anti-inflammatory assays [260]. Kapakahines A–G are also proline-containing cyclic peptides isolated from a Pohnpei sponge *Cribrochalina olemda* (order Haplosclerida) [185–187]. They share a unique structural feature: two tryptophan residues (Trp-1 and Trp-2) are not linked by an amide bond but by a N–C bond from the indole nitrogen of Trp-1 to the β -indole carbon of Trp-2. Kapakahine B (**175**) was the first reported congener, and it exhibited moderate cytotoxicity against P388 cells ($IC_{50} = 5.9 \mu M$) [185]. All other kapakahine derivatives exhibited moderate to weak cytotoxic activity [186, 187]. Their structures, however, were found to be unique and of biogenetic interest.

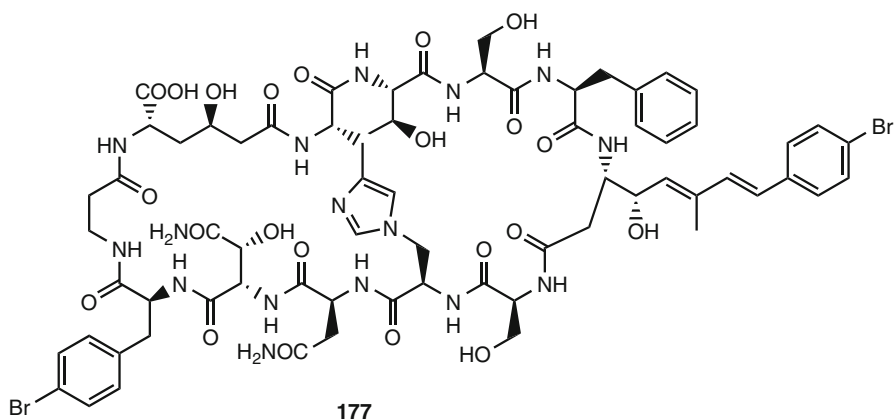
Haligramides A and B were also identified as proline-rich cyclopeptides from the marine sponge *Haliclona nigra* collected from the northern coast of Papua New Guinea [261]. The cyclic depsipeptides, halipeptins (A–D), were isolated from another species of the genus *Haliclona* collected in Vanuatu [262, 263]. Although, haligramides A and B exhibited moderate activity in the cytotoxicity assay against four human tumor cell lines [261], halipeptin A (**176**) revealed no significant results in either cytotoxicity, antifungal, antiviral, or antimicrobial assays [262].



Interestingly, halipeptin A (**176**) was found to possess potent *in vivo* anti-inflammatory activity, causing about 60 % inhibition of edema in mice at the dose of 0.3 mg/kg (i.p.) compared to indomethacin and naproxen (ED_{50} of 12 and 40 mg/kg, respectively) [262].

Recently, euryjanicins (A–D) have been reported from the Caribbean marine sponge *Prosuberites laughlini* [264, 265]. They are cycloheptapeptides containing two or three prolines, an array of apolar residues, and one or two aromatic residues. Euryjanicins A, C, and D each contain a serine residue, whereas euryjanicin B possesses one threonine unit. When tested against the National Cancer Institute 60 tumor cell line panel, all euryjanicins displayed weak cytotoxicity [265].

Theonellamides (A–F) are a group of cytotoxic peptides with novel amino acid residues and complex bicyclic macrocyclic rings isolated from the marine sponge *Theonella* sp. collected off Hachijo-jima Island (Japan) [266, 267].

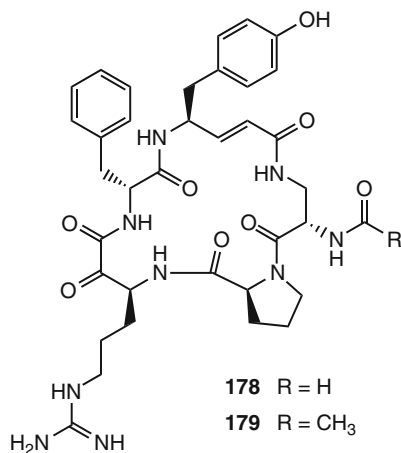


Theonellamide F (**177**) was the first reported congener exhibiting antifungal activity against pathogenic fungi *Candida* sp., *Trichphyton* sp., and *Aspergillus* sp. at MIC values between 1.8 and 7.3 μM . It is also cytotoxic against L1210 and P388 leukemia cells with IC_{50} values of 1.9 and 1.6 μM , respectively [266]. In addition, all other theonellamides (A–E) were cytotoxic against P388 cells (IC_{50} 's between 0.5 and 2.8 μM) [267].

Polytheonamides (A–C) are polypeptides consisting of 20 amino acid residues with unprecedented structural features. They were reported from the marine sponge *Theonella swinhoei* (Hachijo-jima Island, Japan) [268, 269]. Polytheonamides exhibited potent cytotoxic activity against P388 cells ($\text{IC}_{50} = 13.5\text{--}15.5$ pM) [269].

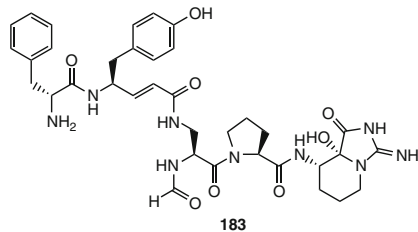
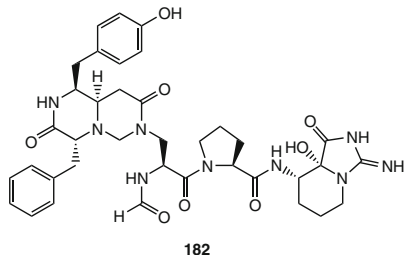
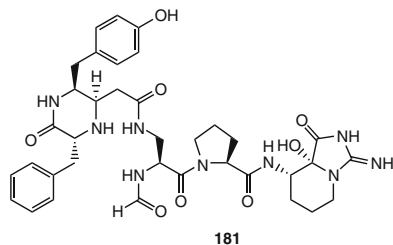
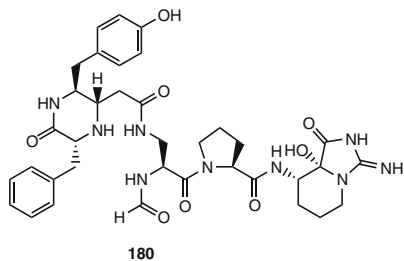
Cyclotheonamides A (**178**) and B (**179**) are cyclic peptides containing unusual amino acid residues, i.e., vinylogous tyrosine (V-Tyr), α -ketohomoarginine (K-Arg), and β -linked-diaminopropionic acid (Dpr). They were isolated from the marine sponge *Theonella swinhoei* (Japan) [270] together with two additional congeners C and D [271], whereas cyclotheonamide E was isolated from a morphologically different specimen of *Theonella swinhoei* [271]. Chemical investigation of the marine sponge *Theonella* sp. collected off Tanegashima Island led to the isolation of cyclotheonamides E2 and E3 [272], while cyclotheonamides E4 and E5 were obtained from the Okinawan marine sponge *Ircinia* sp. [273]. Cyclotheonamides (A–E) and (E2–E5) were found to possess potent inhibitory activity against serine proteases including thrombin, trypsin, and plasmin [270–273]. Their mode of action was elucidated by X-ray crystallography of the complex between cyclotheonamide A (**178**) and human α -thrombin which disclosed that (1) the binding of **178** to the catalytic triad of the enzyme is achieved through forming a network of hydrogen bonds between the α -keto group of the K-Arg residue and the hydroxyl group of Ser195 of the enzyme, (2) V-Tyr residue proved to be involved in the bonding mechanism, and (3) cyclotheonamide D which

possesses D-Leu instead of D-Phe in **178** showed comparable activity against thrombin; thus, a further hydrophobic amino acid can replace D-Phe [271].

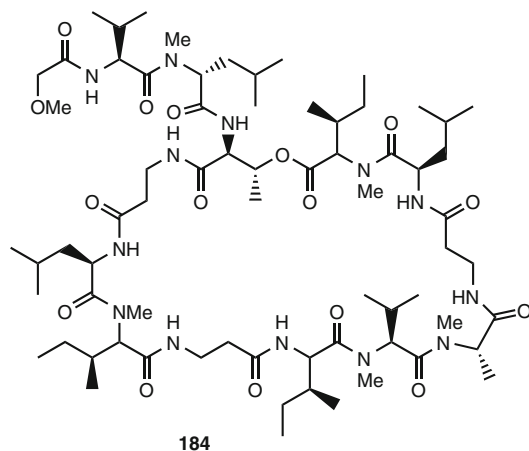


However, a comparative X-ray study against either human α -thrombin or bovine β -trypsin revealed that cyclotheonamide A (**178**) inhibited trypsin stronger than thrombin ($IC_{50} = 16$ and 23 nM, respectively) [272]. These results were substantiated to the more favorable (1) aromatic interaction of the D-Phe in **178** with Tyr39 and Phe41 in trypsin than with Glu39 and Leu41 in thrombin and (2) interaction of *N*-formyl Dpr residue with Gly174 and Gln175 in trypsin than Ile174 and Arg175 in thrombin [272]. Since the cyclotheonamides exhibited potent inhibitory activity against serine proteases, the marine sponge *T. swinhoei* has been thoroughly investigated. From a specimen collected off Hachijo-jima Island in 1993, pseudotheonamides A₁, A₂, B₂, C, D, and dihydrocyclotheonamide A were isolated [273].

Pseudotheonamides A₁ (**180**), A₂ (**181**), and B₂ (**182**) are linear pentapeptides embracing the rare piperazinone and piperidinoiminoimidazolone ring systems, while pseudotheonamide C (**183**) contains V-Tyr instead of a piperazinone ring. Pseudotheonamide D, a tetrapeptide lacking a C-terminal K-Arg unit and dihydrocyclotheonamide A, is a reduction product of cyclotheonamide A (**178**). Peptides **180–183** and dihydrocyclotheonamide A inhibited thrombin with IC_{50} values of 1.0, 3.0, 1.3, 0.19, 1.4, and $0.33 \mu\text{M}$, respectively, whereas they inhibited trypsin with IC_{50} values of 4.5, >10 , 6.2, 3.8, >10 , and $6.7 \mu\text{M}$, respectively [274]. As revealed by a SAR study of cyclotheonamides, potent inhibition of serine proteases is associated with the presence of the α -keto group of K-Arg residue [270–273]. Therefore, it was not surprising that pseudotheonamides, in which the α -keto group was either modified or missing, showed only moderate activity [274]. Thus, cyclotheonamides and pseudotheonamides inhibited serine proteases including trypsin and thrombin. These results suggested that cyclotheonamides and pseudotheonamides may be useful for treatment of asthma and other disorders associated with inflammation of the respiratory tract in addition to coagulatory disorders [273].



Theonellapeptolides are a group of tridecapeptide lactones characterized by the presence of high proportions of D-amino acids, *N*-methyl amino acids and β -amino acids. Theonellapeptolide Id (**184**) was the first reported congener from the Okinawan marine sponge *Theonella swinhoei* [275]. From the same specimen, theonellapeptolides (Ia–Ic, Ie, and Iid) have also been purified [276–280], whereas theonellapeptolide Iie was isolated from an Indonesian specimen of *T. swinhoei* collected using SCUBA in Baranglombo Island [281]. From the same Indonesian specimen, four cyclic depsipeptides named barangamides (A–D) have been reported [281, 282].

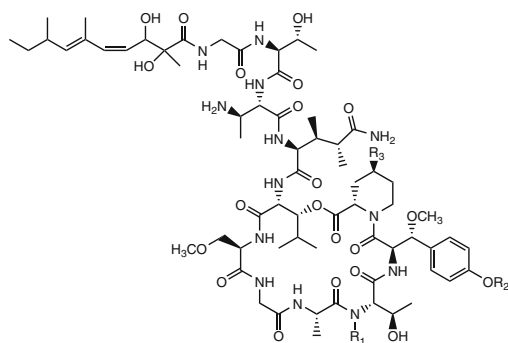


Biological activity of theonellapeptolides include cytotoxicity, ion-transport activity for Na^+ , K^+ , and Ca^{2+} ions [278], Na^+ , K^+ -ATPase inhibitory activity [283], and mild immunosuppressive activity [281]. However, other theonellapeptolide

(III series) exhibiting in vitro cytotoxicity against the P388 cell line ($IC_{50} = 5.2 \mu M$) have also been reported from a New Zealand deep-water sponge, *Lamellomorpha strongylata*, belonging to a different order compared to *T. swinhoei* [284].

The cyclic depsipeptides, papuamides (A–D), were isolated from two-sponge associations of *Theonella mirabilis* and *T. swinhoei* collected in Papua New Guinea [285]. They contain a number of unusual amino acids including 3,4-dimethylglutamine, β -methoxytyrosine, 3-methoxyalanine, and 2,3-diaminobutanoic acid or 2-amino-2-butenoic acid residues. Papuamides also contain a previously undescribed 2,3-dihydroxy-2,6,8-trimethyldeca-(4Z,6E)-dienoic acid moiety linked to a terminal glycine residue. In addition, they were the first marine-derived peptides reported to contain 3-hydroxyisoleucine and homoproline residues [285]. Papuamides A (**185**) and B (**186**) inhibited the infection of human T-lymphoblastoid cells by HIV-1_{RF} in vitro with an EC_{50} of approximately 2.6 nM [285]. Papuamide A (**185**) was also cytotoxic against a panel of human cancer cell lines with a mean IC_{50} of 0.05 μM [285].

Mirabamides (A–D) are cyclic depsipeptides structurally related to papuamides. However, mirabamides were isolated from an aqueous extract of the marine sponge *Siliquariaspongia mirabilis* (Chuuk Lagoon, Micronesia), and they differ from papuamides in either being chlorinated (4-chlorohomoproline) and/or glycosylated (β -methoxytyrosine 4'-*O*- α -L-rhamnopyranoside) derivatives [286]. A comparative study to determine the effects of mirabamides on HIV-1 infection was performed using two different viral strains, namely, HXB2 (T-cell-tropic virus) and SF162 (macrophage-tropic virus) in HIV-1 neutralization assay. In addition, HIV-1 envelope-mediated cell fusion assay was also carried out to determine whether the compounds act at early stages of infection, i.e., viral entry.



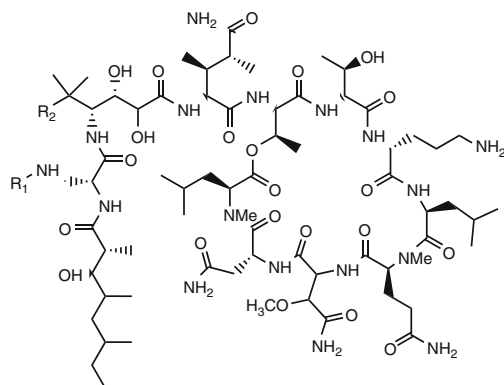
	R ₁	R ₂	R ₃
185	CH ₃	H	H
186	H	H	H
187	CH ₃	β -L-Rha	Cl
188	CH ₃	H	Cl
189	CH ₃	β -L-Rha	H

Results of testing mirabamides (A–D) and papuamide A revealed that mirabamides A (**187**), C (**188**), and D (**189**), as well as papuamide A (**185**) inhibit

HIV-1 envelope-mediated fusion with activities comparable to those observed in the neutralization assays [286]. Mirabamide A (**187**) and papuamide A (**185**) were found to be the most potent inhibitors in the fusion assay, with respective IC_{50} values of 41 and 73 nM, while mirabamides C (**188**) and D (**189**) inhibited fusion at lower micromolar concentrations (IC_{50} 's between 0.14 and 3.9 μ M) [286]. Mirabamide B is the only mirabamide containing a 2,3-dehydro-2-aminobutanoic acid residue instead of the 2,3-diaminobutanoic acid residue (Dab) that is present in other mirabamides as well as in papuamides A (**185**) and B (**186**). Interestingly, mirabamide B was consistently found to be less potent than other mirabamides (**187–189**) in both neutralization and fusion assays. Thus, the Dab residue in this class of peptides appeared to be important for anti-HIV activity [286].

As for the role of β -methoxytyrosine residue (β -OMe Tyr), mirabamide A (**187**), with rhamnosylated β -Tyr residue, was found to be the most potent analogue among the four mirabamides. This indicates that Tyr residues bearing substitutions at the 4' position can be tolerated with no deleterious effect on antiviral activity and that the presence of a free 4' hydroxyl on the Tyr unit is not essential [286]. In summary, the reported results disclosed that mirabamide A (**187**) is equipotent to papuamide A (**185**) (which also contains a β -OMe Tyr residue), whereas theopapuamide A (**190**), which was isolated from a Papua New Guinea lithistid sponge *Theonella swinhoei* and lacks a β -OMe Tyr residue, was inactive [287]. One hypothesis that would be consistent with these results is that the β -OMe Tyr residue imparts a specific conformation required for binding to target protein(s) involved in HIV-1 entry [286]. However, neither 4-chlorohomoproline nor β -methoxytyrosine 4'-*O*- α -L-rhamnopyranoside that are present in mirabamides affected their anti-HIV activities [286].

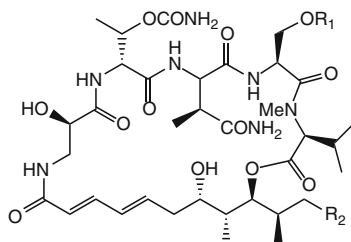
Celebesides A–C (**193–195**) and theopapuamides (B–D) together with **190** were isolated from the marine sponge *Siliquariaspongia mirabilis* (Sulawesi Island, Indonesia) [288].



190 $R_1 = H$ $R_2 = OH$

191 $R_1 = COCH_3$ $R_2 = OH$

192 $R_1 = COCH_3$ $R_2 = H$



193 R₁ = PO₃H₂ R₂ = C₂H₅

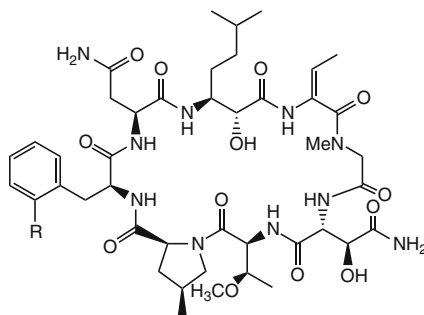
194 R₁ = PO₃H₂ R₂ = CH₃

195 R₁ = H R₂ = C₂H₅

Celebesides are unusual cyclic depsipeptides that comprise a polyketide moiety established as 7,9-dihydroxy-8,10-dimethyltrideca-2,4-dienoic acid (Dtd) and five amino acid residues including an uncommon 3-carbamoyl threonine and a phosphoserine residue in celebesides A (**193**) and B (**194**). Celebeside A (**193**) neutralized HIV-1 in a single-round infectivity assay with an IC₅₀ value of 2.1 μM, while its nonphosphorylated analogue, celebeside C (**195**), was inactive at concentrations as high as 60 μM [288]. This correlates the observed anti-HIV activity of celebesides to the presence of phosphoserine in the molecule.

Theopapuamides A–C (**190–192**) showed cytotoxicity against HCT-116 human colon carcinoma cells in vitro with IC₅₀ values between 1.3 and 2.5 μM, and they also exhibited strong antifungal activity against wild-type and amphotericin B-resistant strains of *Candida albicans* at loads of 1–5 μg/disk [288]. However, celebesides (A–C) displayed neither antibacterial nor antifungal activities against the tested microorganisms at concentrations up to 50 μg/disk [288].

Perthamides (B–D) are further examples of cyclic depsipeptides isolated from two different collections of the lithistid sponge *Theonella swinhoei* [289, 290]. Perthamide B was identified as a cytotoxic peptide [289], while perthamides C (**196**) and D (**197**) lacked antiproliferative activity on KB cell line up to a dose of 10 μg/mL [290].

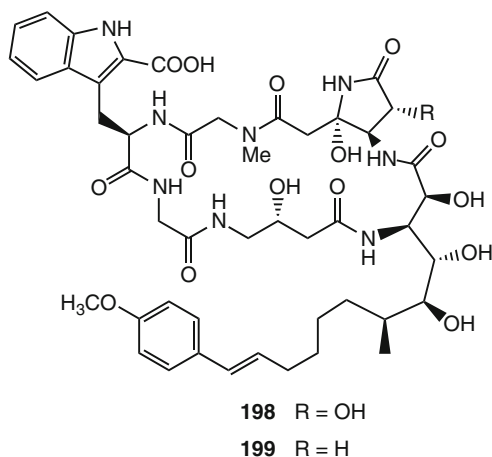


196 R = OH

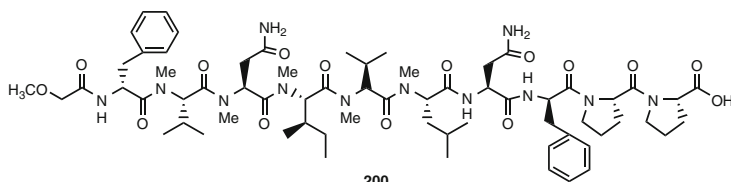
197 R = H

Interestingly, perthamides C (**196**) and D (**197**) reduced carrageenan-induced mouse paw edema significantly in vivo causing 60% and 46% reduction of edema at a dose of 300 $\mu\text{g}/\text{kg}$ (i.p.) similar to halipeptin A (**176**) [290]. These data compare well with the most common NSAID sold in the pharmaceutical market, naproxen ($\text{ED}_{50} = 40 \text{ mg}/\text{kg}$), and clearly indicate that perthamides C and D in addition to halipeptin A are about 100 times more potent. Furthermore, the observed in vivo activity implies that these compounds are able to access the site of inflammation [262, 290].

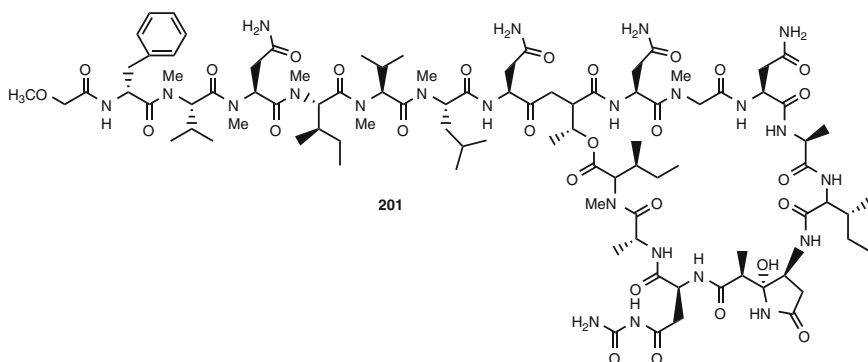
The microsclerodermins (A–I) are a family of antifungal cyclic hexapeptides which have been isolated from different collections of the lithistid sponges *Theonella* sp. and *Microscleroderma* sp. [291–293]. Microsclerodermins A (**198**) and B (**199**) were the first reported members of this family from the New Caledonian lithistid sponge *Microscleroderma* sp. [291]. Both of them, together with microsclerodermin F, showed potent antifungal properties by inhibiting the growth of *C. albicans* at 2.5 and 1.5 $\mu\text{g}/\text{disk}$, respectively [291–293]. In addition, microsclerodermins F–I showed nearly similar in vitro cytotoxic activity against HCT-116 cell line (IC_{50} 's of 1.0–2.5 μM) [293].



Koshikamide A₁ (**200**) and A₂ are linear peptides that were isolated from the sponge *Theonella* sp. collected off the Koshiki-jima Island (Japan) [294, 295]. Koshikamide B (**201**) was isolated from two separate collections of the marine sponge *Theonella* sp. [296]. Koshikamide B (**201**) is a 17-residue peptide lactone composed of six proteinogenic amino acids, two D-isomers of proteinogenic amino acids, seven N-methylated amino acids, and two unusual amino acid residues, namely, N^δ-carbamoylasparagine and 2-(3-amino-2-hydroxy-5-oxopyrrolidin-2-yl) propionic acid. Koshikamides A₁ (**200**), A₂ and B (**201**) exhibited cytotoxicity against P388 murine leukemia cells in vitro with IC_{50} values of 1.7, 4.6, and 0.2 μM , respectively [294–296].



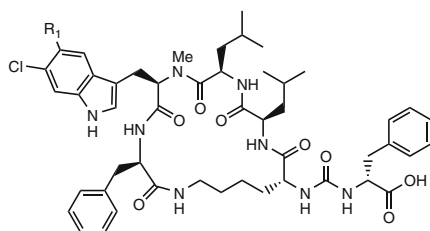
200

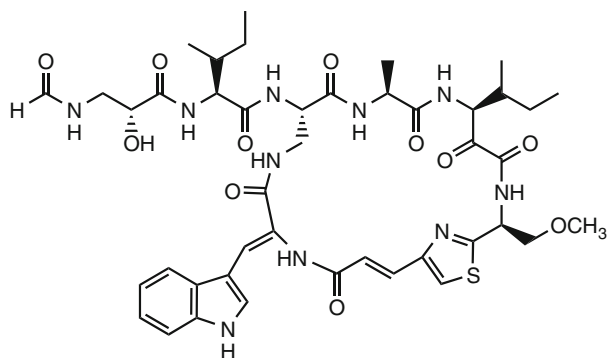


201

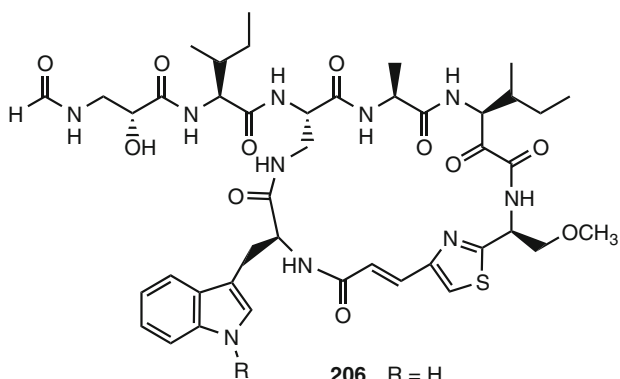
Keramamides (A–J and K–N) are a group of cyclic peptides isolated from different collections of the Okinawan marine sponge *Theonella* sp. [297–302]. They were named after the location of the first collection of the sponge which was Kerama Island, Okinawa. Keramamides A (202) and L (208) are characterized by having an ureido bond and a 6-chloro-*N*-methyltryptophan residue. Keramamides B (203) and (C–E) contain an oxazole ring as a structural feature, while keramamides (F–H) and (J–K) share the presence of a thiazole ring. Keramamides M (209) and N (210) are sulfate esters of keramamides D (204) and E (205), respectively.

Most of the known keramamides feature *in vitro* cytotoxic activity when tested against L1210 murine lymphoma (IC₅₀'s between 0.5 and 2.3 μ M) and KB human epidermoid carcinoma (IC₅₀'s between 0.45 and 6.2 μ M) cell lines [299–302]. Among the tested congeners, keramamides K (207) and L (208) were the most potent derivatives with IC₅₀ values of 0.77 and 0.5 μ M against L1210 cells and 0.45 and 0.97 μ M against KB cells, respectively [301].

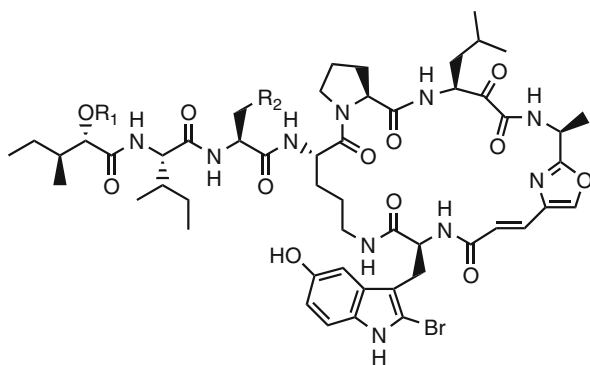
202 R₁ = OH208 R₁ = H



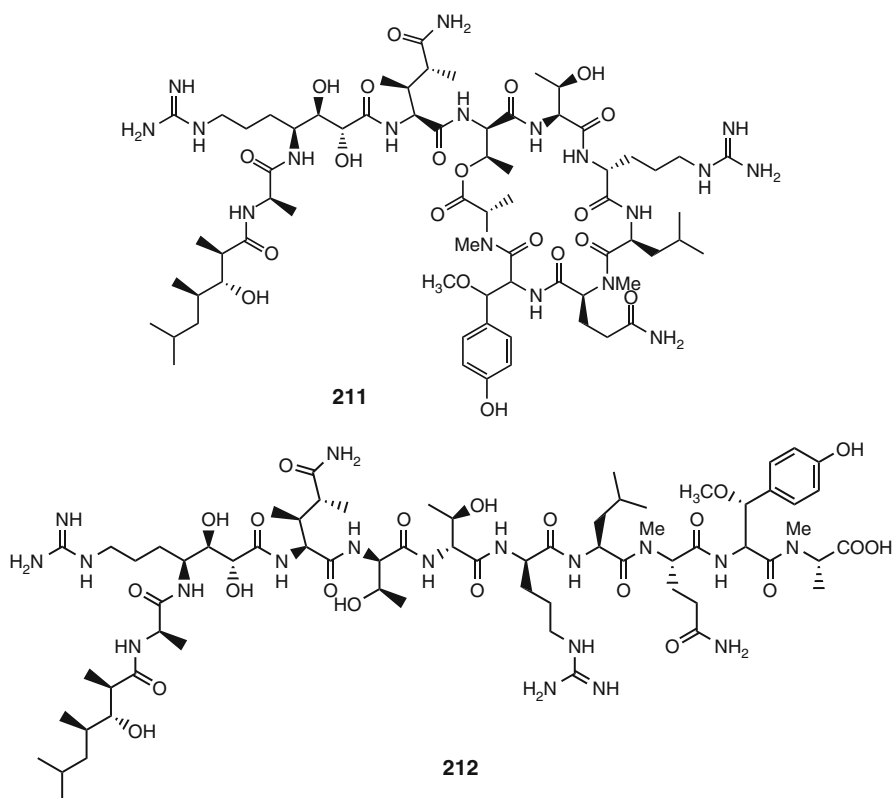
203



206 R = H

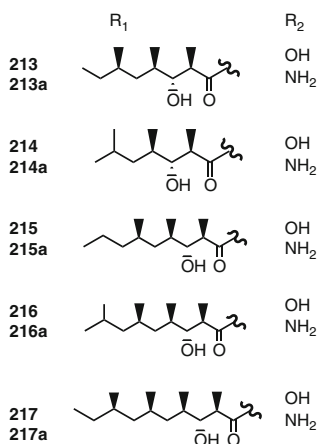
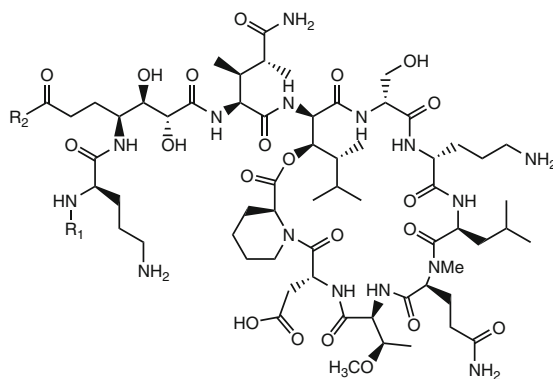
207 R = CH₃204 R₁ = H R₂ = CH₃205 R₁ = H R₂ = C₂H₅209 R₁ = SO₃H R₂ = CH₃210 R₁ = SO₃H R₂ = C₂H₅

Callipeltins are a group of marine peptides with unusual structural features and remarkable biological activities isolated from the marine sponges *Callipelta* sp. [303, 304] and *Latrunculia* sp. [305–307]. Callipeltin A (**211**) is the parent compound of this family which comprises 12 further congeners (B–M). Apart from the cyclic congeners, callipeltins A and B, all the other callipeltins are linear derivatives structurally related to callipeltin C (**212**) which, in turn, represents the acyclic counterpart of callipeltin A (**211**). Structurally, the most distinctive feature of callipeltins is the presence of several nonproteinogenic units while from a biological point of view, callipeltin A displays a broad range of bioactivities, including antiviral, antifungal, and cytotoxicity against several human tumor cell lines and regulatory activity of the myocardial force of contractions [303–309]. The unusual structural features of callipeltins and the interesting biological activities have aroused considerable interest among the synthetic chemistry community.



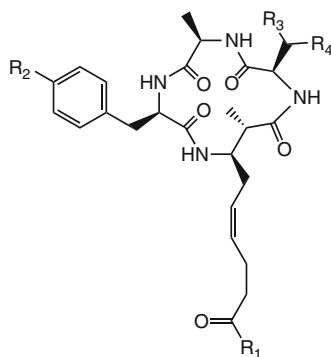
As a result, all nonproteinogenic units in this group of metabolites, namely, (3*S*,4*R*)-3,4-dimethyl-L-pyrrolysine (the N-terminus unit in callipeltin B) [310], (2*R*,3*R*,4*S*)-4-amino-7-guanidino-2,3-dihydroxyheptanoic acid [311], (2*R*,3*R*,4*R*)-3-hydroxy-2,4,6-trimethylheptanoic acid [312] linked to the N-terminus of callipeltins A, C, D, and F–I; and (*R*)- β -methoxy-D-tyrosine were obtained in a stereoselective manner [313].

Homophymine A (**213**) was isolated as the principal active constituent of the New Caledonian lithistid sponge *Homophymia* sp. [314]. Homophymine A is a cyclic depsiundecapeptide structurally related to other aforementioned marine peptides isolated from the order Lithistida such as callipeltin A, papuamides, theopapuamides, and mirabamides which are well known for their potent HIV-inhibitory activity. In addition to the common structural features, homophymine A (**213**) contains two hitherto unprecedented residues, i.e., the 4-amino-2,3-dihydroxy-1,7-heptandioic acid and 2-amino-3-hydroxy-4,5-dimethylhexanoic acid. Homophymine A exhibited cytoprotective activity against HIV-1 infection with an IC_{50} of 75 nM [314]. Recently, nine additional homophymines, namely, B–E (**214–217**) and A1–E1 (**213a–217a**) have been isolated from the same sponge [315]. From the structural point of view, homophymines (A1–E1) feature the 4-amino-6-carbamoyl-2,3-dihydroxyhexanoic acid residue compared to the corresponding (A–E) possessing the same residue in its carboxy form.



All homophymines were subjected to an antiproliferative activity assay against a wide panel of cell lines including human and simian cancer and noncancer cells and displayed potent cytotoxicity (IC_{50} values between 2 and 100 nM) [315]. A comparison of activities against different tumor cell lines showed a moderate selectivity toward PC3 human prostate and OV3 ovarian carcinoma cell lines. However, when the sensitive and their resistant counterpart cell lines were compared (MCF7/MCF7R, HCT116/HCT15, HLC60/HL60R), no significant difference was observed [315]. Homophymine A1–E1 (**213a–217a**) exert stronger biological activity compared to the corresponding congeners A–E (**213–217**) [315]. Further extensive biological investigations were carried out to distinguish whether the homophymines possess antiproliferative and/or acute toxic activity. The results strongly suggested that the toxic effect of homophymines was due to an acute and a nonspecific toxicity toward various tested human cell lines [315].

Azumamides A–E (**218–222**), isolated from the Japanese marine sponge *Mycale izuensis*, are five cyclic tetrapeptides that exhibit potent histone deacetylase (HDAC) inhibitory activity (IC_{50} 's of 0.045–1.3 μ M) [316]. Furthermore, azumamide A (**218**) at a concentration of 19 μ M significantly inhibited angiogenesis [316]. Only few examples of marine HDAC inhibitors are known up to date such as psammaphin A (PsA, **109**) (see Section 4.2.3) obtained from marine sponge *Pseudoceratina purpurea* [133], whereas azumamides A–E (**218–222**) were the first examples of cyclic peptides with HDAC inhibitory activity isolated from marine organisms.



	R ₁	R ₂	R ₃ = R ₄	IC ₅₀ (μ M) (HDAC)
218	NH ₂	H	CH ₃	0.045
219	NH ₂	OH	CH ₃	0.11
220	OH	OH	CH ₃	0.11
221	NH ₂	H	H	1.3
222	OH	H	CH ₃	0.064

After the crystal structure of the complex between a HDAC-like protein and the HDAC inhibitor, trichostatin A (TSA) [317], had been solved, interesting insights into the binding modes of HDAC inhibitors were disclosed [318]. According to the TSA structure, a plausible binding mode to the enzyme is by inserting the long aliphatic chain of TSA into the hydrophobic pocket of the enzyme. Then, the terminal hydroxymic group coordinates with a zinc ion at the polar bottom of the pocket while the aromatic dimethylaminophenyl portion of TSA makes contact with the pocket entrance and an adjacent surface group thereby capping the pocket. Trapoxin A [319] and apicidin [320] are the parent congeners of two classes of HDAC inhibitory cyclic tetrapeptides containing groups that may be analogous to the aliphatic side chain of TSA. Trapoxins possess a 2-amino-8-oxo-9,10-epoxy-decanoic acid, in which the epoxide moiety is thought to bind irreversibly to the enzyme [317], while the apicidins comprise a 2-amino-8-oxo-decanoic acid, with the keto group being responsible for zinc chelation [321].

The corresponding terminal function for azumamides is probably the amide or the carboxylate group. Despite that the affinity of an amide group to zinc is much weaker than that of a carboxylic acid, azumamides A (**218**) and B (**219**) with an amide end showed equivalent levels of HDAC inhibitory activity as C (**220**) and E (**222**) congeners, which have carboxylate functionality [316].

In conclusion, many peptides from marine sponges showed potent activities such as antitumoral, antiviral, immunosuppressive, antifungal as well as cardiac stimulant properties. However, these bioactivities cannot clearly explain their *in situ* role inside the marine sponges. Interestingly, the most striking feature of this class of metabolites is the preponderance of nonproteinogenic amino acids suggesting that these metabolites are the result of the NRPS/PKS pathways of microorganisms, proposing that symbiotic microorganisms, including cyanobacteria, are the real producers of these metabolites. Therefore, the symbiotic associations within sponges and other marine invertebrates need further intensive research which will ultimately unravel the innate sources of these bioactive metabolites.

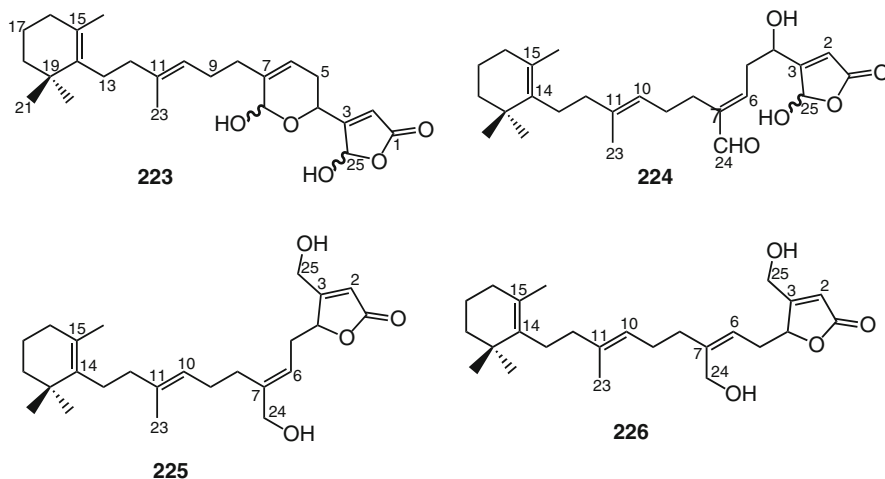
4.4 Terpenes

Terpenes include primary and secondary metabolites, all biosynthesized from the five carbon isoprene building units [322]. Structural modification of these isoprene units leads a massively diverse range of derivatives with a wide array of chemical structures and biological properties.

Steroidal terpenoids were the first marine isoprenes to be discovered by Bergmann during the 1930s–1940s, particularly sterols that were obtained from various marine macroorganisms [323]. Since then, a huge number of terpenoidal secondary metabolites have been obtained from marine resources. In addition to our recent review on this topic [324], we will survey two major classes of marine isoprenes from sponges, namely, the sesterterpenoids (C₂₅) and triterpenoids (C₃₀) with particular attention of their biological activities.

4.4.1 Sesterterpenes (C₂₅)

Manoalide (**223**) is the parent compound of a series of marine sponge metabolites belonging to the sesterterpene class. Manoalide was first reported in 1980 by Scheuer from the marine sponge *Luffariella variabilis* (class Demospongiae; order Dictyoceratida; family Thorectidae) collected in Palau [325] with activity as an antibiotic against *Streptomyces pyogenes* and *Staphylococcus aureus*. One year later, Scheuer reported three additional related metabolites from the same Palauan sponge, namely, secomanoalide (**224**), (*E*)-neomanoalide (**225**), and (*Z*)-neomanoalide (**226**) [326].



All three compounds, as well as the parent compound (**223**), displayed antibacterial activity against Gram positive bacteria (*Staphylococcus aureus* and *Bacillus subtilis*) but were inactive against *Escherichia coli*, *Pseudomonas aeruginosa* and *Candida albicans* [326].

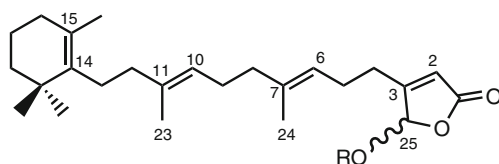
Later, marine sponges belonging to the family Thorectidae, including species of the genera *Luffariella* [327–339], *Hyrtios* [340, 341], *Thorectandra* [342], *Cacospongia* [343, 344], *Fasciospongia* [345–348], *Acanthodendrilla* [349], and *Aplysinopsis* [350], were also found to be rich sources of novel bioactive sesterterpenoids related to manoalide.

Manoalide was further investigated and found to be a potent inhibitor of phospholipase A₂ (PLA₂) [351–358]. Subsequently, many structurally related metabolites with PLA₂ inhibitory activity were also reported [328, 359–365]. PLA₂ is an enzyme that specifically catalyzes the hydrolysis of phospholipids at the *S_N*-2 position to produce a lysophospholipid and arachidonic acid, which in turn provides the substrate for proinflammatory mediators such as leukotrienes, prostaglandins, and thromboxanes, collectively known as the eicosanoids [361]. Since manoalide revealed an irreversible inhibition of phospholipase A₂ (PLA₂) [353], the structure-activity relationships (SAR) of this compound attracted scientific interests to study

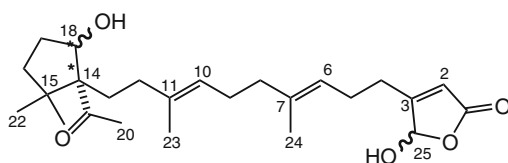
and to understand both PLA₂ function and mechanism of action in the whole cell. Therefore, several studies were successfully performed to determine the contributions of the various functional groups incorporated in **223** and its analogues, such as the γ -hydroxybutenolide, α -hydroxydihydropyran, and trimethylcyclohexenyl ring systems, to the efficacy as PLA₂ inhibitors [356, 361, 365]. These studies indicated that (1) the existence of the hemiacetal in the α -hydroxydihydropyran ring is crucial for irreversible binding, (2) the γ -hydroxybutenolide ring is involved in the initial interaction with PLA₂, and (3) the hydrophobic nature of the trimethylcyclohexenyl ring system allows nonbonded interactions with the enzyme that enhances the potency of these analogues. These studies suggested that the closed ring form of manoalide is the predominant molecular moiety that accounts for the selective and potent inhibition of PLA₂ [356].

Manoalide analogues also exhibited other bioactivities including molluscicidal [330], cytotoxicity [333, 334, 336, 340, 343, 346, 349, 350, 367–369], inhibitory activity of Cdc25 phosphatase [366], nicotinic antagonistic activity [332], and fish deterrent properties [346, 369]. Therefore, chemical synthesis and derivatization of manoalide attracted much interest leading to a better understanding of the structure-activity relationships (SAR) and/or for the plausible mechanism of action [355, 358–360, 363, 364, 370, 371]. Manoalide (**223**) was licensed to Allergan Pharmaceuticals and reached phase II clinical trials as a topical antipsoriatic. Its development was, however, discontinued due to formulation problems. The compound is now commercially available as a biochemical standard tool to block the action of PLA₂ [372].

Luffariellolide (**227**) is a sesterterpenoid analogue of secomanalide (**224**), which was first reported from a Palauan sponge *Luffariella* sp. [328]. Structurally, luffariellolide differed in having C-24 as methyl group instead of an aldehyde functionality as in secomanalide, and it was obtained as the (*Z*) isomer as well.



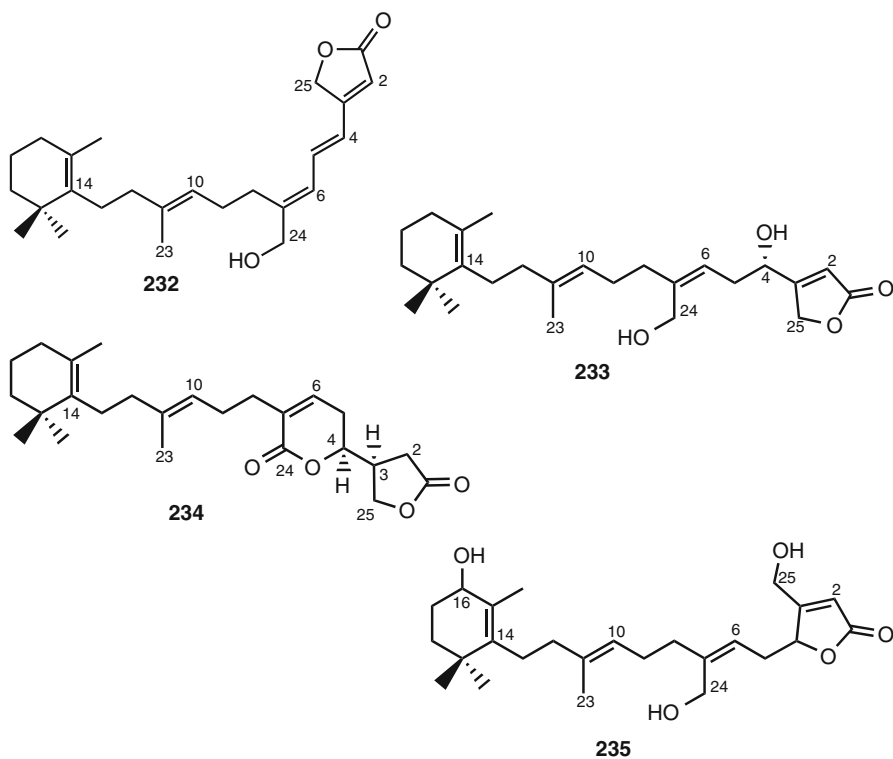
- 227** R = H
228 R = CH₃
229 R = CH₂CH₃



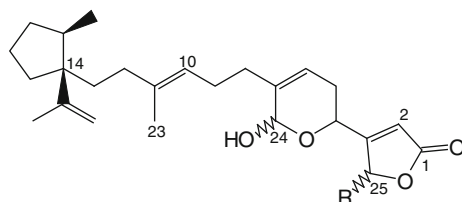
- 230** 18- β -(OH)
231 18- α -(OH)

In contrast to the irreversible inhibitory action of manoalide (**223**) toward PLA₂, luffariellolide (**227**) is a slightly less potent but a partially reversible inhibitor. This meant that **227** became a more preferable anti-inflammatory agent for potential pharmacological investigation [328]. In addition to luffariellolide (**227**), its 25-*O*-methyl (**228**) and 25-*O*-ethyl derivatives (**229**), five related sesterterpenes, acantholides (A–E), were obtained from the Indonesian sponge *Acanthodendrilla* sp. [349]. Acantholide D (**230**) and E (**231**) represent rare variants for the C₁₄–C₂₀ segment in this type of linear sesterterpenes in which they have the 1-acetylcyclopentan-5-ol moiety replacing the trimethylcyclohexenyl ring. Luffariellolide (**227**) and its 25-*O*-methyl congener (**228**), as well as acantholide E (**231**), were cytotoxic against the mouse lymphoma L5178Y cell line with IC₅₀ values of 8.5, 1.8, and 16.8 μM, respectively. Interestingly, these results suggest that the 25-*O*-methyl group in **228** and the stereochemistry of 1-acetylcyclopentan-5-ol in **231** play an important role [349]. Luffariolides (A–J) represent a related group of sesterterpenoidal analogues, which have been obtained from different collections of the Okinawan marine sponge *Luffariella* sp. [333, 334, 336].

All luffariolides exhibited significant cytotoxicity against murine lymphoma L1210 cells with IC₅₀ values ranging between 2.9–19.3 μM. Among them, luffariolides A (**232**, IC₅₀ 2.9 μM), B (**233**, IC₅₀ 3.23 μM), E (**234**, IC₅₀ 3.0 μM), and F (**235**, IC₅₀ 3.8 μM) were the most active ones [333, 334, 336].



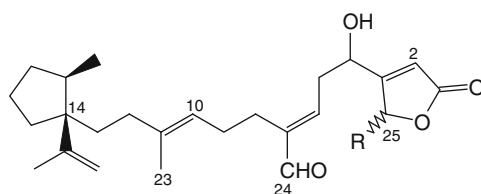
Luffariellins A (**236**) and B (**237**) [327] together with their respective 25-acetoxy derivatives (**240** and **241**) [338] were isolated from the marine sponge *Luffariella variabilis* collected off different locations in Palau and in Australia, whereas luffariellins C (**238**) and D (**239**) were obtained from the shell-less marine mollusc *Chromodoris funerea* collected from the Kaibakku lake shores in Palau [373].



236 R = OH

238 R = H

240 R = OAc



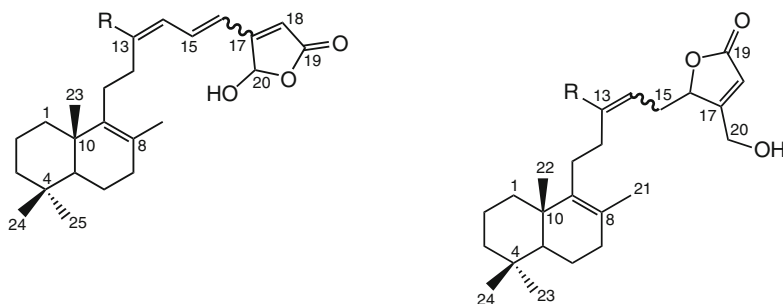
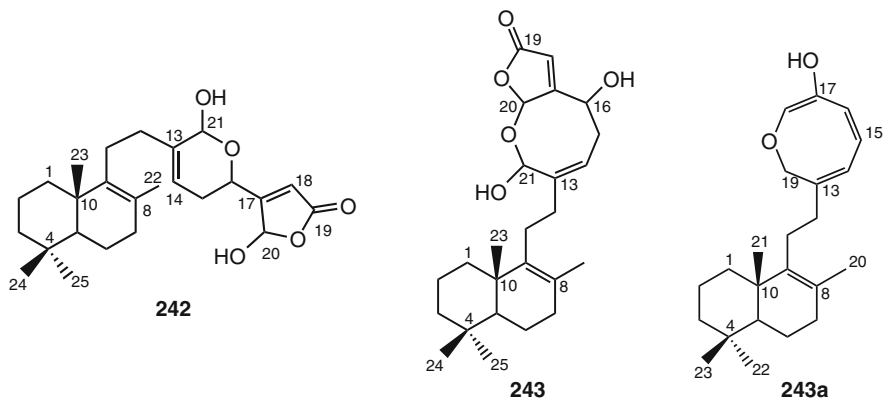
237 R = OH

239 R = H

241 R = OAc

Luffariellins (**236–241**) are all characterized by the 1-isoproprenyl-2-methylcyclopentane ring system replacing the trimethylcyclohexenyl moiety in other manoalide analogues. Despite this discrepancy in chemical structure, luffariellins A (**236**) and B (**237**) retain identical functional groups as present in manoalide (**223**) and secomanoalide (**224**), respectively. Therefore, not surprisingly, each respective pair was shown to have similar anti-inflammatory properties to **223** and **224** [327]. Luffarin metabolites comprise another group of compounds represented by 28 derivatives. Twenty-six of them, luffarins (A–Z), have been reported from the Australian marine sponge *Luffariella geometrica* [332], while the other two were obtained from the Adriatic Sea sponge *Fasciospongia cavernosa* [348]. Based on the chemical structures, luffarins have been classified into 14 bicyclic sesterterpenes, luffarins (A–N); one bicyclic bisnorsesterterpene, luffarin O; one monocyclic sesterterpene, luffarin P; and six acyclic sesterterpenes, luffarin (Q–V), in addition to four diterpenoidal derivatives, luffarin (W–Z) [332]. All luffarins were tested for antimicrobial activity against *Staphylococcus aureus*, *Micrococcus* sp., and *Saccharomyces cerevisiae*. Only luffarins C–F (**244–247**), K (**248**), and L (**249**) showed activity against both *S. aureus* and *Micrococcus* sp. [332], whereas luffarins

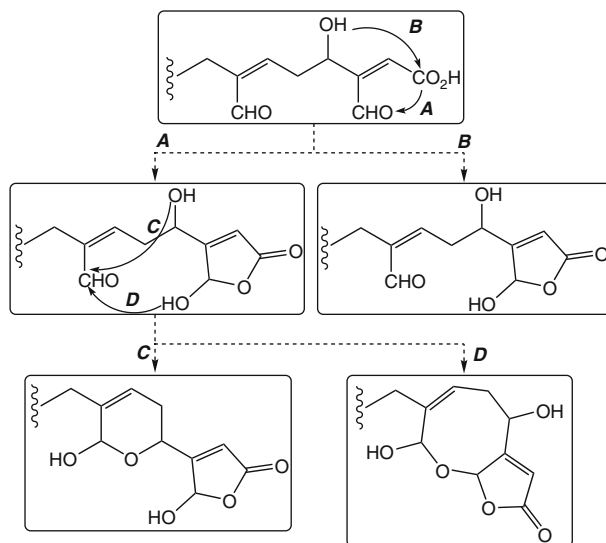
A (**242**) and M (**250**) revealed only mild activity against the latter. Moreover, some luffarins were also found to be effective inhibitors of nicotinic receptors [332].



244	R = CHO	15(16)-trans	248	R = CH ₂ OH	13(14)-trans
245	R = CH(OCH ₃) ₂	15(16)-trans	249	R = CH ₂ OH	13(14)-cis
246	R = CH ₂ OH	15(16)-trans	250	R = CHO	13(14)-trans
247	R = CH ₂ OH	15(16)-cis			

Biosynthetically, a relationship could be recognized between the various luffarins as illustrated in Scheme 4.5. Luffarins appear to belong to the same enantiomeric series as reported for manoalide-type marine natural products. It is also curious to note that no acyclic luffarins incorporated the hydroxylated butenolide functionality. Perhaps the most interesting luffarins from a biosynthetic point of view are luffarins B (**243**) and O (**243a**), which were the first examples of a hitherto unknown cyclization pattern in compounds of this class [332].

Another example of bicyclic sesterterpenes are thorectandrols A–E (**253–257**) that were isolated from a Palauan collection of the marine sponge *Thorectandra* sp. [367, 368] together with the parent compounds of this group palauolide (**251**) and



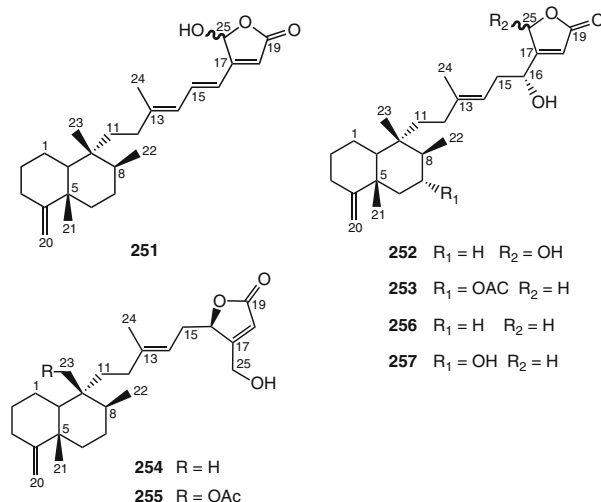
Scheme 4.5 Postulated biosynthetic relationship between all known *Luffariella* metabolites [332]

palauolol (**252**). Palauolide (**251**) was obtained first as an antimicrobial sesterterpene from a three-sponge association collected in Palau [374], while palauolol (**252**) was identified as an anti-inflammatory sesterterpene from the Palauan sponge *Fascaplysinopsis* sp., and chemically, it was recognized as being a secondary alcohol that upon dehydration yields **251** [375].

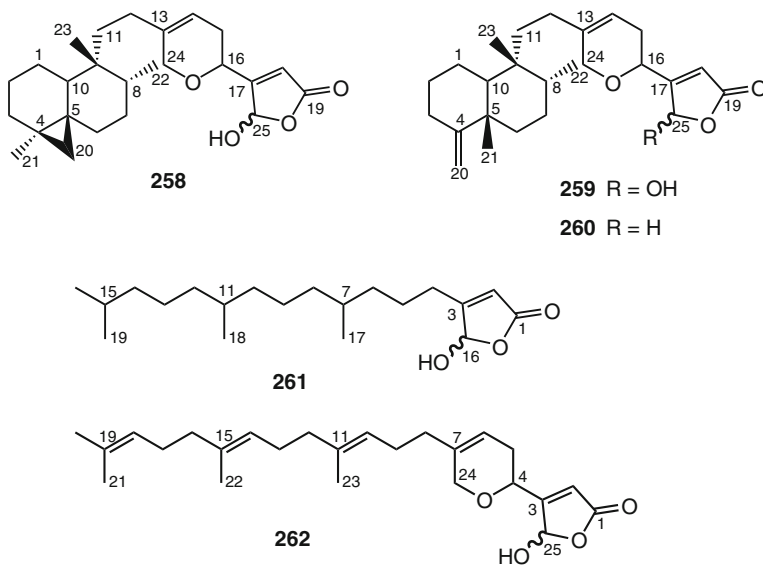
All thorectandrols (**253–257**) in addition to palauolide (**251**) and palauolol (**252**) were tested for antiproliferative activity against 6 to 12 human tumor cell lines depending on sample availability [368]. Palauolol (**252**) was active against all tested cell lines except A549 (non-small cell lung cancer), with IC_{50} values in the range 1.2–1.7 μM , while palauolide (**251**) showed a diminished activity. On the other hand, thorectandrols (A–E) revealed only weak to no cytotoxicity against the tested cell lines (IC_{50} 's 70–100 μM). While firm deductions on the structural requirements for activity were not possible, it appeared that the presence of both the hemiacetal lactone functionality and the 16-hydroxyl group in palauolol (**252**) enhanced cytotoxicity compared to palauolide (**251**) and other thorectandrols [368].

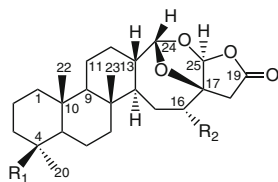
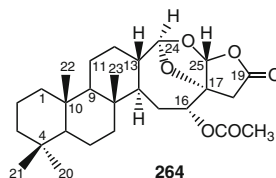
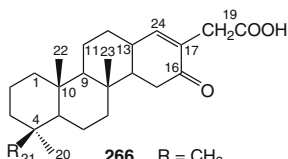
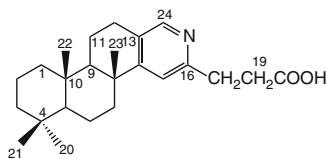
Cacospongionolides (**258–262**) were isolated from different collections of the marine sponge *Fasciospongia cavernosa* (= *Cacospongia mollior*) collected from the Mediterranean Sea [343, 346, 369, 376]. Cacospongionolides A (**258**), B (**259**), and its 25-deoxy derivative (**260**) revealed a bicyclic sesterterpenoidal skeleton, resembling luffarins and thorectandrols, with the addition of a γ -hydroxybutenolide moiety. The other cacospongionolides C (**261**) and D (**262**) are acyclic diterpenoidal derivatives. Despite the structural relation with luffarins and thorectandrols, cacospongionolides (**258–260**) together with cacospongionolide D (**262**) exhibited significant cytotoxicity [343, 346, 369, 376]. This notion

suggested a possible relation between the presence of the γ -hydroxybutenolide moiety and the cytotoxicity.

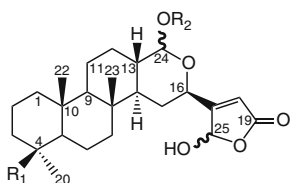
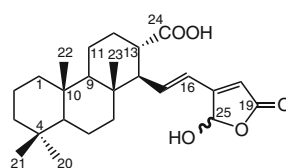


Petrosaspongiolides A (**263**) and B (**264**) were the first cheilantane sesterterpene lactones to be isolated from a New Caledonian sponge incorrectly assigned to the genus *Dactylospongia* [377] and then reassigned as a new genus and a new species: *Petrosaspongia nigra* (Bergquist 1995 sp. nov., class Demospongiae; order Dictyoceratida; family Spongidae) [378]. From another New Caledonian collection of the same sponge, 15 additional petrosaspongiolide congeners (C–R) were isolated [379, 380].

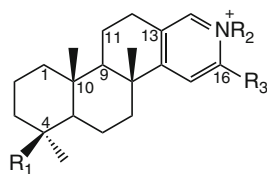


**263** R₁ = CH₃ R₂ = OAc**265** R₁ = CH₂OAc R₂ = OAc**264****266** R = CH₃**266a** R = CH₂OH**267**

From the chloroform extract of another Dictyoceratida sponge of the genus *Spongia*, 21-hydroxy derivatives of petrosaspongiolides K (**266a**) and P (**270a**) were isolated in addition to four other pyridinium alkaloids named spongidines A–D (**273–276**) [381]. Spongidines were found to be structurally related to petrosaspongiolide L (**267**) particularly in the presence of pyridine ring. Petrosaspongiolides (A–L) were subjected to in vitro cytotoxicity assay against the human bronchopulmonary NSCLC-N6 carcinoma cell line. They revealed IC₅₀ values ranging between 1.0–32.2 μM [379]. Petrosaspongiolides C (**265**) and K (**266**) exhibited the highest potency with IC₅₀ values of 1.0 and 3.5 μM, respectively. However, petrosaspongiolides A (**263**) and B (**264**) were the least cytotoxic congeners in vitro with IC₅₀ values of 28.0 and 32.2 μM, respectively; **263** inhibited tumoral proliferation in vivo at 20 mg/kg without significant toxicity when tested on immunosuppressed rats carrying a bronchopulmonary tumor (NSCLC-N6) [379].

**268** R₁ = CH₃ R₂ = OAc**269** R₁ = CH₂OAc R₂ = OAc**270** R₁ = CH₃ R₂ = H**270a** R₁ = CH₂OH R₂ = H**271** R₁ = CH₂OAc R₂ = H**272**

Petrosaspongiolides M–R (**268–272**) revealed the presence of a γ -hydroxybutenolide moiety and a hemiacetal function. Due to these structural similarities to manoalide (**223**), petrosaspongiolides (M–R) have received special attention from the scientific community to study their inhibitory activity against PLA₂ from different resources to point out their specificity. Two main groups of PLA₂ enzymes have been reported [382], the secretory PLA₂ (sPLA₂ groups I, II, III, V, IX, and X with relatively small molecular weights) and the cytosolic PLA₂ (cPLA₂ groups IV, VI, VII, and VIII with higher molecular weights). Inhibition of specific PLA₂ constitutes a potentially useful approach for treating a wide variety of inflammatory disorders such as septic shock, adult respiratory distress syndrome, arthritis, and acute pancreatitis [381]. Petrosaspongiolides M–R (**268–272**) together with 21-hydroxy derivatives of petrosaspongiolides K (**266a**) and P (**270a**), and spongidines A–D (**273–276**) were tested on five different sPLA₂s belonging to the groups I (*Naja naja* venom and porcine pancreatic enzymes), II (human synovial recombinant and rat air-pouch secretory enzymes), and III (bee venom enzyme) [380, 381].



273	R ₁ = CH ₃	R ₂ = CH ₂ COOH	R ₃ = H
274	R ₁ = CH ₂ OAc	R ₂ = CH ₂ COOH	R ₃ = H
275	R ₁ = CH ₃	R ₂ = CH ₂ COOH	R ₃ = CH ₂ CH ₂ COOH
276	R ₁ = CH ₃	R ₂ = CH ₂ CH ₂ SO ₃ H	R ₃ = H

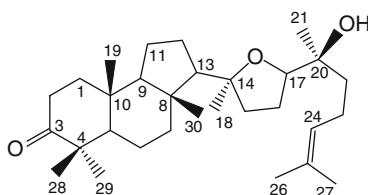
Among petrosaspongiolide derivatives, **268** and **270a** inhibited mainly human synovial PLA₂ with IC₅₀ values of 1.6 and 5.8 μ M, respectively, compared to manoalide (**223**) (IC₅₀ = 3.9 μ M) [380, 381]. Petrosaspongiolide M (**268**) also inhibited bee venom PLA₂ enzyme with IC₅₀ of 0.6 μ M, compared to **223** (IC₅₀ of 7.5 μ M) [380]. The mechanism of action of petrosaspongiolides M–R (**268–272**) as anti-inflammatory marine metabolites has been the topic for many research articles [383–388]. The covalent binding of **268** to bee venom PLA₂ has been investigated by mass spectrometry and molecular modeling. The mass increment observed was consistent with the formation of a Schiff base by reaction of a PLA₂ amino group with the hemiacetal function at the C-25 atom of the petrosaspongiolide M γ -hydroxybutenolide ring [383]. The molecular mechanism of inactivating the bee venom and the human type IIA secretory PLA₂s by petrosaspongiolides R (**272**) [387] and M (**268**) [388], respectively, has been investigated. In both cases, either covalent (imine formation) and/or noncovalent (van der Waals) interactions contributed to the inhibitory activity against PLA₂ enzymes [387, 388]. Due to potent anti-inflammatory properties of petrosaspongiolides, their chemical synthesis has been investigated. Recently, the first enantioselective synthesis of petrosaspongiolide R (**272**) has been successfully performed [389].

4.4.2 Triterpenes (C₃₀)

Steroidal triterpenes were the first marine isoprenes to be discovered in the 1930s. Scientific interest has been driven toward these metabolites due to the isolation of biosynthetically unprecedented derivatives possessing a broad spectrum of bioactivity (ies). Marine triterpenoids have been reported from various marine macroorganisms. In this section, we survey two examples of triterpenoidal metabolites, namely, isomalabaricane triterpenes and steroidal saponins obtained from marine sponges, with particular attention being drawn to their pharmacological significance.

4.4.2.1 Isomalabaricane Triterpenes

Malabaricol (**277**) is the chief triterpene constituent of a yellow pigment obtained from the wood of the terrestrial plant *Ailanthus malabarica* (family Simaroubaceae), after which the whole group of related compounds was named [390–392]. Malabaricane, the trivial name of this group of compounds, was given to the hydrocarbon system (3*S*^{*},3a*R*^{*},5a*S*^{*},9a*S*^{*},9b*S*^{*})-3a,6,6,9a-tetramethyl-3-(1,5,9-trimethyldecyl)perhydr-obenz[*e*]indene, where the tricyclic nucleus has a *trans-anti-trans* ring junction [391, 392].

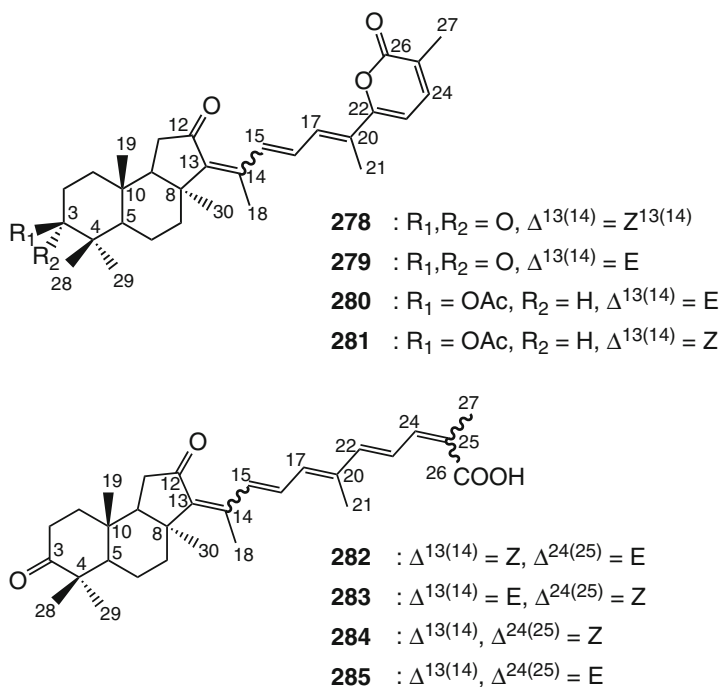


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The malabaricanes are structurally characterized by a tricyclic triterpenoid core and a conjugated polyene side chain [390–392], whereas the isomalabaricane skeleton is embedded in a 4,4,8,10-tetramethyl-perhydrobenz[*e*]indene with a *trans-syn-trans* ring junction, that leads to an unfavorable twist-boat conformation for the central ring [393, 394]. Isomalabaricane triterpenes were first reported from a Fijian collection of the sponge *Jaspis stellifera* [393] and the Somalian marine sponge *Stelletta* sp. [394]. Since then, they have been isolated from several genera of marine sponges belonging to the order Astrophorida including members of the genera *Rhabdastrella* [395, 400, 402, 406, 413, 414, 416, 420], *Stelletta* [397–399, 405, 408, 412], *Jaspis* [401, 407, 409, 418, 419, 421, 422], and *Geodia* [403, 410, 415]. Isomalabaricane triterpenoids having polyene conjugated functionality can be classified into three groups: (1) stelletins principally possessing the γ -pyrone functionality, which could be ring-opened in some of its congeners yielding the side chain with terminal free carboxylic acid and methyl moieties, (2) stelliferins oxygenated at C-22, and (3) globostellatic acids whose main feature is a carboxyl group at C-4. In addition to triterpenoids, the isomalabaricane core has also been recognized in some sesqui- and/or sesterterpenes. The isomalabaricane terpenoids were sometimes trivially named according to their sponge origin. Upon light exposure, the isomalabaricane-type terpenes readily isomerize at the C-13 position.

Therefore, during isolation and characterization processes, they rapidly equilibrate into a 1:1 mixture of the 13*E* and 13*Z* isomers [398–400, 408, 409, 418, 419]. Nevertheless, these compounds continue to gain a great deal of attention because of their significant cytotoxic activity [399, 409], whereas the nature of the natural isomer, either 13*E* or 13*Z* or both, is still unresolved. Recently it was reported that the ¹H NMR spectrum of a crude extract obtained from the fresh sponge *Rhabdastrella* aff. *distinca* (Hainan, the South China Sea) revealed that it mostly contained isomalabaricanes with the 13*E*-configuration (H-15 of most derivatives appeared around 7.0 ppm). Thus, the 13*Z* isomers were suggested in this case to be formed through isomerization during the isolation and analytical procedures [406].

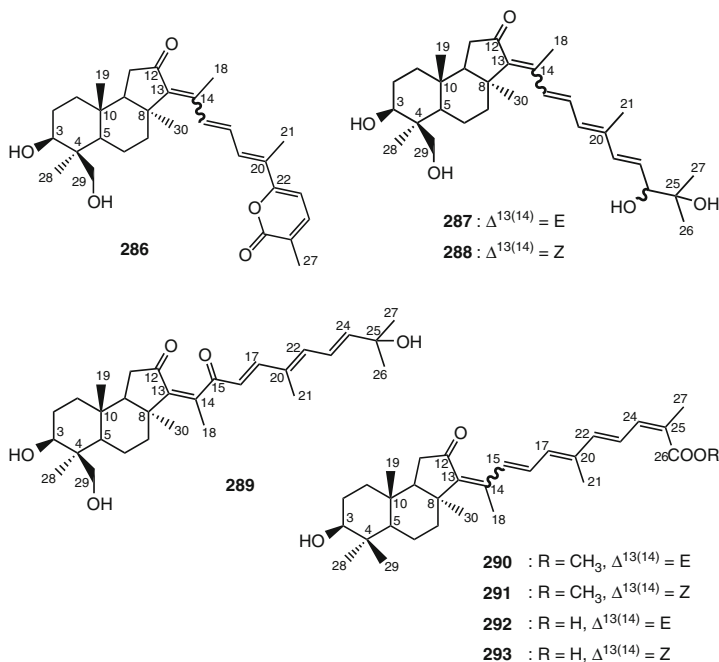
Stelletins comprise the first group of isomalabaricane-type triterpenoids. Stelletin A (**278**) was recognized in 1981 as a yellow triterpenoidal pigment from the Fijian marine sponge *Jaspis stellifera* [393]. Later, it was obtained together with its *E* isomer, stelletin B (**279**), from the marine sponge *Stelletta tenuis* collected off Hainan Island, China [397]. Stelletin A (**278**) revealed significant cytotoxicity against murine leukemia P388 cell line with IC₅₀ of 2.1 nM [397].



Stelletin G (**284**), with an opened γ -pyrone and featuring terminal -COOH and -CH₃ functionalities, was isolated together with **278** from *J. stellifera* [393]. Later, stelletins G (**284**) was reported from the Australian marine sponge *Stelletta* sp. together with stelletins E (**282**) and F (**283**) [398]. The *E* isomer of stelletin G (**284**) was isolated from the marine sponge *Rhabdastrella globostellata* collected from the South China Sea, and it was given the trivial name rhabdastrellic acid-A (**285**)

[395, 396]. Research interests have been intensively driven toward this group of triterpenoidal derivatives, which led to the isolation of eight further stelletins C, D, and H–M [398–400, 402, 405] in addition to 22,23-dihydrostellatin D [401].

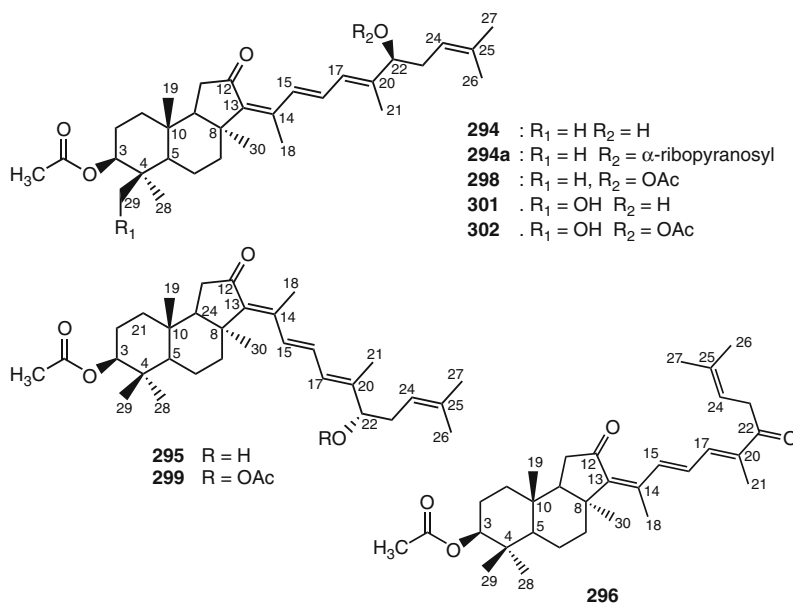
Rhabdastrellins A–F (286–291), along with stelletins L (292) and M (293), were obtained from the marine sponge *Rhabdastrella* aff. *distinca* collected from a coral reef off Hainan in the South China Sea [406]. Four of the rhabdastrellins (286–289) exhibited a primary alcohol moiety at C-29 instead of a methyl group as for the stelletins and the other two rhabdastrellins E (290) and F (291). All rhabdastrellins and stelletins L and M share a hydroxyl group at C-3 instead of a carbonyl group as in other stelletins [406]. The antiproliferative profile of stelletins A–F (278–283) has been examined at the National Cancer Institute (NCI, Australia) against 60 cell lines. Due to the rapid isomerization upon light exposure, stelletins were tested as isomeric pairs. Stelletin C(280)/D(281) pair was the most potent derivative with a mean panel GI₅₀ of 0.09 μM. The stelletin E(282)/F(283) pair was approximately ten times less potent (mean GI₅₀ of 0.98 μM) [399]. Apoptotic cell death is a stress response of cells to cytotoxic agents that might be executed either through a receptor-mediated pathway that activates caspase-8 or through a receptor-independent pathway that involves the cyclin-kinase inhibitors p53/p21. Both pathways lead to a translocation of proapoptotic Bax protein to the mitochondria, thereby resulting in a dissipation of mitochondrial membrane potential, activation of caspase-3, and execution of the apoptotic machinery [404].

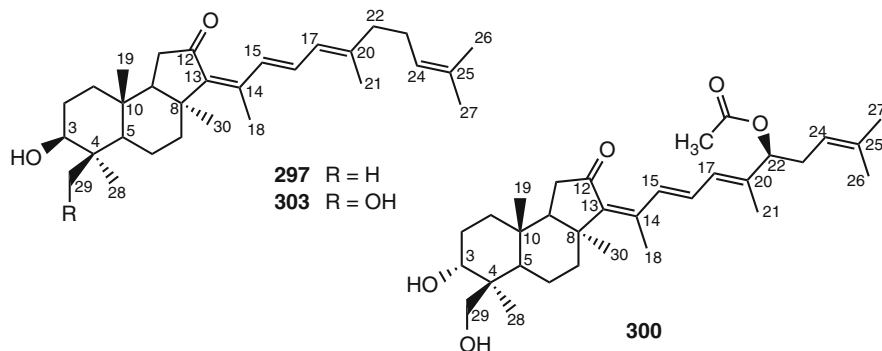


Stelletin A (**278**) demonstrated a differential cytotoxicity against human leukemia HL-60 cells (IC_{50} 0.9 μ M) compared to human prostate cancer LNCaP cells (IC_{50} 260 μ M) by activation of NADPH oxidase, which induces oxidative cell death through a FasL–caspase-3–apoptotic pathway [403]. Stelletins B (**279**) and E (**282**) revealed selective cytotoxicity toward p21-deficient human colon tumor HCT-116 cells with IC_{50} values of 0.043 and 0.039 μ M, respectively [400]. Stelletins L (**292**) and M (**293**) exhibited selective cytotoxicity against stomach cancer AGS cells with IC_{50} values of 3.9 and 2.1 μ M, respectively [405]. Rhabdastrellic acid–A (**285**) also inhibited proliferation of human leukemia HL-60 cells with an IC_{50} value of 1.5 μ M through inhibition of the PI3K/Akt pathway and induction of caspase-3–dependent apoptosis [396]. Only rhabdastrellin A (**286**) possessed moderate inhibitory activity toward human leukemia HL-60 cells (IC_{50} = 8.7 μ M) while other rhabdastrellins were inactive (IC_{50} > 20 μ M) [406].

Stelliferins are the second group of isomalabaricane triterpenes. To the best of our knowledge, 13 compounds belonging to this group have been reported. In addition to stelliferins A–F (**294**–**299**), which have been isolated from the Okinawan marine sponge *Jaspis stellifera* [407], stelliferin G (**300**) and 29-hydroxy derivatives of stelliferins A (**301**) and E (**302**) have been isolated from an unidentified species of the genus *Jaspis* collected near Tonga [409].

The 29-hydroxy derivative of stelliferin D (**303**) together with 3-epimeric isomers of **301** and **302** were reported from the marine sponge *Stelletta globostellata* collected by SCUBA off Mage-jima Island, Japan [408], whereas stelliferin riboside (**294a**), the first example of a glycosylated stelliferin, was isolated from the Fijian sponge *Geodia globostellata* [410].





Stelliferins A–F (**294–299**) exhibited potent *in vitro* antineoplastic activities against murine lymphoma L1210 cells (IC_{50} of 1.1–5.0 μM) and human epidermoid carcinoma KB cells (IC_{50} of 2.8–13.0 μM) [407], while the isomeric mixture of stelliferin G (**300**) and 29-hydroxystelliferin A (**301**) showed the highest inhibitory activity against the melanoma MALME-3 M cell line with IC_{50} values of 0.2 and 0.4 μM , respectively [409]. Stelliferin riboside (**294a**) displayed moderate cytotoxicity against ovarian A2780 cancer cells ($IC_{50} = 60 \mu\text{M}$) [410].

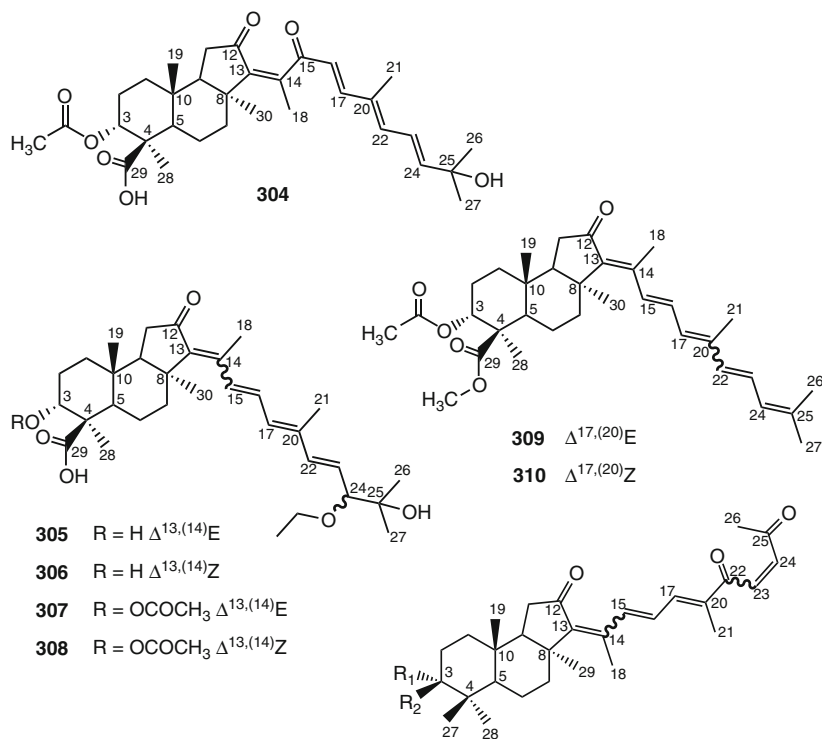
Due to the significant antiproliferative activity exhibited by stelletins and stelliferins, research efforts have been directed toward their chemical synthesis. In 1999, Raeppl et al. successfully synthesized the common *trans-syn-trans* perhydrobenz[e]indene moiety in the isomalabaricane-type terpenoids, which enabled the chemical synthesis of stelletins and stelliferins [411].

Globostellatic acid (**304**) is the prototype of the third group of isomalabaricane-type triterpenoids sharing carboxylation at C-4. It was first isolated together with three other derivatives, globostellatic acids (B–D), from the marine sponge *Stelletta globostellata* collected off Mage Island near Kagoshima, Japan [412]. Other globostellatic acid congeners, (F–M), and X methyl esters, have been reported from different collections of the Indonesian marine sponge *Rhabdastrella globostellata* [413, 414]. Globostellatic acids revealed potent cytotoxicity similar to the stelletins and stelliferins. Globostellatic acids (A–D) demonstrated significant cytotoxicity against murine leukemia P388 cells with IC_{50} values of 0.2–0.8 μM [412]. For cytotoxicity toward mouse lymphoma L5178Y cells, the 3-*O*-deacetyl congeners, globostellatic acids H/I (**305/306**) were the most active with an IC_{50} of 0.31 nM. However, acetylation of the C-3 hydroxyl group decreases its bioactivity abruptly, as in globostellatic acids J/K (**307/308**), with an IC_{50} of 8.28 nM. The reverse was found for the 13*Z* isomer of stelliferin riboside (**294a**) that revealed higher activity than its 3-*O*-deacetyl congener with IC_{50} values of 0.22 and 2.40 nM, respectively [413].

On the other hand, globostellatic acids showed only moderate or no cytotoxicity against either human cervix carcinoma HeLa or rat pheochromocytoma PC-12 cell lines [413]. Two globostellatic acid X methyl esters (**309** and **310**), possessing the 13*E*-geometry, inhibited proliferation of human umbilical vein endothelial cells

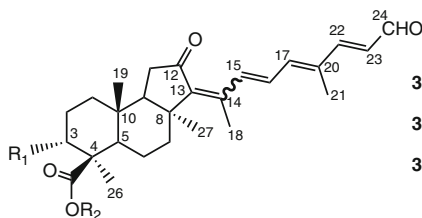
(HUVECs), 80- to 250-fold greater in comparison to several other cell lines and hence inhibited angiogenesis which, if pathologically uncontrolled, accompanies several diseases such as atherosclerosis, arthritis, diabetic retinopathy, and cancer. 13*E*,17*E*-Globostellatic acid X methyl ester (**309**) also inhibited basic fibroblast growth factor (bFGF)-induced tubular formation and vascular endothelial growth factor (VEGF)-induced migration of HUVECs. In addition, **309** induced apoptosis of HUVECs without affecting their VEGF-induced phosphorylation of ERK1/2 kinases [414].

Geoditins, which are stelliferin-related isomalabaricane triterpenoids, are mainly oxygenated at both C-22 and C-25. Five geoditins (**311–315**) were obtained from the marine sponges *Geodia japonica* [415] and *Rhabdastrella* aff. *distinca* [416] collected at different locations in the South China Sea.



Geoditins (**311–315**) were submitted for bioassays against several human tumor cell lines including HL-60 (promyelocytic leukemia), PC-3MIE8 (prostate carcinoma), BGC-823 (gastric carcinoma), MDA-MB-423 (breast carcinoma), Bel-7402 (hepatocellular carcinoma), and HeLa (cervical carcinoma) cells. Isogeoditin A (**313**) showed significant cytotoxicity toward the former three cell lines with IC_{50} values of 0.3, 0.2, and 1.0 μM , respectively. 13*E*-isogeoditin A (**314**) revealed no cytotoxic activity, implying that the *Z*-geometry at C-13 enhances antiproliferative activity compared to the *E*-form [416]. Geoditin A (**311**) proved to be cytotoxic against HL-60 cells ($IC_{50} = 6.7 \mu\text{M}$), while geoditin B (**312**) exhibited relatively weak cytotoxicity. Mechanistically, geoditin A (**311**) markedly induced reactive oxygen species (ROS), decreased mitochondrial membrane potential, and mediated a caspase-3 apoptosis pathway [417].

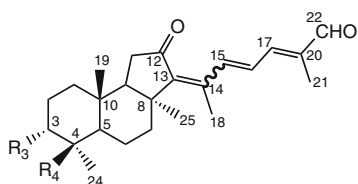
Jaspiferals (**316–325**) and aurorals (**326–329**) are isomalabaricane-type terpenoids differentiated into norriterpenoids, norsesterterpenoids, and norditerpenes possessing a 3α -hydroxy group. Jaspiferals A–G (**316–322**) were purified from the Okinawan marine sponge *Jaspis stellifera* [418], while the 3-*O*-acetyl and methyl ester derivatives of jaspiferals B (**323**), D (**324**), and E (**325**) were obtained from a new species of *Jaspis* collected at the Vanuatu Islands [419]. Aurorals (**326–329**) have been isolated from the New Caledonian marine sponge *Rhabdastrella globostellata* [420]. Jaspiferals A–G (**316–322**) exhibited in vitro cytotoxicity against murine lymphoma L1210 cells with IC_{50} values of 1.6–10.4 μM , whereas only jaspiferals E–G (**320–322**) revealed antineoplastic activity against human epidermoid carcinoma KB cells (IC_{50} of 5.2–14.7 μM) [418]. Jaspiferal G (**322**) exhibited antifungal activity against *Cryptococcus neoformans* (MIC, 144 μM) and *Trichophyton mentagrophytes* (MIC, 36 μM) and antibacterial activity against *Sarcina lutea* (MIC, 144 μM), while the mixture of jaspiferals E (**320**) and F (**321**) showed antifungal activity against *T. mentagrophytes* (MIC, 134 μM) [418]. On the other hand, the 3-*O*-acetyl, methyl ester derivatives of jaspiferals B (**323**), D (**324**), and E (**325**) revealed weak cytotoxicity against L1220 cells ($IC_{50} > 8.8 \mu\text{M}$) [419].



316: $R_1 = \text{OH}$ $R_2 = \text{H}$, $\Delta^{13(14)} = Z$

317: $R_1 = \text{OH}$ $R_2 = \text{H}$, $\Delta^{13(14)} = E$

323: $R_1 = \text{OAc}$ $R_2 = \text{CH}_3$, $\Delta^{13(14)} = E$



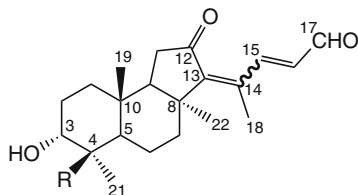
318: $R_1 = \text{OH}$ $R_2 = \text{COOH}$, $\Delta^{13(14)} = Z$

319: $R_1 = \text{OH}$ $R_2 = \text{COOH}$, $\Delta^{13(14)} = E$

324: $R_1 = \text{OAc}$ $R_2 = \text{COOCH}_3$, $\Delta^{13(14)} = E$

326: $R_1 = \text{OH}$ $R_2 = \text{CH}_2\text{OH}$, $\Delta^{13(14)} = Z$

327: $R_1 = \text{OH}$ $R_2 = \text{CH}_2\text{OH}$, $\Delta^{13(14)} = E$

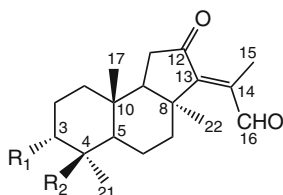


320: R = COOH, $\Delta^{13(14)} = Z$

321: R = COOH, $\Delta^{13(14)} = E$

328: R = CH₂OH, $\Delta^{13(14)} = Z$

329: R = CH₂OH, $\Delta^{13(14)} = E$



322: R₁ = OH R₂ = COOH

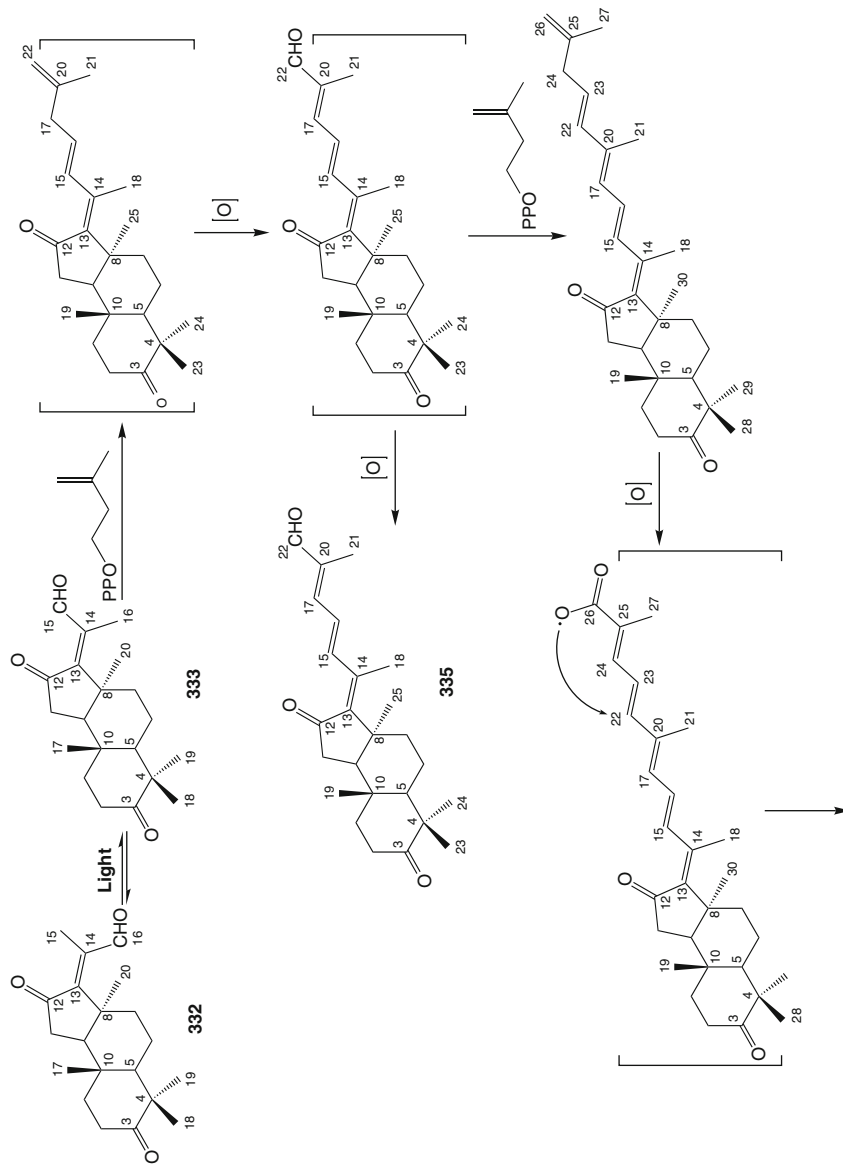
325: R₁ = OAc R₂ = COOCH₃

Aurorals (**326–329**), which differ from jaspiferals C–F (**318–321**) by the presence of a primary alcohol group at the C-4 position, exhibited stronger cytotoxicity against KB cells. The isomeric mixtures of aurorals (**326/327**), (**328/329**), and jaspiferals C/D (**318/319**) showed IC₅₀ values of 0.5, 22.2, and 13.3 μM , respectively, while jaspiferals E/F (**320/321**) were inactive up to 27 μM [420].

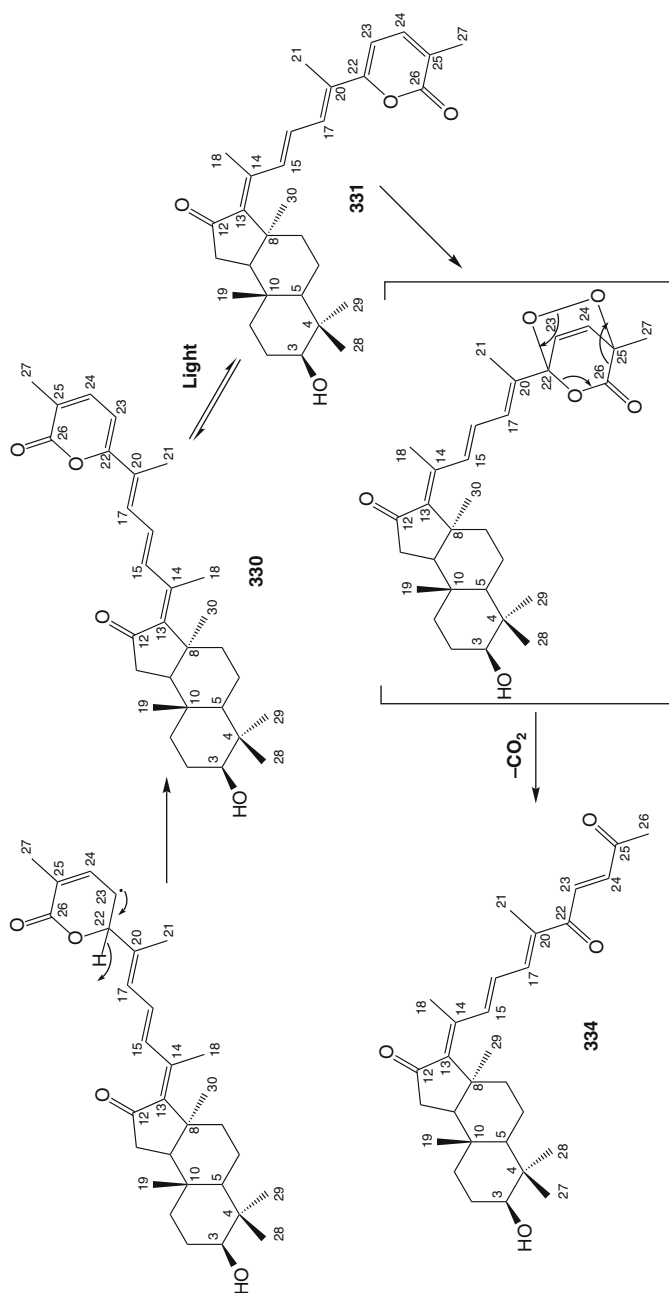
Jaspolides represent another example of isomalabaricane-type terpenoids of either monomeric or dimeric congeners. Monomeric congeners of jaspolides could be classified into triterpenes, jaspolides A (**330**) and B (**331**); sesterterpene, jaspolide F (**335**); diterpenes, jaspolides C (**332**) and D (**333**); and nortriterpene, jaspolide E (**334**) which were all isolated from the marine sponge *Jaspis* sp. collected from the South China Sea [421]. A presumable biogenetic transformation scheme of jaspolides A–F (**330–335**) (Scheme 4.6) revealed that light-induced isomerization is responsible for the jaspolides A/B (**330/331**) and C/D (**332/333**) isomeric pairs. In addition, it substantiated jaspolide D (**333**) as a precursor to jaspolide F (**335**), formed through condensation with an isoprenyl pyrophosphate (IPP) followed by oxidation at a terminal methyl group [421]. Jaspolides G (**336**) and H (**337**) are dimeric isomalabaricane congeners which were isolated from the same Chinese sponge *Jaspis* sp., and their proposed biogenetic pathway (Scheme 4.7) suggested that they were derived from stelletin A (**278**) yielding the left moiety and the nortriterpene, geoditin A (**311**) yielding the right moiety [422].

Jaspolide B (**331**) arrested HL-60 cells in the G₂/M phase of the cell cycle and induced apoptosis in a dose- and time-dependent manner. Jaspolide B with an IC₅₀ value of 0.61 μM exhibited a comparable efficacy to that of paclitaxel (IC₅₀ = 0.78 μM). These results suggested **331** to be a promising anticancer agent for chemotherapy of leukemia by prohibiting cell cycle progression at the G₂/M phase and triggering apoptosis [423].

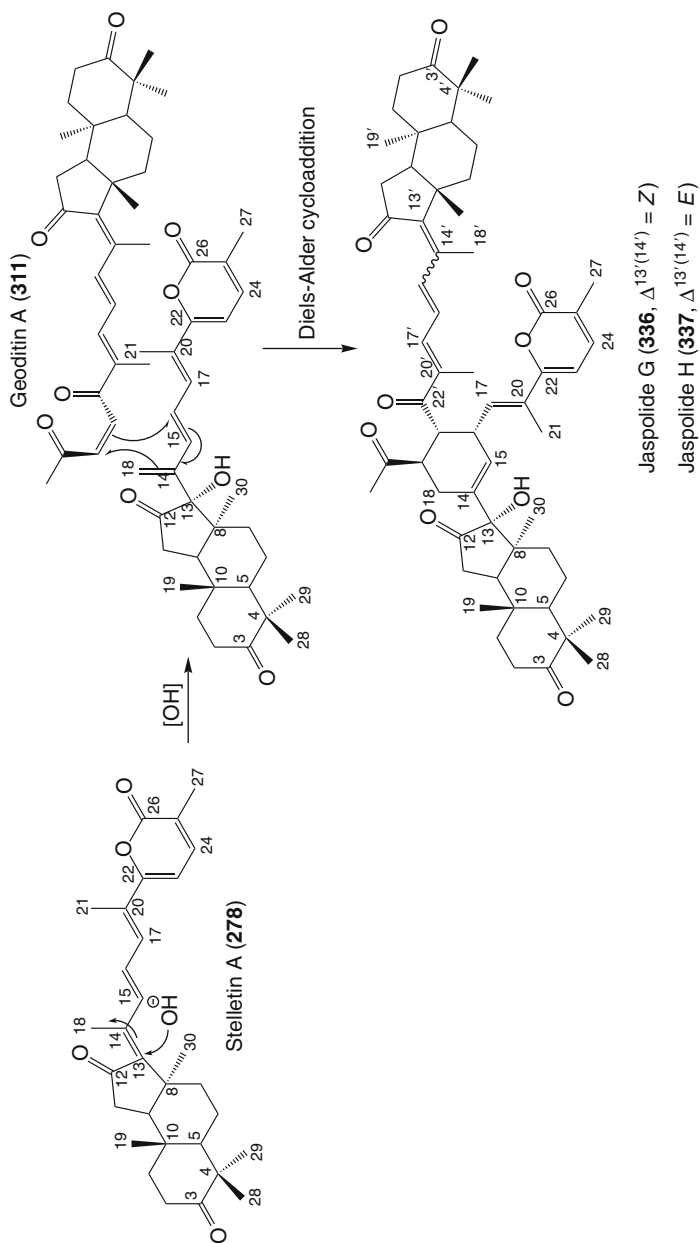
In a further study with human hepatoma cells, jaspolide B (**331**) inhibited the growth of Bel-7402 and HepG2 cells with IC₅₀ values of 29.1 and 29.5 μM , respectively. Incubation with 0.5 μM of **331** caused time-dependent induction of



Scheme 4.6 (continued)



Scheme 4.6 Proposed biogenetic transformation of jaspolides (A-F) [421]



Scheme 4.7 Postulated biogenetic pathway of jaspolidides G and H [422]

apoptosis in Bel-7402 as confirmed by the enhancement of mitochondrial masses, cell membrane permeability, and nuclear condensation. In conclusion, the anticancer effect of jaspolid B involves multiple mechanisms including apoptosis induction, cell cycle arrest, and microtubule disassembly, but these were weaker than observed for colchicine, a well-known microtubule-disassembly agent [424]. These multiple mechanisms of jaspolid B, especially the apoptosis induction, pose interesting perspectives for further exploration of the isomalabaricane-type terpenes as potential anticancer agents.

Since the class of isomalabaricane terpenoidal metabolites has been reported in the literature from different sponge species of the genera *Rhabdastrella*, *Stelletta*, *Jaspis*, and *Geodia* as shown above, the identity of these sponges has been questioned and reevaluated. Interestingly, the taxonomic reevaluation of these sponges revealed that they all might be reassigned to *Rhabdastrella globostellata* (class Demospongiae; order Astrophorida; family Ancorinidae) [400]. However, this could not be ascertained for the isomalabaricane producing *Stelletta* sp. from Somalia [394] and *Stelletta tenuis* from China [397]. The latter, collected from an identical location (Hainan Island), was taxonomically recognized as *R. globostellata* [395].

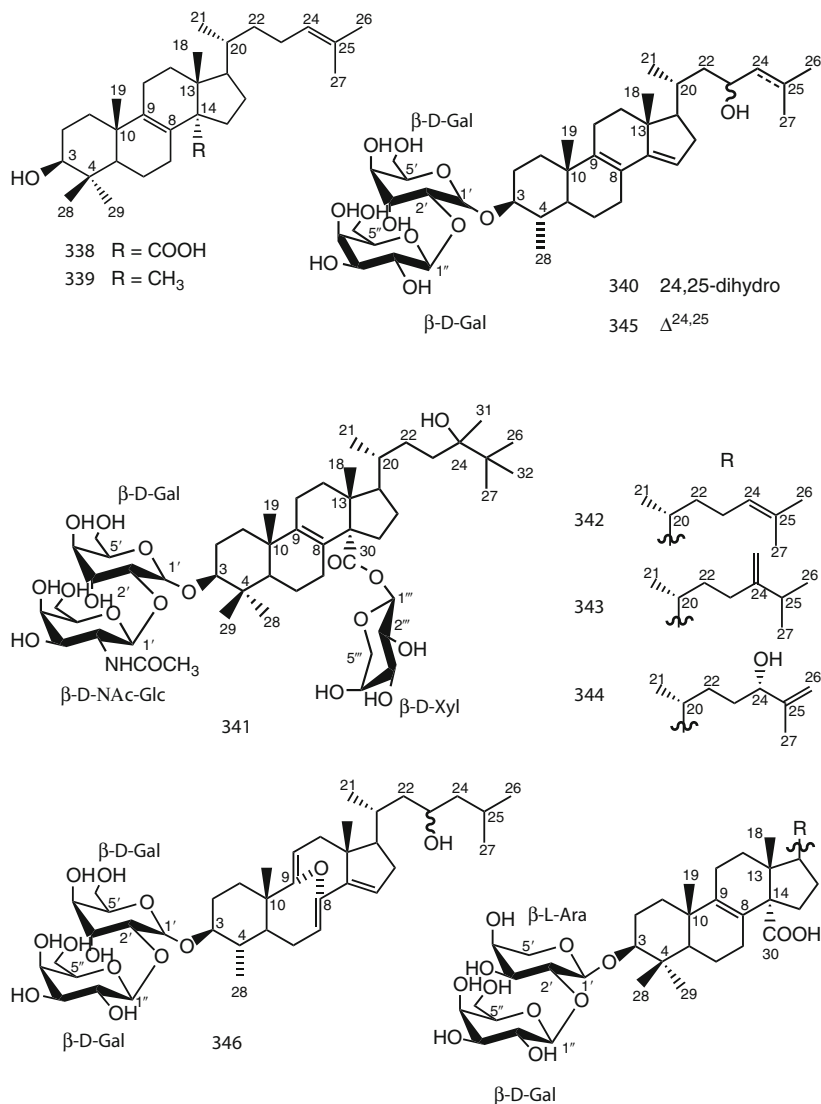
4.4.2.2 Steroidal Saponins

In the Kingdom Animalia, steroidal and triterpene glycosides are predominant metabolites of starfishes and sea cucumbers, respectively [427]. In addition, these types of glycosides have also been isolated from marine sponges. To the best of our knowledge, around 80 triterpenoidal sponge glycosides have been reported to date, including erylosides [427–434], formosides [435, 436], nobiloside [437], and sokodosides [438] from different sponge species of the genus *Erylus*; sarasinosides from the marine sponges *Asteropus sarasinosum* [440–443], *Meloplus isis* [444], and *M. sarassinorum* [445]; mycalosides from *Mycale laxissima* [446–448]; ectyoplasides and feroxosides from the Caribbean marine sponge *Ectyoplasia ferox* [449, 450]; ulososides from *Ulosa* sp. [451, 452]; wondosterols from a two-sponge association [453]; and pachastrelloside A from a marine sponge of the genus *Pachastrella* [454]. The majority of these glycosides belong to norlanostane-triterpenoidal saponins, derived from lanosterol or related triterpenes as a result of oxidative elimination of one or two methyl groups.

Penasterol (338), an acidic steroidal metabolite closely related to lanosterol (339) and possessing potent antileukemic activity, was originally isolated from the Okinawan marine sponge *Penares* sp. in 1988 [425]. Penasterol together with its analogues penasterone and acetylpensterol, isolated from the Okinawan marine sponge *Penares incrustans*, inhibit IgE-dependent histamine release from rat mast cells [426].

Eryloside A (340) was the first eryloside congener isolated from the Red Sea sponge *Erylus lendenfeldi* (class Demospongiae; order Choristida; family Geodiidae) [427]. Twenty-eight additional erylosides (A–F, F₁–F₇, G–V) have been reported from different species of the genus *Erylus* including *E. goffrilleri* [429, 434], *E. formosus* [430, 433], *E. nobilis* [431] in addition to another collection

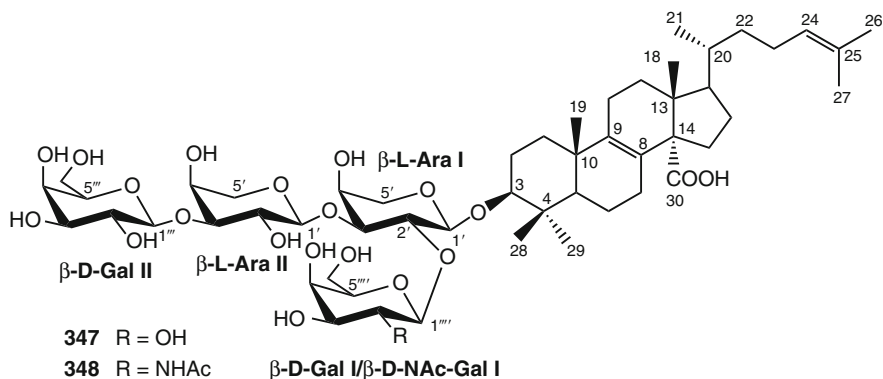
of *E. lendenfeldi* [432]. For eryloside A (**340**), antitumor activity against murine leukemia P388 cells with an $IC_{50} = 5.7 \mu\text{M}$ and antifungal activity against *Candida albicans* ($MIC = 21.1 \mu\text{M}$) have been reported [427]. Eryloside E (**341**), glycosylated at C-30 through an ester linkage with the rare *t*-butyl substitution of the side chain, was isolated from an Atlantic sponge *Erylus goffrilleri* [429]. It revealed immunosuppressive activity with an EC_{50} of $1.8 \mu\text{M}$ and a therapeutic index (TI) of 9.5, which indicated that the immunosuppressive effect is specific and is not due to a general cytotoxic effect [429].

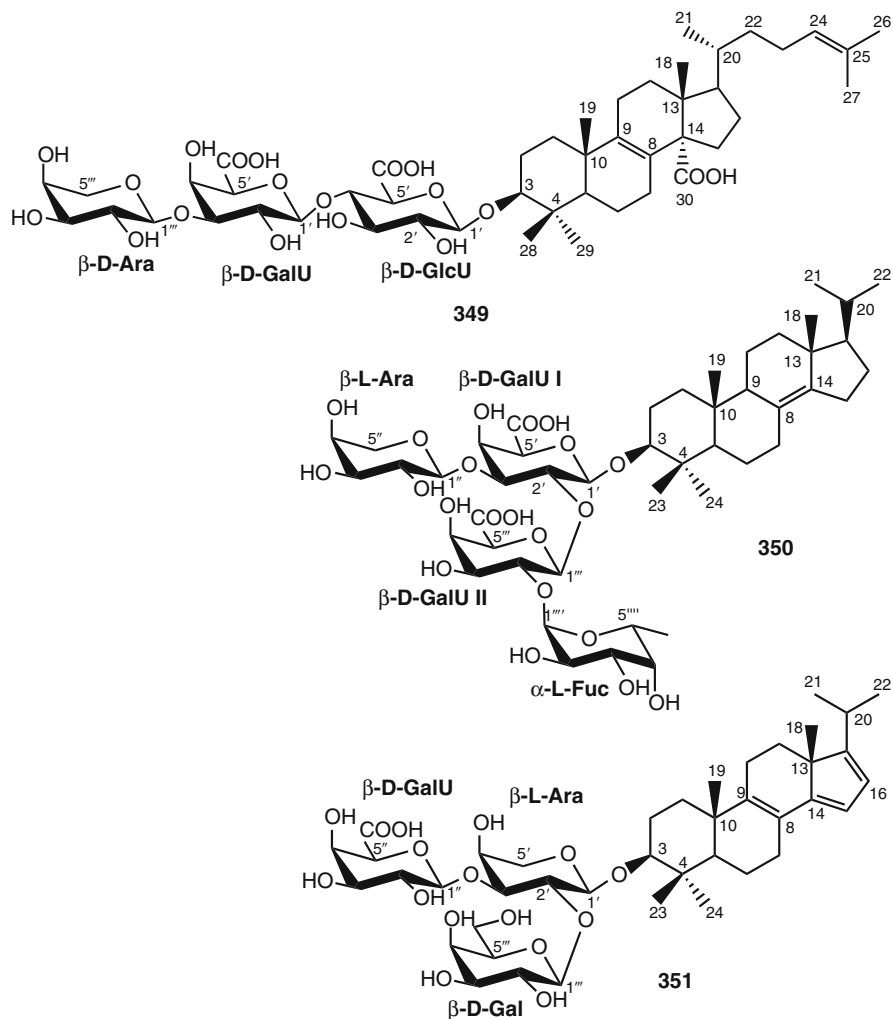


Eryloside F (**342**) was reported from two collections of the marine sponge *E. formosus* [430] and exhibited potent thrombin receptor antagonistic activity. Furthermore, it inhibited platelet aggregation in vitro. Against hepatocyte HepG2 cells, **342** possessed little activity [430]. Erylosides F₁ (**343**) and F₃ (**344**) were isolated along with nine other congeners from the Caribbean sponge *E. formosus* [433]. In contrast to its 24-epimer, eryloside F₃ (**344**) induced early apoptosis in Ehrlich carcinoma cells at 130 μM , while erylosides F (**342**) and F₁ (**343**) activated the Ca^{2+} influx into mouse splenocytes at the same doses [433].

Erylosides K (**345**) and L (**346**) have been obtained together with **340** from another collection of the Red Sea marine sponge *Erylus lendenfeldi* [432]. While **345** was identified as the 24,25-didehydro congener of eryloside A, eryloside L (**346**) incorporated a naturally unprecedented $8\alpha,9\alpha$ -epoxy- 4α -methyl-8,9-secocholesta-7,9(11),14-triene skeleton [432]. Erylosides A (**340**) and K (**345**) led to a 50% mortality rate in the brine shrimp assay at a concentration of 0.14 mM. Eryloside L (**346**) was inactive at the same concentration [432]. In addition to erylosides, the marine sponges *E. formosus* and *E. nobilis* produced other steroidal saponins identified as formosides A (**347**) [435] and B (**348**) [436] and nobiloside (**349**) [437], respectively, whilst sokodosides A (**350**) and B (**351**) have been obtained from the marine sponge *Erylus placenta* [438]. A convergent synthesis of the trisaccharides of **351** has been successfully performed [439]. Formoside A (**347**) was first reported by Jaspars and Crews in 1994 from the Caribbean marine sponge *Erylus formosus* [435]. Later, it was isolated together with formoside B (**348**) from another collection of the same sponge from the Bahamas [436]. Formoside A (**347**) and its *N*-acetyl galactosamine derivative, formoside B (**348**) possess deterrent properties against predatory fish. Therefore, they were suggested to have important ecological functions, resembling those ascribed to similar compounds present in sea stars, sea cucumbers, and terrestrial plants [436].

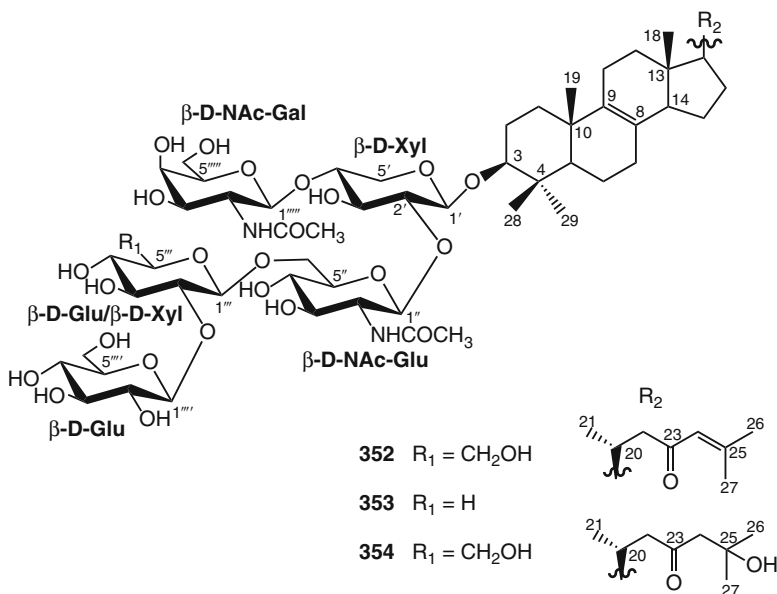
Nobiloside (**349**), a penasterol saponin, was reported from the marine sponge *E. nobilis* collected off Shikine-jima Island, Japan [437], and revealed the presence of a carboxylic group at C-30 in addition to uronic acid moieties. Nobiloside (**349**) inhibited neuraminidase from the bacterium *Clostridium perfringens* with an IC_{50} of 0.5 μM [437].





Sokodosides A (**350**) and B (**351**) were obtained from the marine sponge *E. placenta* collected off Hachijo Island, Japan [438]. They possessed a novel carbon skeleton as characterized by the presence of a combination of an isopropyl side chain and the 4,4-dimethyl steroid nucleus. Moreover, sokodoside B (**351**) exhibited double bonds at unusual positions $\Delta^{8(9),14(15),16(17)}$.

Both sokodosides displayed moderate antifungal activity against the fungus *Mortierella ramanniana* and the yeast *Saccharomyces cerevisiae* but no antibacterial activity was found. Additionally, sokodosides A (**350**) and B (**351**) exhibited cytotoxic activity against P388 cells with IC_{50} values of 103 and 62 μM , respectively [438].



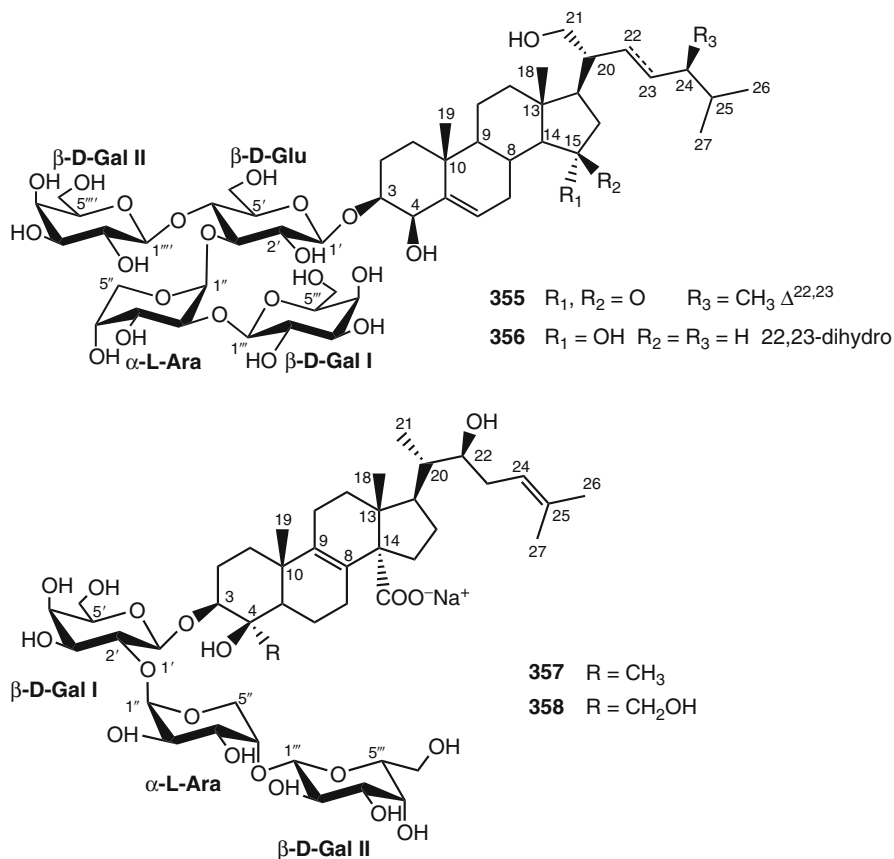
Sarasinosides follow erylosides in the number of isolated metabolites. To date, 21 sarasinoside congeners have been reported, which all feature a carbonyl group at C-23 position. Sarasinoside A₁ (**352**) was the first steroidal saponin reported in the literature, even before eryloside A (**340**), from the Palauan marine sponge *Asteropus sarasinum*, together with other eight new congeners that had been described [440–442]. Then, from the same sponge collected in the Solomon Islands, four additional sarasinosides (D–G) were reported [443]. From each of the marine sponges *Melophlus isis* (Guam) [444] and *M. sarassinorum* (Indonesia) [445], four sarasinoside congeners were isolated. Among the sarasinoside congeners known to date, sarasinoside A₁ (**352**) and B₁ (**353**) exhibited piscicidal activity against *Poecilia reticulata* with LD₅₀ values (48 h) of 0.3 and 0.6 μM, respectively [440, 442]. Sarasinoside A₁ is known to possess moderate cytotoxicity in vitro against leukemia P388 [441] and K562 [444] cell lines with IC₅₀ values of 2.2 and 5.0 μM, respectively. Sarasinoside A₃, which differs from A₁ (**352**) in having Δ^{8(9),14(15)} instead of Δ⁸⁽⁹⁾ unsaturation, exhibited mild cytotoxic activity with an IC₅₀ of 13.3 μM [444]. In the agar diffusion antimicrobial assay (10 μg/disk), sarasinoside A₁ showed strong and selective activity against the yeast *S. cerevisiae* but was inactive against *B. subtilis* and *E. coli*. On the other hand, sarasinoside J (**354**) was active against *S. cerevisiae* and showed moderate antibacterial activity against *B. subtilis* and *E. coli* [445].

Mycalosides include 11 steroidal saponin congeners that were isolated from the Caribbean marine sponge *Mycale laxissima* (class Demospongiae; order Poecilosclerida; family Mycalidae) collected near San Felipe Island,

Cuba [446–448]. They were all characterized by having oxygenated C-4, C-15, and C-21 positions.

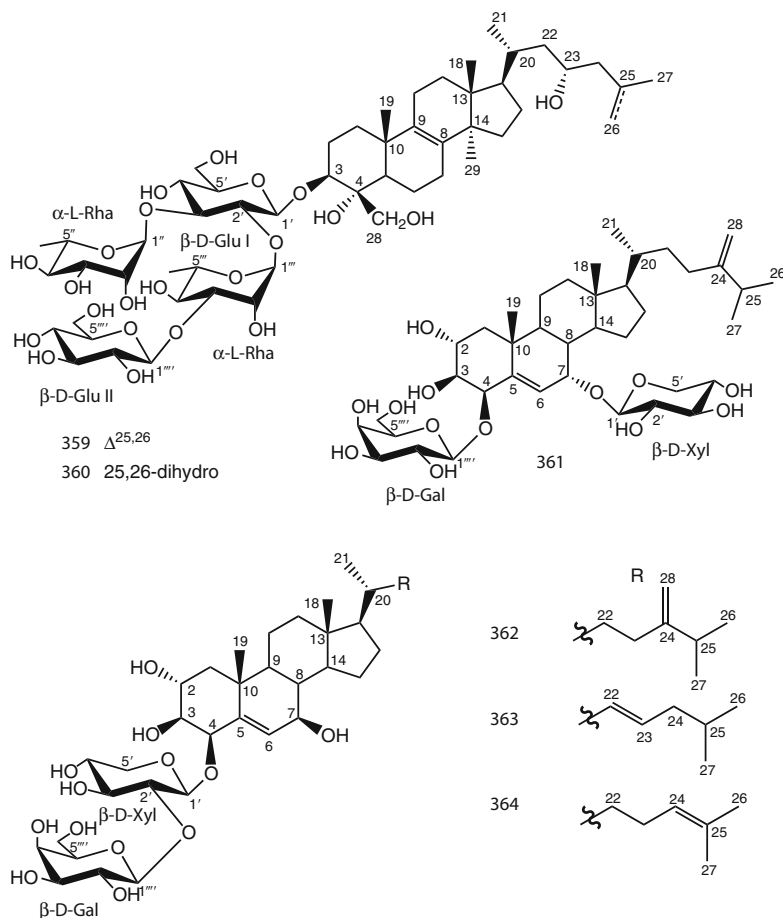
Mycaloside A (**355**) and G (**356**) as well as the total glycoside fraction did not influence nonfertilized eggs and the developing embryo up to the 8-blastomere stage at concentrations of up to 94.6 μM . However, these compounds were effective as spermatostatics when preincubated for 15 min with sea urchin sperm with an EC_{50} of 3.04 μM . The total glycoside fraction generated a less toxic effect ($\text{EC}_{50} = 7.03 \mu\text{g/mL}$) [447].

Ectyoplasides A (**357**) and B (**358**) were first isolated from the Caribbean sponge *E. ferox* (class Demospongiae; order Axinellida; family Raspaliidae) collected along the coasts of San Salvador Island, Bahamas [449]. The compounds are C-4 norpenasterol triterpenoidal derivatives. Later, ectyoplasides were reisolated together with feroxosides A (**359**) and B (**360**) from the same sponge collected along the coasts of Grand Bahama Island [450]. Feroxosides have been shown to be unusual C-4 norlanostane triterpenes glycosylated with a rhamnose-containing tetrasaccharide chain.



Against murine fibrosarcoma WEHI164, murine leukemia P388, and murine monocyte-macrophage J774 cell lines, both ectyoplasides (**357** and **358**) exhibited moderate in vitro cytotoxic activity with IC_{50} values ranging from 9.0 to 11.4 μM [449], while against the latter cell line, feroxosides (**359** and **360**) were mildly cytotoxic ($IC_{50} = 17.6 \mu M$) [450].

Pachastrelloside A (**361**) was obtained from the marine sponge *Pachastrella* sp. (Kagami Bay, Japan) and revealed the presence of a cholest-5,24-diene- $2\alpha,3\beta,4\beta,7\alpha$ -tetraol aglycone that was glycosylated at the C-4 and C-7 positions with β -D-xylopyranose and β -D-galactopyranose moieties, respectively [454]. A Korean sponge association composed of *Poecillastra wondoensis* and *Jaspis wondoensis* resulted in the isolation of wondosterols A–C (**362–364**), which are structurally related to **361** [443]. Wondosterols were shown to have a β -OH group at C-7, and they were all diglycosylated at C-3 with β -D-xylopyranose connected to β -D-galactopyranose.



Wondosterols A–C (**362–364**) were weakly cytotoxic against P388 cells ($IC_{50} = 63 \mu\text{M}$), and at a concentration of $10 \mu\text{g}/\text{disk}$, only **362** and **364** showed antibacterial activities against *P. aeruginosa* and *E. coli* [453]. Pachastrelloside A (**361**) inhibited cell division of fertilized starfish (*Asterina pectinifera*) eggs at $35 \mu\text{M}$ [454].

4.5 Concluding Remarks

The enormous diversity of marine natural products combined with improved global concerns to find new therapeutic agents for the treatment of different ailments provide the stimulus to evaluate marine natural products in clinical trials. Marine drug discovery faces many obstacles including a sufficient supply and the low concentrations of some compounds that may account for less than $10^{-6}\%$ of the wet weight [6]. However, there have been substantial advances, suggesting that sustainable sourcing could be achievable. Since the continuous and exhaustive harvesting of terrestrial drug lead resources proved to be unreliable and resulted in the frequent re-isolation of known compounds, researchers from academia and from pharmaceutical companies alike are now turning their focus to the sea in search for new lead structures from nature. Nevertheless, the large-scale production of marine natural products for clinical use is a real challenge, and, therefore, environmentally sound and economically feasible alternatives are required.

Chemical synthesis is among the first strategies to be explored, but unfortunately, the structural complexity of marine metabolites with novel mechanisms of action and high selectivity has resulted in only a few successful examples of this strategy such as the conus toxin ziconotide [455]. A second strategy, but also as labor-intensive, is to study the pharmacological significance of marine natural product pharmacophores and then attempt to define the critical pharmacophore that can result in practical drugs based on a marine prototype via chemical synthesis, degradation, modification, or a combination of these.

Aquaculture of the source organisms, including sponges, tunicates, and bryozoans, with an aim at securing a sustainable supply of the active constituent(s), has progressed notably in cancer applications. However, in most cases, the biomass currently generated is still far from that required should a marine-based drug finally enter the pharmaceutical market [456]. Furthermore, the cultivation of invertebrates in their natural environment is subject to several hazards and threats, such as destruction by storms or diseases. An intriguing strategy has been to identify the true producers of bioactive compounds and to explore whether or not they are of microbial origin including bacteria, cyanobacteria, or fungi that are known to thrive within the tissues of marine invertebrates.

If bacterial or other associated microorganisms prove to produce the compounds of interest, a careful design of special culture media would be crucial for large-scale fermentation, e.g., ET-743 production. Currently, only 5% or less of the symbiotic bacteria present in marine specimens can be cultivated under standard

conditions [457]. Consequently, molecular approaches offer particularly promising alternatives through the transfer of biosynthetic gene clusters to a vector suitable for large-scale fermentation, thereby avoiding the obstacles in culturing symbiotic bacteria. Oceans will play a potential role in the future to control and relieve the global disease burden. In spite of the substantial development that has been achieved in disclosing novel drug leads from marine resources, more efforts are still required for more chemical entities to reach to clinical applications.

4.6 Study Questions

1. Considering that oroidin is believed to be the precursor of most of the spongal bromopyrrole alkaloids, delineate a plausible biogenetic pathway connecting oroidin with other bromopyrrole alkaloids.
2. What are the main molecular targets of hymenialdisine and analogues, and what are the structural requirements that are responsible for the biological activities of these compounds?
3. Depict the biogenetic relationships between the sponge-derived alkaloids aerophysinin-1, aerophobin-2, and isofistularin-3. What is the amino acid precursor for these alkaloids? Depict the wound-induced biotransformation of brominated isoxazoline alkaloids in *Aplysina* sponges.
4. The bastadins are important bromotyrosine-derived sponge metabolites. Depict a plausible biogenetic scheme that explains the formation of bastadins in sponges. What are the most important biological activities of bastadin derivatives?
5. The jaspamides are important sponge-derived depsipeptides. What are the most promising biological activities of these compounds? Do they bear structural resemblances to other natural products that might support the notion that some sponge metabolites are derived from microorganisms?
6. Azumamides are the first cyclic peptides with histone deacetylase (HDAC) inhibitory activity isolated from marine organisms. Briefly discuss the structural resemblance between azumamides and trichostatin A (TSA) and their relevance for HDAC inhibitory activity.
7. To which group of terpenes does manoalide belong? What are the most prominent biological activity and mode of action of manoalide?
8. Isomalabaricane triterpenes comprise a group of marine sponge natural products with polyene conjugated functionality. Briefly enumerate with examples the different classes of isomalabaricane triterpenes.
9. Jaspolides represent an example of isomalabaricane-type terpenoids including both monomeric and dimeric congeners. Classify different jaspolides based on their chemical structures and depict a plausible biogenetic pathway of the dimeric jaspolide congeners.

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M. Menna (✉) • A. Aiello

Dipartimento di Chimica delle Sostanze Naturali, Università degli Studi di Napoli "Federico II",
Via D. Montesano 49, Naples, Italy

e-mail: mlmenna@unina.it, aiello@unina.it

Abstract

The chapter illustrates the chemistry which has been generated through the investigation of marine ascidians in the last 30 years, highlighting the structural diversity of the compounds produced by these organisms. About 600 structures are here discussed in terms of their occurrence, structural type, and reported pharmacological activity. The chemistry of ascidians is presented in an order based on the general compound type of the metabolites and/or their likely biosynthetic origin.

5.1 Introduction

The tunicates include a wide variety of invertebrates that are classified within the Phylum Chordata based on the presence of a larval notochord during their early development. They are about 3% of the 45,000 or so species of chordates and contain about 3,000 species, usually divided into Ascidiacea (Aplousobranchia, Phlebobranchia, Stolidobranchia), Thaliacea (Pyrosomida, Doliolida, Salpida), Appendicularia (Larvacea), and Sorberacea classes. The great majority are benthic sac-like filter feeders (Ascidiacea and Sorberacea); they live on the ocean floor and filter water by a variety of mechanisms to extract fine planktonic food particles. Those within the two much smaller classes (Thaliacea and Appendicularia) have abandoned the benthic existence in favor of a holoplanktonic lifestyle, that is they live in the pelagic zone as adults.

Despite their simple appearance, they are closely related to vertebrates, and therefore, they represent the most highly evolved group of animals commonly investigated by marine natural products chemists. Most chemical studies have been performed on Ascidiacea (commonly known as the ascidians). An interest in ascidians' chemistry was kindled as early as 1847, when unusual color changes in ascidian blood from yellow-green to deep blue were observed upon exposure to air [1]. A German physiologist discovered that the blue coloring was due to relatively large amounts of vanadium and sulfuric acid, along with an uncharacterized nitrogenous metabolite. Early researchers proposed that the pigmentation was due to oxygen-carrying proteins called hemovanadins. This postulate has proven wrong, but the conquest to understand the role of vanadium in ascidian blood has led to a huge amount of chemical and biological studies [2]. The possible mode of complexation of vanadium was proposed to be by very unstable hydroquinoid compounds, called tunichromes, isolated from the blood cells of several species of ascidians; however, the biological function of these pigments as well as the functional role of the vanadium to the ascidians remains still unclear [3, 4].

Then, attention has focused on ascidians because of their biologically active metabolites, and it has been stimulated by the frequent discovery of antineoplastic agents. Although the birth of the field of marine natural products is generally credited to Bergmann, who in 1950 isolated several modified arabino-nucleosides from a *Tedania* sponge, it was not until 1974 that Fenical isolated the first ascidian metabolite, the geranylhydroquinone, from *Aplidium* sp. [5]. This compound

exhibited chemopreventive activity against some forms of leukemia, Rous sarcoma, and mammary carcinoma in test animals. The occurrence of an anticancer compound in a marine organism, coupled with the general absence of neoplasms in ascidians, provided a powerful incentive to further expand research on these organisms. Since that time, ascidians have been the source of numerous natural products, many with interesting biological activities. The chemistry of ascidians has become one of the most active fields of marine natural products; it has been amply demonstrated that these sea creatures are prolific producers of unusual structures with significant bioactivities [6, 7]. Most of these products fall within the area of cancer therapy, and a significant number of ascidian-derived compounds have entered into preclinical and clinical trials as antitumor agents [8, 9].

The overall goal of this review is not to numerate all the known ascidians metabolites; its primary focus is rather to illustrate the chemistry which has been generated through the investigation of marine ascidians in the last 30 years, highlighting the structural diversity of the compounds produced by these organisms. The metabolites discussed in this review are presented in an order based on their general structural type or on a plausible biosynthetic origin (amino acid origin). As it will be evident, ascidians' chemistry is dominated by the presence of nitrogenous metabolites, among which there is a large variety of structures. There is an extensive range of modified peptides and depsipeptides, sometimes containing unusual amino acids. Heterocyclic alkaloids are also numerous and include pyridoacridines, tryptophan-derived alkaloids (i.e., β -carboline-, and indole-based alkaloids), alkaloids derived from phenylalanine and tyrosine (i.e., isoquinolines), and lysine-derived alkaloids. Nonnitrogenous secondary metabolites are few in number. However, apart from few examples of carotenoids (both common ones and some rarer ones, probably derived from metabolic alteration of commoner carotenoids present in the filtered plankton), steroids (mostly straightforward cholestanes and ergostanes, with some 5,8-epidioxysteroids and secosteroids), and terpenoids, a significant number of acetogenins have been described, including families of macrocyclic lactones, polyethers, cyclic peroxides, and simple alkyl sulfates. Ascidians have also proved to be the source of a sizeable number of terpene-quinone derivatives (meroterpenes), compounds of mixed biogenesis, as well as of a broad spectrum of sulfur-containing metabolites, with fascinating structures and different biological activity.

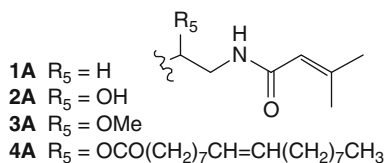
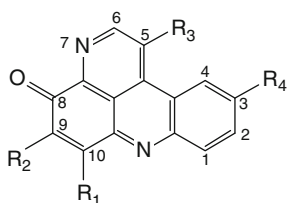
5.2 Alkaloids

5.2.1 Polycyclic Aromatic Alkaloids with Pyridoacridine-Based Nucleus

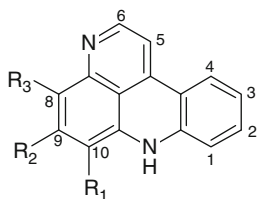
Pyridoacridine alkaloids isolated from ascidians are typically fused tetra- or pentacycle aromatic alkaloids based on the pyrido [*k,l*] acridine skeleton, usually possessing a functionalized alkylamine side chain; more complex polycyclic

pyridoacridines have been reported, too. There has been considerable interest on the biological activity of these compounds, mainly on their potential as antitumor agents [10, 11]. Almost all natural pyridoacridines have been reported to possess significant cytotoxic activity against tumor cells, in part due to their capacity to intercalate into DNA [10]. However, the most intriguing property of the pyridoacridine compounds is their capacity to interfere with the catalytic functions of topoisomerase (TOPO) II; the great chemical diversity in this family of alkaloids provided a large set of tools to manipulate the activity of this enzyme, either stimulating cleavage of DNA through stabilization of covalent TOPO II-DNA complexes or promoting the catenation of DNA [12]. During the past 25 years, both natural pyridoacridines and their analogues have constituted excellent targets for synthetic works [11], confirming that this family of alkaloids as a whole is of interest as a source of new lead structures for drug development.

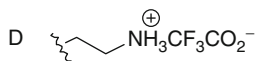
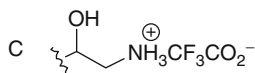
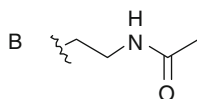
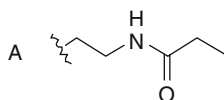
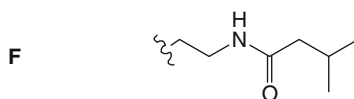
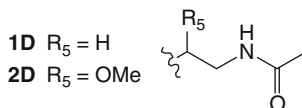
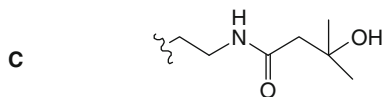
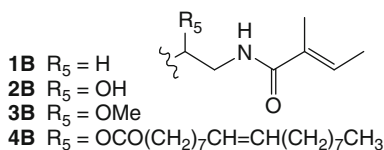
The known tetracyclic pyridoacridine alkaloids from marine sources are dominated by those isolated from ascidians. They show an oxygen function at C-8, which can be a carbonyl group, a hydroxyl, or an ether moiety. Pantherinine (**1**), a cytotoxic brominated alkaloid isolated from *Aplidium pantherinum* [13], can be considered the simplest member of the immiquinone series, which include also cystodytins A–K (**2–12**), a large family of strongly cytotoxic molecules [14–17]. Cystodytins A–C, isolated from an Okinawan *Cystodytes dellechiaiei*, were shown to possess, in addition to a potent cytotoxic activity, powerful Ca^{2+} -releasing activity in the sarcoplasmic reticulum [14]. Diplamine A (**13**), isolated from a *Diplosoma* sp. [18], possesses a thio-methyl functionality on the aromatic nucleus at C-9, like its deacetyl analogue diplamine B (**14**), isolated from *Lissoclinum* cf. *badium* [19]. The S-methyl group seems to be important for cytotoxicity; furthermore, movement of this function from C-9 to C-5 in isodiplamine (**15**), isolated from *L. notti* [17] reduces cytotoxicity. Lissoclins A and B (**16** and **17**), isolated from an Australian collection of *Lissoclinum* sp. [20], are strictly related to diplamine, but no cytotoxic activity data have been reported for these two alkaloids. Nor-segoline (**18**) possesses the 11H-pyrido [4,3,2-*m,n*] acridine nucleus; it was isolated from a purple tunicate from the Red Sea, *Eudistoma* sp. [21, 22], and exhibited potent antileukemic properties [23]. The same aromatic skeleton has been found again in varamines A and B (**19** and **20**), cytotoxic thioalkaloids isolated from a Fijian collection of *L. vareau* [24], and in styelsamines A–D (**21–24**), isolated from an Indonesian collection of *Eusynstyela latericius* [25].



	R ₁	R ₂	R ₃	R ₄
1	H	NH ₂	H	Br
2	1A	H	H	H
3	1B	H	H	H
4	C	H	H	H
5	2A	H	H	H
6	2B	H	H	H
7	3A	H	H	H
8	3B	H	H	H
9	4A	H	H	H
10	4B	H	H	H
11	1D	H	H	H
12	2D	H	H	H
13	1D	SCH ₃	H	H
14	E	SCH ₃	H	H
15	1D	H	SCH ₃	H
16	F	SCH ₃	H	H
17	1B	SCH ₃	H	H

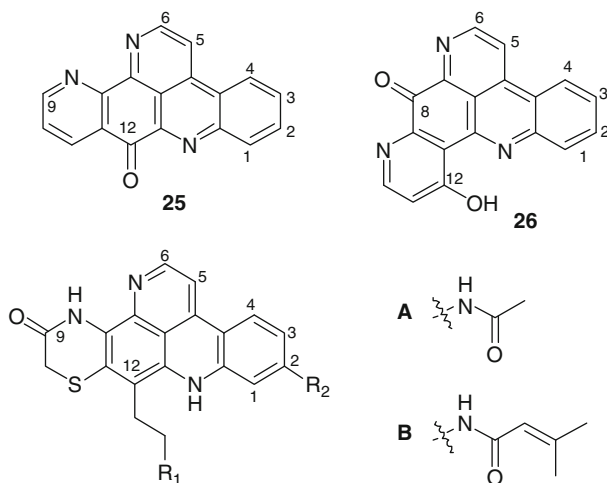


	R ₁	R ₂	R ₃
18	COOMe	H	OMe
19	A	SCH ₃	OMe
20	B	SCH ₃	OMe
21	C	H	OH
22	B	H	OH
23	CHO	H	OH
24	D	H	OH



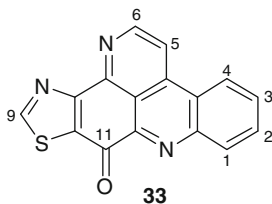
Pentacyclic pyridoacridine alkaloids isolated from ascidians possess an additional ring of various kind, generally fused at C9,10 or at C8,9 of the acridine ring C. Examples are the highly cytotoxic alkaloids ascididemin (**25**), from *Didemnum* sp. [26], and meridine (**26**) [27], from *Amphicarpa meridiana*, both containing a further pyridine moiety. The shermilamines (**27–32**), isolated from a purple

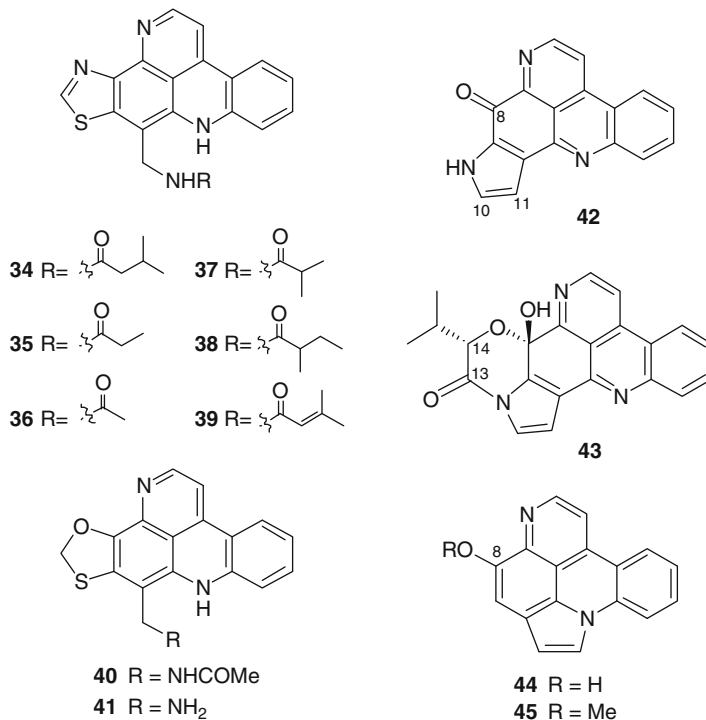
tunicate *Trididemnum* sp., collected in Guam, are thiazinone-containing pentacyclic alkaloids differing in their C-12 side chain [28–31].



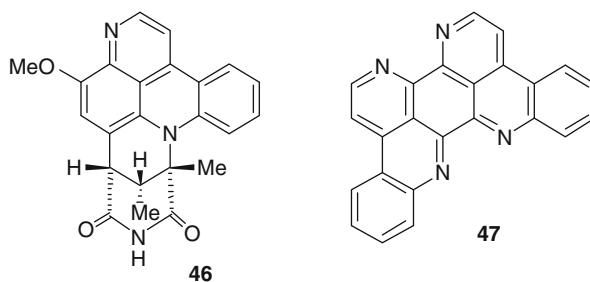
	R ₁	R ₂	R ₃	R ₄
27	A	Br	H	Br
28	A	H	H	H
29	B	H	H	H
30	NMe ₂	H	H	H
31	N(O)Me ₂	H	H	H
32	NH ₂	H	H	H

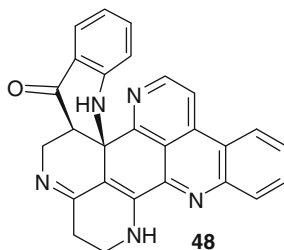
A series of thiazole-containing compounds, kuanoniamines A–F (33–39), was isolated from both an unidentified Micronesian ascidian and the Lamellariidae mollusk *Chelynotus semperi*, believed to be a predator of the ascidian [32, 33]. The structure of kuanoniamine A contains the same tetracyclic iminoquinone-containing pyridoacridine ring system found in ascididemin (25), while the remaining kuanoniamines differ in their acylated phenethylamine side chains. Lissoclinidines (40, 41), isolated from ascidians of *Lissoclinum* genus [17, 19], feature a benzoxathiole moiety, while both sebastianines (42 and 43), from a Brazilian collection of *Cystodites dellechiaiei* [34], and arnoamines (44 and 45), from a *Cystodites* sp. [35], contain a pyrrole ring.





Among the more complex pyridoacridines from ascidians, segolines (**46**, segoline A), possessing a benzo-1,6-diazaphenanthroline ring system, eilatin (**47**), having an unusual symmetrical heptacyclic structure, and eudistones (**48**, eudistone A), can be mentioned. All these alkaloids have been isolated from *Eudistoma* ascidians [20, 21, 36–38]; they have been shown to be potent regulators of cellular growth and differentiation and affect cAMP-mediated processes [39].

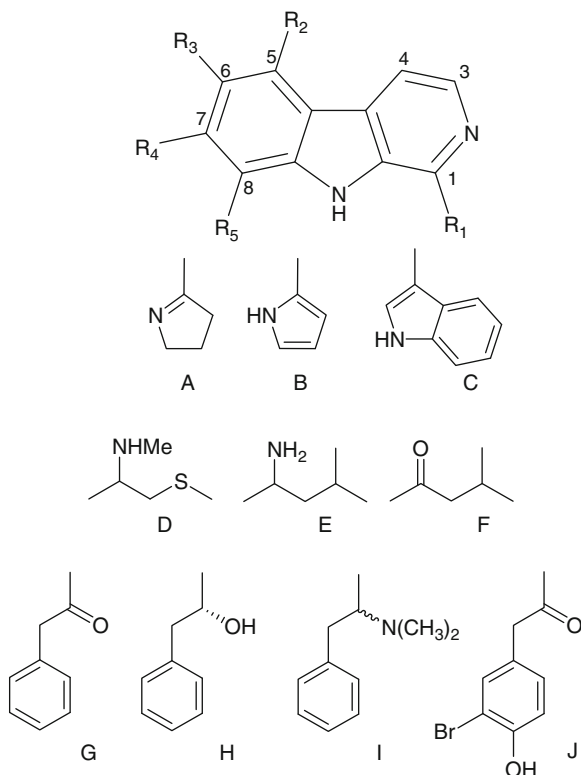




5.2.2 Polycyclic Aromatic Alkaloids with Carboline-Based Nucleus

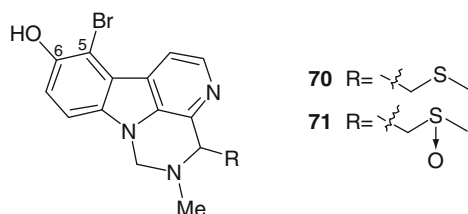
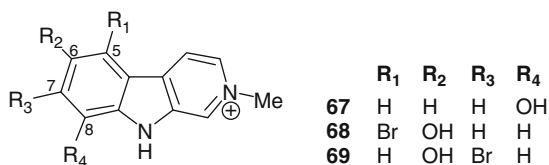
Polysubstituted β -carbolines, as well as dihydro-, and tetrahydro- β -carbolines form a large group of tryptophan-derived ascidian metabolites. The majority of these alkaloids have been isolated from tunicates belonging to the genus *Eudistoma*; they include most of the large group of eudistomins, **49–62** [40–44] and **91–95** [45], eudistomidins (**64**, **65**, **70–72**, **83** **84**) [46–49], eudistalbins (**65** and **66**) [50], the N-methyl β -carbolinium derivatives **68** and **69** [51], woodinine (**85**) [52], and the tryptargine derivatives **87** and **100** [53]. Alkaloids based on a β -carboline ring system have also been reported from other tunicate genera, such as *Ritterella* [54, 55], *Pseudodistoma* [56–68], *Didemnum* [59–63], *Synoicum* [64], and *Lissoclinum* [20, 65]. Almost all the reported compounds are hydroxylated and/or brominated at C5, C6, C7, and C8; apart from few members of the group, which are unsubstituted at C1, they show different substituents at this position, such as pyrrole, pyrroline, or indole rings, as well as hydroxylated, carboxylated, or thiomethylated alkyl residues. Actually, all of the β -carboline metabolites isolated thus far are related biosynthetically; the production of these metabolites is generally believed to involve the coupling of tryptophan with a second amino acid, whose nature clearly affects C1 substitution. For example, eudistomins A (**54**) and M (**55**), as well as G (**50**) and P (**52**), may be considered to be derived from tryptophan and glutamine [40], while the 2-phenylacetyl- β -carbolines, eudistomines R (**56**) and T (**57**), are, in addition to tryptophan, made up of phenylalanine or phenylpyruvic acid. Similarly, the unusual amino acids, *p*-methylphenyl-L-alanine and S-methyl-D-cysteine have been supposed to be involved in the production of eudistomidins B (**83**) and C (**64**) [47], respectively. A proline-derived precursor is evident in eudistomins G, I, P (**50–52**), A (**54**), and M (**55**); eudistomidin A (**63**); and woodinine (**85**). In vivo studies with *E. olivaceum* confirmed that tryptophan and proline are the primary precursors of eudistomin I (**51**) [66]. Some of the most intriguing members of these alkaloids are those bearing an oxathiazepine ring (eudistomins C, E, F, K, and L, **91–95**) which apparently originate from condensation of tryptophan with cysteine [45]. Eudistalbins A (**65**) and B (**66**) likely derive from leucine.

Examples of simple β -carboline alkaloids are the eudistomins **49–62** [40–44], eudistomidins A (**63**) and C (**64**) [46, 47], and eudistalbins (**65** and **66**) [50].

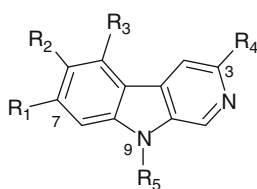


name		R1	R2	R3	R4	R5
Eudistomin J	49	H	H	OH	Br	H
Eudistomin G	50	A	H	H	Br	H
Eudistomin I	51	A	H	H	H	H
Eudistomin P	52	A	H	OH	Br	H
Eudistomin V	53	A	H	Br	Br	H
Eudistomin A	54	B	H	OH	Br	H
Eudistomin M	55	B	H	OH	H	H
Eudistomin R	56	G	H	H	Br	H
Eudistomin T	57	G	H	H	H	H
Eudistomin U	58	C	H	H	H	H
Eudistomin W	59	H	H	OH	H	H
Eudistomin X	60	I	H	OH	H	H
Eudistomin D	61	H	Br	OH	H	H
Eudistomin Y4	62	J	H	Br	H	H
Eudistomidin A	63	A	H	Br	H	OH
Eudistomidin C	64	D	Br	OH	H	H
Eudistalbin A	65	E	H	H	Br	H
Eudistalbin B	66	F	H	H	Br	H

Pseudodistamine (**67**) [58] as well as 2-methyleudistomins D (**68**) and J (**69**) [51] are rare examples of N-methyl β -carbolinium derivatives described from marine sources, while eudistomins I (**70**) and F (**71**) are structurally unique, with a tetrahydropyrimidine ring fused to the β -carboline skeleton [48].



Eudistomidin D (**72**) as well as didemnolines A–D (**73–76**) differ from the other ascidian β -carboline metabolites in that they are substituted at the N9 position of the β -carboline ring, rather than at the C1 position [47, 59]. Tiruchanduramine (**77**) is a β -carboline guanidine alkaloid, and it is the sole 3-substituted β -carboline isolated to date from ascidians [64].



72 R₁=R₄=H; R₂=OH; R₃=Br; R₅=Me

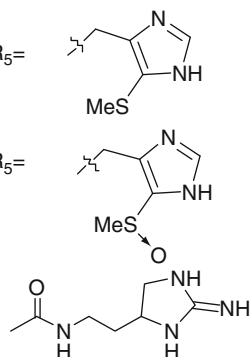
73 R₁=Br R₂=R₃=R₄=H; R₅=

74 R₁=R₂=R₃=R₄=H; R₅=

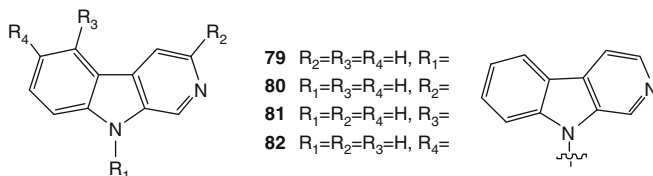
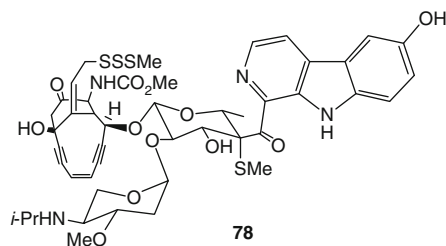
75 R₁=Br R₂=R₃=R₄=H; R₅=

76 R₁=R₂=R₃=R₄=H; R₅=

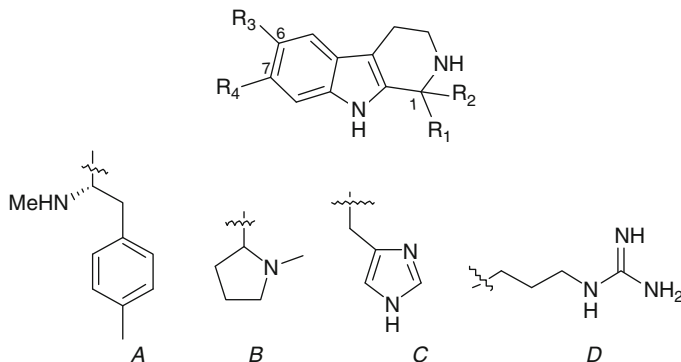
77 R₁=R₂=R₃=R₅=H; R₄=



Shishijimicins (shishijimicin A, **78**) are perhaps the most complex β -carbolines from ascidians; they belong to the enediyne class of antibiotics, which are also potent antitumor agents [60]. Both symmetrical and nonsymmetrical β -carboline dimers (**79–82**) have been reported from *Didemnum* sp., and their structures were confirmed by synthesis [61, 62].



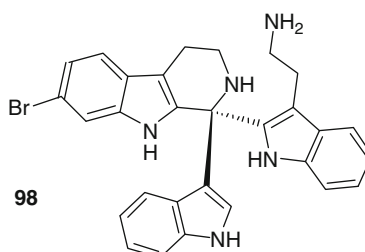
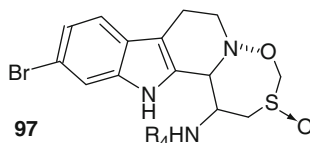
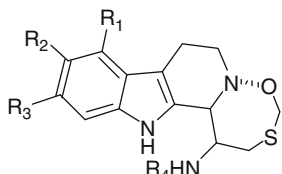
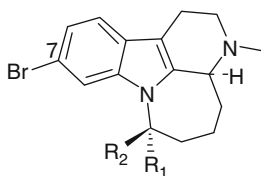
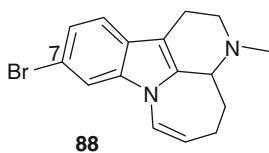
A number of tetrahydro- β -carbolines with various substituents at C1 have been reported; they include eudistomidins B (**83**) and G (**84**) [47, 49], woodinine (**85**) [52], lissoclin C (**86**) [20], and compound **87** the 1-carboxyl analogue of tryptargine, a tetrahydro- β -carboline previously isolated from the skin of the African frog *Kassina senegalensis* [53].



	R_1	R_2	R_3	R_4
83	A	H	Br	H
84	A	H	H	Br
85	B	H	Br	H
86	C	H	H	Br
87	D	CO ₂ H	H	H

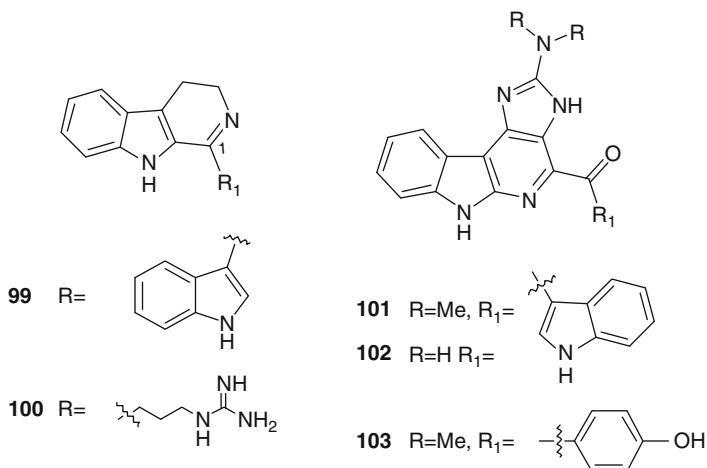
Arborescidines B–D (**88–90**) [57]; eudistomins C, E, F, K, L (**91–95**) [45]; K-sulfoxide (**97**) [54]; and debromo-eudistomin K (**96**) [55] contain a 7-membered additional ring attached to the tetrahydro β -carboline moiety which, in the case of the eudistomins, is an oxathiazepine ring. Bengacarboline (**98**) is

a tetrahydro- β -carboline with two indole units attached to C1 of the carboline nucleus; it resulted cytotoxic toward a 26 cell line human tumor panel in vitro and inhibited the catalytic activity of TOPO II [63].



The eudistomins display a variety of biological activities, including a broad spectrum of antibiotic activity and cytotoxicity, but they are notable for the strong antiviral properties displayed by some members of the family [67, 68]. The tetrahydro- β -carboline generally exhibited higher levels of biological activity than their fully aromatic relatives; the oxathiazepino-eudistomins **88–94**, for example, exhibit the highest level of antiviral activity and were also endowed with antimicrobial activity. Eudistomin K (**91**) is significantly active against *Herpes simplex* Type I (HSV-1) and *Polio* virus, while the sulfoxide (**94**) and debromo (**90**) derivatives are active against both virus but less potent. Enhancement of antiviral activity correlates to bromination at C7. Eudistomidin A (**66**) and C (**67**) display calmodulin antagonistic activity, while eudistomidin B (**81**) activates rabbit heart muscle actomyosin ATPase [69].

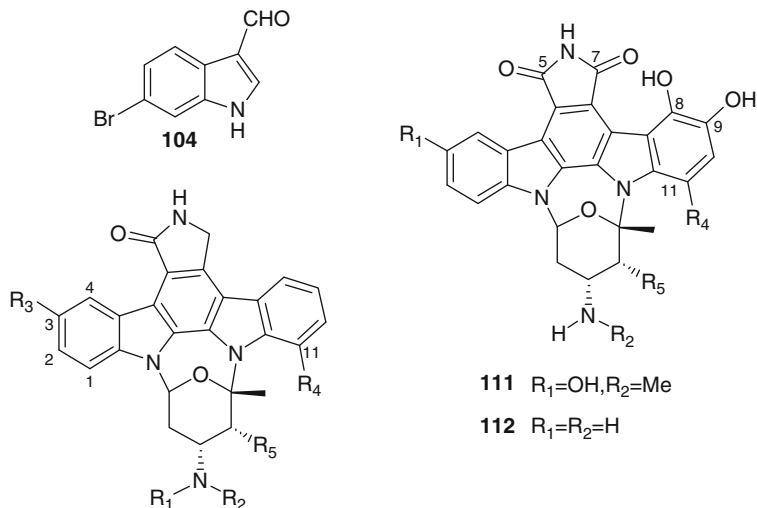
There are only few reported examples of dihydro- β -carboline from ascidians. The first was isoeudistomin U (**99**) which was initially reported to be a 4-substituted dihydro- α -carboline derivative [65], but whose structure was revised after total synthesis to 3,4-dihydroeudistomin U [70]; the bioactivity of isoeudistomin U was reported to be similar to that of the related eudistomin U (**59**). A 1,2-dehydro analogue of trypargine, named trypargimine (**100**), has been reported from a previously undescribed *Eudistoma* sp. [53].



Also α -carbolines are not common ascidian metabolites. The grossularines (**101–103**) from *Dendrodia grossularia* are the sole representatives of this structural class and are the first α -carbolines to be isolated from a natural source. The initial structure reported for grossularine (=grossularine-1) [71] was incorrect, and it was revised when data for both grossularine-1 (**101**) and -2 (**103**) were reported [72]. Both grossularines are cytotoxic and cause accumulation of cells in the G1-phase; grossularine-2 appears to act on DNA as a mono-intercalating agent. N,N-didesmethylgrossularine-1 (**102**) has been reported from *Polycarpa aurata*, but no activity data were presented [73].

5.2.3 Indole-Based Alkaloids

The structures of indole-based alkaloids isolated from ascidians span a wide range of complexity, spreading from the simple 6-bromoindole-3-carbaldehyde (**104**), isolated from *Pyura sacciformis* [74] which was previously found in a marine pseudomonad [75] to the complex indolocarbazoles of the staurosporine type (**105–112**) isolated from some Polycitoridae species [76–81]. Staurosporine and its derivatives have been isolated from various actinomycete strains as well as from some marine organisms, including ascidians [82]. These alkaloids were shown to be strong inhibitors of several kinases, in particular protein kinase C (PKC); other activities include inhibition of platelet aggregation and smooth muscle contraction, induction of cell cycle arrest and apoptosis, and the reversal of multidrug resistance in some cancer cell lines. The potential of these derivatives as anticancer agents is supported by the example of 7-hydroxystaurosporine which is in clinical phase I trials at the NCI [79].



105 $R_1=H, R_2=Me, R_3=H, R_4=OH, R_5=OMe$

106 $R_1=H, R_2=Me, R_3=OH, R_4=H, R_5=OH$

107 $R_1=H, R_2=H, R_3=H, R_4=OH, R_5=OMe$

108 $R_1=Me, R_2=Me, R_3=OH, R_4=H, R_5=OMe$

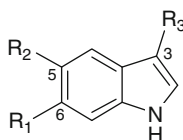
109 $R_1=H, R_2=H, R_3=OH, R_4=H, R_5=OMe$

110 $R_1=H, R_2=H, R_3=H, R_4=H, R_5=OH$

111 $R_1=OH, R_2=Me$

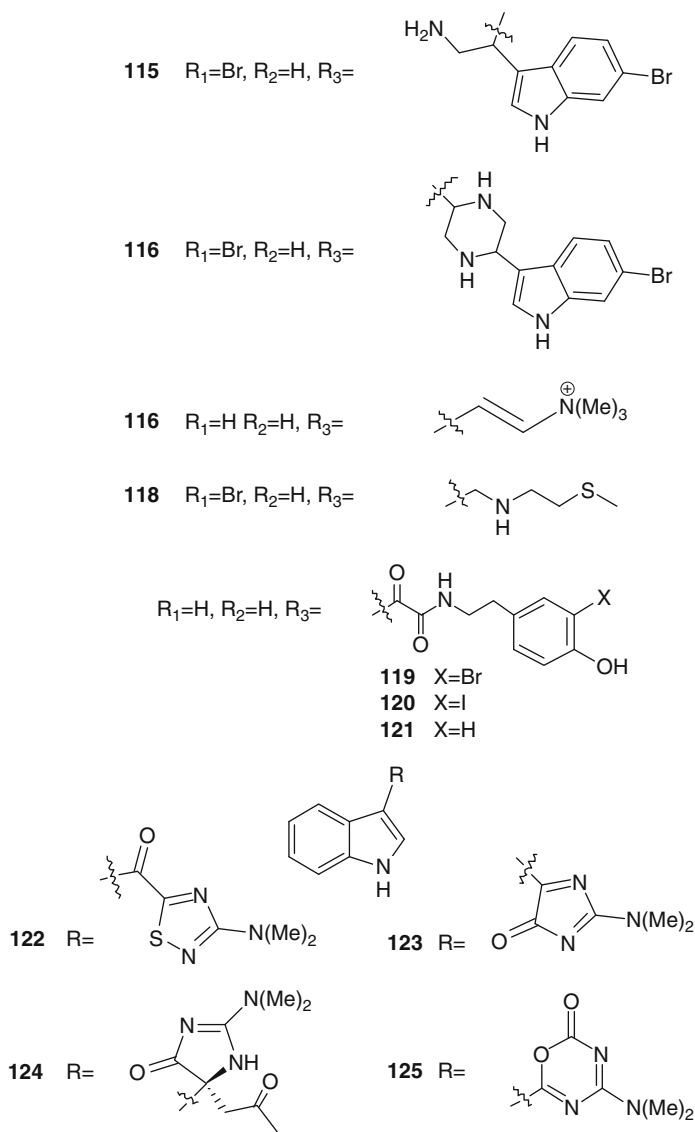
112 $R_1=R_2=H$

A number of 3-substituted indoles have been isolated from ascidians. Examples are 6-bromotryptamine (**113**) and its derivatives (**114–116**), isolated from *Didemnum candidum* [83], conicamin (**117**), from *Aplidium conicum*, with histamine-antagonistic activity [84], citorellamine (**118**), from *Polycitrella mariae*, the first indole disulfide dihydrochloride from a marine organism [85, 86], and the indolyl-3-glyoxylic acid derivatives polyandrocarpamides A–C (**119–121**) [87]. *Dendrodoa grossularia* was the source of several indole alkaloids with different heterocyclic moieties linked at three position (compounds **122–125**) [88–91]. Among them, alboinon (**125**) contained an oxadiazinone system, found in nature for the first time [90].



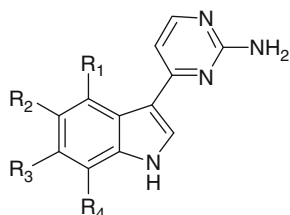
113 $R_1=Br, R_2=H, R_3=-CH_2CH_2NH_2$

114 $R_1=H, R_2=Br, R_3=-CH_2CH_2N(Me)_2$

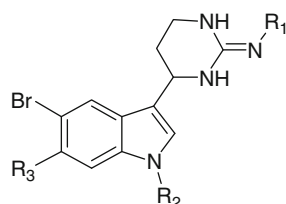


Meridianins are brominated and/or hydroxylated 3-(2-aminopyrimidine)-indoles which have been isolated from *Aplidium meridianum* [92, 93]. Seven meridianins A–G (**126–132**) have been discovered so far, differing in the bromine and/or hydroxyl substitution. They constitute a new family of protein kinase inhibitors, inhibiting various protein kinases such as cyclin-dependent kinases, glycogen synthase kinase-3, cyclic nucleotide-dependent kinases, and casein kinase 1; they also prevent proliferation and induce apoptosis probably due to their ability to enter

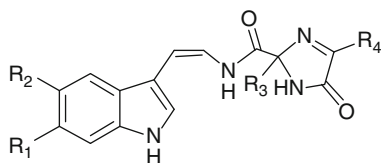
cells and to interfere with the activity of kinases important for cell division and death [94]. Structurally related to meridianins are aplicyanins A–F (**133–138**), isolated from *Aplidium cyaneum* and containing a 6-tetrahydropyrimidine substituent at C-3; these alkaloids can be considered reduced forms of the relevant meridianins and, thus, their biogenetic precursors [95].



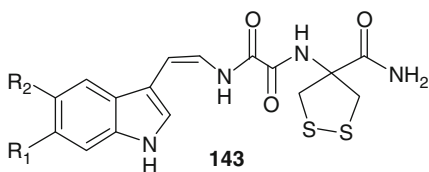
- 126** R₁=OH; R₂=R₃=R₄=H
127 R₁=OH; R₂=R₄=H; R₃=Br
128 R₁=R₃=R₄=H; R₂=Br
129 R₁=R₂=R₄=H; R₃=Br
130 R₁=OH; R₂=R₃=H; R₄=Br
131 R₁=R₄=H; R₂=R₃=Br
132 R₁=R₂=R₃=R₄=H



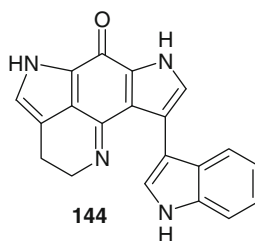
- 133** R₁=R₂=R₃=H
134 R₁=Ac; R₂=R₃=H
135 R₁=R₃=H; R₂=OMe
136 R₁=Ac; R₂=OMe; R₃=H
137 R₁=H; R₂=OMe; R₃=Br
138 R₁=Ac; R₂=OMe; R₃=Br



- 139** R₁=R₂=Br; R₃=2-propyl; R₄=2-butyl
140 R₁=Br; R₂=H; R₃=2-propyl; R₄=2-butyl
141 R₁=H; R₂=Br; R₃=2-propyl; R₄=2-butyl
142 R₁=R₂=Br; R₃=2-Butyl; R₄=Methyl



143

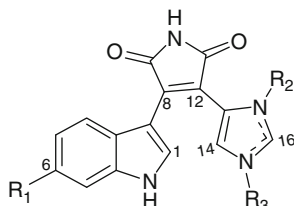


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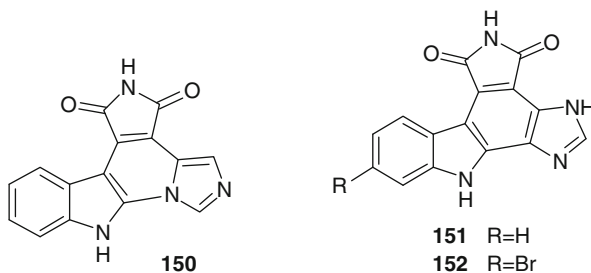
Kottamides (**139–142**) have been isolated from a New Zealand collection *Pycnoclavella kottae* [96, 97]; kottamides A–D (**139–142**) are imidazol-4-one containing alkaloids; their biogenesis could involve stereospecific imidazolone ring formation from modified Trp-Val-Ile and Trp-Ile-Ala tripeptide precursors [96]. Kottamide E (**143**) represents the first report of a natural product bearing

a 4-amino-1,2-dithiolane-4-carboxylic acid residue [97]. Wakayin (**144**), from *Clavelina* sp., provides the first example of a pyrroloiminoquinone alkaloid to be isolated from an ascidian. It is also one of the first camptothecin (CPT)-like TOPO I inhibitors isolated from a marine organism, the indole ring linked to the bispyrrole iminoquinone core playing a significant role in this activity [98].

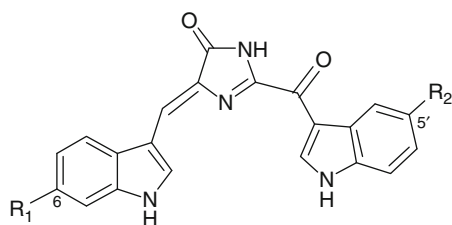
Four predator-deterrent alkaloids possessing a novel indole–maleimide–imidazole carbon skeleton, didemnimides A–D (**145–148**), were isolated from a Caribbean collection of *Didemnum conchyliatum* [99]. They were the first examples of a new alkaloid structural class and add to a relatively small group of naturally occurring maleimides. Successively, didemnimide E (**149**) was isolated from *Didemnum granulatum* collected in Brazil together with a less polar and deep purple cyclized didemnimide alkaloid, isogranulatimide (**150**) [100]. Almost at the same time, Fenical's group independently obtained this compound from *D. conchyliatum* [101]. Compound **150** is the cyclization product of didemnimide A (**145**) formed via a C-2 indole condensation with the imidazole nitrogen and represented the first alkaloid to be isolated with this cyclized indole–maleimide–imidazole structure. Isogranulatimide (**150**) and its isomer granulatimide (**151**) could be biomimetically synthesized involving the photocyclization of **145**. Subsequently, **151** and its 6-bromo derivative **152** were obtained as naturally occurring compounds from a new collection of Brazilian *D. granulatum* [102]. Isogranulatimide **150** was reported as the first noncytotoxic, specific G2 cell cycle checkpoint inhibitor, and the mechanism of this antitumor action was elucidated at molecular level [100, 103].



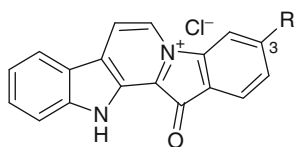
- 145** $R_1=R_2=H$
146 $R_1=Br; R_2=H$
147 $R_1=H; R_2=Me$
148 $R_1=Br; R_2=Me$
149 $R_1=H; R_3=Me$



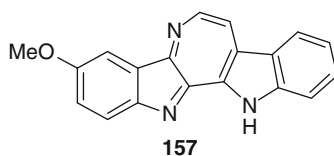
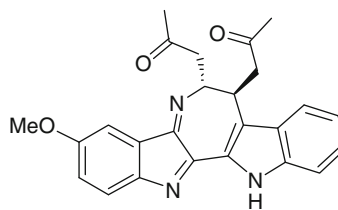
Apart from the above mentioned staurosporine derivatives **105–112**, other examples of bisindole alkaloids are rhopaladins (**153–156**), from *Rhopalaea* sp., possessing an imidazolinone moiety [104], and iheyamines A (**157**) and B (**158**), from a *Polycytorella* sp., with a new heteroaromatic skeleton composed of an azocine unit fused onto a bisindole system [105]. The 12H-pyrido[1,2-a:3,4-b0]diindole ring system forms the framework of the red pigment faspaplysins (**159**), which was isolated in 1988 from the sponge *Faspaplysinsopsis Bergquist* and successively found in other Thorectidae sponges; this compound, together with its 3-bromo derivative (**160**), has been found in some *Didemnum* collections [63, 106, 107]. Faspaplysins and its derivatives exhibit a broad range of bioactivities including antibacterial, antifungal, antiviral, HIV-1-RT, p56 tyrosine kinase, antimalarial, cytotoxicity against numerous cancer cell lines, specific inhibition of Cdk 4, and DNA intercalation, demonstrating a huge potential for therapeutic assays [108].



- 153** R₁=OH; R₂=Br
154 R₁=OH; R₂=H
155 R₁=H; R₂=Br
156 R₁=R₂=H



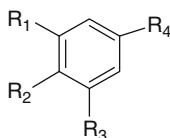
- 159** R=H
160 R=Br

**157****158**

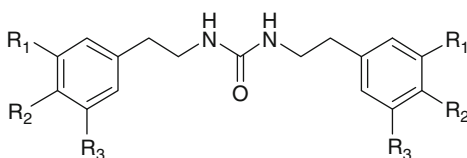
5.2.4 Tyrosine- and Phenylalanine-Derived Alkaloids

Tyrosine is the precursor of a wide number of alkaloids whose structures are characterized by possessing the Ar-C₂-N subunit derived from Tyr, commonly via dopamine; often, additional Ar-C₁ and Ar-C₂ moieties are present, derived from a partial degradation of the amino acids Phe or Tyr. Furthermore, the aromatic ring of all these subunits is usually oxygenated at 4-, 3,4-, or

3,4,5-positions. The amino acid DOPA [2-amino,3-(3',4'-dihydroxyphenyl) propionic acid] in particular, appears to play an important role in the metabolism of ascidians, serving as the apparent precursors not only of peptide products but also of several alkaloid metabolites. In this group fall simple aromatic alkaloids, derived directly or indirectly from phenylalanine, tyrosine, phenylethylamine, tyramine, or dopamine, as well as complex highly condensed structures. Phenylethylamine itself (**161**) and its urea derivative (**162**) have been found in a *Lissoclinum* sp. and in *Didemnum ternatanum*, respectively [20, 109]. Iodinated and/or brominated tyramine derivatives, such as compounds **163–172**, are often found within ascidians metabolites [53, 110–114]. The guanidine derivatives tubastrine (**173**) and its saturated analogue **174** have been found in a New Zealand collection of *Aplidium orthyum* [115]; an Australian collection of *Polycarpa aurata* contained the three *p*-methoxybenzoyl derivatives **175–177** [116].



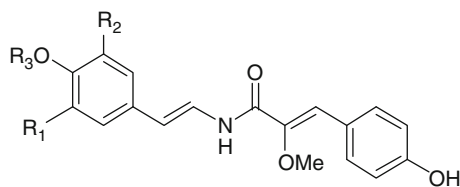
- 161** $R_1=R_2=R_3=H; R_4=-CH_2CH_2NH_2$
163 $R_1=I; R_2=OMe; R_3=I; R_4=-CH_2CH_2NH_2$
165 $R_1=I; R_2=OMe; R_3=I; R_4=-CH_2CONH_2$
166 $R_1=I; R_2=OMe; R_3=I; R_4=-CH_2CH_2NHCOH$
167 $R_1=I; R_2=OMe; R_3=I; R_4=-CH_2CH_2NHCOPhe$
168 $R_1=I; R_2=OH; R_3=H; R_4=-CH_2CH_2NH_2$
169 $R_1=I; R_2=OH; R_3=H; R_4=-CH_2CH_2N(Me)_3+$
170 $R_1=Br; R_2=OH; R_3=H; R_4=-CH_2CH_2NH_2$
171 $R_1=Br; R_2=OH; R_3=Br; R_4=-CH_2CH_2NH_2$
172 $R_1=Br; R_2=OH; R_3=H; R_4=-CH_2CH_2N(Me)_3+$
173 $R_1=OH; R_2=OH; R_3=H; R_4=-CH=CHNHCNHNH_2$
174 $R_1=OH; R_2=OH; R_3=H; R_4=-CH_2CH_2NHCNHNH_2$
175 $R_1=H; R_2=OMe; R_3=H; R_4=-CONHCNHNH_2$
176 $R_1=H; R_2=OMe; R_3=H; R_4=-COCOO(CH_2)_3CH_3$
177 $R_1=H; R_2=OMe; R_3=H; R_4=-COCONHCH_3$



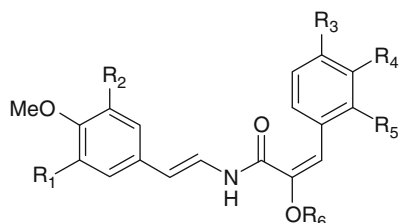
- 162** $R_1=R_2=R_3=H$
164 $R_1=I; R_2=OMe; R_3=I$

Botryllamides (A–J, **178–187**) are a series of brominated tyrosine derivatives isolated from several *Botryllus* species [117–120]; they form a new class of

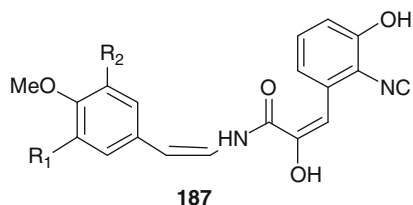
selective inhibitors of ABCG2, a human ATP-binding cassette (ABC) transporter gene usually associated with multidrug resistance in cancer [119, 121].



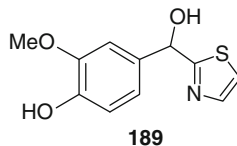
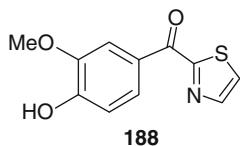
- 178** $R_1=R_2=Br$; $R_3=Me$
180 $R_1=Br$; $R_2=H$; $R_3=Me$
182 $R_1=R_2=H$; $R_3=Me$
183 $R_1=R_2=H$; $R_3=H$
184 $R_1=R_2=Br$; $R_3=H$

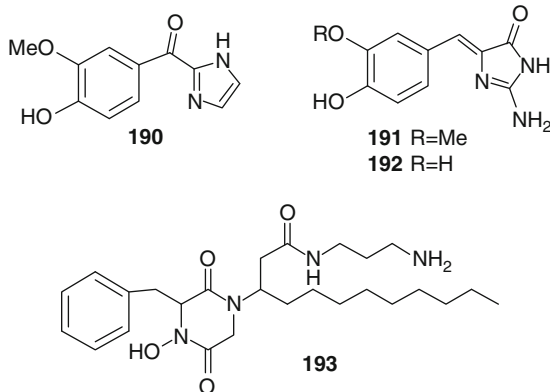


- 179** $R_1=R_2=Br$; $R_3=OH$; $R_4=R_5=H$; $R_6=Me$
181 $R_1=Br$; $R_2=H$; $R_3=OH$; $R_4=R_5=H$; $R_6=Me$
185 $R_1=R_2=R_3=H$; $R_4=OH$; $R_5=NC$; $R_6=H$
186 $R_1=R_2=H$; $R_3=OH$; $R_4=R_5=H$; $R_6=Me$

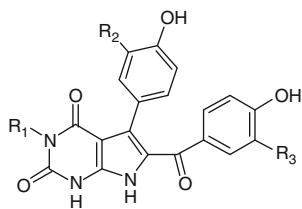


In some metabolites, the amino group of what initially was the amino acid residue has ended up as a part of a heteroaromatic ring. Examples are the thiazole and imidazole metabolites **188–190** isolated from *Aplidium pliciferum* [122] as well as the polyandrocarpamines A and B (**191** and **192**), from a Fijian *Polyandrocarpa* sp. possessing a 2-aminoimidazolone moiety [123]. A condensation between phenylalanine and glycine is expected to form the 1,4-diketopiperazine unit present in etzionin (**193**), an unusual antifungal metabolite isolated from an unidentified Red Sea tunicate [124].

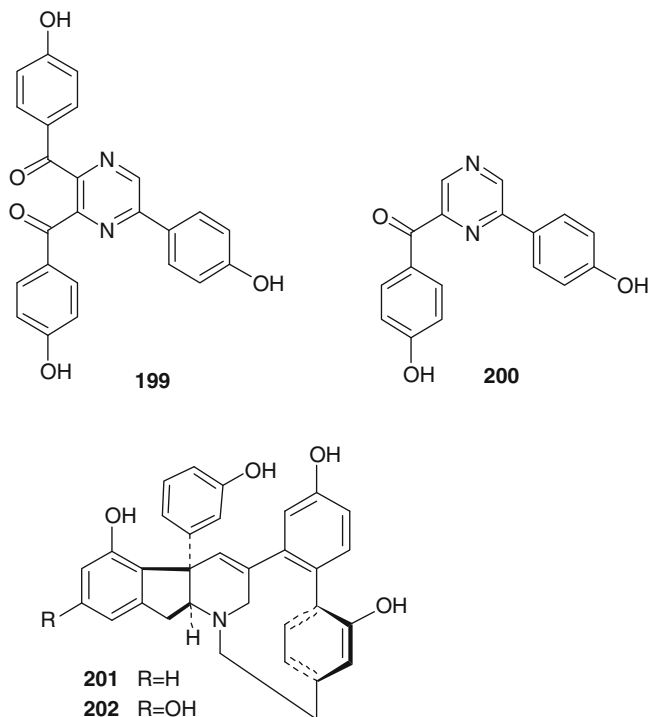




Rigidin (**194**), isolated from the Okinawan tunicate *Eudistoma cf. rigida*, was the first pyrrolopyrimidine alkaloid to be isolated from a marine source; it exhibited calmodulin antagonistic activity for inhibition of calmodulin-activated brain phosphodiesterase [125]. Four rigidin congeners, rigidins B–E (**195–198**), have been successively isolated from *Cystodites* and *Eudistoma* species [126, 127]. Botryllazines A and B (**199** and **200**) have been isolated from *Botryllus leachi*; the structure of botryllazine A is unprecedented since three tyrosine precursors are involved in the formation of a pyrazine nucleus. It has been proposed that the biogenetic pathway leading to botryllazine B from two tyrosine units involves amide formation and, subsequently, cyclization *via* imine formation [128]. Haouamines A and B (**201** and **202**), isolated from *Aplidium haouarianum* [129], demonstrate intriguing stereochemical features; in solution, each haouamine exists as an inseparable mixture of two interconverting isomers derived by the presence of a highly strained 3-aza-[7]-paracyclophane moiety in their structures. Even if one Ar–C2–N and three Ar–C2 subunits can be readily identified in the structures of haouamines, the oxygenation pattern of all these units, hydroxylated at the meta position with respect to the C2 chain, does not allow establishing a relationship between these alkaloids and the amino acid tyrosine. Thus, the biosynthesis of these alkaloids should imply either an unusual loss of the C4 hydroxyl group of tyrosine along the biosynthetic pathway or the involvement of an undescribed natural amino acid precursor exclusively meta hydroxylated [129].



- 194** R₁=R₂=R₃
195 R₁=R₂=H; R₃=OMe
196 R₁=R₃=H; R₂=OMe
197 R₁=H; R₂=R₃=OMe
198 R₁=Me; R₂=R₃=H



The lamellarins form a group of more than 50 highly condensed DOPA- and TOPA-derived pyrrole alkaloids; they were first isolated from the proso-branch mollusk *Lamellaria* sp. in 1985 [130] and, since then, they have been reported from diverse marine organisms, mainly but not exclusively ascidians and sponges, which suggests a potential microbial link to their biosynthesis [131].

The lamellarins fall into two structural groups, depending on whether the central pyrrole ring is fused (group I) or unfused (group II) to adjacent aromatic rings (Fig. 5.1). Group I could be further divided into two subgroups, Ia, including compounds with an olefin at C5/C6, and Ib, with compounds in which this olefin is saturated. The family also includes sulfated members. Most of lamellarins have shown a wide range of bioactivities, such as antibiotic activity, HIV-1 integrase inhibition, immunomodulation, antioxidant activity; a considerable number of lamellarins have been found to be cytotoxic and, more interestingly, some of them were reported to act as nontoxic inhibitors of acquired multidrug resistance (MDR) in various cancer cell lines. In light of their fascinating novel structures and intriguing biological properties, lamellarins have got to be a particularly important subject for synthetic as well

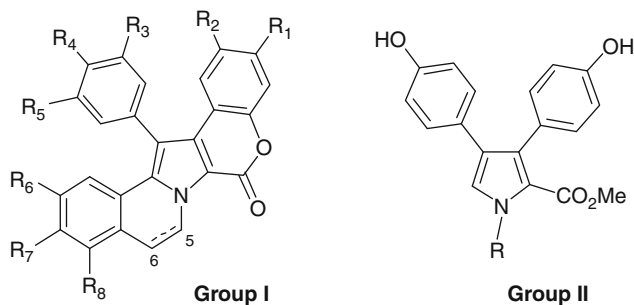
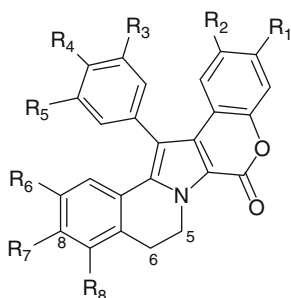
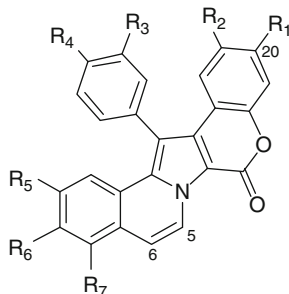


Fig. 5.1 Core structures of lamellarins

as SAR studies [131, 132]. A number of lamellarins have been isolated from ascidians belonging to *Didemnum* genus, all with the hexacyclic skeleton of group I; examples are lamellarins E–M (203–211) [133, 134], Z (212) [135], α , ϵ , ζ , η , and ϕ (213–217) [136, 137]; triacetate of lamellarin N (218) [134]; lamellarin G 8-sulfate (219) [135]; the 20-sulfate derivatives of lamellarins B, C, L, and α (220–223) [135, 138].

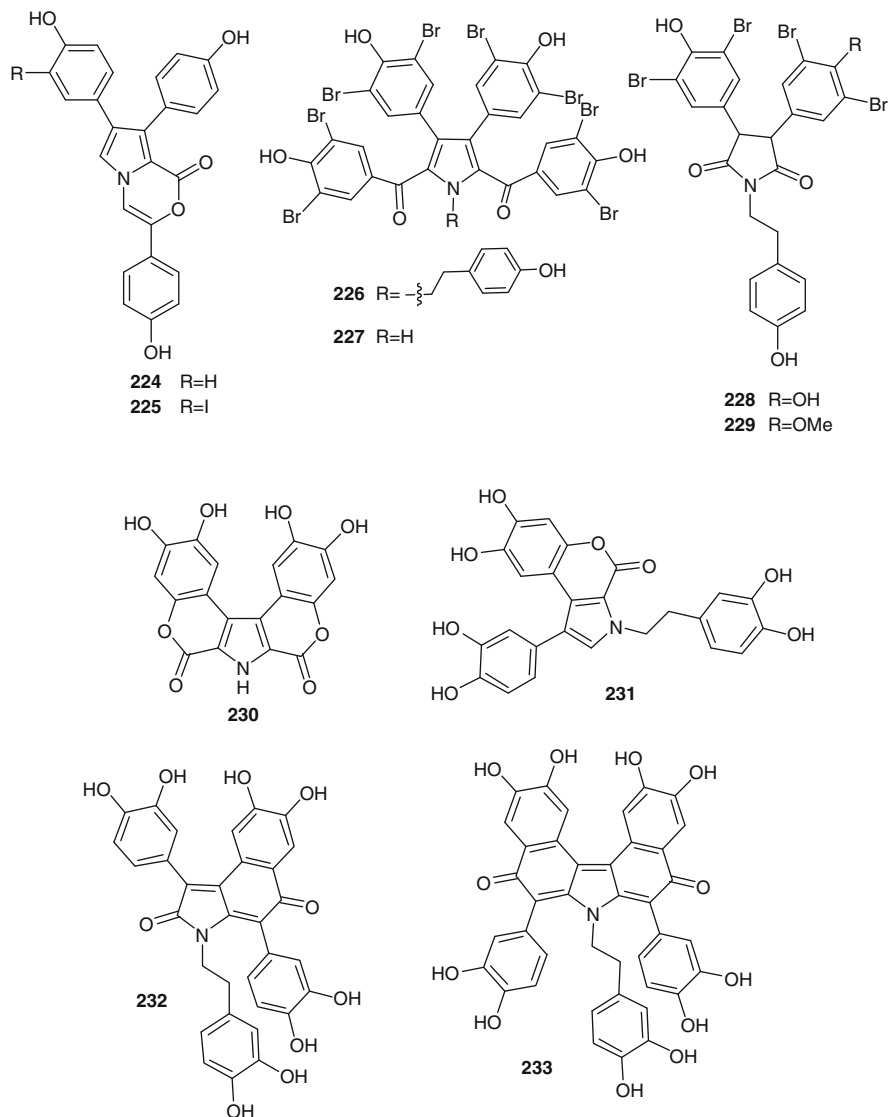


Lamellarin E	203	$R_1=R_8=OH$; $R_2=R_4=R_5=R_6=R_7=OMe$; $R_3=H$
Lamellarin F	204	$R_1=R_5=R_8=OH$; $R_2=R_4=R_6=R_7=OMe$; $R_3=H$
Lamellarin G	205	$R_1=R_4=R_6=OMe$; $R_2=R_5=R_7=OH$; $R_3=R_8=H$
Lamellarin I	207	$R_1=OH$; $R_2=R_4=R_5=R_6=R_7=R_8=OMe$; $R_3=H$
Lamellarin J	208	$R_1=R_7=OH$; $R_2=R_4=R_5=R_6=OMe$; $R_3=H$
Lamellarin K	209	$R_1=R_4=R_8=OH$; $R_2=R_5=R_6=R_7=OMe$; $R_3=H$
Lamellarin l	210	$R_1=R_5=R_7=OH$; $R_2=R_4=R_6=OMe$; $R_3=R_8=H$
Lamellarin α	213	$R_1=R_6=OMe$; $R_2=R_4=R_5=R_7=OH$; $R_3=R_8=H$
Lamellarin ζ	215	$R_1=OSO_3^-$; $R_2=R_5=R_6=R_7=R_8=OMe$; $R_4=OH$; $R_3=H$
Lamellarin η	216	$R_1=OSO_3^-$; $R_2=R_4=R_6=OMe$; $R_5=R_7=OH$; $R_3=R_8=H$
Lamellarin ϕ	217	$R_1=R_4=R_6=OMe$; $R_2=R_5=OH$; $R_7=OSO_3^-$; $R_3=R_8=H$



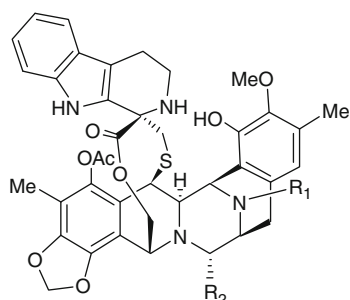
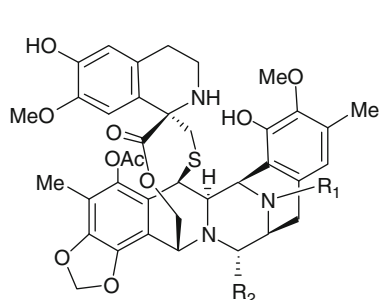
Lamellarin H	206	$R_1=R_2=R_3=R_4=R_5=R_6=OH$; $R_7=H$
Lamellarin M	211	$R_1=R_3=R_7=OH$; $R_2=R_4=R_5=R_6=OMe$;
Lamellarin Z	212	$R_1=R_4=R_6=OAc$; $R_2=R_3=R_5=OMe$; $R_7=H$
Lamellarin ϵ	214	$R_1=OSO_3^-$; $R_2=R_4=R_5=R_6=R_7=OMe$; $R_3=OH$
Lamellarin N triacetate	218	$R_1=OSO_3Na$; $R_2=R_3=R_5=R_6=OMe$; $R_4=OH$; $R_7=H$
Lamellarin G 8-sulfate	219	$R_1=R_4=OH$; $R_2=R_3=R_5=R_6=OMe$; $R_7=H$
Lamellarin B 20-sulfate	220	$R_1=R_7=OH$; $R_2=R_3=R_4=R_5=R_6=OMe$
Lamellarin C 20-sulfate	221	$R_1=OH$; $R_2=R_3=R_4=R_5=R_6=R_7=OMe$
Lamellarin L 20-sulfate	222	$R_1=OH$; $R_2=R_3=R_4=R_5=R_6=OMe$; $R_7=H$
Lamellarin α 20-sulfate	223	$R_1=R_3=R_5=OAc$; $R_2=R_4=R_6=R_7=OMe$

Pyrrole-derived alkaloids related to lamellarin include lukianols (**224–225**) [139], polycitones (**226–227**) [140, 141], polycitrins (**228–229**) [140], and ningalins (**230–233**) [142]. The structures of the lukianols A and B, isolated from an unidentified Pacific tunicate, contained a pyrrolooxazinone moiety; they appear to arise by the same biogenetic pathways leading to lamellarin O and P isolated from the marine sponge *Dendrilla cactos*. Lukianol A (**224**) inhibited DNA synthesis in L1210 lymphocytic leukemia cell lines with less effect on RNA and protein synthesis, demonstrating a therapeutic profile very similar to current clinically used anticancer agents [139]. Polycitone A (**226**) was isolated from a *Polycitor* sp., together with polycitrins A and B (**228** and **229**), containing a maleimide unit; polycitone B (**227**) was successively isolated from *Polycitor africanus*. Ningalins A–D (**230–233**) are condensed aromatic systems with the unifying theme that all appear derived from the condensation of two, three, four, and five DOPA precursors, respectively. Although a potential role for these alkaloids in metal sequestration has not been demonstrated, they are structurally related to other metal binding ascidian-derived *o*-catechols; it is thus conceivable that they too participate in the metal chelating phenomena characteristic of this class of marine invertebrates [131, 139].



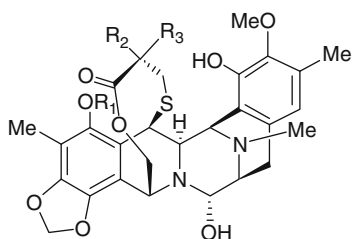
Tetrahydroisoquinoline alkaloids are uncommon in ascidians, but the sole representatives of this class, ecteinascidins, mainly from the Caribbean ascidian *Ecteinascidia turbinata*, are probably the most useful anticancer agents found to date in marine source. Their lead compound, Yondelis[®] (trabectedin, ET-743), is the first marine anticancer agent approved in the European Union for patients with soft tissue sarcoma (STS). Positive results of a large randomized phase III clinical trial in ovarian cancer have recently been presented [143]. The first description and structural

characterization of six new chemical entities called ET 729 (**234**), ET 743 (**235**), ET 745 (**236**), ET 759A (**237**), ET 759B (**238**), and ET 770 (**239**) was reported by the Rinehart group in 1990 of which ET-743 was the most abundant representative [144]. Simultaneously, Wright and coworkers described compounds **234** and **235** [145], but the unequivocal assignment of the absolute stereochemistry was achieved only when the X-ray crystal structures of the natural N¹²-oxide of ET-743 (**240**) and a synthetic O-methyl analogue of N¹²-formyl ET-729 (**241**) were solved [146]. Successively, a number of additional new members of this class of molecules have been isolated, such as compounds **242** and **243** [147], **244–247** [148], **248** [149], **249–252** [150].

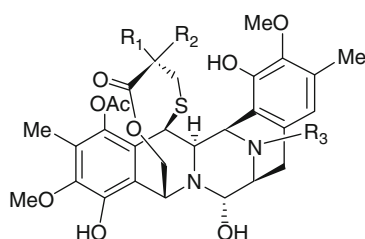


ET 729	234	R ₁ =H; R ₂ =OH
ET 743	235	R ₁ =Me; R ₂ =OH
ET 745	236	R ₁ =Me; R ₂ =H
ET 759 A	237	R ₁ =Me; R ₂ = =O(lactam)
ET 759 B	238	R ₁ =Me; R ₂ =OH, S-oxide
ET 770	239	R ₁ =Me; R ₂ =CN
ET 743 N ¹² -oxide	240	R ₁ =Me; R ₂ =OH, N-oxide
ET 729 N ¹² -formyl	241	R ₁ =CHO; R ₂ =OH
ET 815	245	R ₁ =Me; R ₂ =CH(CHO) ₂
ET 731	246	R ₁ =R ₂ =H
ET 745 B	247	R ₁ =H; R ₂ =OH, S-oxide
ET 786	248	R ₁ =Me; R ₂ =CN, S-oxide

ET722	242	R ₁ =H; R ₂ =OH
ET736	243	R ₁ =Me; R ₂ =OH
ET808	244	R ₁ =Me; R ₂ =CH(CHO) ₂



ET594 **249**



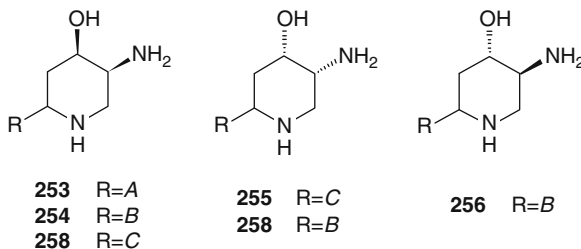
ET583	250	R ₁ =H; R ₂ =NH ₂ ; R ₃ =H
ET597	251	R ₁ =H; R ₂ =NH ₂ ; R ₃ =Me
ET596	252	R ₁ =R ₂ =O; R ₃ =Me

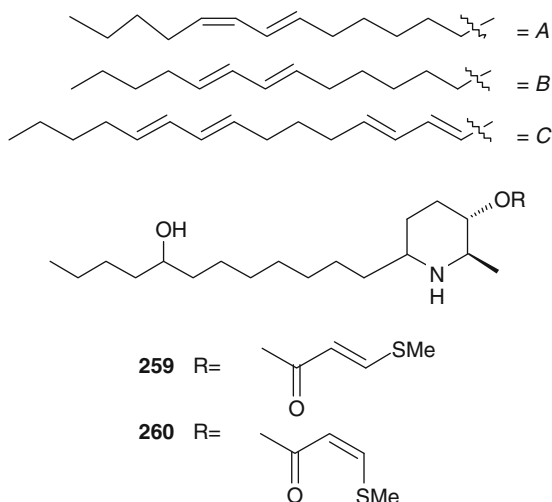
The interesting biological properties as well as the extraordinary three-dimensional molecular architecture of these compounds have made them a fascinating target for the synthetic organic chemist, allowing a number of original synthetic and semisynthetic methodologies for the preparation of a wide variety of ecteinascidins to be discovered [151]. The unique structure of ecteinascidins consists of a monobridged pentacyclic skeleton composed of two fused tetrahydroisoquinoline rings (subunits A and B) linked to a 10-membered lactone bridge through a benzylic sulfide linkage. Most ecteinascidins have an additional tetrahydroisoquinoline or tetrahydro- β -carboline ring (subunit C) attached to the rest of the structure through a spiro-ring. As for the biogenesis of the ecteinascidins, it has been proposed that A–B units could be formed by condensation of two DOPA-derived building blocks, and the tetrahydroisoquinoline ring in unit B is closed by condensation with a serine- (or glycine)-derived aldehyde as in the case of the related saframycins. *S*-Adenosylmethionine is the likely source of methyl groups at C-6, O-7, C-16, O-17, and N-12 [150].

5.2.5 Lysine-Derived Alkaloids

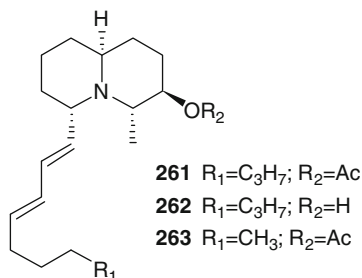
Alkaloids based on a 2-amino-3-hydroxyoctadecane moiety, generally referred to as lysine-derived metabolites, have been found in several genera of ascidians. Monocyclic examples are the piperidine alkaloids, which are among the most abundant metabolites of terrestrial plants, but there are relatively few examples isolated from marine organisms.

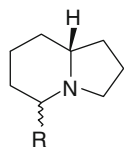
Pseudodistomins A (253) and B (254), isolated from the Okinawan ascidian *Pseudodistoma kanoko*, represent the first piperidine alkaloids obtained from marine sources [152]. The structure of the side chains of 253 and 254 has been revised after the first disclosure of the molecules [153, 154], while the stereostructure of the piperidine nucleus has been established by synthesis of their tetrahydroacetyl derivatives [155, 156]. Other members of the group have been successively isolated, from other *Pseudodistoma* species, including pseudodistomin C (255), with the absolute configuration at C-4 and C-5 opposite to those found in 253 and 254 [157], and pseudodistomins D–F (256–258) [158]. Pseudodistomins A and B exhibited cytotoxic activity with calmodulin antagonistic activity; pseudodistomins B–F were found to be active in a cell-based assay for DNA damage induction. Uoamines A (259) and B (260) also are monocyclic piperidine alkaloids isolated from *Aplidium uouo*; in these compounds, the 3-hydroxyl group present on the piperidine nucleus is esterified by (*E*)- or (*Z*)-3-thiomethylacrylic acid, respectively [159].





Bi- and tricyclic members of the lysine-derived alkaloids group have been most often found in *Clavelina* species and include quinolizidines and indolizidines derivatives. Clavepictines A (**261**) and B (**262**) and pictamine (**263**) are homologous quinolizidine alkaloids isolated from Bermudan and Venezuelan collections of the tunicate *C. picta* respectively [160, 161]. With the use of NOE experiments, **261** was determined to have a cis ring junction in the quinolizidine moiety, with the decadienyl side chain in the equatorial orientation, and the methyl and acetoxy substituents oriented trans-diaxial. An X-ray analysis of clavepictine B (**262**) confirmed the proposed relative stereochemistry and conformation. Both clavepictines inhibited the growth of murine leukemia and human solid tumor cell lines at concentrations less than 9 $\mu\text{g/mL}$. Pictamine (**263**) is a bis-nor analogue of clavapictine A, bearing two less carbons on the side-chain. *C. picta* has also been the source of a series of indolizidine metabolites, piclavines A–C (**264–266**) [162]. They consist of three series of isomeric compounds differing in the number of double bonds on the side chain. Each group is composed of an inseparable mixture of stereoisomers, which differ at the C2 chiral center, as well as at each of the double bonds. The piclavines are the first indolizidines isolated from a marine source; they exhibited antifungal and antimicrobial activity against Gram-positive bacteria.



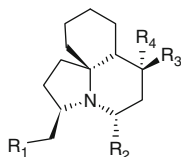


264 R=CH₂CH=CH(CH₂)₆CH₃

265 R=CH=CHCH=CH(CH₂)₅CH₃

266 R=CH=CHCH=CHCH=CH(CH₂)₃CH₃

Tasmanian collections of *C. cylindrica* yielded the tricyclic alkaloids cylindricines A–K (**267–277**) [163–165]; cylindricine B (**268**) represented the first example of the new perhydropyrido[2,1-*j*]quinoline ring system, while cylindricine A (**269**) is the first perhydropyrrolo[2,1-*j*]quinoline known from nature. The skeleton of cylindricines A (**267**), C–I (**269–275**), and K (**277**) is closely related to the indolizidine system of piclavines by having an extra 6-membered carbocyclic fused ring. In the same way, structures of cylindricines B (**268**) and J (**276**) are related to the quinolizidine system of the clavepictines and pictamines. Cylindricines F (**272**) and G (**273**) are the first thiocyanates from an ascidian. Closely related to cylindricines A and B are polycitorols A (**278**) and B (**279**), isolated from a marine ascidian of the family Polycitoridae [166]; they lack C-4 oxygenation found in cylindricines and have a OH group instead of a chlorine atom at C-13 and a butyl instead of a hexyl appendage at C-2. Other analogous metabolites are lepadiformines A–C (**280–282**) isolated from *C. lepadiformis* and *C. moluccensis* [167, 168] and fascicularin (**283**) from *Nephteis fascicularis* [169]. The initially reported structure of lepadiformine A was revised through its total synthesis; in the same study fascicularin (**283**) was also synthesized, allowing its absolute configuration to be assigned [170]. Early biological experiments on fascicularin suggested that its cytotoxic properties may stem from its ability to damage cellular DNA [169]. Successive studies revealed fascicularin as the first natural product found to generate a DNA-alkylating aziridinium ion via a mechanism analogous to the clinically used anticancer drugs mechlorethamine, melphalan, and chlorambucil [171]. Biological studies on lepadiformines showed that they have marked effects on the cardiovascular system when tested on frog atrial myocytes, the potency varying with the alkaloid structure [168].



267 R₁=Cl; R₂=C₆H₁₃; R₃,R₄=O

269 R₁=OH; R₂=C₆H₁₃; R₃,R₄=O

270 R₁=OMe; R₂=C₆H₁₃; R₃,R₄=O

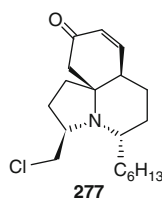
271 R₁=OAc; R₂=C₆H₁₃; R₃,R₄=O

272 R₁=SCN; R₂=C₆H₁₃; R₃,R₄=O

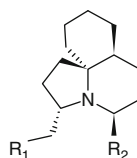
274 R₁=SCN; R₂=C₄H₉; R₃=H; R₄=OAc

275 R₁=NCS; R₂=C₄H₉; R₃=H; R₄=OAc

278 R₁=OH; R₂=C₄H₉; R₃=R₄=H



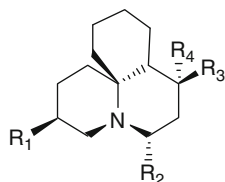
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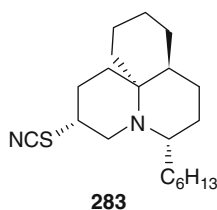
280 R₁=OH; R₂=C₆H₁₃

281 R₁=OH; R₂=C₄H₉

282 R₁=H; R₂=C₄H₉

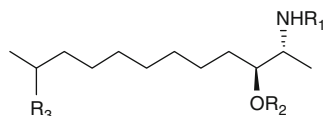
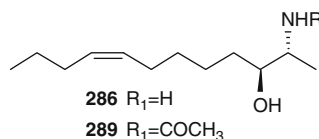
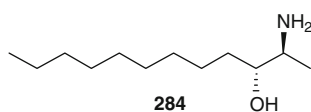


- 268** $R_1=Cl$; $R_2=C_6H_{13}$; $R_3=O$
273 $R_1=SCN$; $R_2=C_4H_9$; $R_3=O$
276 $R_1=NCS$; $R_2=C_4H_9$; $R_3=H$; $R_4=OAc$
279 $R_1=OH$; $R_2=C_4H_9$; $R_3=R_4=H$

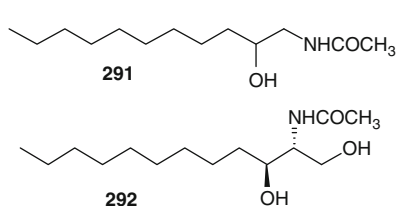
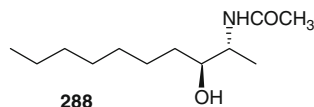


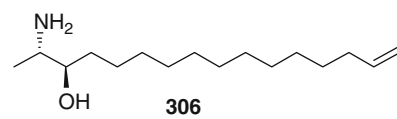
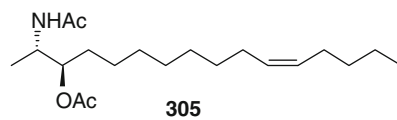
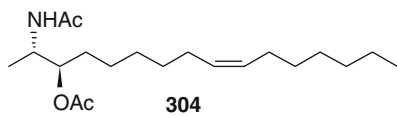
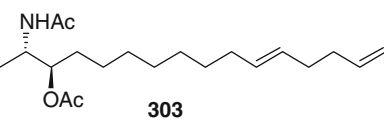
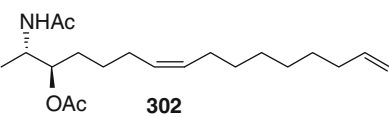
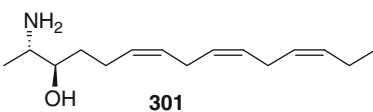
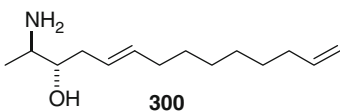
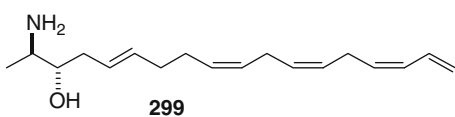
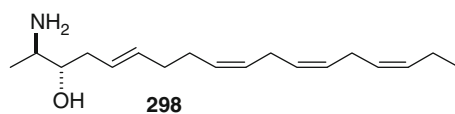
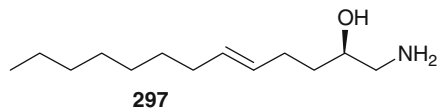
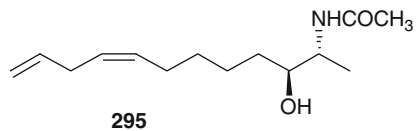
5.2.6 Protoalkaloids

Ascidians have been also the source of protoalkaloids, simple amines in which the nitrogen is not in a heterocyclic ring. *Clavelina* and *Pseudodistoma* genera have been prolific in the production of linear 2-amino-alkanols and their unsaturated and/or acetylated derivatives. Structurally, these compounds are related to the sphingosine derivatives, which are central structural elements of sphingolipids and important constituents of the lipid portion of cell membranes in living organisms. The carbon chain length of these sphingolipid derivatives vary from C12 to C18 amino alcohols. Examples are the C12 saturated amino alcohol (2*S*,3*R*)-2-aminododecanol-3-ol (**284**) isolated from *C. oblonga* [172], the clavaminols A–N (**285–296**), twelve saturated and unsaturated cytotoxic sphingoids isolated from the Mediterranean *C. phlegraea* [173, 174], and the antifungal 2-amino alcohol **297** isolated from an Australian *Didemnum* sp. [175]. Crucigasterins 277, 275, and 225 (**298–300**) and A–E, and obscuraminols A–F (**301–306**) are examples of polyunsaturated 2-amino-3-alkanols; they have been isolated as their diacetyl derivative from *P. crucigaster* and *P. obscurum*, respectively [176, 177].

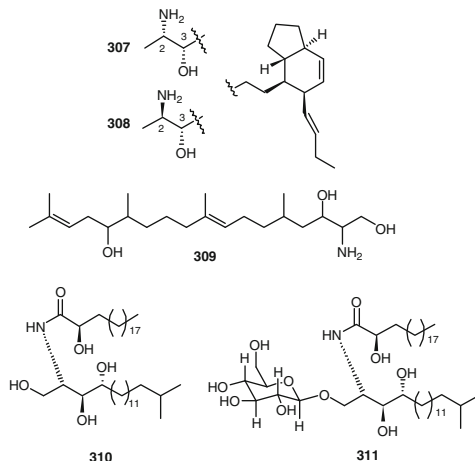


- 285** $R_1=H$ $R_2=H$ $R_3=H$
287 $R_1=COCH_3$ $R_2=H$ $R_3=H$
290 $R_1=H$ $R_2=COCH_3$ $R_3=H$
293 $R_1=COCH_3$ $R_2=COCH_3$ $R_3=H$
294 $R_1=CHO$ $R_2=COCH_3$ $R_3=H$
296 $R_1=COCH_3$ $R_2=COCH_3$ $R_3=CH_3$

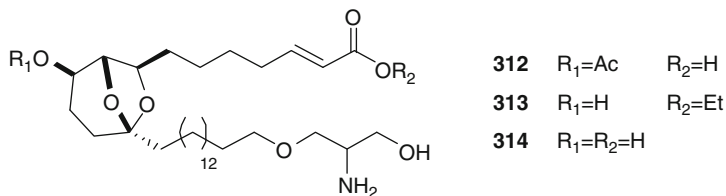


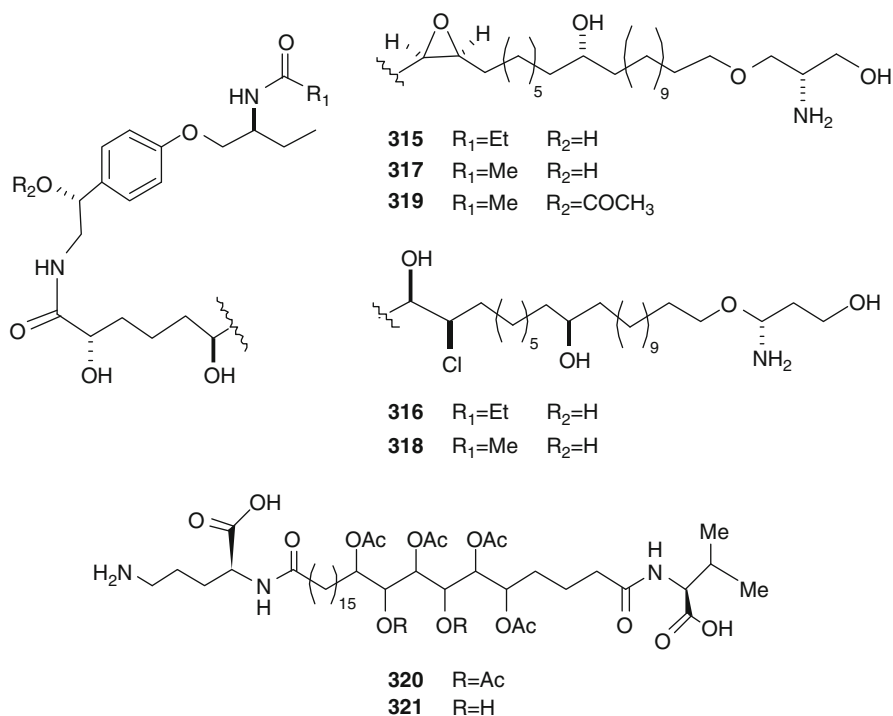


Two bicyclic amino alcohols, amaminols A e B (**307–308**) have been isolated from an unidentified tunicate of the family Polyclinidae [178]. Total synthesis of amaminol A (**307**) allowed to establish its absolute stereochemistry [179]. Other sphingosine-related compounds are apidiasphingosine (**309**), and the two lipids (**310–311**) isolated from *Cystodytes* cf. *dellechiajei* as PLA2 inhibitors [180, 181].



Didemniserinolipids A–C (**312–314**) are unprecedented serinolipids, compounds containing a unique serinol component and a 6,8-dioxabicyclo[3.2.1]octane core, isolated as antibacterial constituents of a tunicate of the family Didemnidae [182]. En route to proving the absolute and relative stereochemistry, through synthesis, of (+)-didemniserinolipid B (**313**), it was discovered that the isolated natural product was in fact its 31-sulfate configured *8R,9R,10R,13S,30S*. This structural reassignment was only possible after the development of a microwave-assisted method for the sulfation of unreactive hydroxyl groups [183]. Further serinolipid derivatives, shishididemniols A–E (**315–319**) have been isolated as antibacterial constituents of a tunicate of the family Didemnidae [184, 185]; they are complex lipids with tyramine-derived tether and two serinol units. An unidentified tunicate from Pohnpei Micronesia yielded sagittamides A (**320**) and B (**321**), with a C26 dicarboxylic acid that acylates terminal L-valine and L-ornithine groups [186]; the structures contain an unprecedented internal *O*-hexacetyl-1,2,3,4,5,6-hexaol moiety. The stereochemistry of sagittamide A has been extensively investigated; its absolute configuration has been established through a detailed ^1H NMR analysis of the two remote diastereomers, followed by doping experiments of them with the authentic natural product [187].



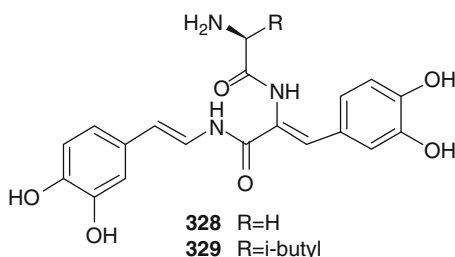
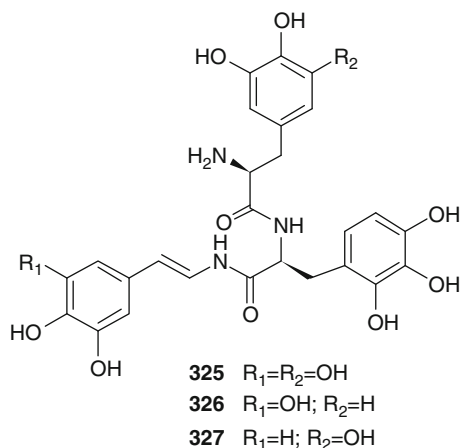
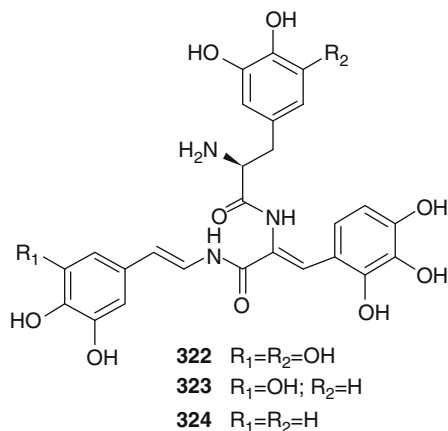


5.3 Peptides

5.3.1 Tunichromes and Related Compounds

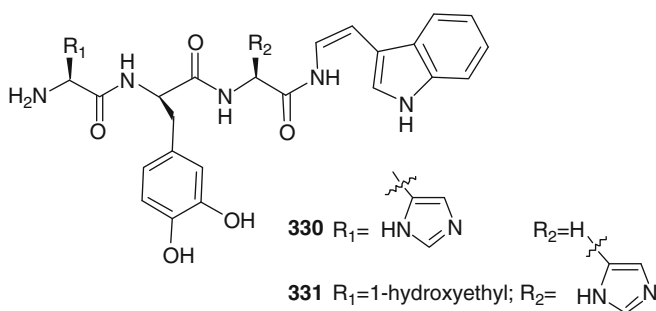
While the vast majority of ascidian metabolites have been isolated from whole-body extractions, several investigations have concentrated on compounds isolated from specific tissues or physiological fluids. A series of very unstable compounds, called the tunichromes, was isolated from the blood of several species of ascidians. Tunichromes are small modified peptides containing one or more DOPA (3,4-dihydroxyphenylalanine) or TOPA (3,4,5-trihydroxyphenylalanine) residues or their unsaturated derivatives; they have been isolated from *Ascidia*, *Phallusia Molgula* and *Styela* genera. The biological function of these pigments remains unclear; they appear to be involved in the vanadium and, to a lesser extent, iron accumulation and storage in ascidian blood cells [3, 4, 188]. Because these compounds are extremely sensitive to air and water, the original isolation was carried out under totally anaerobic and anhydrous conditions. Synthetic studies have yielded a breakthrough in the isolation methodology which involves protection of the hydroxyl groups as their tert-butyldimethylsilyl ethers and free amino groups as their tert-butyloxycarbonyl derivatives. In addition to allowing the straightforward

separation of individual tunichromes, the protecting groups may be subsequently removed, providing native tunichromes for further biological studies [189].



The first isolated member of the series was tunichrome B-1, which is now referred to as *An*-1 (**322**), since it was isolated from *A. nigra* [190]. Its structure consisted of a modified tripeptide of three DOPA-derived fragments. Later, the structures of *An*-2 (**323**) and *An*-3 (**324**) were determined, differing only in the degree of

hydroxylation [191]. More recently, three tunichromes, *Pm-1*, *Pm-2*, and *Pm-3* (325–327), have been identified from the blood cells of *P. mamillata* [192]; the structural difference between these tunichromes and those from *A. nigra* is that *Pm* tunichromes are saturated at the C11–C12 bond. A third group of tunichromes, *Mm-1* (328) and *Mm-2* (329) have been isolated from the iron-accumulating ascidian *M. manhattensis* [191]; they bear only two DOPA residues linked to a glycine (Mn-1, 328) or a leucine (Mn-2, 329) residue. Recently, a modified pentapeptide has been isolated from *S. plicata* [193]; it was designated as a tunichrome (tunichrome *Sp-1*) since (1) it was a linear low molecular weight peptide, (2) it was recovered in the ascidian hemocytes, and (3) it has an oxidatively decarboxylated C-terminus derived from a hydroxylated aromatic amino acid residue and two hydroxylated amino acid in its sequence. Related to the tunichromes are halocyamines A and B (330 and 331) isolated from the hemocytes of the solitary ascidian *Halocynthia roretzi* [194]; they are tetrapeptides which contain a DOPA residue which showed antimicrobial as well as cytotoxic properties.

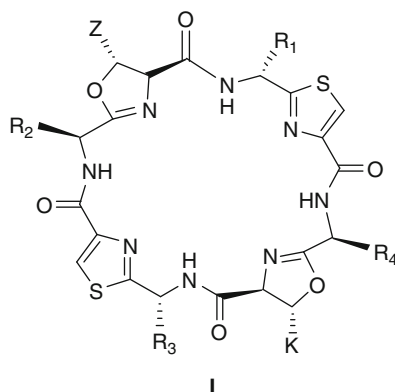


5.3.2 Cyclic Peptides

A variety of cyclic peptides have been isolated from ascidians and have shown to exhibit moderate to high cytotoxicity. Structure elucidation of these compounds has been fraught with difficulty and minor or major revisions have been made for a number of the originally proposed structures. Ascidians of the genus *Lissoclinum* are a prolific source of unusual cyclic peptides containing both D- and L-amino acids, many modified in the form of thiazole, oxazole, thiazoline, or oxazoline rings. The cyclic peptides that have been isolated from *L. patella* belong to two general families of compounds, the octapeptide patellamide family, **I**, and the heptapeptide lissoclinamide family, **II**, according to the number of amino acids and inclusion of thiazole (Thz), thiazoline (Thn), and oxazoline (Oxn) rings within their structure [195].

Compounds of the patellamide family, (**I**: 332–340) [196–203], are characterized by thiazole alternating with oxazoline rings, and some of their structures have been confirmed by synthesis [204–211]. Structure-activity studies of the sets 332–334 and 338–339 and related synthetic or semisynthetic compounds have revealed that the oxazoline ring is vital for the cytotoxic activity of these compounds and that the bridging disulfide unit in 339 greatly enhances cytotoxicity [212]. Studies of the

conformation ofazole-based marine cyclic peptides, both in solution and in solid state, have provided valuable insights into the factors which may affect the reactivity and the biology of these metabolites [213–219]. An X-ray crystal structure determination of the C₂-symmetric ascidiacyclamide (**338**), for example, showed that it has a “square” (also sometimes referred to as “saddle-shaped”) conformation with its thiazole and oxazoline rings occupying the corners of a rectangle with all of the NH bonds directed to the interior of the macrocyclic ring [213, 220–222]. Patellamide A (**332**) has a similar rectangular shape in the solid state [216, 223], but, by contrast, X-ray analysis of the closely related patellamide D (**335**) shows that it assumes a “twisted figure of eight” conformation stabilized by intramolecular hydrogen bond and by π -stacking between its thiazole rings [214].

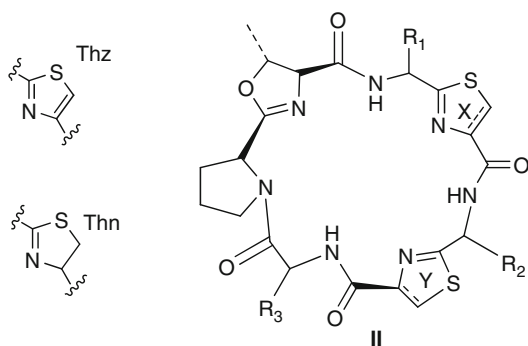


name	Z	K	R ₁	R ₂	R ₃	R ₄	
patellamide A	332	H	Me	D-Val	L-Ile	D-Val	L-Ile
patellamide B	333	Me	Me	D-Ala	L-Leu	D-Phe	L-Ile
patellamide C	334	Me	Me	D-Ala	L-Val	D-Phe	L-Ile
patellamide D	335	Me	Me	D-Ala	L-Ile	D-Phe	L-Ile
patellamide E	336	Me	Me	D-Val	L-Val	D-Phe	L-Ile
patellamide F	337	Me	H	D-Ala	L-Val	D-Phe	L-Val
ascidiacyclamide	338	Me	Me	D-Val	L-Ile	D-Val	L-Ile
ulithiacyclamide	339	Me	Me	D-Leu	L-1/2Cys	D-Leu	L-1/2Cys
ulithiacyclamideB	340	Me	Me	D-Phe	L-1/2Cys	D-Leu	L-1/2Cys

There is now a substantial literature which demonstrates that these marine metabolites have a high propensity to chelate metal ions [224–229]. A large number of analytical and spectroscopic methods have been used to study the metal complexation behavior of *Lissoclinum* peptides. Thus, it was established that although patellamides A (**332**), B (**333**), and E (**336**) could bind comfortably to Zn²⁺ and Cu²⁺, they showed no affinity for binding to such metals as Mg²⁺ and Ca²⁺ [230]. There is no doubt that copper is the preferred metal for the patellamide family of cyclic peptides in ascidians that adopt a “square” conformation [231, 232].

Peptides of lissoclinamide family, (**II: 341–351**) [197, 201, 214, 233–235], show structures which feature an oxazoline ring together with one or more thiazole and/or thiazoline units, derived from unusual amino acids residues,

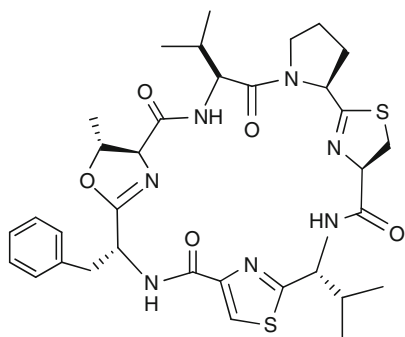
incorporated in a cyclic heptapeptide, e.g., lissoclinamide 4 (**344**), lissoclinamide 5 (**345**), and lissoclinamide 7 (**347**). The lissoclinamides 1–8 (**341–348**) and the ulicyclamide (**351**) [236] are all derived from a cyclic heptapeptide in which a threonine has been cyclized to an oxazoline and two cysteines have been cyclized to give a thiazole or thiazoline [235]. The correct assignment of the chiral centers adjacent to the thiazole, and especially the thiazoline rings in lissoclinamide 4, 5, and 7 was particularly problematic since these centers are prone to undergo epimerization during the usual methods of cyclopeptide hydrolytic degradation and during their synthesis [234, 237]. Based on a total synthesis, the stereochemistries published for natural lissoclinamide 4 and lissoclinamide 5 [194] were re-assigned as **344** and **345**, respectively [238, 239]. The cytotoxicity of the lissoclinamides was tested in vitro using transitional bladder carcinoma cells (T24), SV40-transformed fibroblasts (MRC5CV1), and normal peripheral blood lymphocytes. Lissoclinamide 7 (**347**) is by far the most cytotoxic with an IC_{50} value of 0.04 $\mu\text{g/mL}$ for a 1 h exposure against MRC5CV1 cell line [234].



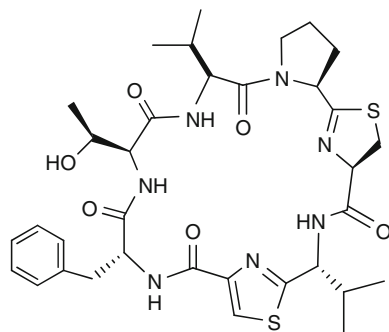
name		X	Y	R ₁	R ₂	R ₃
lissoclinamide 1	341	Thz	Thz	L-Val	D-Ile	L-Phe
lissoclinamide 2	342	Thn	Thz	D-Ile	D-Ala	L-Phe
lissoclinamide 3	343	Thn	Thz	D-Ile	L-Ala	L-Phe
lissoclinamide 4	344	Thn	Thz	L-Val	L-Phe	L-Phe
lissoclinamide 5	345	Thz	Thz	L-Val	L-Phe	L-Phe
lissoclinamide 6	346	Thn	Thz	D-Val	D-Phe	L-Phe
lissoclinamide 7	347	Thn	Thn	D-Val	D-Phe	L-Phe
lissoclinamide 8	348	Thn	Thz	Val	Phe	L-Phe
lissoclinamide 9	349	Thn	Thz	L-Ile	D-Val	D-Phe
lissoclinamide 10	350	Thn	Thn	L-Ile	L-Ile	D-Phe
ulicyclamide	351	Thz	Thz	L-Ile	D-Ala	L-Phe

The heptapeptide cyclodidemnamide (**352**), isolated from *Didemnum molle* collected in the Philippine Islands, possesses both oxazoline and thiazole rings together with a thiazoline-proline unit [240]. The stereochemistry of **352** has been revised through a synthetic work [241–243]. The stereochemical structure of cyclodidemnamide B (**353**), isolated from the same species collected in Mozambique, has been established on the basis of its total synthesis [244]. A feature common to the four cyclic peptides patellamide G (**354**) and ulithiacyclamides

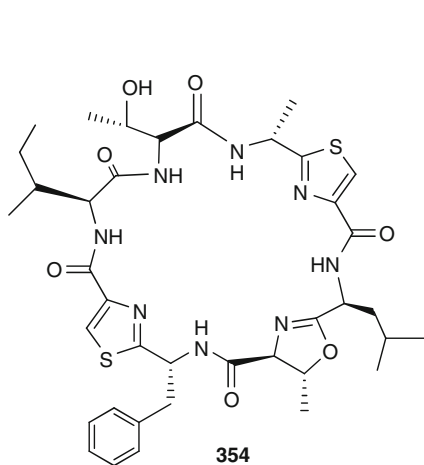
E–G (355–357), isolated from *L. patella* collected in Micronesia, is that one or more of the threonine units is not cyclized to an oxazoline ring [245].



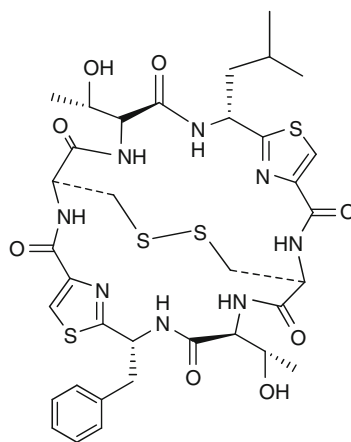
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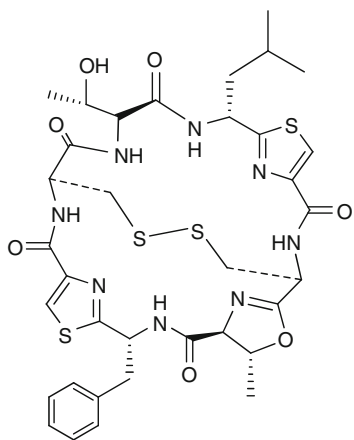
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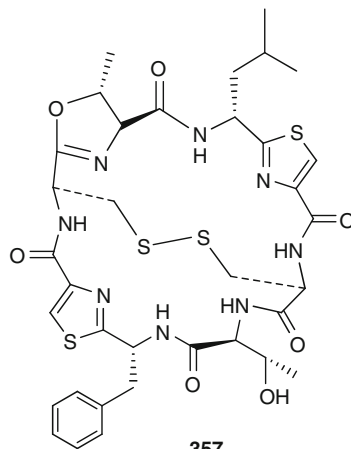
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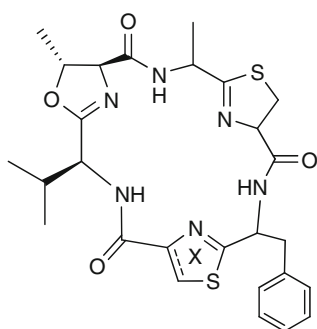


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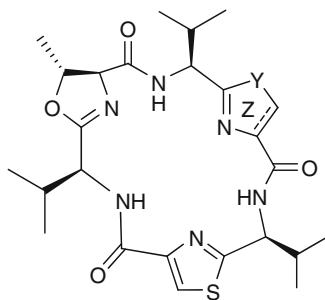


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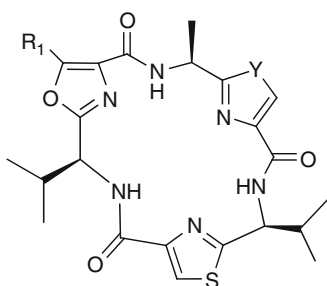
The cyclic hexapeptides bistratamides A (**358**) B (**359**), D (**361**), E (**362**), and F (**363**), isolated from *L. bistratum* collected in Australia and Philippines, possess the modified amino acid residues methyloxazoline (mOxn), thiazole (Thz), thiazoline (Thn), oxazole (Oxz), and oxazoline (Oxn) [246–248]. From the same species collected in Philippines, bistratamide C (**360**) and bistratamides G–J (**364–367**) were also isolated [247, 248]. The total synthesis of **360**, **361**, and **363–366** has been performed [249–251]. Bistratamide D (**361**) showed depressant effects when introduced directly into the central nervous system of mice by intracerebral injection [252]; at a 65 μg dose, mice exhibited decreased motor activity, sluggishness, and sedation relative to control [247]. Bistratamides E–J showed weak to moderate activity against human colon tumor (HCT-116) cell line; the compounds **365** and **367**, containing two thiazole rings, are more active than those containing a thiazole ring and an oxazole ring (**364** and **366**) [248].



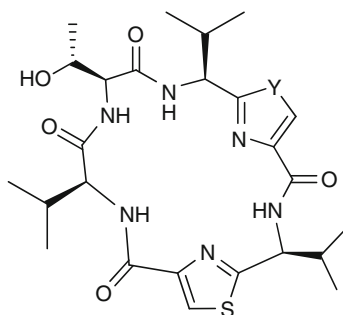
358 X=Thn
359 X=Thz



361 Y=O Z=Oxz
362 Y=S Z=Thz
363 Y=O Z=Oxn



	Y	R ₁
360	S	H
364	O	Me
365	S	Me

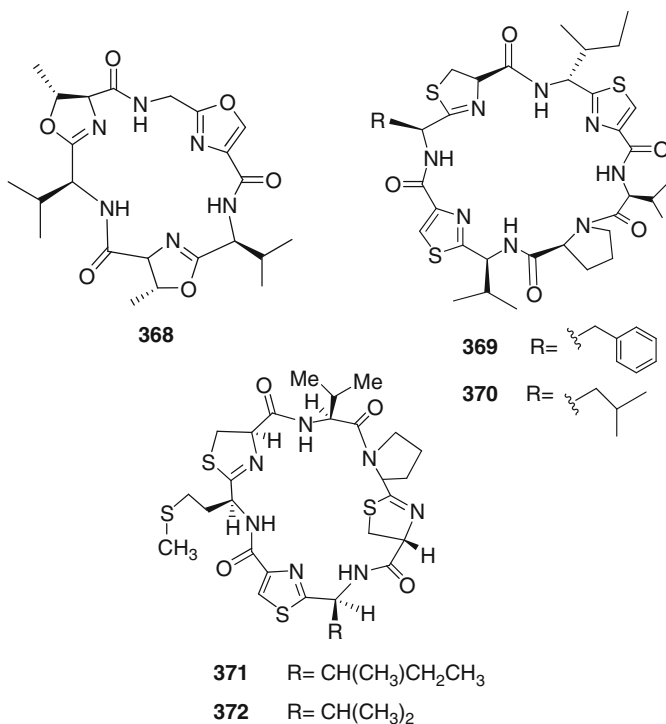


366 Y=O
367 Y=S

Two cyclic hexapeptides, didmolamide A and B, strictly related to bistratamides, were isolated from *D. molle* collected in Madagascar [253]. The total synthesis of didmolamides has been reported [254]. In addition, a quite similar hexapeptide **368**

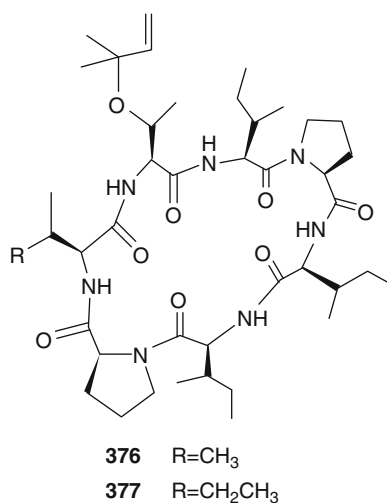
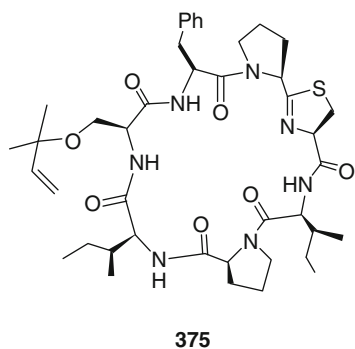
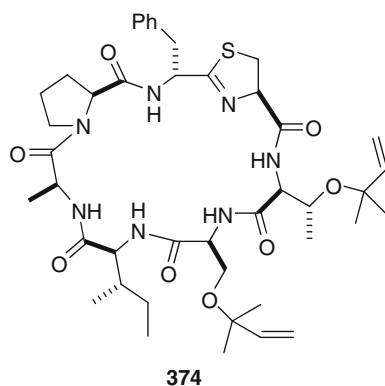
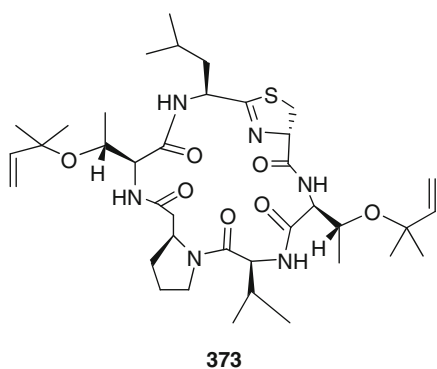
has been reported under two different names from both *L. bistratum* (cycloazoline) [255] and the terrestrial cyanobacteria, *Westiallopsis prolifica* (westiellamide) [256], which led to the suggestion that the peptides were produced by symbiotic cyanobacteria. This hypothesis has not yet been confirmed. On the other hand, Faulkner et al. found that the peptides are not stored in cyanobacterial cells and are instead present in significant quantities throughout the ascidian tunic. The best approach to this problem would be to determine the cellular location of the peptides using an antibody to a specific peptide or to determine the location of the biosynthetic genes, both of which are technically difficult procedures [203]. The copper (II) coordination chemistry of westiellamide as well as of three synthetic analogues has been investigated [257]. Because cyclic peptides with oxazole building block in the cyclic backbone have been proposed to be useful structures for the construction of molecular receptors, the structural investigation of westiellamide analogues has been performed [258].

Tawicyclamides A (369) and B (370), isolated from *L. patella* collected in the Philippine Islands [259], and mayotamides A (371) and B (372), isolated from *D. molle* collected in the North-West of Madagascar [260], belong to another set of cytotoxic cyclic peptides, possessing thiazole- and thiazoline-amino acids but lacking the oxazoline ring characteristic of patellamide (I) and lissoclinamide (II) families. A characteristic feature of mayotamides A–B is the presence of a methionine unit.



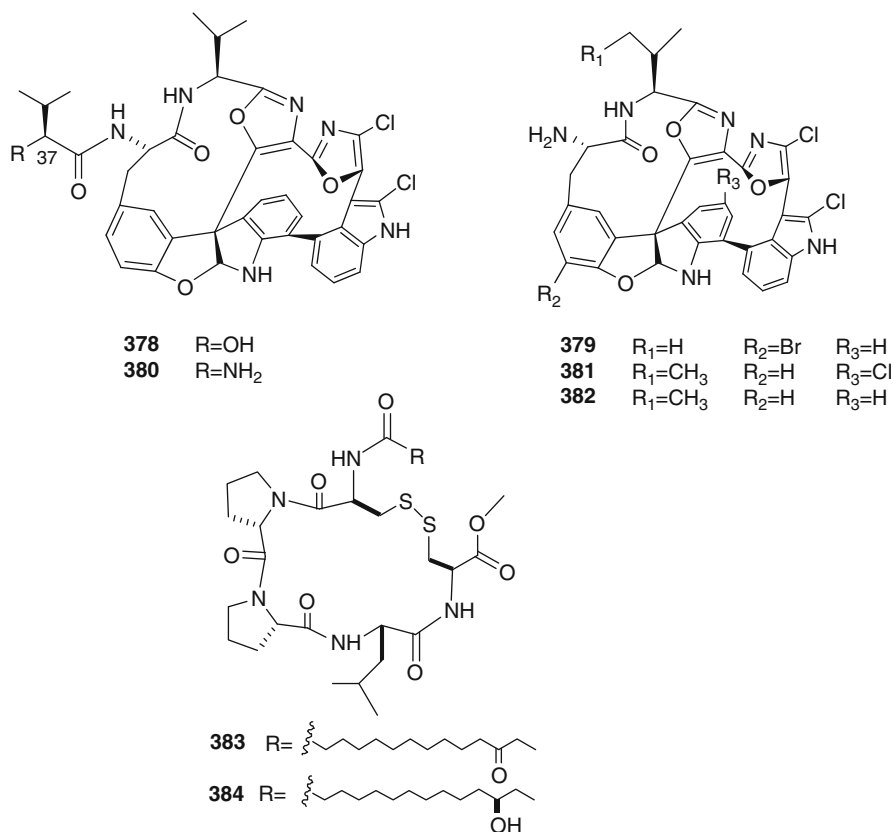
Several cyclopeptides isolated from ascidians of the genera *Lissoclinum* and *Didemnum*, patellins 1–6 [261], trunkamide A (374) [261], mollamide (375)

[262, 263], mollamides B–C [264], as well as hexamollamide [265] and comoramides A–B [260], are structurally uniquely characterized by the presence of a single thiazoline heterocycle in the peptide backbone, as well as of threonine and serine residues whose side chains have been modified as dimethylallyl (reverse prenylated) ethers. Patellin 2 (**373**), containing a thiazoline and two threonine residues modified as dimethylallyl ethers, was shown to exist in different conformations in solution and in the crystal on the basis of X-ray crystallography, NMR spectroscopy, and molecular modeling [266]. The structure of trunkamide A (**374**) initially suggested was incorrect in terms of the configuration of the Phe residue. The total synthesis performed by Wipf showed that the correct configuration was D by comparison of the synthetic and natural products [267]. Nairaiamides A (**376**) and B (**377**), two heptapeptides isolated from a Fijian *L. bistratum*, possess two proline residues, several isoleucines and a dimethylallylthreonine (daT); **376** possesses a Val residue in place of an Ile in **377** [268].



The diazonamides (**378–382**) [269, 270] are a family of halogenated cyclic peptides isolated from *Diazona angulata* (originally misidentified as *D. chinensis*). The first structural proposal for diazonamides A–B (**378–379**) [269] was later revised, and the final structures of diazonamides A (**378**) and B (**379**) have been established after reinterpretation of the NMR and X-ray data and total synthesis of diazonamide A [271–273]. The cytotoxic activity of diazonamides A–E (**378–382**) has been evaluated against a panel of three human tumor cell lines, including lung (A549), colon (HT29), and breast (MDA-MB-231). The potent activity, with values in the low nanomolar range, observed for diazonamide A suggested that the hydroxyl group at C-37 must play a key role in the cytotoxicity of these metabolites [269, 270].

The lipopeptides eudistomides A (**383**) and B (**384**) have been isolated from the Fijian ascidian *Eudistoma* sp. They are the first ascidian-derived peptides cyclized solely by a disulfide bridge [274].

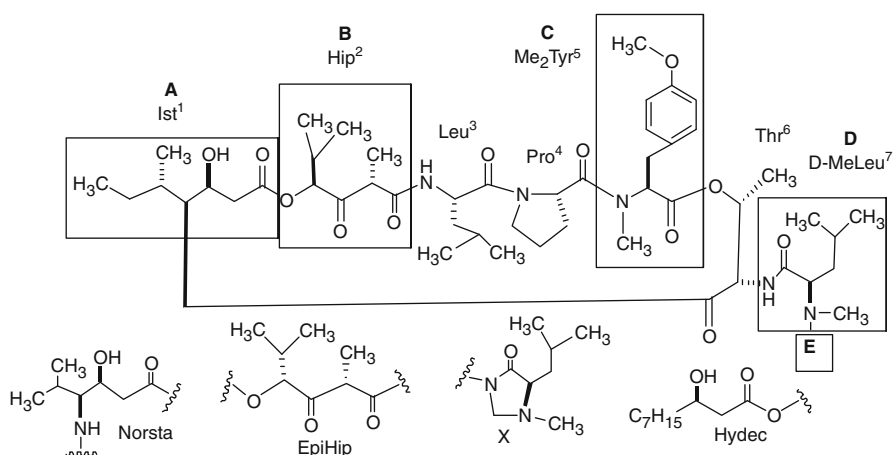


5.3.3 Depsipeptides

Depsipeptides are natural metabolites, having sequences of amino and hydroxy carboxylic acid residue, in which one or more of the amide (–CONHR–) bonds

are replaced by ester (COOR) bonds; in cyclodepsipeptides, the residues are connected in a ring.

In 1981, a new class of cyclic depsipeptides, the didemnins A–C, was isolated from a Caribbean tunicate of the genus *Trididemnum* by K.L. Rinehart et al. [275, 276]. Later, *Trididemnum solidum* and *T. cyanophorum* both have been reported to contain didemnins [277, 278]. Additional cyclic depsipeptides, didemnins D (388), E (389), nordidemnins A and B (395–396), and the formaldehyde adduct methylenedidemnin A (398), as well as didemnin G (390), were also reported [279]. *T. cyanophorum* ether extract was shown to contain didemnin H (=M) (391) [280]. Seven didemnins – didemnin M (=H) (391), N (392), X (393), and Y (394), nordidemnin N (397), and epididemnin A₁ (399), as well as a ring-opened form of didemnin A, acyclodidemnin A (400) – were isolated by Sakai et al. from an extract of the Caribbean tunicate *T. solidum* [281].



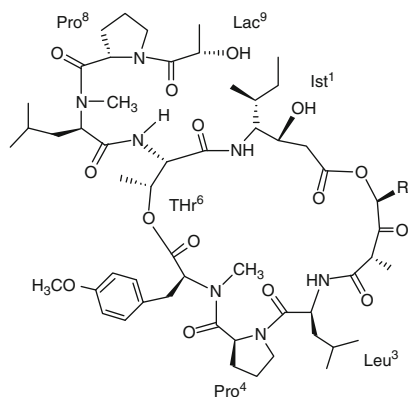
name		A	B	C	D	E
didemnin A	385	Ist	Hip	Me ₂ Tyr	D-MeLeu	-H
didemnin B	386	Ist	Hip	Me ₂ Tyr	D-MeLeu	-Pro-Lac
didemnin C	387	Ist	Hip	Me ₂ Tyr	D-MeLeu	-Lac
didemnin D	388	Ist	Hip	Me ₂ Tyr	D-MeLeu	-Pro-Lac-Gln-Gln-Gln-pGlu
didemnin E	389	Ist	Hip	Me ₂ Tyr	D-MeLeu	-Pro-Lac-Gln-Gln-pGlu
didemnin G	390	Ist	Hip	Me ₂ Tyr	D-MeLeu	-CHO
didemnin H (=M)	391	Ist	Hip	Me ₂ Tyr	D-MeLeu	-Pro-Lac-Gln-pGlu
didemnin N	392	Ist	Hip	Tyr	D-MeLeu	-Pro-Lac
didemnin X	393	Ist	Hip	Me ₂ Tyr	D-MeLeu	-Pro-Lac-Gln-Gln-Gln-Hydec
didemnin Y	394	Ist	Hip	Me ₂ Tyr	D-MeLeu	-Pro-Lac-Gln-Gln-Gln-Gln-Hydec
nordidemnin A	395	Norsta	Hip	Me ₂ Tyr	D-MeLeu	-H
nordidemnin B	396	Norsta	Hip	Me ₂ Tyr	D-MeLeu	-Pro-Lac
nordidemnin N	397	Norsta	Hip	Tyr	D-MeLeu	-Pro-Lac
methylenedidemnin A	398	Ist	Hip	Me ₂ Tyr	X	-H
epidemnin A ₁	399	Ist	epiHip	Me ₂ Tyr	D-MeLeu	-H
acyclodidemnin A	400	Ist	Hip	Me ₂ TyrOH	D-MeLeu	-H

The originally reported suggestion for the structure of didemnin B (**386**) [277] has been revised several times: (1) The configuration of the N-methyl-leucine in the side chain has been identified as *R* [282]. (2) M. Joullie et al. established the *2S,4S*-configuration for the hydroxyisovalerylpropionic acid [= (*2S,4S*)-4-hydroxy-2,5-dimethyl-3-oxohexanoic acid; Hip] [283]. (3) By means of NMR investigations, B. Castro et al. demonstrated that isostatin [= (*3S,4R,5S*)-4-amino-3-hydroxy-5-methyleptanoic acid; Ist] and not statine is a ring building block [284]. A reliable elucidation of the structure has been achieved by X-ray crystallography and total synthesis [285, 286]. Didemnins A–C were efficiently prepared in a stereocontrolled manner, producing the common macrocycle and introducing the substituents on the amino group of L-threonine as optically pure units [287].

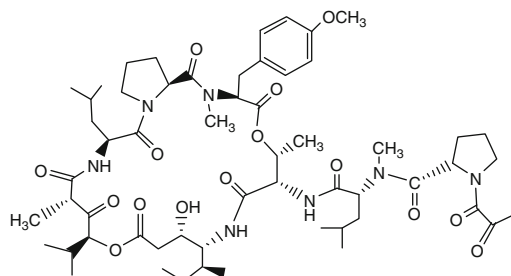
All didemnins (**385–400**) contain the same basic structure consisting of a 23-membered macrocycle, with an attached side chain. The macrocycle is made up of six subunits, (*S*)-Leu, (*S*)-Pro, (*1S2R*)-Thr, (*S*)-N(Me)-O(Me)-Tyr, (*3S,4R,5S*)-isostatine, and (*2S 4S*)-HIP. The side chain, whose first amino acid is always (*R*)-N(Me)-Leu, is joined to the threonine of the macrocycle, and its structure differentiates the various didemnins: In the simplest member of the family, didemnin A (**385**), it consists only of (*R*)-N(Me)-Leu, whereas in other cases, it can be appreciably more complex. Certain didemnins exhibit significant antiproliferative and immunosuppressive activity. Didemnin B (**386**) exhibited strong antiviral, immunosuppressive, and cytotoxic activities. Didemnin B inhibited DNA viruses *Herpes simplex* types I and II in vitro at 0.05 μM concentrations, and it has demonstrated in vivo anticancer activity in mice against P388 murine leukemia (T/C 199 at 1.0 mg/kg) and B16 melanoma (T/C 160 at 1.0 mg/kg). Didemnin B was tested against a number of tumors in a human tumor stem-cell assay, and significant activity was observed after 1 h of exposure at concentrations as low as 0.1 $\mu\text{g/mL}$ in ovarian, sarcoma, kidney, and breast cells [288]. Phase I and phase II clinical and pharmacological studies indicated that didemnin B had little or no significant antitumor activity in some of the common carcinomas and showed significant toxic side effects such as nausea, vomiting, and neuromuscular toxicity [289]. Despite the limited clinical promise of didemnin B as anticancer agent, there was widespread interest in didemnins. In order to understand the marked difference of the biological activity of didemnins, conformational analysis of them has been performed [290].

[Pyruvyl⁹] didemnin B was discovered in a Mediterranean tunicate *Aplidium albicans* [291], whereas [Tyr⁵]didemnin B (described by Sakai as didemnin N) and [D-Pro⁴]didemnin B were reported by E. Abou-Monsour et al. [292]. Later, the structure elucidation of [Hysp²] (**401**) and [Hap²]didemnin B (**402**), two[Hip²]-modified didemnin B isolated from the tunicate *T. cyanophorum*, have been reported [293]. In 1990, a new member of this family was isolated from the Mediterranean tunicate *A. albicans* (application PCT/GB 90/01495) [294–296]; this depsipeptide was named dehydrodidemnin B (**403**); it has a piruvoyl-proline residue instead of the lactyl-proline residue found in the linear peptide moiety of didemnin B. Dehydrodidemnin B (=aplidine) was shown to possess higher anti-neoplastic activity than didemnin B both in vitro and in vivo [297]. Total synthesis of dehydrodidemnin B was performed [298].

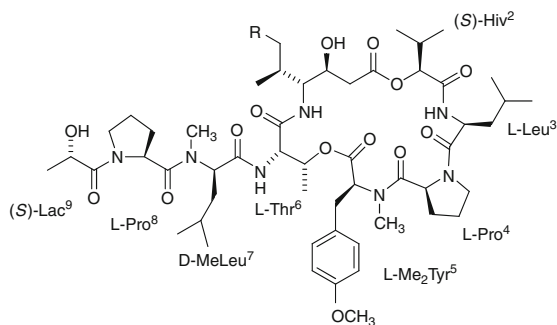
Two cytotoxic depsipeptides, tamandarin A (**404**) and B (**405**), were isolated from an unidentified Brazilian marine ascidian of the family Didemnidae [299]. Tamandarin A (**404**), similar in structure to didemnin B (**386**), was shown to be somewhat more active *in vitro* than **386** against pancreatic carcinoma with an ED₅₀ value 1.5–2 ng/mL. Total syntheses and biological evaluation of tamandarins A and B and of their respective analogues have been reported [300–302].



[Hisp²]didemninB **401** R=sec-butyl
[Hap²]didemninB **402** R=H



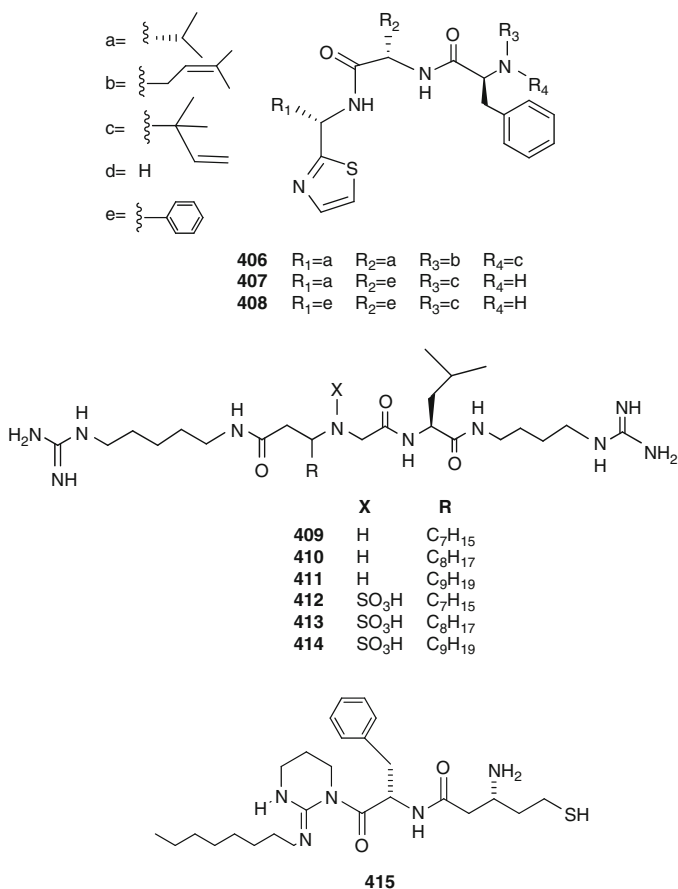
dehydrodidemnin B (aplidin) **403**



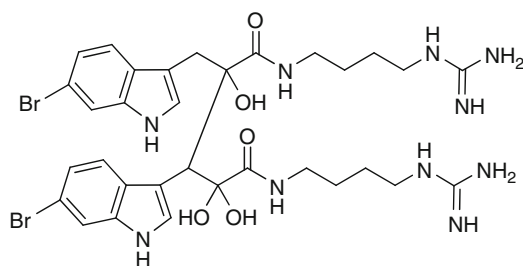
404 R=CH₃; (3*S*, 4*R*, 5*S*)-Ist¹
405 R=H; (3*S*, 4*R*)-Nst¹

5.3.4 Linear Peptides

Three linear cytotoxic peptides, virenamides A–C (**406–408**) have been isolated from *Diplosoma virens* collected on the Great Barrier Reef, Australia. Virenamides A–C showed modest cytotoxicity toward a panel of cultured cells; virenamide A also exhibited TOPO II inhibitory activity (IC₅₀ of 2.5 μg/mL) [303–305]. Six peptide guanine derivatives, named minalemines A–F (**409–414**), have been isolated from *Didemnum rodriguesi* [306, 307]. These compounds incorporate one agmantine (Aγμα) and one homoagmantine (Hagma) terminal unit with their guanidine groups free and the primary amino groups linked through a peptidic bond to L-Leu and a very rare β-N-carboxymethyl amino acid (Ncma) bearing a saturated long chain. Minalemines D–F are the sulfamic acid derivatives of minalemines A–C and constitute the first examples of such a functional group in a marine organism. From the same ascidian, caledonin (**415**) was also isolated; this linear peptide possesses a unique β-amino acid residue and a cycloguanidine group. It exhibited strong metal-complexing properties [308].



A highly modified dimer peptide, eusynstyelamide (**416**), was the major component of an aqueous extract of *Eusynstyela misakiensis*. It is a modified tryptophan–arginine dipeptide dimer [309].



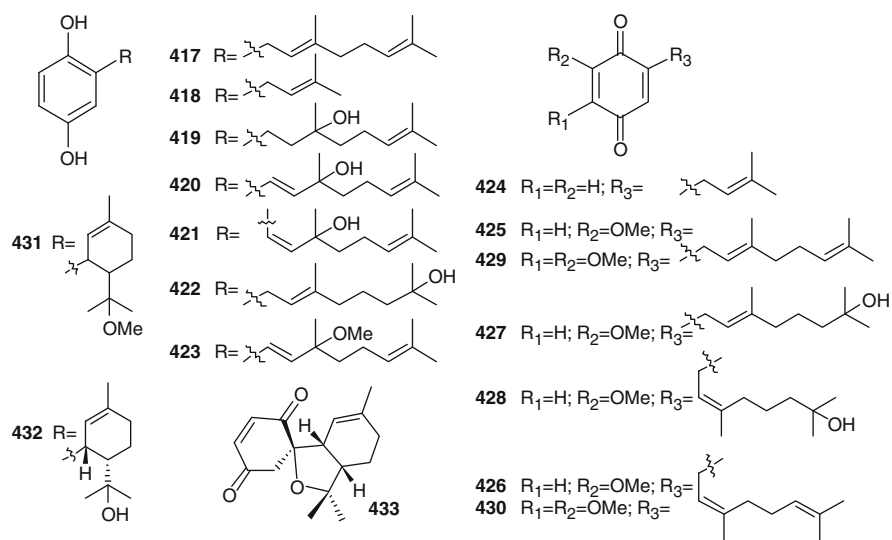
416

5.4 Meroterpenes

Meroterpenes are compounds of mixed biosynthesis, mostly quinones or hydroquinones bonded with a terpenoid portion ranging in size from one to nine isoprene units. In the marine environment, these secondary metabolites are isolated mainly from brown algae, but other sources include microorganisms, soft corals, and invertebrates [310]. Among marine ascidians, they have been found almost exclusively in species belonging to the genus *Aplidium*, which have been the source of a vast array of prenyl-quinone, -hydroquinone, -chromene, and/or -chromane derivatives, either linear or cyclic, originated from intra- and intermolecular cyclizations and/or rearrangements, thus giving macrocyclic or polycyclic skeletons, often linked to amino acids or taurine residues [311].

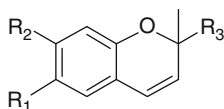
The first biologically active tunicate metabolite, geranylhydroquinone (**417**), was isolated from an *Aplidium* sp. and, successively, found in many others *Aplidium* species; it was shown to offer protection against leukemia and tumor development in test animals [5]. Several isoprenoid hydroquinones have been then reported, such as compounds **419** and **420** from *A. multiplicatum* [312], **421** from *A. savignyi* [313], **422** and **423** from *A. conicum* [314]. *A. californicum* has been the source of the simple monoprenyl hydroquinone **418** and the relevant quinone **424** [315]. An *Aplidium* sp. collected in French Atlantic waters was shown to contain verapliquinone **B** (**426**) and **D** (**428**) as the first examples of linear diprenylquinones of the neryl type, besides their respective isomers verapliquinones A (**425**) and C (**427**) of the geranyl type [316]. Glabruquinone B (**429**), isolated from *A. glabrum* together with its isomer glabruquinone A (desmethylubiquinone Q₂, **430**) is a further but rare example of neryl derivative, the majority of natural prenyl benzoquinones possessing a linear side chain of the geranyl type [317]. Compound **430** is closely related to the ubiquinones, although lacking the methyl group in the quinoid moiety; it is not a cytotoxin but demonstrated good cancer-preventive activity on JB6 Cl 41 cells

transformation activated by epidermal growth factor (EGF). Structure-activity relationships studies on its synthetic analogues demonstrated that this activity depend on the length of the side chain and on the position of the methoxyl groups in the quinone part of the molecule [318]. In vivo anticancer properties of **430** and its analogues as well as the molecular mechanism of its action against tumor cells have been examined; it was shown to inhibit the growth of the solid Ehrlich carcinoma in mice and to induce apoptosis in various human tumor cell lines [319]. Cyclo-diprenyl hydroquinones/quinones have been isolated from *A. aff. densum* (methoxyconidiol, **431**) [320] and from *A. conicum* (conitriol, **432** and conidione, **433**) [315]. Methoxyconidiol (**431**) displayed an antimetabolic action on the first division of sea urchin embryos, disrupting M-phase progression and completely blocking cytokinesis without having any effect on DNA replication [321].



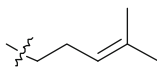
The occurrence of chromenols has been reported in *A. californicum* (**434**) [315], *A. costellatum* (**435**) [322], *A. multiplicatum* (**436**) [312], and *A. solidum* (**437** and **438**) [323]. The chromane derivative **439** has been isolated from *Synoicum castellatum* [324], a species closely allied to the genus *Aplidium*, and successively found in *A. conicum* together with its C-1' epimer, conicol (**440**) [314]. Didehydroconicol (**441**) has been isolated from *A. aff. densum* [320]. Chromene derivatives clearly arise from the relevant prenylated para-quinones via tautomerization/electrocyclization [325]. The formation of cyclized compounds such as **431–433** and **439–441** from the relevant quinones/hydroquinones can be easily rationalized through a sequence of acid-catalyzed cyclizations. With the data available, it is not possible to argue whether the above mentioned transformations

occur in the organism, either enzymatically or not, prior to its extraction, or they take place during isolation and/or chromatographic purification.

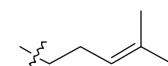


434 $R_1=OH; R_2=H; R_3=Me$

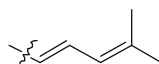
435 $R_1=OH; R_2=H; R_3=$



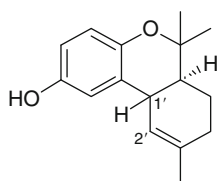
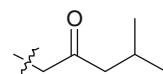
436 $R_1=OH; R_2=OMe; R_3=$



437 $R_1=OH; R_2=H; R_3=$

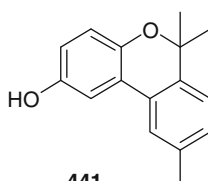


438 $R_1=OH; R_2=Me; R_3=$



439 H-1' a

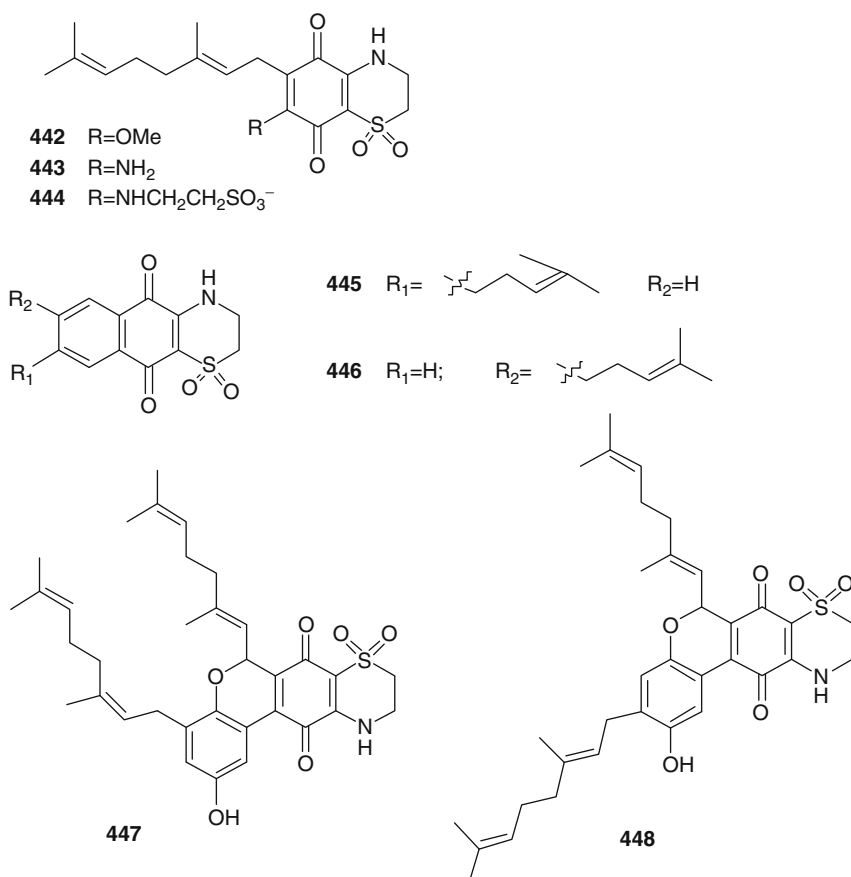
440 H-1' b



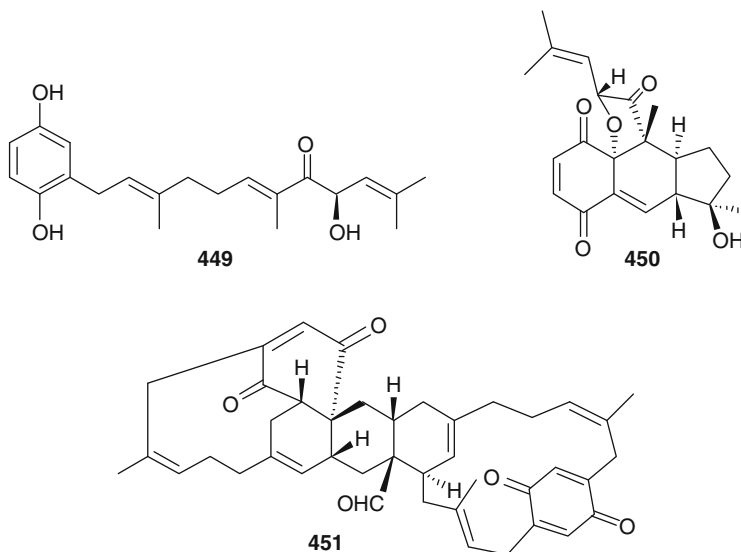
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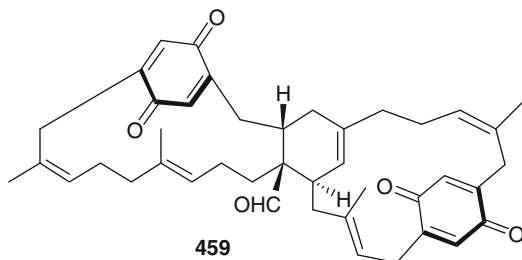
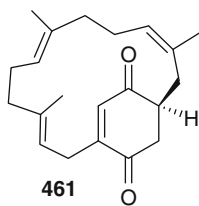
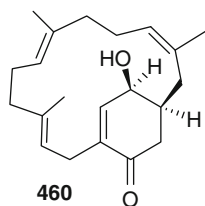
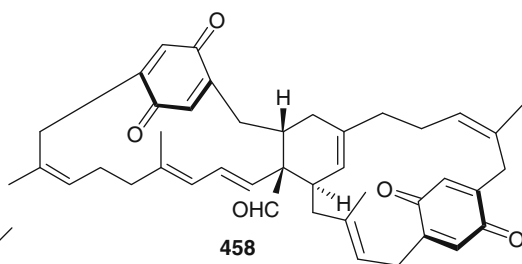
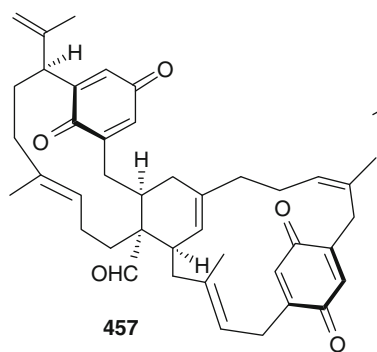
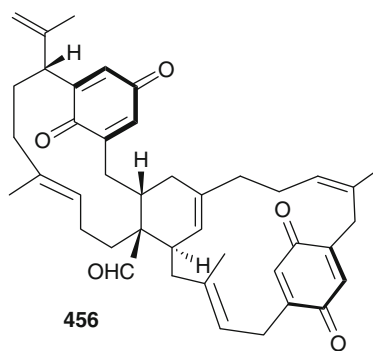
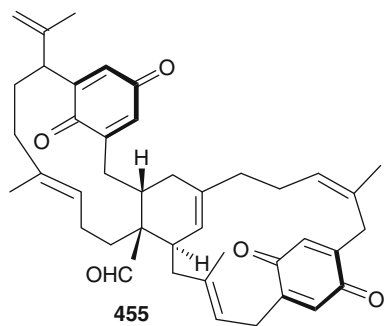
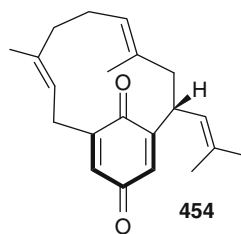
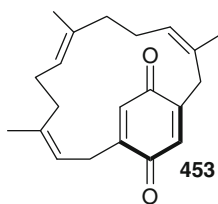
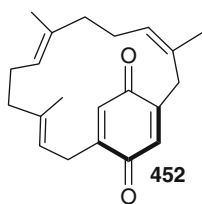
Interestingly, *A. conicum* showed a metabolic content that is different depending on the geographical place of collection. Apart from the meroterpenes **417**, **419**, **422**, **423**, **432**, **433**, **435**, **439**, and **440** above reported, isolated from a Spanish collection of the ascidian, a sample of *A. conicum* collected along Sardinia coasts gave rise to the isolation of a large group of unique meroterpenes, compounds **442–448**, whose structures all feature an unusual 1,1-dioxo-1,4-thiazine ring fused with the quinone portion [326–328]. Aplidinones A–C (**442–444**) and conicaquinones A and B (**445** and **446**) possess a benzoquinones and a naphthoquinone moiety, respectively; thiaplidiaquinones A and B (**447** and **448**) possess an unprecedented tetracyclic core and visibly are composed of two geranylated benzoquinones that have fused together. Both conicaquinones A and B showed marked and selective cytotoxic effects on rat glioma cells [326]; thiaplidiaquinones were strongly cytotoxic against Jurkat cell line, derived from a human T lymphoma, inducing cell death by apoptosis. The pro-apoptotic mechanism of thiaplidiaquinones involves the induction of a strong production of intracellular reactive oxygen species (ROS) in the

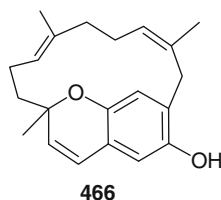
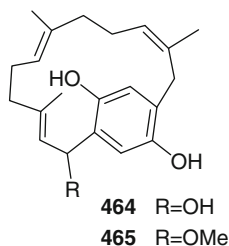
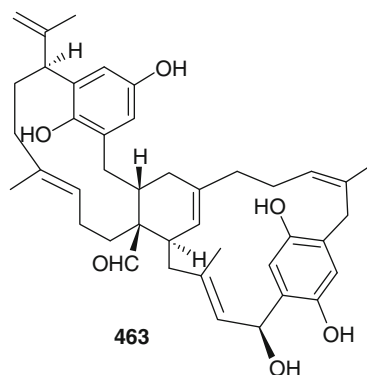
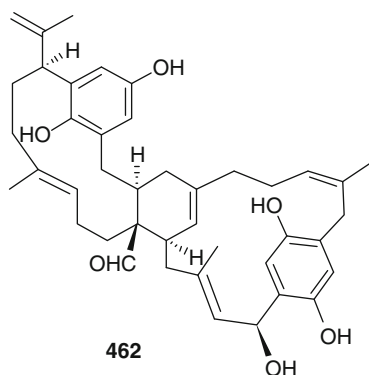
cells, likely due to the inhibition of the plasma membrane NADH-oxidoreductase (PMOR) system, an important target for anticancer drugs, through interference with the coenzyme Q-binding site [328]. In order to validate the structural assignment made for aplidinones by theoretical means, a synthetic approach has been undertaken which yielded some synthetic analogues of aplidinone A in which the geranyl chain is replaced by other alkyl chains; these compounds as well as the natural metabolite **442** were subjected to cytotoxicity assays and preliminary structure-activity relationships (SAR) studies. Both aplidinone A and its synthetic analogues were shown to possess interesting cytotoxic effects; SAR studies revealed that cytotoxic activity depends on the nature and the length of side chain linked to the benzoquinone ring and, mainly, on its position with respect to the dioxothiazine ring. The study evidenced also one of the synthetic analogues as a potent cytotoxic and pro-apoptotic agent against several tumor cell lines which also inhibits the TNF α -induced NF- κ B activation in a human leukemia T cell line [329].



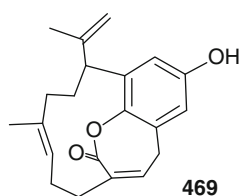
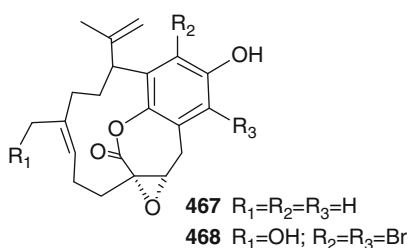
Rossinones A (**449**) and B (**450**) are triprenylated (farnesyl) hydroquinone and quinone, respectively. They have been isolated from an Antarctic *Aplidium* species and exhibited anti-inflammatory, antiviral, and antiproliferative activities [330]. *A. longithorax* has been the source of longithorones A–K (**451–461**) and longithorols A–E (**462–466**), a unique class of macrocyclic C_{21} or C_{42} prenylated quinone/hydroquinone derivatives featuring unprecedented carbocyclic skeletons formed by an unusual cyclization of the farnesyl chain with the hydroquinone unit to give [9] and [10]metacyclophane, as well as [12]paracyclophane structures [331–335]. Longithorones A (**451**) and E–I (**455–459**) are dimeric compounds; it has been speculated that they may arise by Diels–Alder reactions of suitable unsaturated precursors, and the discovery of the monomers longithorones B–D (**452–454**), J (**460**), and K (**461**) supports this suggestion. The stereochemistry of the central carbocyclic rings in **451** and **455–459** is consistent with such a fusion [332]. Longithorones A–I have restricted rotations in their macrocyclic rings, resulting in atropisomerism; longithorone J is the first example of a γ -hydroxy-cyclohexenone in this class of compounds. Longithorols (**462–466**) are hydroquinone derivatives; longithorols A (**462**) and B (**463**) were isolated as their pentaacetates because of their rapid decomposition occurring under purification conditions [334]. Longithorol E (**466**), a macrocyclic chromenol, is possibly an artifact of the isolation process as it can be envisaged that longithorol C (**464**) could undergo an intramolecular cyclization followed by dehydration to yield **466** [335]. To date, the only biological activity reported for longithorones/longithorols class of marine metabolites pertains to longithorone A (**451**), which was shown to display cytotoxicity against P388 murine leukemia cells.





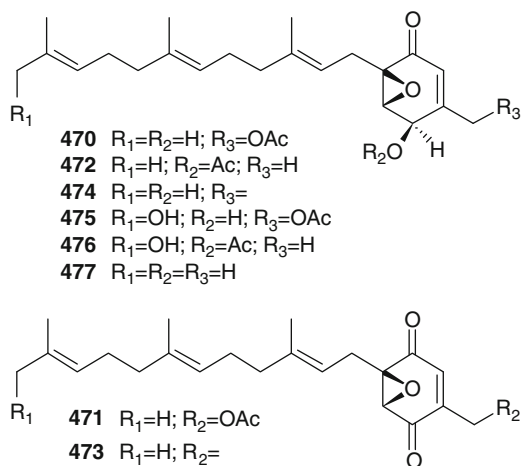


Floresolides A–C (**467–469**) are three further cyclofarnesylated hydroquinones cytotoxic against KB cells isolated from an Indonesian *Aplidium* sp.; they are unique relatives of longithorols, possessing an endocyclic ϵ -lactone bridging the aromatic ring and a [10]metacyclophane moiety [336].



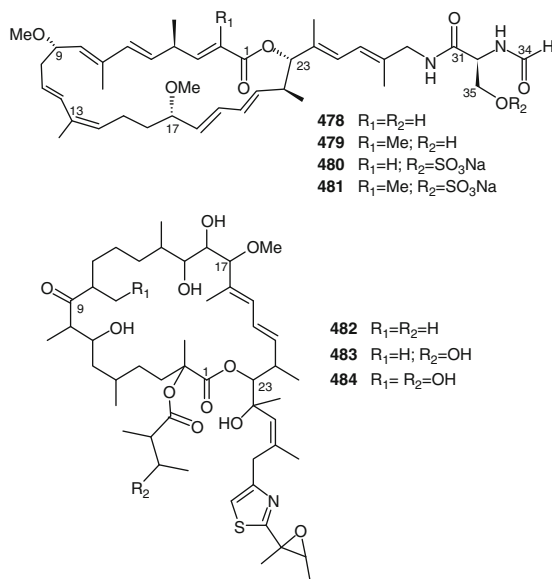
Eight bioactive farnesylated epoxy cyclohexenones closely related to some of the above reported meroterpenes, yanuthones A–E (**470–474**), 1-hydroxyyanuthones A (**475**) and C (**476**), and 22-deacetylanuthone A (**477**) have been reported from an *Aspergillus niger* isolate obtained from tissue homogenates of an *Aplidium* ascidian [337]. The structural similarities between yanuthones and the meroterpenes isolated

from ascidians raise some question about the origin of the latter compounds; the possibility exists that they or, at least, a portion of their structure could be a microbial product.

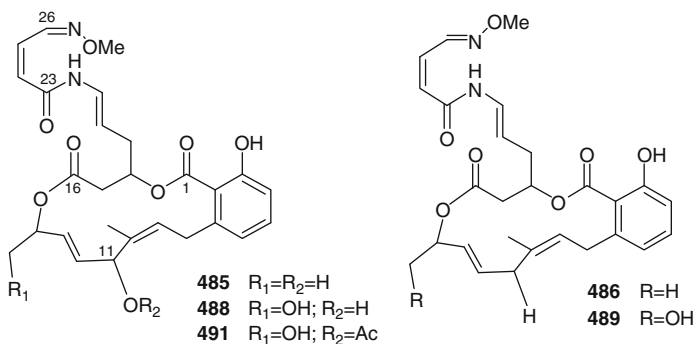


5.5 Macrolides

A significant number of large macrocyclic lactones (macrolides) have been found in ascidians; they constitute another family of ascidians metabolites which have attracted great interest because of their potent antineoplastic properties, thus becoming one of the challenging targets for total synthesis or as candidate of new antitumor drugs. Iejimalides (**478–481**) are a group of 24-membered macrolides isolated from *Eudistoma* cf. *rigida* [338, 339] and from *Cystodites* sp. [340]; they exhibited strong cytotoxic properties in vitro and antitumor activity in vivo. Iejimalides A (**478**) and B (**479**) represent the first macrocyclic lactones isolated from a tunicate; a rare *N*-formyl-L-serine unit (C-31–C-35) is included in their side chains. Iejimalides C (**480**) and D (**481**) are the C-35 sulfates of **478** and **479**, respectively. *Lissoclinum patella* has been the source of patellazoles (A–C, **482–484**), a family of cytotoxic and antifungal 24-membered macrolides having a pendant thiazole-epoxy group [341, 342]. Although patellazoles appear predominantly polyketide-derived, the thiazole moiety probably originates from an amino acid. The patellazoles are potent cytotoxins; they are extremely cytotoxic toward HCT 116 human colon tumor cells; treatment with nanomolar amounts of these compounds results in immediate inhibition of protein synthesis and cell cycle arrest at the G1 and S phase. The opening of the epoxide ring does not greatly affect the bioactivity although the cellular toxicity is generally decreased [343].



Lobatamides A–F (485–490) are a group of macrocyclic lactones which have been isolated from three different shallow water Australian collections of *Aplidium lobatum* [344], from a deep water collection of an *Aplidium* sp. [345], and from an unidentified Philippine ascidian [345]. The overall structures of the lobatamides are unique, due primarily to the unusual enamide-oxime methyl ether moiety which terminates the side chain of the macrolide. Lobatamides A, B, D, and E have been shown to be the same compounds as those previously isolated from an Australian *Aplidium* sp. and named aplidites A, B, C, and D, respectively, whose structures were incorrectly assigned [346]. The Australian authors also reported the isolation of further aplidites, E–G; the earlier reported structures and nomenclature of these compounds have been revised to those for lobatamides G–I (491–493) [345].



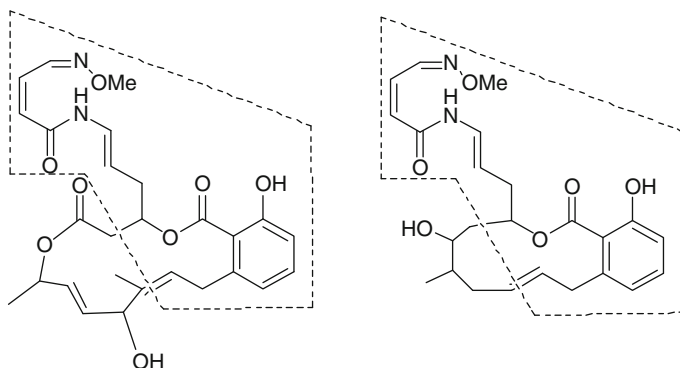
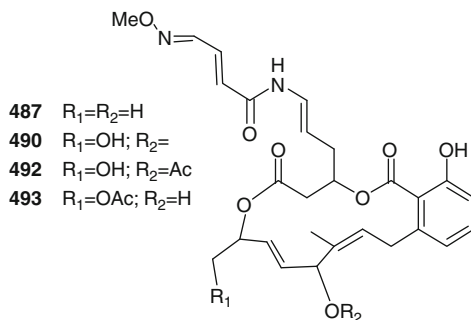
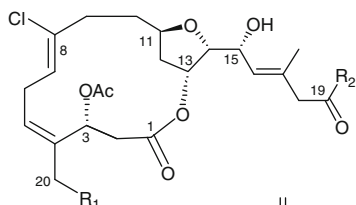


Fig. 5.2 Common core structural component shared by the lobatamides (*left*, lobatamide A9) and the salicylihalamides (*right*, salicylihalamide A)

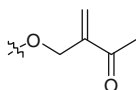


Lobatamides are related to salicylihalamides (Fig. 5.2) isolated from a sponge *Haliclona* sp.; while the size of the macrolide ring differs (12 for salicylihalamides and 15 for lobatamides), both families contain the common core structure depicted in Fig. 5.2. Lobatamides and salicylihalamides are member of the salicylate enamide macrolides class, an emerging group of antitumor natural products that have attracted considerable interest especially due to their mechanism of action [347]. Like the salicylihalamides, the lobatamides display high potency against tumor cell lines [345] which may be derived from their ability to inhibit vacuolar-ATPase (V-ATPase), largely responsible for cellular and organellular pH regulation but also implicated in cancer treatment [347].

Haterumalide B (**494**) and biselides A–D (**495–498**) are rare examples of halogenated marine macrolides. Haterumalide B is a chlorinated 14-membered ring macrolide and has been found in an Okinawan *Lissoclinum* sp. [348]; biselides A–D are haterumalide B close analogues and have been recovered in the organic extract of an Okinawan Didemnidae sp., together with the structurally related haterumalide NA (**499**) previously isolated from an Okinawan sponge [349, 350].

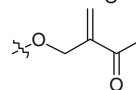


494 $R_1=H$; $R_2=$



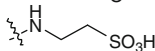
495 $R_1=OAc$; $R_2=OH$

496 $R_1=OAc$; $R_2=$



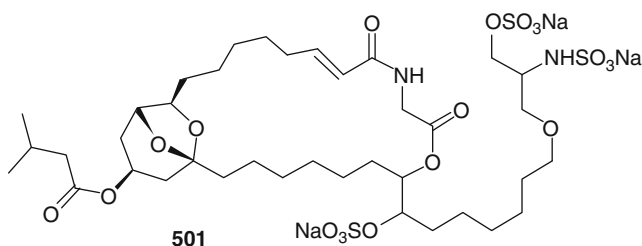
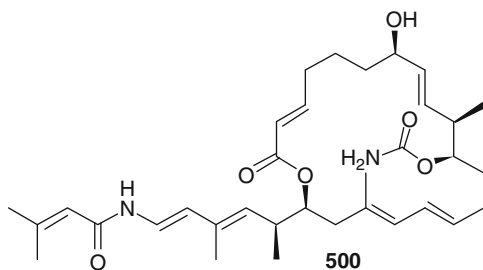
497 $R_1=R_2=OH$

498 $R_1=H$; $R_2=$



499 $R_1=H$; $R_2=OH$

Palmerolide A (**500**) is a 20-membered macrolide decorated with a polyunsaturated N-acyl dienamine side chain distinct from the N-acyl enamine found in lobatamides. It has been isolated from a sample of *Synoicum adareanum* collected in Antarctica, one of the most inaccessible areas of the world [351]. Its earlier reported structure was successively revised to a diastereomer of that previously proposed [352]. Palmerolide A is a potent and selective inhibitor of melanoma cell growth; it also targets transmembrane proton pump, the V-ATPase, for which it is a potent inhibitor. Cyclodidemniserinol trisulfate (**501**), isolated from the Palauan ascidian *Didemnum guttatum*, is an inhibitor of HIV-1 integrase, which is an attractive target for anti-retroviral chemotherapy [353].

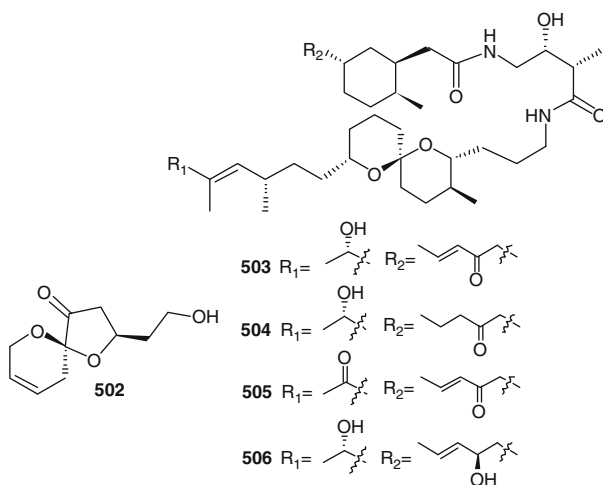


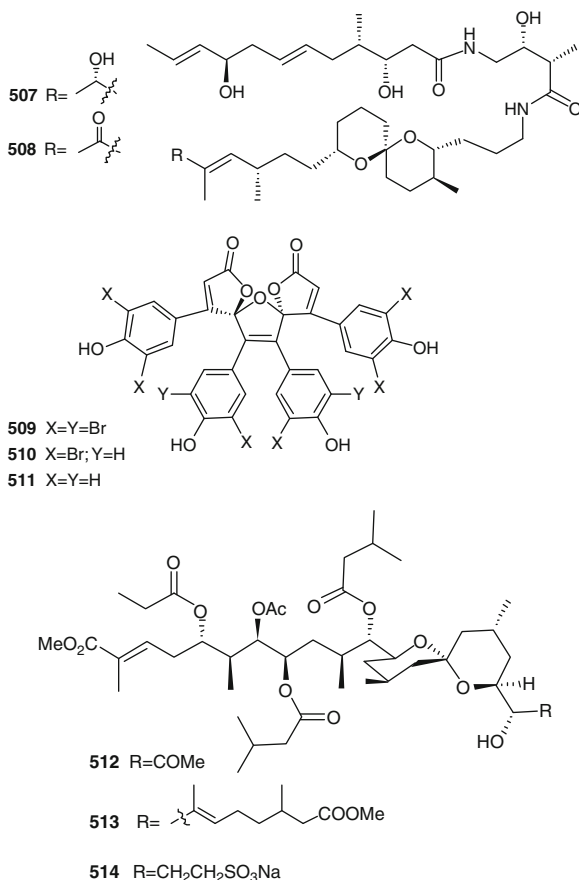
The question about the real producers of marine natural products is today an open question; macrolides such as those found in ascidians have been isolated from many other marine microorganisms (sponges, nudibranch eggs, and bryozoans). Lobatamide A (**485**) is identical to the structure of YM-75518 reported from a terrestrial *Pseudomonas* sp. cultured from an Indonesian soil sample [354]. The occurrence of identical and/or biosynthetically related compounds in collections of different tunicates from distinct geographical locations (e.g., iejimalides and lobatamides), in different organisms (e.g., haterumalides, salicylihalamides), and in terrestrial source suggests the possibility of their biosynthesis by associated microorganisms or of accumulation through dietary intake.

5.6 Other Nonnitrogenous Compounds

5.6.1 Spiroketal-Containing Products

Most marine natural products, especially polyketides, possess polyhydroxy and polyoxy substituents in their structures. A number of bicyclic (bridged ring) and/or spirocyclic acetals have been isolated from marine organisms [355], these motifs being the result of intramolecular dehydration of their hydroxy ketone precursors. In addition to the previously mentioned didemnerinolipids A–C (**312–314**, see Sect. 5.2.6) from *Didemnum* sp., spiroketal-containing metabolites isolated from ascidians include small molecules like lissoketal (**502**), isolated from *Lissoclinium voeltzkowi* and endowed with a 1,6-dioxaspiro[4, 5]dec-8-en-4-one moiety [356] as well as families of complex molecules, biosynthetically unrelated, such as bistramidides (**503–508**), prunolides (**509–511**), and didemnaketals (**512–514**).





Bistramides are a family of polyether toxins possessing a 1,7-dioxaspiro [5] undecane spiroketal unit. The first of the series, bistramide A (bistratene A, **503**) was isolated from *Lissoclinum bistratum* [246, 357]; additional bistramides (B–D and K, **504–507**) were later recovered also from *L. bistratum* [358], while the only report of these compounds from another source is 39-oxobistramide K (**508**) from *Trididemnum cyclops* [359]. The bistramides have been shown to display diverse bioactivities, including immunomodulating and weak antimalarian activity, but their most notable trait is their antitumor properties. Bistramide A (**503**) promises to become a useful agent with which to dissect the complex processes controlling cell growth, differentiation, and death [360, 361]. Unfortunately, high toxicity prevents them from therapeutic use; among bistramides, compounds **506** and **507** are less toxic but far less abundant in nature.

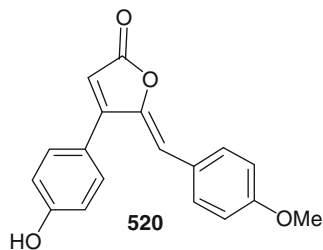
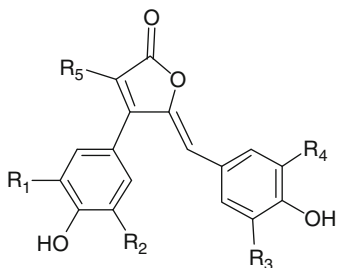
Prunolides A–C (**509–511**) are tetraphenolic bis-spiroketal containing a unique 1,6,8-trioxadispiro[4.1.4.2]trideca-3,10,12-triene-2,9-dione carbon

skeleton which have been isolated from an Australian collection of *Synoicum prunum* [362]. They represent a structurally novel family of ascidian metabolites; they have been frequently co-isolated with rubrolides (515–529, see Sect. 5.6.2), suggesting that they probably arise from an oxidative dimerization of a rubrolide precursor. The prunolides also bear some resemblance to the alkaloids polycitone A (226) and polycitrins A and B (228–229), and they probably share a common biogenesis.

In 1991, Potts et al. reported that an unidentified Palauan ascidian of the genus *Didemnum* contained two polyisoprenoid, didemnaketal A and B (512–513) containing a 1,7-dioxaspiro [5]undecane spiroketal unit; both of them inhibited the activity of HIV-1 protease [363]. A reinvestigation of the same organisms yielded as the major secondary metabolite: the isoethonic ester 514, didemnaketal C [364]. It was therefore assumed that compounds 512 and 513 had been produced from didemnaketal C during prolonged storage in methanol by mechanisms involving oxidation and methanolysis, respectively. Unfortunately, didemnaketal C (514) did not inhibit HIV-1 in a peptidolysis assay.

5.6.2 Nonnitrogenous Phenylalanine- or Tyrosine-Derived Metabolites

The rubrolides (515–529) are a structurally unique family of biologically active ascidians metabolites. Rubrolides A–H (515–522) were first described as antibacterial, phosphatase-inhibiting metabolites of *Ritterella rubra* [365], followed by the discovery of six new members of the family, rubrolides I–N (523–528) in *Synoicum blochmani* with rubrolides I, K, L, and M exhibiting significant cytotoxicity [366]. A New Zealand *Synoicum* n. sp. contained rubrolide O (529) which, unlike the others rubrolides reported solely as the Z isomers, exists as a mixture of E/Z isomers; moreover, it is the first anti-inflammatory rubrolide reported [367]. A related biogenesis from either phenylalanine or tyrosine appears most likely for rubrolides; therefore, even though they are part of the very small minority of tunicate metabolites that do not contain nitrogen, rubrolides probably share an amino acid biogenetic origin with the majority of the other tunicate metabolites. Rubrolides B (516), H (522), I (523), and K–O (525–529) are rare examples of chlorinated tunicate metabolites; rubrolide N (528) displays an unprecedented halogenation pattern among the rubrolides since it contains an α -bromo- β -lactone ring and a chlorinated aromatic substituent. Rubrolide A (515) has also been detected in the Australian *S. prunum*, from which were isolated the related prunolides (509–511, see Sect. 5.7) [362], and from an ascidian of the genus *Botryllus*, which also yielded the cadiolides (530–531) [368], other furanone metabolites structurally related to the rubrolides but possessing a novel carbon skeleton probably originated from three molecules of phenylalanine.



515 R₁=R₂=R₃=R₄=Br; R₅=H

516 R₁=R₂=R₃=R₄=Br; R₅=Cl

517 R₁=R₂=R₅=H; R₃=R₄=Br

518 R₁=R₂=Br; R₃=R₄=R₅=H

519 R₁=R₂=R₃=R₄=R₅=H

523 R₁=H; R₂=R₃=R₄=Br; R₅=Cl

524 R₁=H; R₂=R₃=R₄=Br; R₅=H

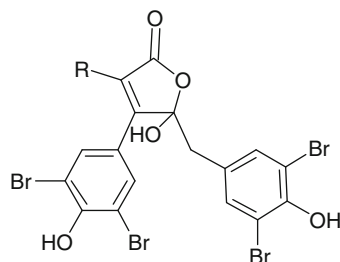
525 R₁=R₃=H; R₂=R₄=Br; R₅=Cl

526 R₁=R₂=H; R₃=R₄=Br; R₅=Cl

527 R₁=R₂=R₃=H; R₄=Br; R₅=Cl

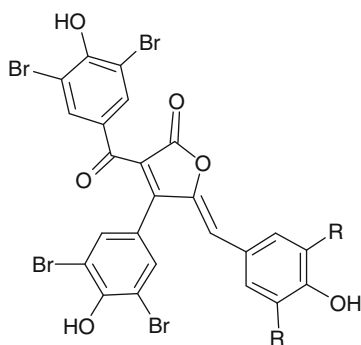
528 R₁=R₃=H; R₂=Cl; R₄=R₅=Br

529 R₁=R₂=R₃=Br; R₄=H; R₅=Cl (mixture of E/Z isomers)



521 R=H

522 R=Cl

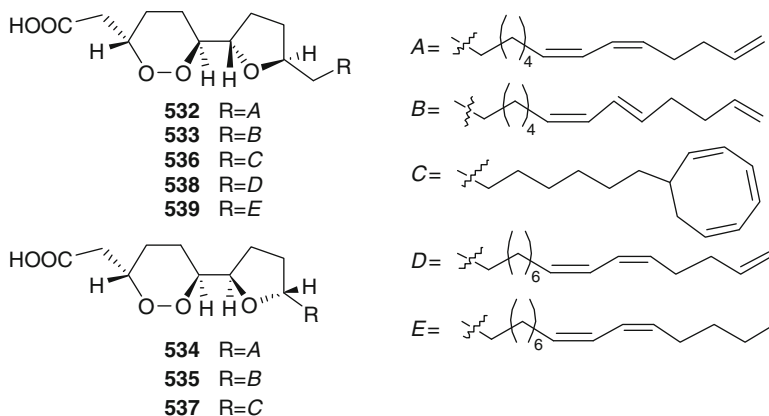


530 R=H

531 R=Br

5.6.3 Stolonoxides and Stolonic Acids

Linear and cyclic peroxides have been encountered in marine organisms, but they are mainly confined to sponges of the genera *Chondrilla*, *Plakortis*, and *Xestospongia*. However, *Stolonica* ascidians have been showed to be an additional source of fatty acid-derived cyclic peroxides, like stolonoxides and stolonic acids (**532–539**) which constitute a family of aliphatic endoperoxides with an unprecedented molecular arrangement.



Differently from other known peroxides, stolonoxides display an unusual structure with a 1,2-dioxane ring directly linked to a tetrahydrofuranyl (THF) moiety. Stolonoxide A (**532**), the first member of the series, has been isolated as its methyl ester from *Stolonica socialis* [369]; compound **532**, together with three new analogues, stolonoxides B–D (**533–535**), were independently isolated from another sample of the same species [370]. Two further stolonoxides, E and F (**536**, **537**), have been recently isolated also from *S. socialis* [371]; while being members of the stolonoxide family, they incorporate a 1,3,5-octatriene ring in their molecules, an element of structural novelty with only one precedent in marine natural products. This ring seems to originate from an unstable tetraene at the end of the aliphatic chain of a potential precursor. There is also the probability that 1,3,5-octatriene ring could be formed during the process of extraction and purification of the compounds [371]. Stolonoxenic acids A and B (**538**, **539**), possessing a longer aliphatic chain, have been isolated from an undescribed *Stolonica* species collected in the Indian Ocean [372]. Both stolonoxenic acids and stolonoxides were strongly cytotoxic against several mammalian tumor cell lines; interestingly, the activity displayed by stolonoxides E (**536**) and F (**537**) was weaker than that measured for their analogues stolonoxides A–D (**532–535**) and for stolonoxenic acids (**538** and **539**). This suggests that the presence of the diene and the vinyl terminal group in these latter compounds plays a key role in the cytotoxic activity displayed by members of this family [371]. The molecular arrangement of compounds **532–539** resembles the adjacent bis-THF group of Annonaceous acetogenins, a class of antitumor and pesticidal compounds whose main mode of action is the inhibition of the mitochondrial respiratory chain, the fundamental process that drives the ATP synthesis under anaerobic metabolism in cells. Based on this structural analogy, stolonoxides A (**532**) and C (**534**) were tested in beef heart submitochondrial particles (SMP) and were found to be inhibitors of the mitochondrial respiratory chain, affecting specifically the functionality of complex II (succinate:ubiquinone oxidoreductase) and complex II (ubiquinol:cytochrome *c* oxidoreductase) in mammalian cells [373].

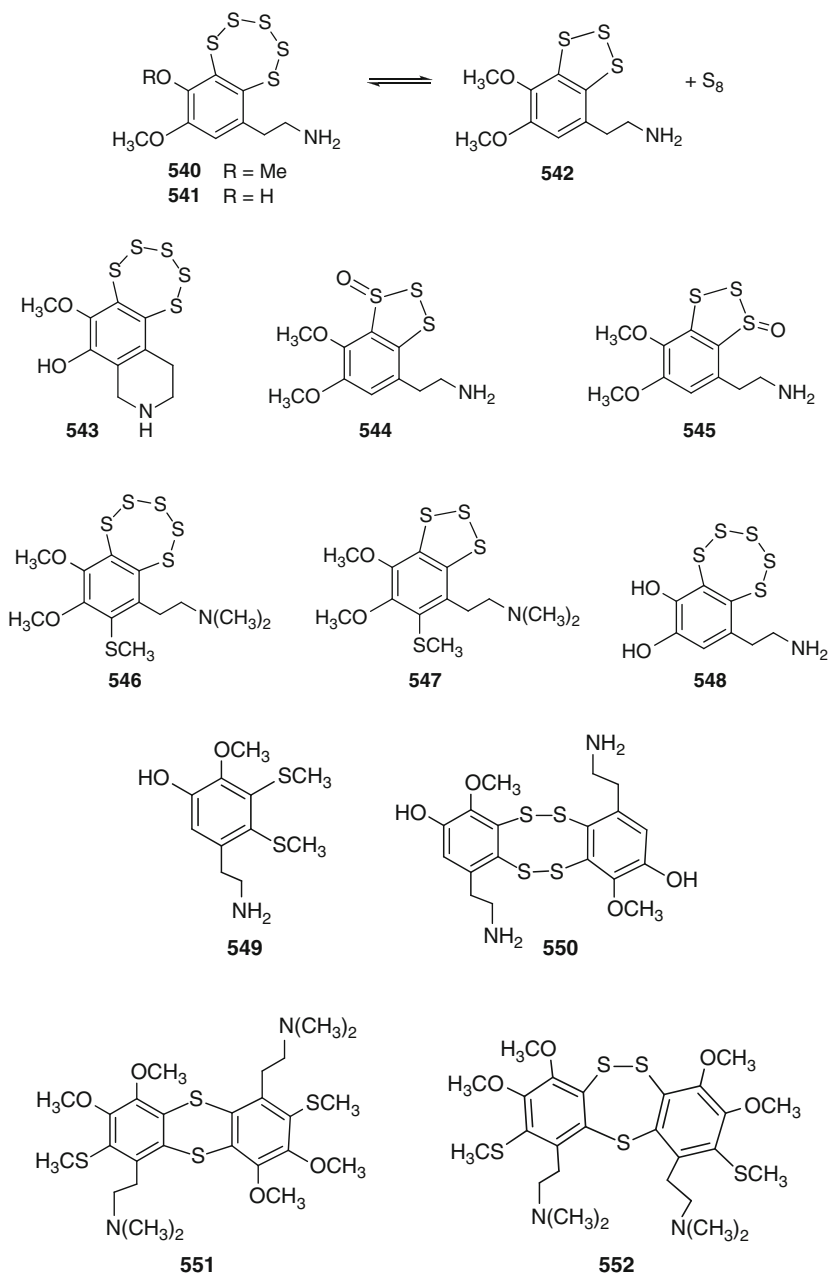
5.7 Sulfur-Containing Metabolites

Sulfur-containing compounds, although relatively unusual, occur in marine organisms. Ascidians have been an extremely rich source of sulfur-containing molecules; they include sulfides/polysulfides, sulfur-heterocycles, sulfoxides, and alkyl sulfates. Some of these compounds (mostly molecules with sulfur-heterocycle, methyl sulfide, and sulfoxide moieties) have been already showed in the previous sections since they flatly fell into one of the main structural groups identified. Here described are essentially sulfides, polysulfides, and simple alkyl sulfates.

A number of unique cyclic polysulfides derived from dopamine have been reported from ascidians of the genera *Lissoclinum*, *Polycitor*, and *Eudistoma* [17, 374–378]; they have received considerable attention both for their unique chemical structures and for their often significant biological activities. Varacin (**540**), the first naturally occurring benzopentathiepin, has been isolated from *L. vareau*, a lavender-colored encrusting species collected in the Fiji Islands [375]. Compound **540** has been synthesized from vanillin providing unambiguous confirmation of the structure proposed [379, 380]. Similar compounds, lissoclinotoxin A (**541**), originally reported to have a cyclic trithiane structure [381], and lissoclinotoxin B (**542**) [376], have been isolated from *L. perforatum* collected in northern Brittany. Evidences have been provided indicating that unsymmetrically substituted benzopentathiepins, such as varacin and lissoclinotoxin A, are chiral because of a high activation barrier to interconversion of the low energy chair conformations of the polysulfide ring [382]. In addition to having unique structures, varacin and lissoclinotoxin A exhibit significant biological activities. Varacin was originally reported to have antifungal activity against *Candida albicans* (14-mm zone of inhibition of 2 µg of varacin/disk) as well as cytotoxicity toward human colon tumor cell line HCT 116 (IC₉₀ 0.05 µg/mL) [375], while lissoclinotoxin A was reported to have antimicrobial and antifungal activity (*S. aureus*, Ø inhibition: 15 mm/300 µg) [381]. Furthermore, a differential cytotoxicity toward the CHO cell lines EM9 (chlorodeoxyuridine sensitive) versus BR1 (BCNU resistant) indicated that varacin's mechanism of action may involve the formation of single-stranded DNA breaks [375, 383]. It has been reported that some aromatic fused benzopentathiepins are capable of decomposing into sulfur and the corresponding benzotrithioles in solution [384]. Examination of varacin (**540**) as well as varacin A (**543**) by ¹H NMR and MS revealed that both of these compounds readily equilibrate to a mixture of **540** and **543**. In fact, the reaction “**540** = **543** + S₈” was observed to occur in CHCl₃, MeOH and pyridine [383]. Varacin B e C (**544 e 545**), isolated from *Polycitor* sp. [380] are the 3'-S-oxide and the 1'-S-oxide, respectively, of varacin A.

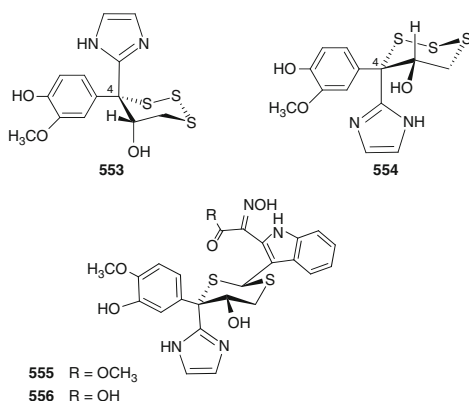
Compagnone et al. reported the isolation and protein kinase C inhibitory activity of N,N-dimethyl-5-(methylthio)varacin (**546**) and the corresponding trithiane **547** from a Palauan collection of *Lissoclinum japonicum* and 3,4-desmethylvaracin (**548**) from *Eudistoma* sp. from Pohnpei [374]. Lissoclinotoxin C (**549**) and the dimeric lissoclinotoxin D (**550**) have been isolated from *Lissoclinum* sp. collected from the Great Reef, Australia [20], while lissoclinotoxins E and F (**551, 552**) have been found

in a Philippine didemnid ascidian. Montecarlo conformational searching using MM2 force field suggested that the *N*-alkyl chains about the tricyclic systems of lissocli-notoxins E and F had *trans* and *cis* orientations, respectively [385].

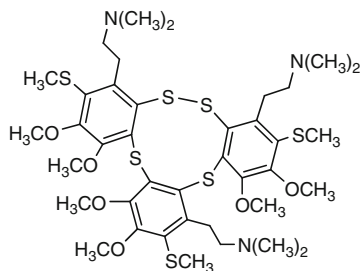
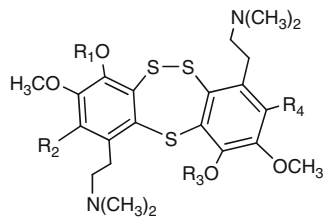


Another trithiane derivative (**553**) was isolated from the New Zealand ascidian *Aplidium* sp. [386]. Compound **553** was observed to be unstable in slightly alkaline solutions or even in neutral CD₃OD, giving a mixture of two new components, one of which was shown to be the diastereomer **554** bearing the opposite configuration at the central chiral carbon (C-4). Both trithiane derivatives **553** and **554** exhibited modest cytotoxic activity against P388 murine leukemia with IC₅₀ values of 13 and 12 µg/mL, respectively, in addition to inhibiting the growth of *Bacillus subtilis* and *Candida albicans* (−20 µg/disk) [386].

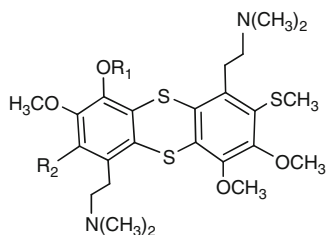
Enantiomeric marine natural products are uncommon, and it is rare to find enantiomers with two or more chiral centers. The (−)-**553** enantiomer of compound (+)-**554** was isolated from the delicate pink stalked ascidian *Hypsistozoa fasmeriana* collected at Tutukaka, North Island, New Zealand [387]. Another collection of *H. fasmeriana* collected at Leigh Harbor, Northland, New Zealand afforded (−)-**553** and two dithiane metabolites **555** and **556** named fasmerianamine A and B, respectively [387].



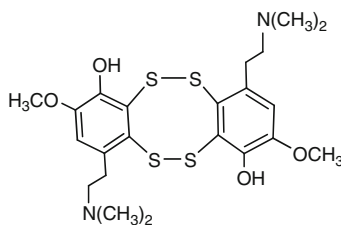
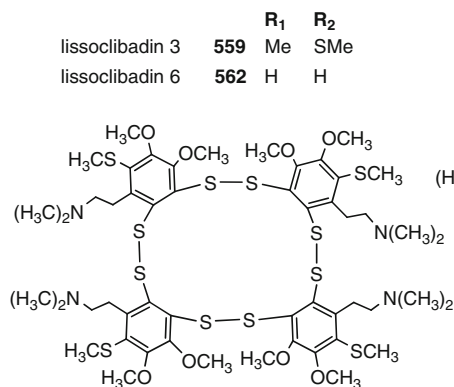
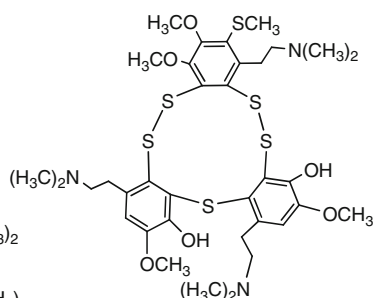
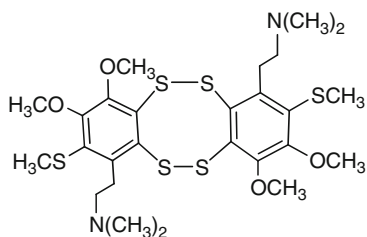
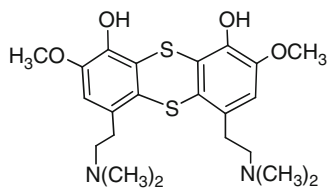
Fourteen polysulfur dopamine-derived compounds lissoclibadin 1–14 (**557–570**) have been isolated from *Lissoclinum* cf. *badium*, collected in Indonesia [388–391]. Lissoclibadins 1 and 2 (**557** and **558**) and lissoclinotoxin F (**552**) showed a very strong activity against human solid tumor cell lines and are more potent than the anticancer drug cisplatin. Lissoclibadin 2 (**558**) was the most interesting compound possessing potent inhibitory activity against colon cancer cell lines (DLD-1 and HCT116), breast (MDA-MB-231), renal (ACHN), and non-small-cell lung (NCI-H460) cancer cell lines and showing no toxicity following a 50 mg/kg single treatment to mice, and preferable stability in rat plasma. Therefore, the activities of compounds possessing a dimeric or trimeric structure with a disulfide bond are stronger than those of the dimeric compound with two sulfide bonds (**559**) and monomeric compounds (**546**, **547**) [392].

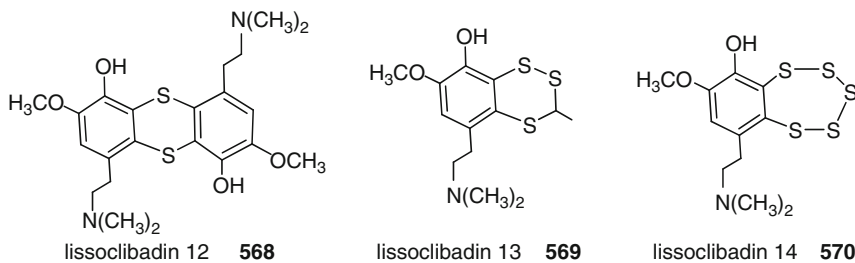
lissoclibadin 1 **557**

	R₁	R₂	R₃	R₄
lissoclibadin 2	558	Me	SMe	Me
lissoclibadin 4	560	H	H	H
lissoclibadin 5	561	H	H	Me

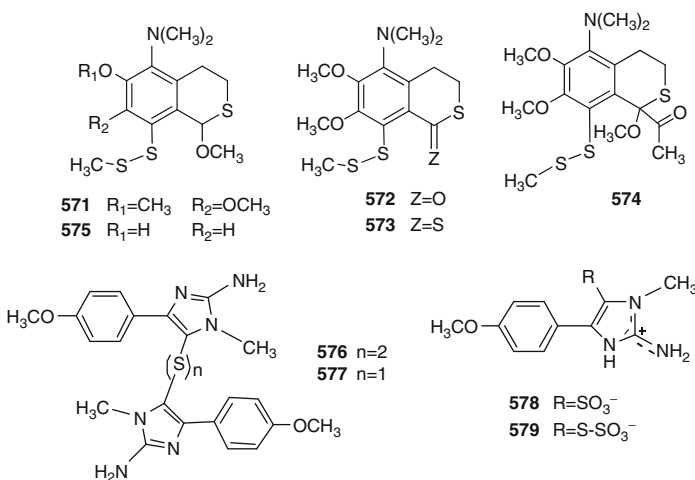


	R₁	R₂
lissoclibadin 3	559	Me
lissoclibadin 6	562	H

lissoclibadin 7 **563**lissoclibadin 8 **564**lissoclibadin 9 **565**lissoclibadin 10 **566**lissoclibadin 11 **567**

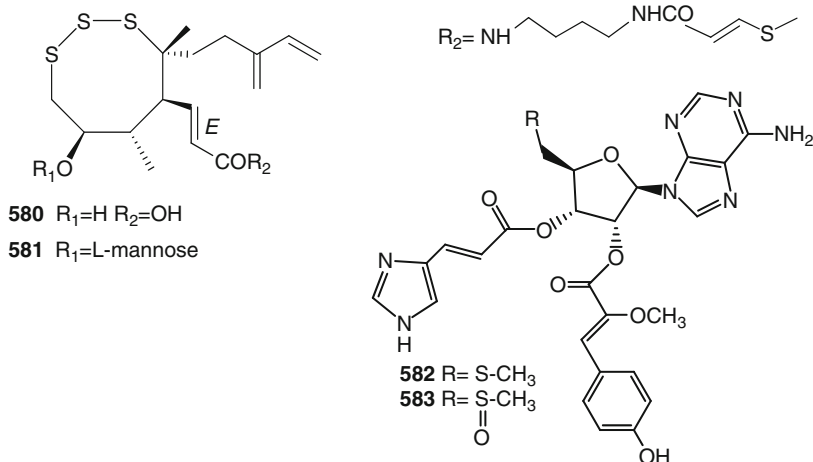


Several disulfides compounds have been isolated from ascidians of the genus *Polycarpa*. They include polycarpamines A–E (**571–575**), found in *P. auzata* [393], and polycarpine (**576**), a cytotoxic metabolite isolated from several collections of *P. aurata* and subsequently reported from *P. clavata* [73, 394, 395]. Polycarpamines as well as polycarpine presented various biological activities, such as antifungal activity [393], cytotoxicity [394], inhibition of inosine monophosphate dehydrogenase (IMPDH) [396], and induction of apoptosis in JB6 cells through p53- and caspase 3-dependent pathways [397]. From a sample of *P. aurata* collected in the Lembeh Strait, Indonesia, in addition to polycarpine (**576**), polycarpaurines A (**577**), B (**578**), and C (**579**) have been isolated [398].

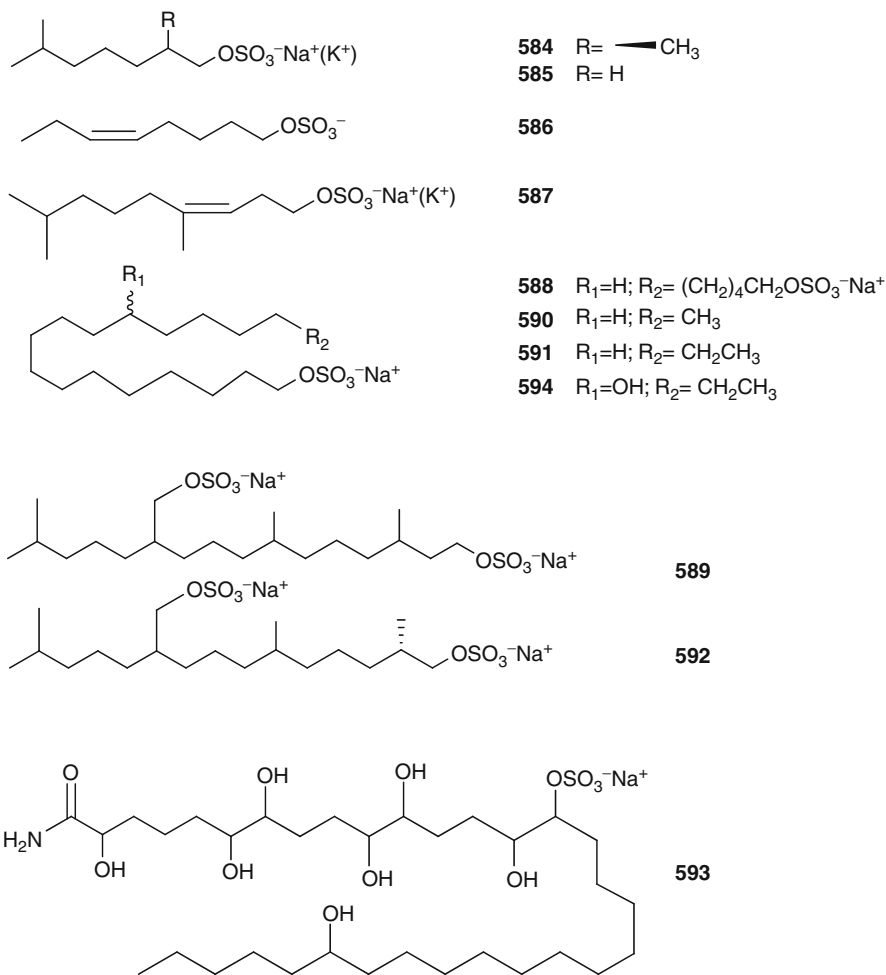


Two sulfur derivatives, **580** and **581**, the latter of which is a glycoside, containing substituted 1,2,3-trithiocane cycles have been isolated from *Perophora viridis* collected off the Atlantic of North Carolina [399].

Two complex nucleosides, (**582–583**) containing the rare methylthioadenosine and methylsulfinyladenosine moieties, were found in *Atrium robustum*. Compound **582** inhibits cAMP accumulation in Chinese hamster ovary (CHO) cell membranes recombinantly expressing the human A_3 adenosine receptor, thus indicating that the adenosine derivative also acted as a partial agonist at A_3 ARs [400].

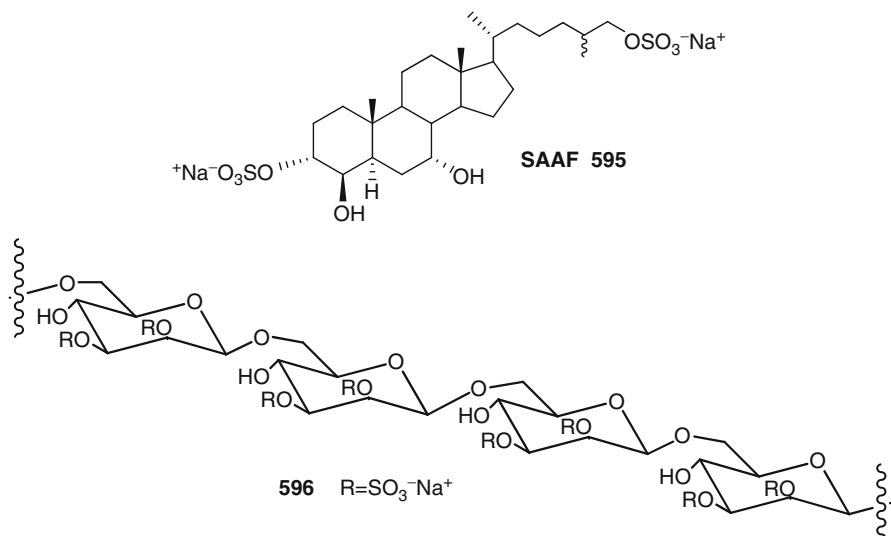


Only a few examples of sulfated alkanes/alkene have been reported from marine sources. Although the isolation of some alkane/alkene sulfate esters from two Japanese ascidians have been reported [401, 402], a series of these metabolites have been isolated from Mediterranean tunicates. Most of these compounds, often having quite simple structures, are cytotoxic or antimicrobial. The first report of a sulfated hydrocarbon from a tunicate was the finding of sodium (or potassium) 2,6-dimethylheptyl sulfate (**584**) from *Policitor adriaticus* in 1994 [403, 404]; it was also isolated, as a racemate, from the hepatopancreas of *Halocynthia roretzi* [401] and from *H. papillosa* together with compounds **585–586**[405]. Further cytotoxic and antiproliferative analogues have been isolated from other Mediterranean ascidians, such as compound **587** from *Microcosmus vulgaris* [406] and **588–589** from *Ascidia mentula* [407]. A selective cytotoxic agent, named turbinamide (**593**) [408] has been isolated from the Mediterranean tunicate *Sidnyum turbinatum* together with tree sulfated alkanes **590–592** [409]. Turbinamide (**593**) showed a potent and selective cytotoxic effect against neuronal rather than immune system cells; C6 rat glioma cells were shown to be very sensible to this metabolite. Gliomas are also considered among the most malignant forms of cancer whose therapeutic treatment is up to now only palliative. Studies on the cellular effects of turbinamide have been performed, and it is demonstrated that turbinamide-induced cytotoxicity in C6 cells is due to apoptosis: The activity of caspase-3 is enhanced in a concentration-dependent manner by this compound, having no effect on J774 cells [410]. Compound **594**, structurally related to the alkyl sulfates isolated from *A. mentula* and *S turbinatum*, has been isolated from a marine tunicate of the family Polyclinidae as a matrix metalloproteinase 2 (MMP2) inhibitor with an IC_{50} value of 9.0 $\mu\text{g/mL}$ [402].



Sperm chemotaxis toward eggs before fertilization has been demonstrated in many animals and plant, and several peptides and small organic compounds acting as chemoattractants have been identified [411]. An endogenous non-peptidic sperm-activating and sperm-attracting factor, SAAF **595**, was isolated from the eggs of *Ciona intestinalis* and *C. savignyi* [412]; the synthesis of **595** allowed to define completely the structure and to provide further biological studies [413]. Spermatozoa of the ascidian *C. intestinalis* are slightly motile when suspended in seawater. However, when an unfertilized egg is set in the sperm suspension, the spermatozoa near the egg are intensely activated and being to show chemotactic behavior toward the egg. A method was established for quantitative analysis of sperm chemotaxis and clearly showed that the chemotactic

behavior of *Ciona* sperm is controlled by the “chemotactic turn” associated with decrease in concentration of SAAF [412]. Kachelokelose (**596**), an unusual sulfated mannose polysaccharide with anti-HIV activity in vitro has been found in *D. molle* [414].



5.8 Study Questions

1. Which structural features of pyridoacridine alkaloids could be principally related to their capacity of intercalate into DNA and cleave the DNA double helix or inhibit the action of topoisomerase II?
2. All complex β -carbolines isolated from tunicates have been considered to be biogenetically related, being derived from tryptophan and a second amino acid. Which amino acid, in addition to the primary biosynthetic precursor tryptophan, could be involved in a plausible pathway leading to eudistomin Y4 (**62**)?
3. Propose a plausible biogenetic pathway for clavaminols A (**285**), G (**291**), and H (**293**), respectively.
4. Explain why the structural features of tunichromes and the related halocyamines could be strongly indicative of their role in vanadium accumulation and reduction in ascidian blood cells.
5. Explain why the occurrence of identical and/or biosynthetically related compounds in collections of different organisms raises a question about the real producer of the metabolites.

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Part 2

Structure Elucidation of Marine Natural Products

The Role of Databases in Marine Natural Products Research

6

John Blunt, Murray Munro, and Meg Upjohn

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J. Blunt (✉) • M. Munro

Department of Chemistry, University of Canterbury, Christchurch, New Zealand
e-mail: john.blunt@canterbury.ac.nz, murray.munro@canterbury.ac.nz

M. Upjohn

Physical Sciences Library, University of Canterbury, Christchurch, New Zealand
e-mail: m.upjohn@gmail.com

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Abstract

Access to suitable databases is essential for the rapid dereplication (assessment of novelty) of crude extracts in natural product research. The efficiency of this dereplication process relies heavily on the interpretation of molecular mass, molecular formula, UV, and NMR spectral data. In this chapter, the availability and the suitability of the available databases for dereplication is critically examined. The chapter concludes with examples of dereplication strategy based on available natural product databases.

6.1 Dereplication

One definition of dereplication is the *differentiation of novel metabolites from known compounds in a natural products extract*. The task of dereplication then is one of instituting approaches that achieve this differentiation as quickly and as efficiently as possible. An added bonus is if the process can be achieved on as small a scale as practical. How difficult a task is this? As of June 2011, the *DICTIONARY OF NATURAL PRODUCTS* [1] listed 159,670 unique naturally occurring compounds. In November 2009, the suggested number of natural products in the CAS database [2] was 250,000 while in *REAXYS* [3] the number was 170,000. While a definitive figure is not possible, it is not unreasonable to assume that there are most probably 175,000 natural products that have been isolated and characterized to date. Thus, the probability that a crude natural products extract will contain new compounds is not high. The history of marine natural products does not extend back as far as that of their terrestrial counterpart, but there are at least 22,000 marine natural products, again offering high odds against the discovery of new compounds. To effectively undertake dereplication of a crude natural product extract, it is first necessary to obtain definitive information about each component of interest in the extract and then compare those data against appropriate chemical and natural product-based databases. The efficiency of this process is very much a function of the quality and accessibility of the relevant data in the available databases. This chapter is focused on surveying the available databases and examining the requirements for dereplication.

6.2 Natural Products Databases

Access to appropriate databases is essential for the efficient study of (marine) natural products whether the aims be the discovery of new compounds, the synthesis of known compounds or analogues, analysis of data relating to taxonomy and distribution of

Table 6.1 A compiled list of databases dealing with natural products

Public domain	Private domain	Commercial
CHEMSPIDER [19]	ALL PHARMA	CAS REGISTRY [2, 4–6]
CSLS [18]	GVK BIOSCIENCES NPD [40]	SPECINFO [11]
PUBCHEM [17]	UC UV DB [24]	REAXYS [3]
NMRS SHIFT DB [25]	DTU UV DB [22]	ACD/LABS [13]
NAPROC-13 [26]	MARINE NP DB [41]	NAPRALERT [20]
SUPER NATURAL [27]	INTERMED UV DB [42]	DICTIONARY OF NATURAL PRODUCTS [1]
SDBS [28]	INTERMED NMR DB [42]	DICTIONARY OF MARINE NATURAL PRODUCTS [8]
	NOVARTIS IR DB [43]	ANTI BASE [10]
	NATIONAL CENTRE PLANT METABOLISM [44]	MARINLIT [12]
	CH-NMR-NP [45]	ANTI MARIN [14]

compounds and source organisms, or studies on bioactivities to name but a few. There are specialized databases of chemical literature, X-ray crystal structure data, NMR spectra, reactions, physicochemical, and bioactivity data. Private domain, free access, and commercial databases abound with an array of different content, coverage and access restrictions. A selection of those considered most relevant is depicted in Table 6.1.

Recent developments in open access and open source resources have generated a rapid increase in the amount of publically available chemical information and the development of sophisticated, free tools to extract these data. Research funded by the US National Institutes of Health (NIH), the Wellcome Trust (British), the Italian National Institute of Health (ISS), the European Research Council, and many other research institutes and universities is required to be made available through a publically accessible repository after acceptance for publication. Freely available data from sources like these provide the core content of other open access databases with specialized search capabilities.

Private Domain databases are those that have been commented on or alluded to in the primary literature. Undoubtedly, there are many more Private Domain databases than those listed in Table 6.1. For dereplication, it is unfortunate that these sources are not generally available as they would be invaluable and would give access to collections of data not otherwise available. The classic examples of this sort of resource are those databases that have been generated by the pharmaceutical companies. Pharmaceutical companies maintain their own extensive libraries of resources, but these are strictly private and inaccessible to other researchers. None of the Private Domain databases will be surveyed here.

There are commercial databases available that contain sufficient substances, data about them, and search capabilities to serve the needs of natural products dereplication, but there is enormous variation in accessibility and fee structure

for access to these resources. Most are very expensive, but academic discounts are often available and pricing options are sometimes offered, catering to occasional users or to those who only need access to a portion of the data. The more expensive of these databases have very broad coverage and contain bibliographic entries and substance information of interest to a wide range of users other than natural products chemists or biologists. The less expensive databases are naturally smaller and more specialized, but among these are resources that provide access to the most comprehensive publically available collections of natural products and they are particularly suited to the process of natural products dereplication.

The challenge is to select a database that returns the best quality and quantity of return for the time and money involved in extracting the needed data. For a commentary on relative costs, see [Sect. 6.9](#). The following discussion describes some of the attributes of the more significant of these commercial and open access databases.

6.3 Commercial Databases

6.3.1 CAS REGISTRY and CAPLUS

Undoubtedly, the most comprehensive compilation of information on natural product substances is the Chemical Abstracts Service CAS REGISTRY database in which each substance is identified by a unique CAS Registry Number (RN). Included are chemical structures, trade names, systematic names, synonyms, molecular formula, and calculated and experimental property data. The companion CAPLUS database contains patent and journal article references with abstracts. CAS REGISTRY contains over 63 million organic and inorganic substances, and it is estimated that more than 250,000 of them are natural products [4]. There are a number of options for gaining access to these databases.

6.3.1.1 STN

STN [5] is an online service that provides a single platform for access to over 200 of the most significant science, technology, and patent databases from different suppliers throughout the world, including CAS REGISTRY and CAPLUS. Various means of access include STN Express which permits desktop access to all STN databases. It uses a powerful but complex STN command-language interface that is intended for experienced online searchers. Similar interaction with the selected databases is also provided through a web interface, STN on the Web. For occasional and novice searchers, an easier search interface that uses keywords and Boolean operators (no special command-language is required) is available via web access with STN Easy. An option for one-off search needs is a mediated search to the user's requirements that will be carried out on STN databases by experts who will send the results to the user. This service is available through the FIZ Karlsruhe's search service.

6.3.1.2 SciFINDER

The other major access pathway to the CAS REGISTRY and CAPLUS files is through SciFINDER [6], a database produced by the American Chemical Society. SciFINDER provides a single, graphical interface to access the CAS REGISTRY and CAPLUS databases, as well as CASREACT (a reaction database), CHEMCATS (chemical supplier listings), CHEMLIST (regulated chemical information), MARPAT (Markush structures of organic and organometallic molecules from patents), and MEDLINE (the National Library of Medicine database). SciFINDER is available on subscription as a web-based and/or client-based system.

Access to the CAS REGISTRY database is mandatory in any MNP investigation that produces a supposedly new compound to ensure that what is being claimed as new is indeed the case. The SciFINDER interface is very versatile, permitting searches in various ways to establish the previous occurrence or novelty of a compound, or its similarity to other known compounds. One of the first pieces of experimental information that is often obtained for a compound under investigation is its molecular mass. Somewhat surprisingly, in SciFINDER it is not possible to search directly for all substances with a particular mass, but this result can be achieved by first carrying out a substructure search for all compounds containing C and then refining the search based on mass.

The CAS REGISTRY and CAPLUS files are updated on a daily basis, with data usually being current to within only a few months from publication.

6.3.2 REAXYS

REAXYS [3] contains an extensive repository of experimentally validated data including structures, reactions (including multistep reactions), and physical properties. These data are derived from CrossFire Beilstein, CrossFire Gmelin, and Patent Chemistry Database. While this combined database is primarily designed to meet the needs of synthetic chemists, the easy-to-use web interface is well-suited to the needs of natural products chemists, providing flexible access to information on an estimated 170,000 natural products. The actual number of MNPs in this database is not readily discernable, but is estimated to be quite significant. REAXYS would be particularly valuable to those researchers interested in the synthesis of natural products.

The REAXYS database is updated monthly with data extracted from over 150 journals and from patent offices (US, WO, EP, class C07). The average time from receipt of an article to its inclusion in the database is 6 weeks.

6.3.3 DICTIONARY OF NATURAL PRODUCTS AND DICTIONARY OF MARINE NATURAL PRODUCTS

The Chapman & Hall/CRC Press DICTIONARY OF NATURAL PRODUCTS (DNP) [1] is a structured database holding information on chemical substances including descriptive and numerical data on chemical, physical, and biological properties of compounds, systematic and common names of compounds, literature references,

and structure diagrams and their associated connection tables. DNP is available by annual subscription with desktop data and supporting software on DVD, or access can be obtained through the web-based CHEMnetBASE [7]. Version 20:1 (June 2011) of DNP contained 220,470 entries, of which 159,670 were ascribed to isolated natural products. The additional 60,800 entries were for derivatives of the actual natural products. THE DICTIONARY OF MARINE NATURAL PRODUCTS (DMNP) [8] is a subset of data from DNP based on the biological source of the compounds. DMNP is available as a book with CD-ROM for a desktop version, and also from the web-based CHEMnetBASE. The web version (November 2009) contains 34,685 entries, of which 22,664 are for isolated MNPs, with the balance being for derivatives. The number of isolated MNPs contains a significant number of compounds that were first isolated from terrestrial sources but were subsequently also found in marine organisms. Both the desktop and web-based versions of DNP and DMNP permit flexible searching and reporting options, including substructure searches. Structure results for many compounds do not show stereochemistry in the diagrams. Only the parent compound in a series of related compounds is represented by a stereodiagram, while the related compounds can be viewed as planar diagrams with text descriptions of the variations in configurations. Linear peptides are shown as sequences rather than as diagrams. A recent reviewer of DMNP found issue with a number of the offered features of the electronic dictionary [9]. Updated DVD and CHEMnetBASE versions of DNP are released every 6 months, while the CHEMnetBASE version of DMNP is updated annually. Each release has data current to within 6–12 months of publication.

6.3.4 ANTI_{BASE}

ANTI_{BASE} 2011 [10] is a comprehensive desktop database of 36,000 natural compounds from microorganisms and higher fungi. ANTI_{BASE} includes descriptive data (molecular formula and mass, elemental composition, CAS registry number), physicochemical data (melting point, optical rotation), some spectroscopic data (UV, ¹³C- and ¹H-NMR, IR, and mass spectra), biological data (pharmacological activity, toxicity), information on origin and isolation, and a summary of literature sources. A feature of ANTI_{BASE} is the use of predicted ¹³C-NMR spectra (SPECINFO [11]) for those compounds where no measured spectra are available. This database is becoming increasingly important for MNP investigations as more MNPs are discovered from microorganisms where the overlap between “marine” microorganisms and “terrestrial” microorganisms can be difficult to determine. Having knowledge of the chemistry of terrestrial microorganisms is therefore highly desirable. ANTI_{BASE} is updated annually with data current to within only a few months of publication.

6.3.5 MARIN_{LIT}

With the exception of CAplus, all of the databases described above are compound-centric. MARIN_{LIT} [12] is a desktop database comprising records relating to

publications covering all aspects of MNP research. Thus, not all entries contain information on newly isolated MNP structures, but they may cover aspects of synthesis, biosynthesis, ecological studies, bioactivity investigations, reisolation of known compounds, and also reviews. MARINLIT currently has 24,000 records of publications, of which 8,500 describe 22,000 structures for compounds isolated for the first time from marine sources. All records contain the usual bibliographic information, an extensive list of keywords, and where appropriate, taxonomy, structures, MW, formulae, UV data, and calculated (ACD/Labs [13]) ^1H and ^{13}C NMR chemical shifts. Very flexible searching and reporting options are available for combinations from all of these data fields including substructure searching. A unique feature in MARINLIT (and ANTIMARIN – see below) is the inclusion of searchable data fields containing the numbers of each structural feature (^1H -SF) that can be determined from inspection of the ^1H -NMR spectrum of a compound. These features include the numbers of methyl groups of various types – singlets, doublets, triplets, or -OMe, -NMe, -SMe, etc., types of substituted benzene rings, and numbers of $\text{sp}^2\text{-H}$, $\text{sp}^3\text{-CH}$ or $\text{sp}^3\text{-CH}_2$ groups to name a few. The value of this feature for MNP dereplication and discovery investigations will be described later in this chapter. MARINLIT updates are released twice each year with the data being current to within 1–2 months of publication.

6.3.6 ANTIMARIN

ANTIMARIN [14] is available to current subscribers to both ANTI-BASE and MARINLIT. It is a compound-centric desktop database containing data for 53,000 compounds from ANTI-BASE and MARINLIT. The compound data from each database is enhanced by the inclusion of searchable data fields containing the numbers of each structural feature that can be determined from inspection of the ^1H -NMR spectrum of a compound, as described above for MARINLIT. This combined database with the structural features data included provides a valuable tool for the process of dereplication, as described later in this chapter. ANTIMARIN is updated annually with data current to within a few months of publication.

6.3.7 Spectroscopic Databases

While the previously described databases contain some spectroscopic data for compounds, or at least reference to the source of experimental spectroscopic data for a compound, there are other databases dedicated to the cataloging and/or calculation of spectroscopic properties. Access to these data can be particularly helpful in the investigation of MNPs, either to establish that the experimental data obtained in an investigation is the same as that previously found for a proposed structure, or to determine if the observed data for a new proposed structure is reasonable. The following descriptions do not include packages that attempt to generate a structure from experimentally obtained data.

6.3.7.1 SPECINFO

SPECINFO [11] is a spectroscopic database whose primary aim is to assist with spectral interpretation and structure elucidation. These functions are supported by facilities for searching the database for compounds with NMR and/or IR spectra, or fragments of spectra, matching the experimental data. Additionally, compounds can be searched for using structures or substructures or other structurally related information such as CAS numbers. NMR spectrum prediction for a proposed structure is also an integral part of SPECINFO. These capabilities are supported by a knowledge base of 359,000 ^{13}C NMR spectra, 130,000 ^1H NMR spectra, 90,000 heteroatom (^{15}N , ^{17}O , ^{19}F , ^{11}B and ^{31}P) NMR spectra, 139,000 mass spectra, and 21,000 IR spectra.

6.3.7.2 ACD/Labs

ACD/Labs [13] provide a collection of software packages directed principally at the handling and processing of experimental data, mostly spectroscopic. For the natural products chemists, the packages of most interest would be the HNMR and CNMR Predictors. These permit the calculation of ^1H and ^{13}C NMR spectra from user-inputted structures. These Predictors utilize algorithms based on more than 1.7 million assigned ^1H chemical shifts from more than 210,000 chemical structures and 2.5 million assigned ^{13}C chemical shifts from about 200,000 chemical structures. Use of these Predictors can be very helpful for comparing the calculated spectra for a proposed structure with the experimental data to assess the feasibility of a proposed structure. Further tools are available in ACD/NMR Workbook for more direct comparisons of calculated 2D spectra with the experimental spectra, again assisting with the verification of a proposed structure. Of particular relevance to MNP chemists are the internal databases in the Predictor packages. These contain the published chemical shift data for $\sim 240,000$ compounds. These data are only entered into the internal databases after a rigorous analysis of the data to establish that the assignments as published are consistent with those arrived at by calculation. Presently, over half of the marine natural products have their data included in the internal databases, and these data are being added to on a regular basis so that the proportion of MNPs contained in the internal databases will eventually be much higher. Currently, the ACD/Labs-calculated ^1H and ^{13}C NMR chemical shift data for all MNPs are accessible from within MARINLIT, as described earlier. Additional useful data in the internal databases are the original references, solvents, frequency, NMR techniques, molecular formulae, molecular masses, IUPAC names, and trivial names, all of which can be searched, viewed, and printed.

6.4 Free Access Databases

There are now over 50 databases with free access to chemical structures from various sources [15, 16]. However, of more use to natural products chemists are

those databases containing compound data collected from a wide range of other open access or proprietary databases. In general, these combined databases contain the chemical structures and a limited amount of other associated data but do not refer to the source of the compounds. They do, however, provide links to the source database from which the data were compiled, and thus allowing the user to make their own arrangements for access to the complete information relating to a compound. A particularly valuable feature of these combined databases is that they allow the user to determine if a structure may have been previously characterized, although this will not be a complete substitute for verifying novelty of a compound as necessary through the use of the CAS REGISTRY. In general, these databases do not provide comprehensive classification of compounds that might be natural products. It is not possible to describe all of the databases that are available, and the following descriptions are for those that are likely to be the most generally useful for natural products studies.

6.4.1 PUBCHEM

PUBCHEM [17] includes substance information, compound structures, and bioactivity data in three primary databases: PC Substance, PC Compound, and PCBioAssay, respectively, with data collated from over 80 other databases. PC Compound contains more than 25 million unique structures.

6.4.2 CSLS

The Chemical Structure Lookup Service (CSLS) [18] can be regarded as an address book for chemical structures. It has two major modes of operation: The first mode permits the submission of one or more chemical structures in the form of an SD file, as SMILES strings, or in one of more than 20 other molecular structure formats that CSLS understands. The service will determine whether the submitted structures are present in any of the databases that are currently indexed in CSLS. The second mode allows the submission of a document, from which CSLS will attempt to extract all possible chemical information that this document might contain – InChI string, InChIKey, SMILES string, molecular formula, or NCI/CADD Structure Identifiers (uuuuu, FICuS, or FICTS). It then conducts a search with these extracted chemical data. There are 74 million entries in CSLS collated from about 100 databases, representing 46 million unique structures. In the classification section of CSLS, there is a check box for natural products. However, this refers to about 124,000 entries from the NCI Frederick NP database, of which only about one third are actual natural products. An additional 8,000 natural product structures from the CHMIS-C database are included in this section.

6.4.3 CHEMSPIDER

CHEMSPIDER [19] is a compound-centric search engine and database, now being developed under the auspices of the Royal Society of Chemistry, which is aggregating and indexing chemical structures and their associated information into a single searchable repository. This database aims to capture and manage chemical structures from online resources, from commercial databases, and from users of the CHEMSPIDER platform who have the ability to submit their own data. Users can access the open access data immediately and where possible, the CHEMSPIDER search engine also provides links to commercial resources that contain information matching the users' query. Many additional properties have been added to each of the chemical structures thus enhancing the value of the collection. These include spectral data, links to publications, reaction synthesis details, and various experimental properties. For MNP researchers, perhaps the greatest value will be to determine if there is any information available about a compound of interest. Access to CHEMSPIDER is without charge. Of particular value is the ability to search by substructure, a feature that is not available in CSLS. Currently (2011), there are in excess of 26 million unique entries in CHEMSPIDER from over 300 data sources. There are numerous cases of the same natural product in the database with various levels of partial to complete stereochemistry as provided by a number of the depositors. Members of the CHEMSPIDER team are focused on curating the structure collection. The information in CHEMSPIDER is updated daily as a result of new compound depositions and curation activities, but the currency and accuracy of the data is only as good as that of the databases from which the data is sourced.

6.5 Approaches to Dereplication

In a dereplication exercise, a minimal set of must-know data would include the molecular masses (and molecular formulas) of the components of the mixture, relevant UV data and, if possible, ^1H NMR spectra. The taxonomy of the organism, although very useful, is not an absolute requirement.

The molecular mass and UV data can be generated from an LC/MS analysis of an aliquot of the crude extract using Diode Array Detection (DAD) in combination with electrospray mass spectrometric analysis (ESMS). Under high-resolution conditions (LC/HRESMS), the individual molecular formulas of the components can be obtained. With access to a CapNMR probe or small-tube cryoprobe, it is now possible to obtain a good ^1H NMR spectrum of individual components from the same LC run (see Sect. 6.8). The ideal situation would be to use this minimal set of data, perhaps in combination with taxonomic data if it is available, and make a definitive identification of the compound as either new or known. Of course, there are other ways that

this minimal data set could be generated, for example, by chromatography on the crude extract followed by MS or HRMS, ^1H NMR, and UV measurements on the isolated individual components. Taxonomic identification of marine organisms can be fraught with difficulties, but this knowledge undoubtedly can be of assistance.

6.5.1 Selection of Database

Not all of the natural product databases suggested (Table 6.1) can give definitive answers using part, or even all of this suggested data set. In Table 6.2, a “filtered” list of databases has been provided listing the attributes and the data that can be extracted readily.

In Table 6.2, the databases are arranged from the largest (CAS REGISTRY) to the smallest (MARINLIT). The smaller databases, from NAPRALERT [20] downward, are the dedicated natural product databases. The number of natural products in each database has been listed. In the larger databases such as SCIFINDER and REAXYS this is an estimate only. With the exception of NAPRALERT all of the databases are kept current, or within a few months of current. NAPRALERT’s coverage of MNPs since 2004 has been sporadic only and for this reason has not been covered in this chapter. Within the range of databases in Table 6.2, molecular formula-based searches are possible and, with the exception of CSLS, it is possible to search on a molecular mass range, although doing so within SCIFINDER is not obvious as it is first necessary to have generated a subset from SCIFINDER that contains all compounds containing C and then to initiate a search using the molecular mass range of interest as a filter. All of the databases except NAPRALERT are capable of carrying out substructure searching. This is a particularly helpful feature for using recognizable fragments in searches. These fragments can arise from interpretation of NMR and/or MS data. As well, taxonomic and biological activity data can be searched in most of the databases listed. The distinction between the utility of the various databases comes when the availability of actual UV and NMR data is considered. For UV data (λ and ϵ), the two DICTIONARIES and MARINLIT contain this data with partial coverage included in NAPRALERT, ANTIMARIN and ANTI-BASE. For NMR data within this group of databases, δ_{C} values are searchable within MARINLIT. The only databases available that can provide spectral data are MARINLIT and ANTI-BASE. Through an arrangement with ACD/Labs, *calculated* ^1H , ^{13}C chemical shift data and HSQC/DEPT spectra are accessible in MARINLIT. This is a facility that is particularly useful for comparing actual data from a potential new compound against data that have been generated for known compounds. The last NMR feature listed in this figure is ^1H NMR Structural Features (^1H -SF). This is a unique aspect for searching ^1H NMR data for matching features and is only available using the MARINLIT or ANTIMARIN databases. As noted earlier, these two databases include searchable data fields containing the actual numbers of each

Table 6.2 A “filtered” list of databases that are of potential use for the derpickation of (marine) natural product extracts

DATABASE	Number of compounds ^a				Current up to	NMR data ^b							
	Total	Natural products	MW	MF		UV ^c λ	SSS ^d	Tax. ^e	Biol. ^f	δ	Spectra	¹ H-SF	HSQC/DEPT
CAS REGISTRY	6.3×10^7	~250,000	+ ^g	+	Current	+	+	+	+	-	-	-	-
CSLS	4.6×10^7	?	-	+	Current	+	+	-	?	-	-	-	-
CHEMSPIDER	2.6×10^7	?	+	+	Current	+	+	-	-	-	-	-	-
PUBCHEM	3.7×10^7	?	+	+	Current	+	+	-	+	-	-	-	-
REAXYS	$>10^7$	170,000	+	+	Current	+	+	-	+	?	-	-	-
NAPRALERT		$>150,261$	+	+	~2004	+	+	+	+	+	-	-	-
DICTIONARY OF NATURAL PRODUCTS		159,670	+	+	2011	+	+	+	+	+	-	-	-
ANTIMARIN		43,000	+	+	2010	+	+	+	+	+	-	-	+
ANTIBASE		36,000	+	+	2010	+	+	+	+	+	+	+	-
DICTIONARY OF MARINE NATURAL PRODUCTS		22,691	+	+	2006	+	+	+	+	+	-	-	-
MARINLIT		22,000	+	+	2011	+	+	+	+	+	+	+	+

^aWhere possible an estimate is given for the number of natural products in the database^bFour options for NMR data: the δ values (calculated or actual), spectra, ¹H NMR structural features (¹H-SF) or calculated HSQC/DEPT spectra^cActual λ(ε) values for UV data as opposed to a reference to the data^dSub-structure searching capability^eTaxonomic data^fBiological activity data^gIn the current version of SciFinder the extraction of molecular mass data is not straightforward^hPartial data only

structural feature that can be deduced from the ^1H NMR spectrum of a compound. For example, the numbers of methyl groups of various types – singlets, doublets, triplets, or *-OMe*, *-NMe*, *-SMe*, etc. This unique feature, in combination with mass and perhaps UV data, is very effective in discriminating between alternative structures in the dereplication process, as will be described in Sect. 6.6.

6.5.2 Dereplication Based on Molecular Mass/Molecular Formula

An early step in dereplication is to obtain the MS of compounds isolated by chromatography of the crude extract or by running an LC/MS experiment on the crude sample. Depending on the resolution and/or mode of the MS or LC/MS, two outcomes are possible. If the MS, typically ESMS, has been run under low resolution conditions ($<1:5,000$) then unit mass differentiation is possible. That is the distinction between say m/z 490 and 491. Under higher resolution conditions, the actual molecular formula can be obtained. For example, $\text{C}_{30}\text{H}_{50}\text{O}_5$ which has $m/z = 490.3658$. Either or both of these outcomes can be searched in databases. The results of such a search are shown in Table 6.3. Even for the more specialized databases, the number of “hits” recorded is often too great even when searching for a molecular formula. Sometimes molecular mass data is all that is available, but that alone is not a good discriminator. Ideally, less than ten hits is an acceptable number.

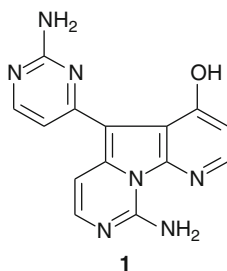
If a new compound that has an unusual or a unique molecular formula, obtaining the molecular formula may be all that is necessary to identify it as a new compound. That was the case with variolin B, a bioactive alkaloid isolated from the Antarctic sponge *Kirkpatrickia variolosa* [21]. Variolin B (**1**) had a molecular formula of $\text{C}_{14}\text{H}_{11}\text{N}_7\text{O}$. At the time a search of the specialist natural product databases gave zero hits thus establishing that this was a new compound. Nearly 20 years later,

Table 6.3 Search of relevant databases from both free access and commercial sources for molecular mass and molecular formula data

Database	m/z 490–491	$\text{C}_{30}\text{H}_{50}\text{O}_5$ (m/z 490.3658)
CHEMSPIDER	58,938	173
CAS REGISTRY	171,904	2,366
CSLS	na ^a	250 (81NP's)
DICTIONARY OF NATURAL PRODUCTS	653	292
DICTIONARY OF MARINE NATURAL PRODUCTS	94	44
MARINLIT	78	35
ANTIMARIN	118	43

^aIt is not possible, at this stage of development, to search CSLS for molecular mass information. Molecular formula searches can be carried out and 250 matches found with 81 of these in the Natural Product section of the database

MARINLIT still records variolin B as the only compound with that molecular formula while in SciFinder there are 79 compounds recorded with that molecular formula. However, it is usually necessary to have more than just molecular mass/molecular formula data for the dereplication process.



When dealing with natural product extracts, there can be problems and uncertainty in obtaining reliable molecular mass/molecular formula data. This could arise because:

- the mass spectrometry sample is only one or two fractionation steps removed from the crude extract, and there are multiple candidates for the supposed molecular ion from impurities;
- such impurities could dominate the ionization giving misleading results;
- there can be ionization suppression problems from traces of TFA (often used as a polar modifier in HPLC);
- of ready fragmentation, even under ESMS conditions;
- of formation of adduct ions (MNa^+ , MNH_4^+ , etc.).

Some of these problems have been very nicely addressed by a group at the Danish Technical University group who, in the area of mycotoxins and fungal metabolites, compiled a database of 474 compounds using standardized HPLC/UV/MS methodology [22] (see Table 6.1).

6.5.3 Dereplication Based on UV Data

UV profiles or maxima are readily acquired using a Diode Array Detector (DAD) as part of the LC or LC/MS examination of a crude extract. That the data are semiquantitative at best is not relevant. What is important are the actual profiles, or the maxima (λ_{max}), as the chromophores that lead to these spectral properties are distinctive and can be searched for. The UV spectra and λ_{max} are indicative of a *chromophore* within a structure, not necessarily the structure itself and therefore offers clues as to potential substructures that can be searched for, for example, the 1,2,3,5-tetrasubstituted aromatic system characteristically found in compounds of polyketide origin. Compounds containing this chromophore have a characteristic UV profile with

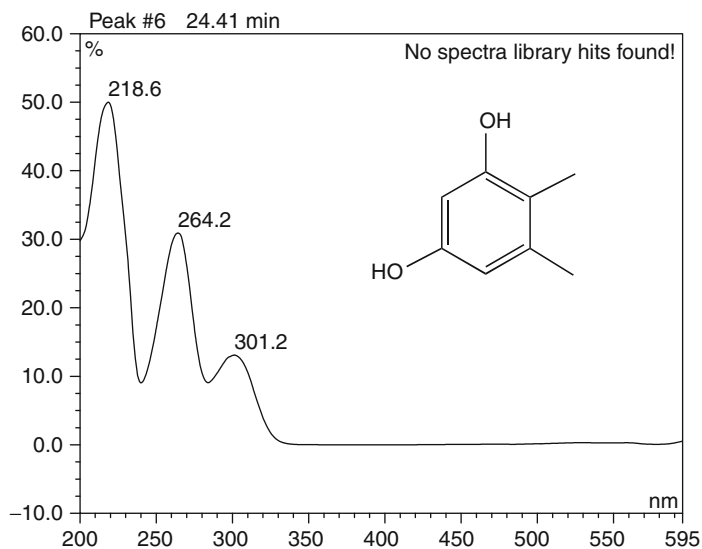


Fig. 6.1 The characteristic UV profile of a 1,2,3,5-tetrasubstituted aromatic system

λ_{\max} at around 220, 265, and 300 nm (see Fig. 6.1) that is easily recognizable. Using UV data with mass data is a powerful and cheap method of dereplication. The one major drawback to this approach is that not all compounds contain UV chromophores.

6.5.3.1 UV λ_{\max} Data

Among the natural product databases, a number contains searchable UV λ_{\max} data, though in some cases this is partial coverage only (see Table 6.2). An example of this approach to dereplication is work that was carried out on a bioactive extract obtained from the deep-water sponge *Lamellomorpha strongylata* [23]. All of the bioactivity associated with this extract eluted in the early fractions from an LH-20 column (higher molecular mass compounds) and the two components in these early fractions each had identical and characteristic chromophores (see Fig. 6.2).

A search was made in MARINLIT using the following search profile: Phylum = Porifera; Mass range 750–2,000; UV = 340 (see Fig. 6.3). The database returned 16 matches from 22,000 possible compounds. Within MARINLIT it is possible to select a second UV maxima and refine the search. This was done using the second maxima at 226 nm and resulted in just nine compounds that matched. All but one of these compounds were calyculin derivatives. Based

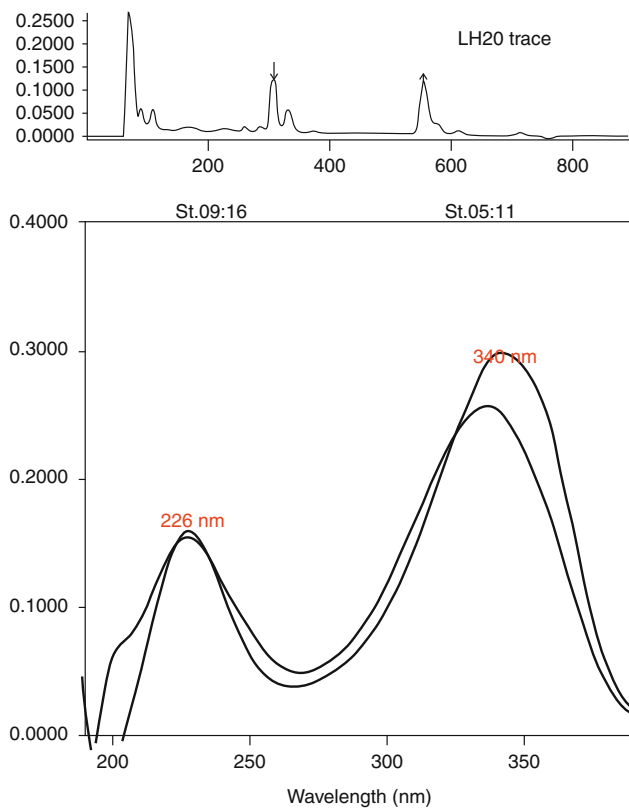


Fig. 6.2 HPLC trace (detection at 340 nm) and extracted UV data for the peaks at 320 and 550 s from an LH-20 column (Fraction 1)

on these data, the two bioactive compounds from *Lamellomorpha strongylata* were rapidly identified as calyculin A and a new, but related compound, calyculinamide A (**2**).

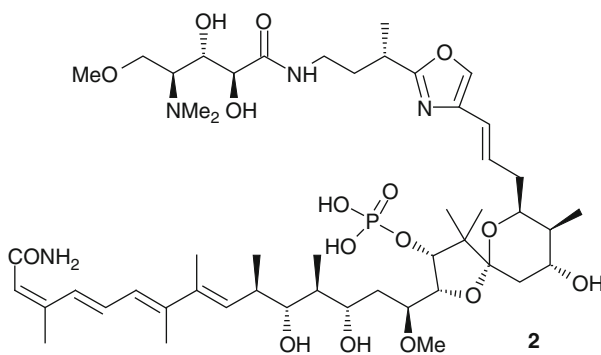


Fig. 6.3 Search profile in MarinLit

The screenshot shows a web-based search interface titled "Search Profile". It is organized into four vertically stacked sections, each with a colored border and a text input field:

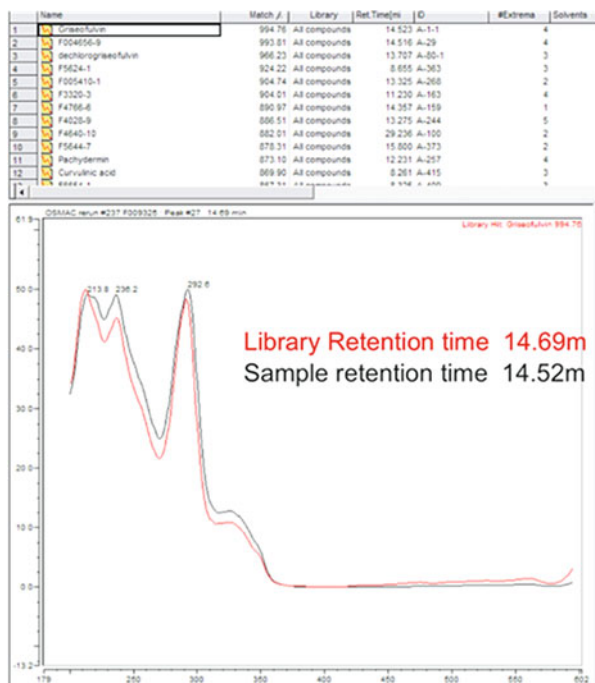
- BIBLIOGRAPHIC DATA** (blue border): An empty text input field.
- COMPOUND DATA** (green border): Labeled "AND (AND operations only)". The input field contains the text "Mass FROM 750 TO 2000 AND UV max = 340e5".
- TAXONOMY DATA** (purple border): Labeled "AND (OR operations only)". The input field contains the text "Phylum IS Porifera".
- SUBSTRUCTURE** (red border): Labeled "AND". The input field contains red text instructions: "Enter substructure in ChemDraw window, select, use command c to put structure on clipboard, then double click on Gen" (with a "Gen" button) and "Paste substructure into Subs.pct window, and then close Subs.pct window.".

On the right side of the interface, there are three buttons: "clear all", "do search", and "home screen".

6.5.3.2 UV Spectra

There is considerably more information contained in the UV spectrum than just the λ_{\max} data. Matching spectra is a superior and more definitive approach to the use of UV spectra in the dereplication exercise. Such approaches have been commented on in the primary literature, and it can be assumed that all pharma carrying out natural product research and quite a number of other natural product laboratories have in-house UV spectral databases. Unfortunately, no UV spectral databases that also contain other information essential to the dereplication process are available. Apart from privacy and IP issues, a major difficulty is the platform to be used for comparing the spectra. Most modern HPLCs have the necessary software for capturing and comparing UV acquired spectral data, but not for comparing that data with spectra acquired on other HPLCs. For the past 10 years in the Marine Group at the University of Canterbury, all UV data from all extracts is archived in a searchable library (All Compounds). Once the identity of compound is established, the UV profile is added to a second library (Known Compounds). As all HPLC runs have been carried out using the same solvents, column manufacturer, and gradient profile the retention times as well as the UV profiles of unknowns can be run against the library and, frequently, unknowns can be identified by UV/retention time correlations only [24]. An example illustrates just how useful this approach can be for compounds with distinctive UV chromophores. By this approach, griseofulvin was identified as a metabolite from a marine fungus (see Fig. 6.4). Note the close match between the retention times of the unknown and the reference sample as well as the comparable UV spectra. The library provides a score, out of 1,000, for the closeness of the spectral match – the griseofulvin score was 994. As appropriate, the retention time window can be widened or eliminated altogether in order to match against the UV spectrum only.

Fig. 6.4 DAD UV spectrum of griseofulvin compared with that stored in the known compounds library



6.5.4 NMR-Based Approaches to Dereplication

^1H NMR spectra are rich in structural information, which in combination with 2D homo- and heteronuclear experiments, molecular mass, molecular formula, and UV data lead to structural assignments. Inherently, there are two drawbacks to the routine use of NMR techniques for dereplication purposes where a rapid answer to the question of novelty is required. The first of these is sensitivity. Of the spectroscopic techniques routinely used in organic structure determination, NMR spectroscopy is by far and away the least sensitive. The limit of detection for routine mass spectrometers is in the 1–10 pg range (10^{-12} g), that for UV spectroscopy 100–1,000 pg, while for most routine NMR spectrometers, 500–1,000 μg are required for ^1H NMR measurements and about five times that for ^{13}C NMR spectroscopy. In recent years, the limit of detection for ^1H NMR has dropped to 1 μg using specialist probes (see Sect. 6.8). This is still 10^6 times less sensitive than mass spectrometry. The implications are that it is possible to obtain excellent LC/MS and associated UV data by the analysis of micrograms of crude extract, but to get NMR data on the components of a crude extract, it is necessary to process mgs or even grams of crude extract.

The second drawback is that of complexity. In order to derive substructures for database searching, interpretation of the 1D and 2D NMR data is required.

Depending on the complexity of the molecule this can sometimes be a complex process, but the derived substructures can then be searched for in any of the natural product databases (Table 6.2). There are also spectral databases available, such as ACD/Labs and SPECINFO, which can be searched to find a match based on molecular formula comparisons. And in the Public Domain arena (Table 6.1), there are other spectral sources that can be searched. These are the likes of NMRSHIFT DB, NAPROC-13, SUPERNATURAL and SDBS [25–28]. From the natural product databases listed in Table 6.1, only ANTI-BASE and MARINLIT have searchable NMR data. MARINLIT, in an arrangement with ACD/Labs, can provide calculated ^1H and ^{13}C chemical shift data for any of the individual compounds in the database along with ^{13}C and HSQC/DEPT spectra based on the ACD predictors (see Sect. 6.3.7.2), allowing the ready checking of actual NMR data against that stored for individual compounds in MARINLIT identified using other parameters. MARINLIT also allows for the direct searching of the database for individual or a series of ^{13}C chemical shifts. ANTI-BASE provides partial lists of actual or calculated ^1H and/or ^{13}C NMR data which are also searchable.

ANTI-MARIN is a combination of parts of the MARINLIT and ANTI-BASE databases. Both this combined database and MARINLIT have a search capability that is not readily available in any other database. This is the capability of searching for the actual numbers of functional groups contained within a molecule. Certain features in a ^1H NMR spectrum are immediately obvious and do not need any interpretation to know what they are. The number and types of methyl groups in a molecule would be a good example. Within these two databases, the number and type of methyl group, alkenes, carbinol protons, acetal, formyl, acetyl, amide, imine, aromatic substitution patterns, sp^3 methines, and methylenes and sp^2 H have been extracted and placed in searchable fields. A simple inspection of a ^1H NMR spectrum and integrals immediately allows the identification of many of the classes of functional group listed above, but *with no consideration* of any relative connectivity. Entry of the relevant numbers for each functional group, along with other relevant data such as taxonomy, molecular mass, molecular formula, provides a very effective method for the dereplication of natural products extracts as the ^1H structural features (^1H -SF) aspect built into ANTI-MARIN and MARINLIT is very discriminating.

6.5.4.1 Why ^1H -SF is Discriminatory

^1H structural features (^1H -SF) allows the examination of combinations of structural features in a molecule. The probability of compounds having identical combinations of ^1H NMR features is low, and if these data are also taken in combination with molecular mass, molecular formula and UV data unique search patterns are generated which can quickly establish the novelty of an isolated compound. The page for each compound in ANTI-MARIN displays the relevant UV, MS, and ^1H -SF features for that compound. This is displayed in Fig. 6.5 which highlights features such as the Me groups and the 1,4-disubstituted benzene. The search data are entered via a simple graphical interface comparable to that shown in the figure.

Two simple examples will serve to demonstrate this selectivity. In the first instance, the simple act of counting the number of methyl groups in a compound

The screenshot displays the ANTIMARIN software interface. On the left, a chemical structure of Kodastalin-A is shown with several methyl groups highlighted in colored circles (red, green, blue, yellow). The right side of the interface is a grid of searchable fields, including:

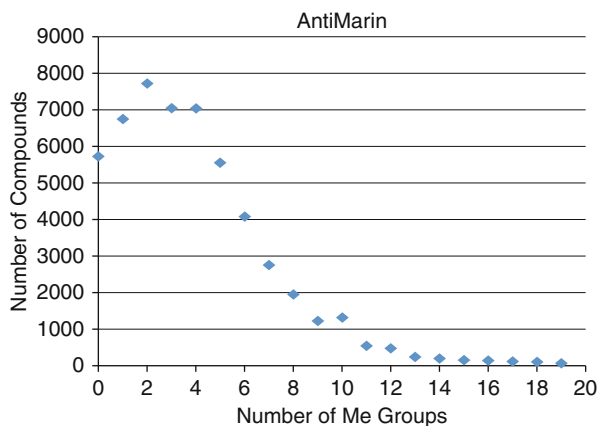
- UV_Neutral: MeOH (292, 45500) (333sh,)
- UV_Basic: (empty)
- UV_Acids: (empty)
- All CH3: 4
- Singlet CH3: 2
- Doublet CH3: 1
- Triplet CH3: 1
- methoxy: 0
- sp3_methylene: 2
- sp3_methine: 2
- all_alkene: 5
- vinyl: 0
- disub11_alk: 0
- trisub_alkene: 2
- all_single_co: 7
- pri_single_co: 0
- sec_single_co: 1
- pri_acetate: 0
- tert_acetal: 0
- all_carbonyl: 4
- aldehyde: 0
- acetyl: 1
- acid_ester: 1
- amide: 0
- B1: 0
- B12: 0
- B13: 0
- B14: 1
- B123: 0
- B135: 0
- B1234: 0
- B1235: 0
- B1245: 1
- B12345: 0
- Py2: 0
- Py4: 0
- Py23: 0
- Py24: 0
- Py25: 0
- Py26: 0
- Py34: 0
- Py234: 0
- Py235: 0
- Py236: 0
- Py245: 0
- Py246: 0
- Py345: 0

Below the grid, the following information is displayed:

- ID Number: 23683
- formula: C₃₅H₃₄O₁₁
- molweight: 630.638
- HRMS: 630.209595
- HRMSP: 631.217407
- HRMSN: 629.202881
- HRMSNa: 653.199402
- Name: Kodastalin-A
- Source: Aspergillus terreus Thom DSM 11847

Fig. 6.5 ANTIMARIN showing a range of the data in searchable fields

Fig. 6.6 Distribution of compounds containing methyl groups in the ANTIMARIN database



is informative. Figure 6.6 shows the distribution of the ~52,000 compounds containing methyl groups in the ANTIMARIN database. Of particular relevance is the large number of compounds (~6,000) with zero methyl groups. The second example focuses on the types of methyl group recognized in the MARINLIT and ANTIMARIN databases. There are eight types in all (singlet Me, doublet Me, triplet Me, -OMe, -SMe, -NMe, vinyl Me, and acetyl Me). For compounds that contain any two methyl

Table 6.4 The distribution of combinations of any two methyl groups in the ANTIMARIN database

	Singlet	Doublet	Triplet	Vinyl	Acetyl	-OMe	-NMe	-SMe
Singlet	1,000							
Doublet	268	1011						
Triplet	153	589	813					
Vinyl	279	385	151	400				
Acetyl	72	168	244	77	93			
OMe	509	435	401	217	148	490		
NMe	78	77	50	30	18	132	223	
SMe	0	4	2	6	5	17	16	91

4 × Me groups (any type) 7,674 hits, or
 1 × formyl group 2,578 hits, or
 1 × 1,4-disubstituted benzene 2,201 hits, or
 1 × 1,2,4-trisubstituted benzene 2,425 hits, or
 1 × 1,2,3,5-tetrasubstituted benzene 3,090 hits

But

4 × Me (any type) + 1 × formyl 358 hits, or
 2 × Me(s) + 2 × Me(d) + 1 × formyl 43 hits, or
 2 × Me(s) + 2 × Me(d) + 1 × 1,4-disubstituted benzene 13 hits, or
 2 × Me(s) + 2 × Me(d) + 1 × 1,2,4-disubstituted benzene 8 hits, or
 2 × Me(s) + 2 × Me(d) + 1 × 1,2,3,5-tetrasubstituted benzene 3 hits

Fig. 6.7 Results from searching on easily recognized functional groups or combinations

groups, 8,385 in the database, there are 36 possible combinations. The distribution from searching all 36 combinations is shown in Table 6.4 and illustrates just how discriminating this approach to dereplication is with all possible combinations of two methyl groups out of eight types being populated to one level or another. That was just using methyl groups as the discriminator. If other easily recognized groups such as formyl, 1,4-disubstituted-, 1,2,4-trisubstituted-, and 1,2,3,5-tetrasubstituted benzenes are now added into the mix, the level of discrimination rises. This is shown in Fig. 6.7. Quite large numbers of possible hits are obtained by searching on individual groups, but by looking at combinations, the number of possible hits is rapidly narrowed (Table 6.4 and Fig. 6.7).

Take the example of the search based on a ^1H NMR spectrum that contained two singlet and two doublet methyl groups and a 1,2,3,5-tetrasubstituted benzene. Using the ^1H NMR data alone, as detailed in Fig. 6.7, the search was narrowed to just three possibilities from 53,000 compounds (see Fig. 6.8) and if low resolution mass data was then added (ESMS: MH^+ $m/z = 321$), the unknown could be tentatively identified as debromohamigeran E (that was originally isolated from the sponge *Hamigera taragensis*) [29]. To confirm that assignment, the original literature would now be consulted and direct comparisons made with the NMR and other relevant spectral data.

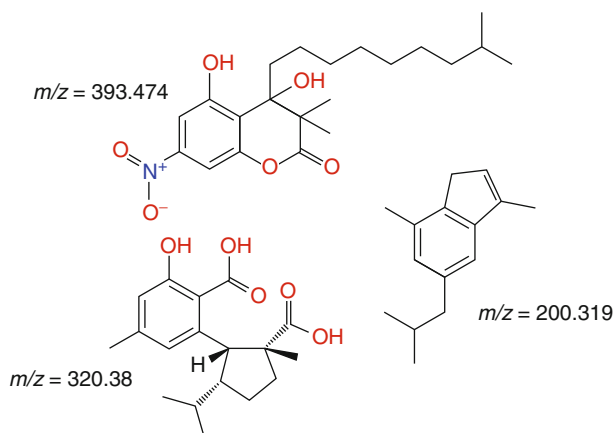


Fig. 6.8 Candidates from search on 2xMe(d) + 2xMe(s) + 1,2,3,5-tetrasubstituted benzene

6.6 Examples of Dereplication

Very seldom is it possible to dereplicate a crude extract without accessing several pieces of information about the components in the extract. Most often these data would be combinations of the source taxonomy, molecular mass/molecular formula, UV, and NMR data. With access to appropriate natural product databases, it is then possible to verify the novelty or not of the components of the extract. In the sections that follow, several worked examples will show how this can be achieved.

6.6.1 Compound Isolated from a Cnidarian

Several compounds were isolated from the crude extract of a cnidarian, possibly a *Minabea* sp. The compound of interest had a low resolution molecular mass of 470, had a UV λ_{max} at 240 nm, and a ^1H NMR spectrum which contained a number of easily recognizable features (see Fig. 6.9).

6.6.1.1 Taxonomy Approach

A search in MARINLIT using Phylum = Cnidaria gave a total of 2,807 articles containing 4,491 compounds. This clearly is not sufficiently discriminating, but if the cnidarian was indeed a *Minabea* sp., the search is narrowed down to just five articles and 21 known compounds. When the mass data of the compound of interest

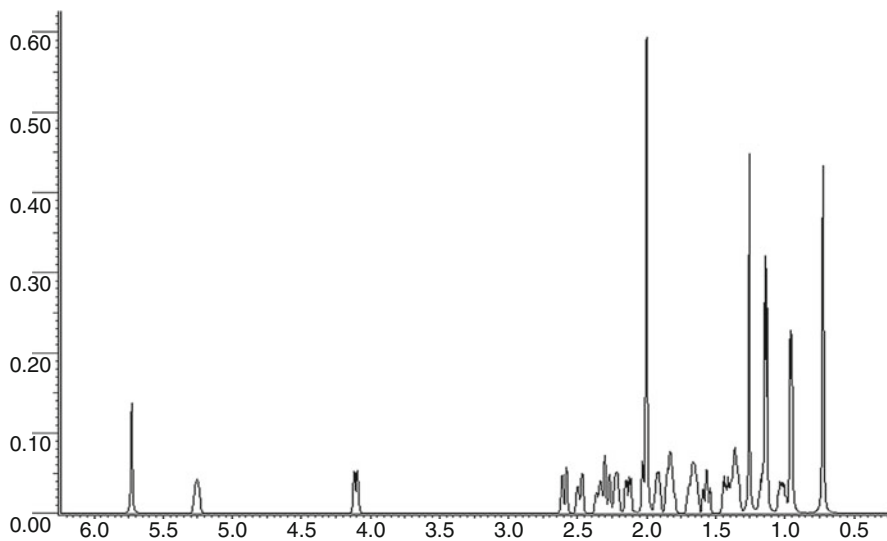
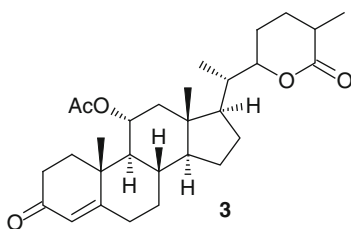


Fig. 6.9 ^1H NMR spectrum of compound isolated from a cnidarian

was searched against the database, four compounds matched and all had the molecular formula $\text{C}_{29}\text{H}_{42}\text{O}_5$. If the UV data, indicative of an $\alpha\beta$ -unsaturated ketone, is added into the profile, only one compound, minabeolide-8 (3), matched. This process would have effectively dereplicated the compound of interest in that extract.



6.6.1.2 Alternative Approaches

If the taxonomic data that in combination with the mass and UV data allowed assignment of structure had not been available, what alternative approaches could have been made? There are several possibilities. Examination of the ^1H NMR data suggests that the compound contains five methyl groups of which three are singlets and two are doublets. Of the singlets, one of these ($\delta = 2.05$) could readily

be assigned as an *-OAc*. Using search profiles in MARINLIT gives the following results:

Cnidaria	2,807 articles/4,491 compounds
Cnidaria + $\lambda_{\max} = 240$ nm	198 articles/355 compounds
Cnidaria + UV + $m/z = 470-471$	5 articles/5 compounds
Cnidaria + UV + $m/z = 470-471 + 5 \times \text{Me groups}$	1 article/1 compound

giving the same answer as before.

An alternative search profile based initially on ^1H NMR data could be

$5 \times \text{Me groups}$	1,774 articles/3,166 compounds
$5 \times \text{Me groups} + 3x \text{ singlet}/2x \text{ doublet}$	264 articles/424 compounds
$5 \times \text{Me groups} + 3x \text{ singlet}/2x \text{ doublet} + 1x\text{-OAc}$	64 articles/77 compounds

If the source phylum is now entered, the number of articles is 42 articles/33 compounds and, finally with the mass data, the numbers drop to 1 article/1 compound.

What if only NMR data were used? There are other resonances that can be used from the ^1H NMR spectrum. For instance, the 1-H resonances at δ 4.2, 5.25, and 5.75 can readily be assigned as $2x\text{-CH-O-}$ and $1x > \text{C} = \text{CH-}$. Using these data produces the following:

$5 \times \text{Me groups} + 3x \text{ singlet}/2x \text{ doublet} + 1x\text{-OAc}$	64 articles/77 compounds
$5 \times \text{Me groups} + 3xs/2xd + 1x\text{-OAc} + 1x > \text{C} = \text{CH-}$	24 articles/26 compounds

If the alternative argument had been used the answer would have been

$5 \times \text{Me groups} + 3xs/2xd + 1x\text{-OAc} + 2x \text{-CH-O-}$	17 articles/19 compounds
--	--------------------------

Using just ^1H NMR data, it was still possible to reduce the number of possible candidates to acceptable levels. Addition of the mass data (m/z 470–471) brought the selection down to one compound from one article.

6.6.2 Dereplication of a *Suberites* sp. Extract

The extract from an Antarctic *Suberites* sp. of sponge collected by SCUBA at 40 m was bioactive against the P388 cell line. The bioactive compound was isolated and partially characterized. The molecular mass was 220.04691 Da ($\text{C}_{10}\text{H}_8\text{N}_2\text{O}_4$), the λ_{\max} was 348, and from the ^1H NMR spectrum, a 1,2,4-trisubstituted benzene

system (doublet, doublet, singlet) and a trisubstituted alkene were recognizable. Notable was the lack of methyl groups in the compound. A search using m/z 220–221 Da in MARINLIT returned 106 matches, but a search with $C_{10}H_8N_2O_4$ gave zero matches and established the possible novelty of the compound. To gain clues as to a possible structural type, the balance of the preliminary structural data was incorporated into a search profile:

λ_{\max} 348	249 matches
λ_{\max} + 0x Me groups	63 matches
λ_{\max} + 0x Me + 1x 1,2,4-trisub. bz	11 matches
λ_{\max} + 0x Me + 1x 1,2,4-trisub. bz + 1x > C = CH–	4 matches
λ_{\max} + 0x Me + 1x 1,2,4-trisub. bz + 1x > C = CH– + m/z 220–221	0 matches

There were matches in the database right up to the point where the mass was entered. If the four matches are now examined (see Fig. 6.10), three can be quickly eliminated on the basis of disparity in mass, leaving one compound that differed by just 1 Da from a known compound: $C_{10}H_8N_2O_4$ (m/z 220) compared with $C_{10}H_9N_3O_3$ (m/z 219) for polyandrocarpamine previously isolated from the Fijian ascidian *Polyandrocarpa* sp. [30] With this structural clue, a hydantoin

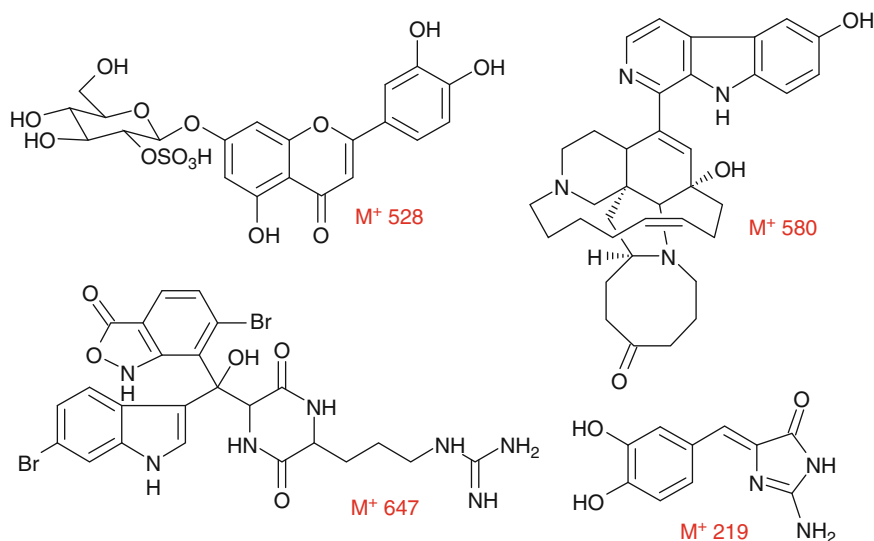
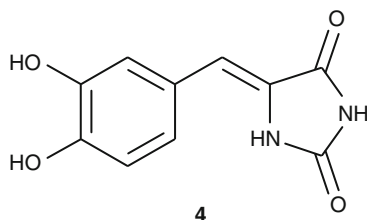


Fig. 6.10 Possible structures matching UV and NMR data from an Antarctic *Suberites* sp.

structure (4) was quickly established for the bioactive compound from the *Suberites* sp.: it was a new compound [31].

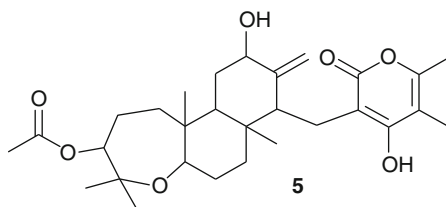


In this instance, just using molecular formula data was sufficient to establish that a new compound had been isolated, but interrogation of the database using other preliminary data gave essential clues as to the identity of the new compound.

6.6.3 Dereplication of an *Aspergillus* sp. Extract

Although not isolated from a marine source, the dereplication of this extract is a good example of the power of the ^1H -SF approach to solving problems. The ^1H NMR spectrum of a bioactive component isolated from the extract of an *Aspergillus* sp. isolated as an endophyte from *Garcinia scortechnii*, a Malaysian medicinal plant, contained seven singlet methyl groups (see Fig. 6.11). As the compound was isolated from a microorganism, the ANTIMARIN database was consulted returning just 387 possible hits out of 53,000 compounds in the database. Consideration of the chemical shift data suggested that of the seven singlet methyl groups, two were vinyl methyls and one an acetoxy group. This refined search reduced the number of hits to five only. If the low resolution mass data (502 Da) was now added, one hit only was returned. Comparison of the ^1H NMR data with published data for this compound (5) [32] established that they were identical and completed the dereplication. The structural elucidation of three further isomers was then trivial based on the established core structure of this unusual triterpene-pyrone [33].

Alternative approaches would have used the low resolution mass data first. That would have given 91 hits reducing to just two if seven singlet methyls were included in the profile of which only one would have matched the ^1H NMR data obtained.



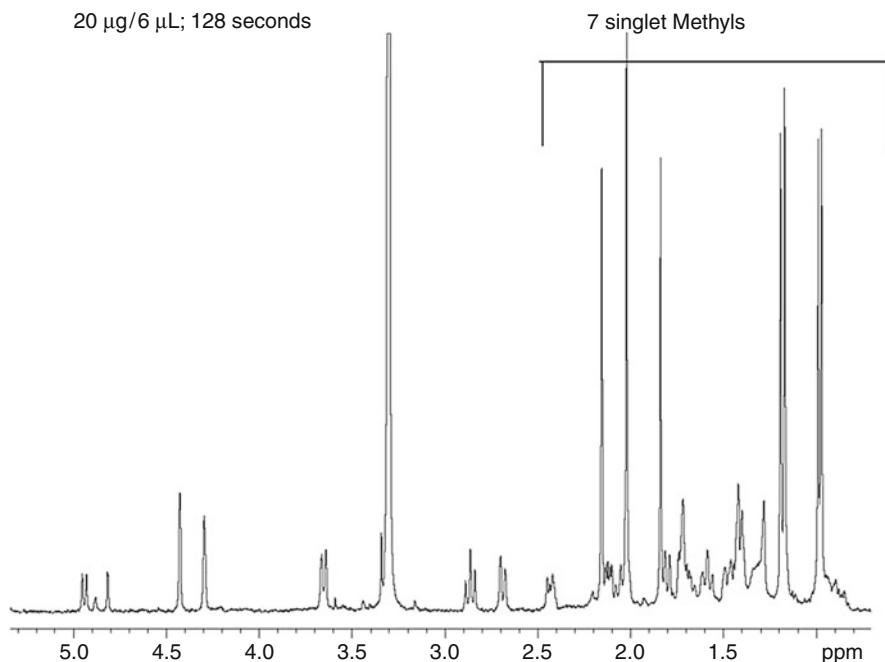


Fig. 6.11 ^1H NMR spectrum for a triterpene pyrone isolated from an *Aspergillus* sp. endophyte

6.7 Commentary on Approaches to Dereplication

In the section above, various approaches to achieving resolution in the dereplication process were considered. The obvious starting point is normally the molecular mass and the molecular formula, but with over 160,000 known natural products, this is not often discriminatory. Adding in taxonomic data can help narrow the dereplication to a class of compound. UV spectral data is a powerful tool in the dereplication process but is not discriminatory as it is the recognition of the chromophore, not the molecule that is occurring, and not all compounds contain chromophores. Fragmentation patterns from mass spectrometry also provide a powerful approach but require experience and skill in interpretation. The MS approach, like that of UV spectroscopy, suffers from a lack of appropriate searchable databases. The ultimate goal in dereplication is full structure determination, but to accomplish that for each and every compound in a crude extract is not a satisfactory approach and requires acquisition and interpretation of full sets of 1D and 2D NMR data in addition to relevant mass and UV data. Such a conventional approach to dereplication is shown diagrammatically in Fig. 6.12a. The alternative approach, as outlined above, is to more productively use a *minimal* set of data that helps define a structure. The recognition that a search

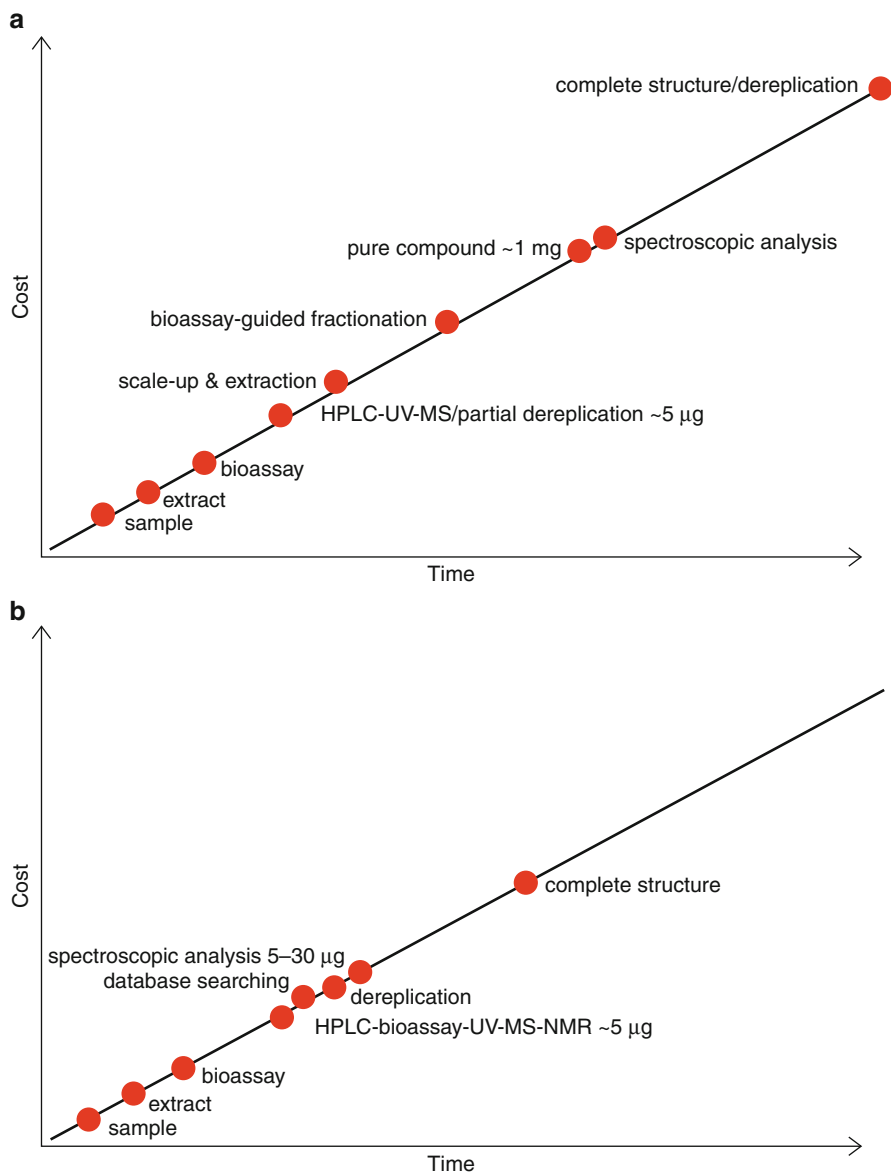


Fig. 6.12 (a) Conventional approach to dereplication; (b) Dereplication based on ^1H -SF approach and nanomole-scale NMR determinations

based on the numbers of functional groups easily recognizable by ^1H NMR spectroscopy was a powerful method for discriminating between alternative structures was the starting point for the development of the ^1H structural features aspect of MARINLIT and subsequently ANTIMARIN. These are the only two databases that have such functionality. This approach allows dereplication to be accomplished and

novelty established shortly after the ^1H NMR spectrum has been obtained and before a full interpretation of the data (see Fig. 6.12b).

This ^1H -SF-based approach to dereplication is well illustrated in one last example. Two isomeric compounds of molecular mass 490.3658 Da, corresponding to the molecular formula $\text{C}_{30}\text{H}_{50}\text{O}_5$ were isolated from a soft coral. Use of the various databases to look for possible structures based on this mass data has already been commented on in Table. 6.3. The ^1H NMR data and interpretation for one of the isomers is shown in Fig. 6.13. Without reference to mass data and simply relying on methyl group count and type, the number of possible hits in MarinLit was reduced to 43. If other information was then used, such as the four 1-H carbinol protons (δ 3.5–4.9) and the trisubstituted alkene (1-H; δ 6.35), the hits were progressively reduced to three and then two hits which corresponded to the 11-acetoxy and 12-acetoxy isomers shown in Fig. 6.13, which were first isolated from the soft coral *Capnella lacertiliensis* in 2003 [34].

If mass data had been used with the NMR interpretation, the same definitive result would have been achieved but with less NMR interpretation ($\text{C}_{30}\text{H}_{50}\text{O}_5$ gave 35 hits; $\text{C}_{30}\text{H}_{50}\text{O}_5 + 3x \text{ Me}$ singlets + $4x \text{ Me}$ doublets gave 7 hits). Either approach would have lead to a full and definitive answer as to whether these were new compounds or not. The actual assignment of structure to the isomers would then be by comparison against the original data. So as with the other cases examined, dereplication has

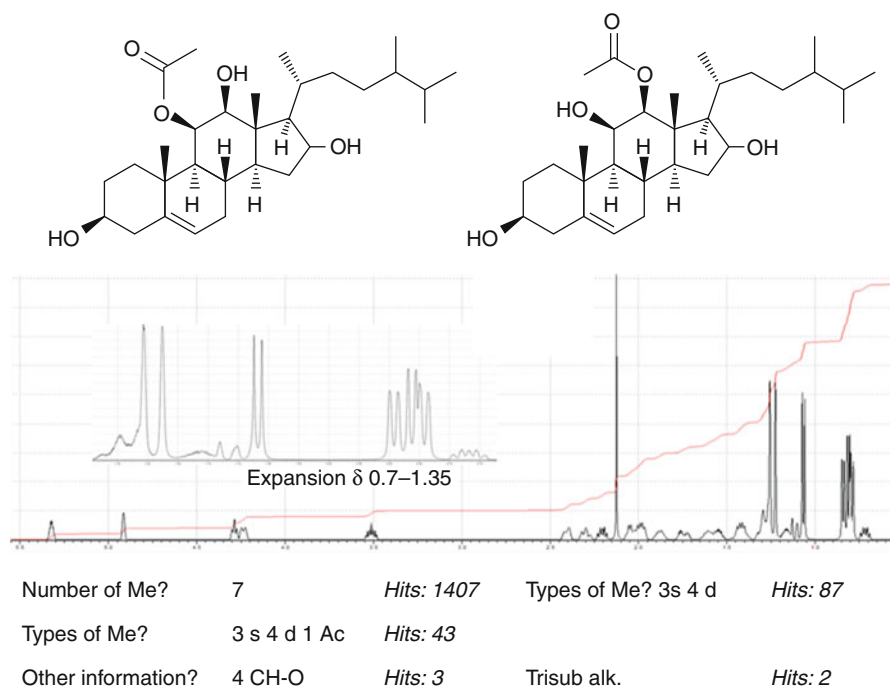


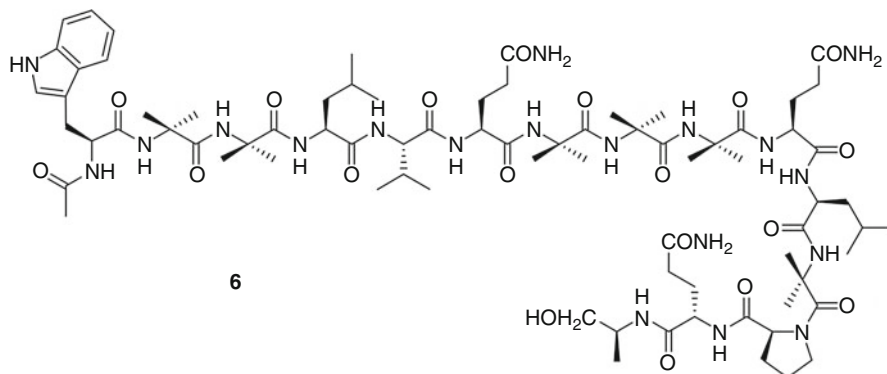
Fig. 6.13 NMR-based dereplication strategy for compounds isolated from a soft coral

been carried through quickly and efficiently and did not rely on a full structural assignment.

6.8 Dereplication at the Nanomole Level

The recent advances in NMR probe design has led to cryoprobes [35] and capillary flow probes [36] that yield 1D and 2D NMR spectra with excellent signal/noise ratios on just 2–20 μg of sample in a matter of minutes for a ^1H NMR spectrum to an hour or so for the likes of a COSY NMR to several hours only for an HMBC spectrum. An example of such a ^1H NMR spectrum is shown above in Fig. 6.11. This spectrum was obtained on 20 μg of material in 6 μL of CD_3OD in less than 2 min. This enormous advance in the relative sensitivity of the NMR experiment quickly led to numerous papers on compounds isolated at the μg level and has led to the description of a microtiter plate–based dereplication built around a Protasis CapNMR probe [37] and the MARINLIT/ANTI-MARIN databases [12, 14]. Essentially, 200–500 μg of extract are injected onto a RP-18 analytical HPLC column using an acetonitrile/water gradient (10–70% acetonitrile over 22 min) with the effluent from the column collected into 88 wells (250 μL /well) after UV and ELSD monitoring. Two daughter plates are prepared by removing 5 μL /well for biological testing and mass spectrometry. The master plate is dried and after bioassay of the daughter plate the MS and ^1H NMR spectra of the bioactive well(s) are obtained. These data can be immediately searched in databases and dereplication achieved. If a new compound has been detected, then further NMR data as necessary can be collected while the sample is still in the probe which meets the optimal pathway suggested in Fig. 6.12b. If a known compound had been detected, the work could be halted at that juncture.

An example of this approach would be the isolation, characterization, and structural elucidation of a new peptaibol, chrysaibol (**6**) from an extract of the fungus *Sepedonium chrysospermum* [38]. This work was carried out with an estimated 30 μg of chrysaibol isolated during HPLC analysis into the microtiter plate. This included obtaining 2D NMR data. Dereplication on the nanomole scale is possible and practicable using the database-assisted processes described in this chapter.



6.9 Relative Costs of the Databases

The cost of database searching is a real consideration. The larger databases such as REAXYS or the various version of CAS, such as SciFinder, are particularly expensive with the actual cost calculated based on factors such as the number of licenses and location. Such databases are usually paid for by central libraries at institutions rather than by individual groups. The specialized natural product databases cost considerably less and, in the main, are initially more useful for the natural product chemist. Estimates of the relative costs of the relevant databases are given in Table 6.5. Gaining access to relevant databases is not cheap, but efficient dereplication procedures can save considerable time and circumvent wasted effort leading to the more efficient throughput of samples by the researchers which is a money saver. Figure 6.12a and b attempt to depict this aspect of efficient dereplication in terms of a time/cost exercise. In Corley's 1994 paper on the strategies for database dereplication, he estimated that "in our laboratory that for each natural product dereplicated, at an average cost of \$300 of online time (using STN databases), a savings of \$50,000 is incurred in isolation and identification time." [39] If that was a true cost/benefit analysis in 1994, imagine the benefits in 2012 and into the future? Databases play an essential role in the dereplication of natural product extracts (Table 6.5).

6.10 Study Questions

1. What are the advantages and disadvantages of using a specialist database to extract specific data in a narrow field such as marine natural products as opposed to using a generalist, all encompassing database such as CAS Registry?

Table 6.5 Relative costings of the databases useful in natural products research

DATABASE	Cost	Number of compounds	
		Total	Natural products
SCIFINDER	>US\$50,000	6.3×10^7	~260,000
CSLS	free	4.6×10^7	extracts
CHEMSPIDER	free	2.6×10^7	?
PUBCHEM	free	3.7×10^7	?
REAXYS	>US\$40,000	$>10^7$	170,000
NAPRALERT	US\$0.5/citation		>150,261
DICTIONARY OF NATURAL PRODUCTS	US\$6,600		159,670
ANTIMARIN ^a	\$0		53,000
ANTIBASE	US\$3,500		36,000
DICTIONARY OF MARINE NATURAL PRODUCTS	US\$625		22,691
MARINLIT	US\$1,850		22,000

^aTo obtain a copy of ANTIMARIN it is first necessary to be a current subscriber to the ANTI-BASE and MARINLIT databases

2. In the dereplication of a natural product extract, suggest a minimal data set that would establish the uniqueness of each compound isolated.
3. What are the pitfalls that may be encountered when using taxonomic data in a dereplication exercise?
4. Outline the problems that would be encountered if molecular mass or molecular formulae only were used in a dereplication exercise?
5. Suggest reasons why a database that includes NMR characteristics for each compound is more likely to be discriminating than any based on other spectral and physical properties such as mass, molecular formulae, UV, MS fragmentation, or IR.

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Contemporary Strategies in Natural Products Structure Elucidation

7

Jaime Rodríguez, Phillip Crews, and Marcel Jaspars

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J. Rodríguez (✉)

Departamento de Química Fundamental, Campus da Zapateira. Universidade da Coruña, A Coruña, Spain

e-mail: jaime.rodriguez@udc.es

P. Crews

Department of Chemistry and Biochemistry, University of California, Santa Cruz, CA, USA

e-mail: crews@chemistry.ucsc.edu

M. Jaspars

Department of Chemistry, Marine Biodiscovery Centre, University of Aberdeen, Aberdeen, UK

e-mail: m.jaspars@abdn.ac.uk

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Abstract

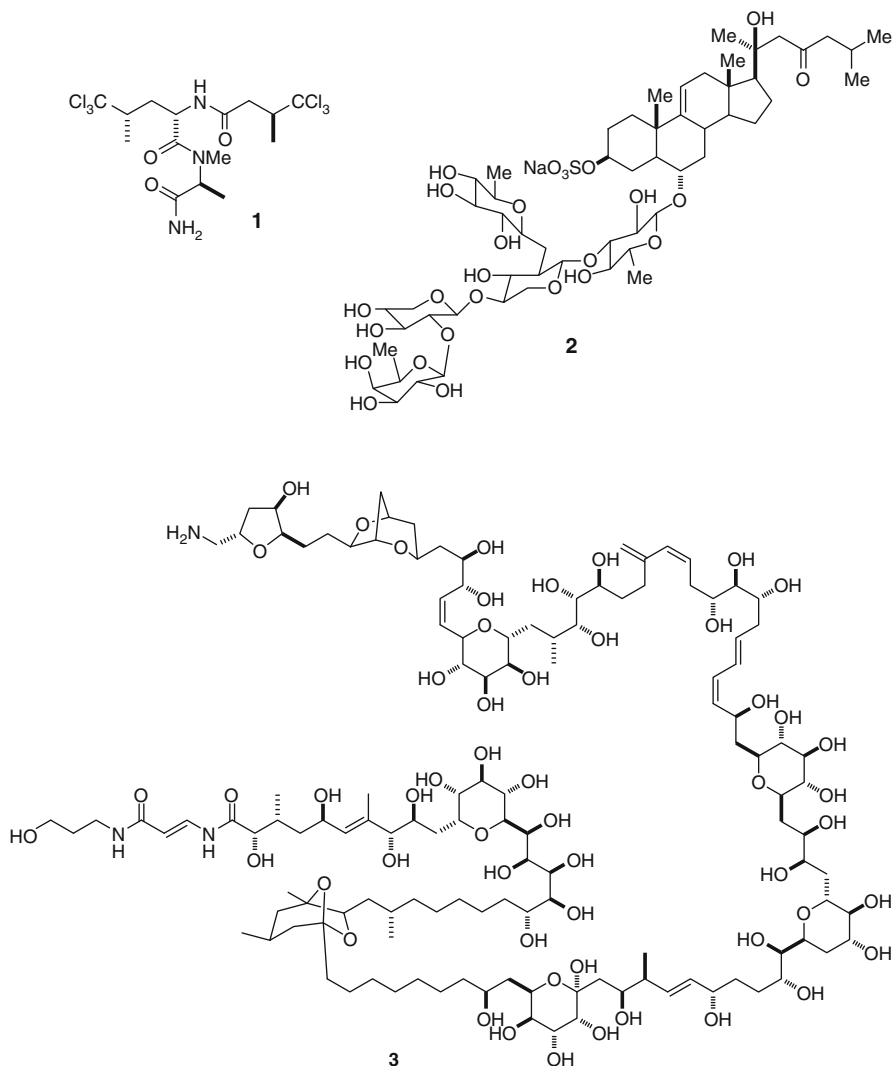
This chapter will describe the four primary spectroscopic techniques utilized for organic structure analysis: *nuclear magnetic resonance* (NMR), *infrared* (IR), *ultraviolet–visible* (UV–VIS), and *mass spectrometry* (MS). Each of these methods is used on a daily basis by most organic chemists in the course of structure elucidation analysis, requiring a very small amount of material in a generally nondestructive approach.

7.1 Methods in Common Use in Structure Elucidation Analysis

Four primary spectroscopic techniques for organic structure analysis have been in use since the early 1960s [1]. They are *Nuclear Magnetic Resonance* (NMR), *Infrared* (IR), *Ultraviolet–visible* (UV–VIS), and *Mass Spectrometry* (MS) [2]. Each of these methods is used on a daily basis by most organic chemists in the course of structure elucidation analysis, requiring a very small amount of material in a generally nondestructive approach. The use of NMR, IR, UV–VIS, and MS should be supplemented by another well-known, powerful tool, *X-ray crystallography*. However to use this technique typically requires well-formed crystals, and liquids or powders are not suitable for analysis.

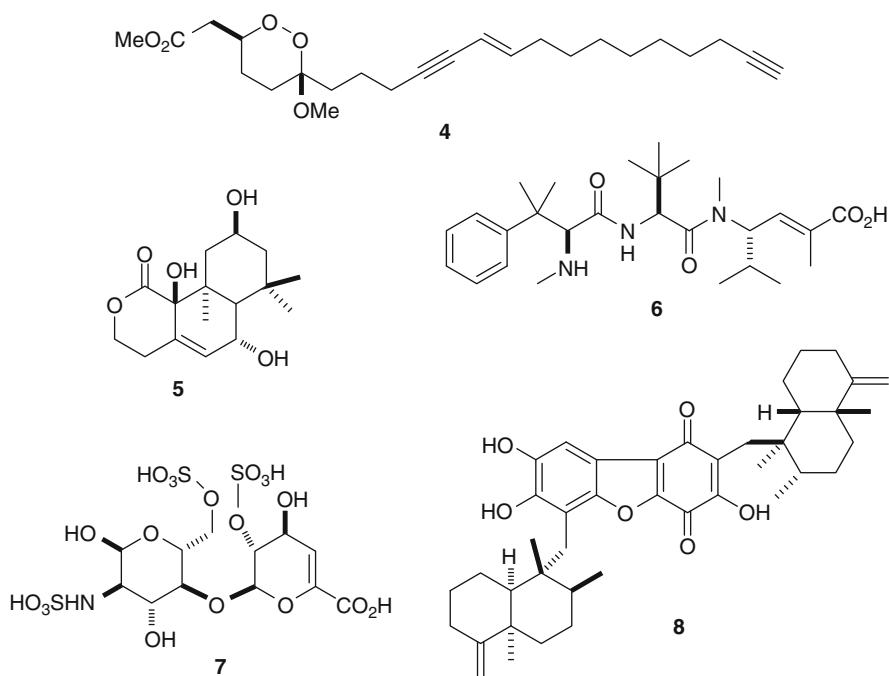
Compounds with molecular weights of less than $\sim 1,500$ amu are excellent candidates for study by the methods of organic spectroscopy, and this is the case for more than 95% of marine natural products. It is generally believed that the unequivocal structure analysis of such small organic compounds by spectroscopic methods is now a routine task. Powerful tools, widely available, consisting of multidimensional NMR, ultrahigh resolution mass spectrometry, tandem mass spectrometry, and chiroptical measurements should all be used in combination. As an illustration, collecting one or more pieces of such data allows a scientist to rapidly recognize the presence of the hexachlorinated dysidenamide (**1**) (504.98 amu, $C_{15}H_{23}Cl_6N_3O_3$), produced from the symbiotic association of the sponge *Dysidea herbacea* with the filamentous cyanobacterium *Oscillatoria spongelliae* [3]. A data set consisting of a mass spectrum alongside a 1H NMR spectrum would help distinguish this structure from other polychlorinated analogs, which are also ubiquitous in the sponge-bacterium association. A synergistic approach of using MS, 1H NMR, and ^{13}C NMR data provides immense power especially in the characterization of substances rich in H atoms and methyl groups. For example, utilizing such data makes it possible to completely assemble the structure of glycoside-steroids such as ophidianoside F (**2**) (1234.54 amu, $C_{56}H_{91}SO_{26}Na$) a sea star derived toxin [4].

Representative of more complex structures that can be solved using one or more of these tools, NMR, IR, UV–VIS, and MS, includes descriptions of the molecular architecture of exceedingly atom rich natural products. Perhaps at the top of the list is the intricate structure of the polyether marine product palytoxin (**3**) of mass 2679.48 amu and molecular formula $C_{129}H_{223}N_3O_{54}$. Its seemingly “never ending” structure was initially proposed based on spectroscopic data. But the process of collecting the appropriate data, making unambiguous interpretations, and reevaluating the data, including that obtained from total synthesis, took some 20 years.



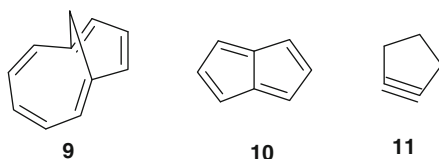
Using multiple pieces of analytical data is the best recipe to efficiently establish or validate an important molecular structure. A brief review of selected examples

from several compound classes provides some useful lessons. The peroxyacarnic methyl ester (**4**) (404.26 amu, $C_{24}H_{36}O_5$), a marine polyketide, whose signature functional groups are identified by NMR, IR and UV data, its molecular formula was determined by the election of the right ionization technique. Laying out the complete list of the functional groups of strobilactone (**5**) (296.16 amu, $C_{16}H_{24}O_5$), a sesquiterpene of marine origin with inhibitory activity against cultured COLO 201 cells, was challenging because no heteroatom protons were visible in the 1H NMR spectrum. The peptide HTI-286 (**6**) (473.32 amu, $C_{27}H_{43}N_3O_4$), a synthetic hemiasterlin-like antitumor agent, is rich in methyl and carbonyl residues [5]. Great atom diversity is present in the major disaccharide heparin-like **7** (576.97 amu, $C_{12}H_{19}NO_{19}S_3$) obtained from the marine mollusk *Callista chione* [6]. Not to be overlooked is that in recent years, advances in NMR and MS instrumentation and in experimental techniques have even made it possible to tackle the structure elucidation of very complex compounds, made up of nonrepeating biosynthetic subunits. However, connoisseurs of this subject recognize that even when all of these tools are applied, errors can be made and other considerations including organic synthesis may be needed. To be discussed later in this chapter are several cases taken from the literature where difficulties were encountered in deriving correct molecular structures.



To be successful in the task of structure elucidation analysis, especially when an exotic compound is in hand, requires several attributes. In addition to chemical common sense [7], five other aspects are important:

- A general knowledge of principles of organic structures is essential. You should also have an understanding of common functional groups. Being able to pick out the quinone alkaloid substructure present in popolophuanone E (**8**), a potent inhibitor of the topoisomerase II [8], provides a simple illustration about dealing with functional groups. It is important to have facility for conceptualizing structures that are especially stable, such as homoazulene (**9**) (a nonbenzenoid aromatic); exceedingly unstable, for instance pentalene (**10**) (a planar $4n$ π -electron system); or immensely strained, such as cyclopentyne (**11**).
- Using an organized and systematic approach (see Figs. 7.1 and 7.2).
- A good understanding of how to interpret spectroscopic information is essential (see Table 7.1).
- An appreciation of the dangers of using negative or unreliable data to make positive conclusions about a molecular structural feature is important (see Table 7.8).
- An ability to maintain a proper perspective in situations where conflicting data sets seem to be in hand. When this occurs, it is helpful to draw on experience gained from past successes in problem solving. Finally, to simultaneously use data from NMR, IR, UV–VIS, and MS and to look repeatedly for multiple pieces of data to support individual conclusions should be considered as an ultimate goal. Taking time to reevaluate a conclusion will also help to avoid mistakes. This can be accomplished by defending the logic of how a structure was elucidated before a critical audience (e.g., the practice of peer review).



Determining a complete organic molecular structure begins with the isolation or synthesis of a *pure* compound. Spectroscopic data is then obtained to derive the following information: (a) molecular formula, (b) identities of functional groups, (c) carbon connectivities, (d) positions of substituents and functional groups on the carbon framework, and (e) stereochemical properties including static and dynamic aspects. The overall flow of information processing is summarized in Fig. 7.1.

The step-by-step approach actually used in organic structure determination will vary greatly as a function of several variables, such as the source of the material under study. In the case of new compounds, an extensive data set must be obtained for a newly isolated natural product when its structure is presumed to be unknown. Undertaking a complete analysis of *all* the data from each of the four spectroscopic methods is not always the most effective way to proceed. An infrared or a mass spectrum can contain more information than can be correlated with specific elements of organic structure, so only a portion of the data obtained is useful. Also, data from the four spectroscopic techniques are not equivalent in the extent to which they will aid the identification of various organic structural elements.

Fig. 7.1 Steps in establishing a molecular structure

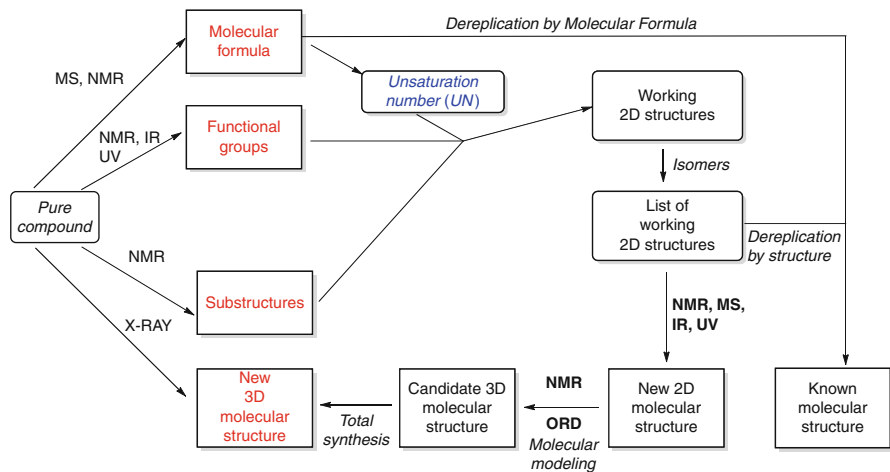
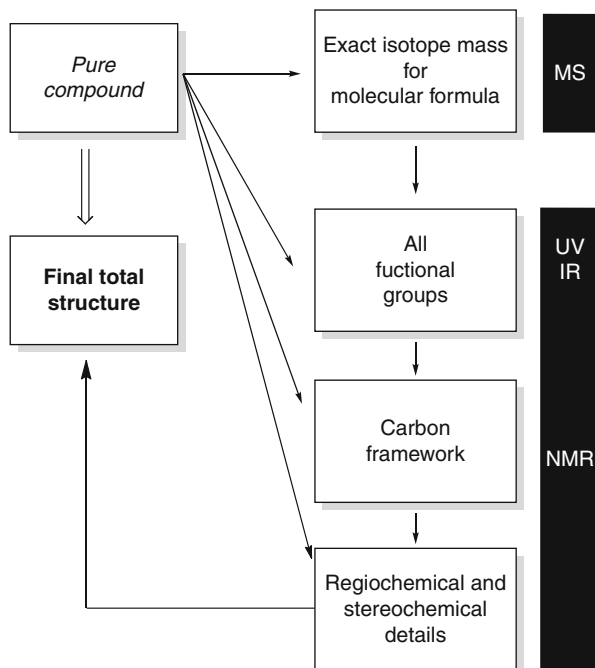
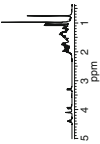
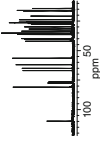

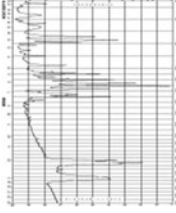


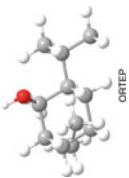


Fig. 7.2 The road map to organic structure analysis

Table 7.1 Characteristics of important spectrometric methods in common use

	^1H NMR	^{13}C NMR	MS	IR/RAMAN	UV-VIS	ORD/CD	X-RAY
Spectral scale	0–15 ppm	0–220 ppm	50–4,000 amu	400–4,000 cm^{-1}	200–800 nm	185–600 nm	Not relevant
Average sample	$\cong 1$ mg	$\cong 5$ mg	< 1 mg	< 1 mg	< 1 mg	< 1 mg	Single crystal
Molecular formula	Partial	Partial	Yes	No	No	No	Yes
Functional groups	Yes	Yes	Limited	Yes	Very limited	Very limited	Yes
Substructures	Yes	Limited	Yes	Limited	Limited	No	Yes
Carbon connectivity	Yes	Yes	No	No	No	No	Yes
Substituent regiochemistry	Yes	Yes	No	Limited	No	No	Yes
Substituent stereochemistry	Yes	Yes	No	Limited	No	No	Yes
Analysis of isomer mixtures	Yes	Yes	Yes	Yes	No	No	Yes
Purity information	Yes	Yes	(by GC/MS LC/MS)	(by GC/IR)	Yes	No	(if separate)
What is measured	Peak areas	Chemical shifts	Singly or multiple charged ions	Vibrational transitions	Electronic transitions	$[\alpha]$	Relative atom positions
	Chemical shifts	Coupling					<i>R/S</i> absolute stereochemistry
	Coupling	Relaxation					
	Relaxation						
Typical units	δ (ppm)	δ (ppm)	<i>m/z</i>	cm^{-1}	nm	nm	–
Typical representations							

It is useful to focus on specific characteristics of the major spectroscopic methods. Summarized in [Table 7.1](#) are properties of nuclear magnetic resonance (NMR), infrared (IR), ultraviolet–visible (UV–VIS), optical rotatory dispersion–circular dichroism (ORD–CD), mass spectrometry (MS), and X-ray crystallography. Take a moment to scan this table, compare the data collected, and become familiar with the limitations of each technique in structure elucidation analysis.

A characteristic of each of these methods, except MS, is that a compound is subjected to irradiation by photons from different regions of the electromagnetic spectrum. It is the electromagnetic waves or photons which initiate the various molecular processes such as nuclear, vibrational, or electronic transitions that result in the various NMR, IR, or UV–VIS “peaks.” In the X-ray method, the very high electromagnetic energy is diffracted by the crystal lattice and a complex pattern results.

Both neutral and charged species can be investigated by NMR, IR, and UV–VIS. As indicated in [Table 7.1](#), the spectral scale in each of these methods is in frequency units. Also, sharp peaks are typically observed in NMR; some regions of the IR spectrum have sharp peaks, while UV–VIS and ORD/CD spectra usually contain very broad peaks. Long-lived radical ions, cations, or anions are generated during MS determinations, but only charged species can be observed by this technique. Some of these ions have the same mass as the original material, but they can also associate to form clusters of higher mass or fragment to species of lower mass. The scale in MS is in units of atomic mass (amu) to charge, or m/z . Overall, it is possible to observe a large number of sharp MS peaks.

Fortunately, both liquid and solid compounds can be easily examined in NMR, IR, and UV–VIS. In addition, no more than just a few mg of a compound are needed for any of these techniques. As a final point, two of the other methods in [Table 7.1](#) have very special sample requirements. A chiral or scalemic compound is needed for ORD/CD, while a crystalline solid is requisite for X-ray analysis.

Nuclear Magnetic Resonance. Many consider NMR to be the most powerful tool in organic structure analysis because it provides direct insight into the backbone of an organic molecule. An NMR spectrum arises from transitions between nuclear spin states, and the ^1H and ^{13}C isotopes are the most common targets although ^{15}N is becoming more common. If one to tens of milligrams of a pure sample is available, then a ^{13}C NMR spectrum or the combination of HSQC/HMBC spectra can be rapidly obtained to provide an analysis of carbon and hydrogen content as accurate as that from either MS or classical combustion analysis [9]. Similarly, ^1H NMR data can also be used to assess hydrogen content, and this can be done on submilligram samples. The identity of various functional groups can often be established entirely by NMR, but this requires careful comparison to data of model compounds from databases or theoretical calculations. Many HC–CH connectivity relationships can be established by two-dimensional homonuclear ^1H – ^1H COSY (correlation spectroscopy) and heteronuclear ^1H – ^{13}C correlation spectra. Finally, nuclear Overhauser enhancement (NOE) data, along with chemical

shift and/or coupling constant data from ^1H and ^{13}C NMR data, can provide stereochemical insights. The use of pulsed field gradients and inverse detection is essential for sample limited situations.

Mass spectrometry is often considered to be second priority in importance for structure elucidation. It involves generating an ionic species of an organic molecule followed by mass analysis with an electric or magnetic field. The data obtained by this process are invaluable for deriving molecular formulas (or partial formulas), and different techniques have been developed to facilitate obtaining a MS peak containing the molecular formula information.

There are several types of *optical spectroscopic methods* in use. Overall, as we saw previously (Table 7.1), their value in organic structure analysis is not as high as data from NMR or MS. These methods are distinguished by the energy of the molecular transition that is examined. Thus, infrared irradiation causes bond vibrational changes, and UV–VIS irradiation causes transitions of the bonding or nonbonding electrons. In general, IR spectroscopy is an excellent tool for identifying certain functional groups, but UV–VIS data can only be applied to molecules with conjugated multiple bonds. The technique of optical rotatory dispersion (ORD) or circular dichroism (CD) is restricted to optically pure (chiral), or enriched (scalemic) compounds, which are subjected to an elliptically polarized source of UV–VIS irradiation. It is the positive or negative nature of ORD or CD spectral peaks which can be used to establish the absolute stereochemistry. This can occur empirically by reference to empirically derived correlation rules, reference spectra, or the results of theoretical calculations.

A lengthy discussion here of X-ray crystallography is not justified, and more information can be obtained from specialized texts [10]. It should be noted that when a suitable crystal is obtained and dereplication efforts have shown that a new compound is in hand, then an X-ray diffraction study ought to be initiated. A major limitation is that many compounds, or their heavy atom derivatives (e.g., *p*-bromobenzoates), are either not crystalline or do not give suitable crystals and thus cannot be subjected to X-ray crystallography.

It is extremely useful to compare data from a sample under study with data of structurally analogous compounds (i.e., standards). Correlation tables serve as an excellent device and are included in many reference sources. One indispensable source of such data is the book by Pretsch et al. *Tables of Spectral Data for Structure Determination of Organic Compounds* [11]. There are many websites emerging that also have such data. Also invaluable are catalogs on paper or online of actual spectra for the major spectroscopic methods.

7.2 Steps in Establishing a Molecular Structure

The process by which a pure compound can be analyzed to establish its molecular structure is outlined in Fig. 7.2. The most direct route would be to obtain a crystal of suitable quality and then subject it to X-ray diffraction analysis. However, this does not represent a practical route for compounds that are resistant to being

crystallized. Thus, for our purposes, the ideal starting point is to obtain the molecular formula (MF). As will be introduced in the next section, an MF can be derived by several methods, and high-resolution mass spectrometry provides the most unambiguous data. The determination of an unequivocal MF is often complicated, so many efforts to establish a molecular structure begin without this information being firmly in hand.

Once obtained the MF is used to calculate the unsaturation number (UN) – the number of multiple bonds and rings. Two other pieces of primary information must also be obtained which include making a list of all functional groups, and conceptualizing the substructures – the frameworks of all carbon/hydrogen containing moieties. It is important to recheck the final list of functional groups and substructures for agreement with the atoms present in the molecular formula. Some common functional groups are easy to pinpoint, such as alkene moieties, aromatic residues, six-membered rings, three-membered carbocyclics, various types of carbonyl groups, alcohol groups, and amines. Alternatively, there are some that can be considered to be harder to recognize. These are headed by cumulenes, ethers and epoxides, thioethers, thiocarbonyls, guanidine groups, isonitriles, imines, and nitro groups.

Combining three elements – the UN, the functional groups, and the substructures – provides the first milestone, creating a *working 2D structure*. This stage in the process is most often reached when there is agreement between the MF, functional groups, and substructures but that does not guarantee that any of these are absolutely correct! The next step is to use the concepts present in the *working 2D structure* to generate a larger list of possible structures. This process will be further illustrated below. Sometimes a compound suspected to be new has already been described in the literature. To check for this possibility, it is wise to engage in a process called “dereplication” [12]. For example, molecular formula searches can be carried out using commercial or proprietary databases. The most comprehensive is the ACS SciFinder, but others such as the Dictionary of Organic Compounds, Chemspider [13], MarinLit [14], and even the Merck Index are useful. The next step involves assessing the properties of the literature “hits” versus those of the compound under investigation. Similar searches can be done using the various *working 2D structures* or *substructures*.

The next hurdle in a structure determination effort is to prune the list of *working 2D structures*. This can also be a difficult task to accomplish and sometimes requires the use of both spectroscopic and chemical data. Assuming that the dereplication efforts have been completed, the compound can be designated as having a *new 2D molecular structure*. To establish the total structure with details of relative stereochemistry (e.g., R^* , S^* designations) and then the absolute stereochemistry (e.g., R , S designations) represents additional steps in this process [15]. Final tests for the overall structure and stereochemistry relationships might include forming a chiral derivative followed by NMR analysis, additional attempts to obtain crystals for X-ray study, a chiral total synthesis of the proposed structure, and/or theoretical study by molecular mechanics or electronic structure calculations.

7.3 Looking for the Molecular Formula (MF) and the Unsaturation Number (UN): Mass Spectrometry

A compound cannot be considered as characterized until its molecular formula has been established [16]. The classical way to obtain this information is from combustion microanalysis on a carefully dried compound [17]. Elemental analysis data (e.g., % C, H, N) can be used to calculate an empirical formula and is still generally required by many chemical journals before the publication of a new compound [18]. However, it is also recognized that such data only provides a proof of purity, because many molecular formulas can be derived from a single empirical formula. In practice, molecular formula information is obtained in another way: by mass spectrometry (MS).

Once the molecular formula has been secured, it is immediately used to calculate another piece of fundamental information, the *unsaturation number* (UN, degree of unsaturation, or double bond equivalent). The UN is important because it is the sum of the number of multiple bonds and rings present, and as such provides information about the relative complexity of a compound. Equation 7.1 shown below can be used to calculate the UN for any type of compound comprised of carbon, hydrogen, nitrogen, oxygen, sulfur, and halogens. Equation 7.1 is based on comparing the known molecular formula to the theoretical formula expected for a completely saturated molecule, which is C_nH_{2n+2} . Thus, stable ionic species (i.e., $(CH_3)_4N^+$) or radical species (i.e., $R_2NO\cdot$) cannot be directly treated by this Eq. 7.1.

$$\begin{aligned} &\text{Calculating an unsaturation number (UN)} \\ &\text{For a compound of } C_aH_bO_cN_dX_e; \quad UN = \frac{[(2a+2)-(b-d+e)]}{2} \end{aligned} \quad (7.1)$$

The unsaturation number can be used to compute the number of rings present. This is accomplished by taking the total count of multiple bonds and subtracting it from the unsaturation number. Quantitative hydrogenation is the classical way to determine a count of multiple bonds, but such data must be carefully interpreted because a cyclopropane can also take up H_2 under mild catalytic conditions.

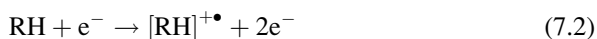
The technique of mass spectrometry does not entail absorption or emission of electromagnetic radiation (review Table 7.1). Rather, it involves visualizing ions of different mass. The essential principle of mass spectrometry is to produce ions from either organic, inorganic, or biomolecules by any suitable methodology, to separate these ions by their *mass-to-charge ratio* (m/z , “m divided by z”), and finally to identify them by their particular m/z values and abundance [19]. Traditionally, the most common technique for producing ions involved electron impact mass spectrometry (EIMS), although electrospray ionization (ESI) has become the most commonly employed technique in the last decade.

7.3.1 Different Ways of Producing Ions: Ionization Techniques

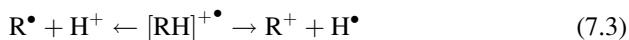
As noted above, the classical way to generate MS ions is by electron impact (EI). However, there are three additional contemporary techniques commonly used for forming ions in mass spectrometry. These are ion molecule reactions, laser desorption, and spray techniques. For the most part, the ionization involves a process that converts analyte molecules into gas-phase ionic species. With so many choices, maximizing the information obtainable from MS depends on matching the compound type to both a particular ionization and an ion detection method.

7.3.1.1 Electron Impact

EIMS analysis involves vaporizing a compound in an evacuated chamber (ca. 10^{-6} – 10^{-5} torr) and then bombarding it with electrons having 25–80 eV (2.4–7.6 MJ/mol) of energy. The high energy electron stream causes a valence electron to be ejected from the compound (symbolized below by RH) under analysis, which generates a radical-cation molecular ion $[RH]^{+\bullet}$ shown below. Since the $[RH]^{+\bullet}$ formed has a great deal of excess energy, this MS method is often referred to as a *hard ionization* process:



In a typical positive ion EIMS, the molecular ion peak is accompanied by numerous additional lower mass fragmentation peaks. However, as is observed in Fig. 7.3 for two C_6H_{14} isomers, in some cases the $[M]^{+\bullet}$ peak can be the base peak and different ionization methods are needed to optimize this situation. The simplest fragmentation of a molecular ion species can occur by a one-bond homolysis or heterolysis, but the former is more common. Each nonequivalent bond in a molecule represents a potential site for such fragmentation, and this can contribute a multitude of distinct species including neutrals, radicals, or ions:



Fragmentation, either by rupture of a bond between two directly connected atoms or by rupture of multiple bonds, will generate many species of discrete mass. Still other new species can arise through molecular rearrangements occurring either before or after a fragmentation event. As might be expected when the number of bonds involved in a fragmentation process increases, the possible combinations of the fragment ion masses will also increase.

The EI mode of ionization is very easy to use and provides library-searchable spectra for a large range of organic compounds. However, a very serious limitation of EI is that many compounds are not stable under these conditions. Another limitation of EI is the requirement that analytes must be in the gas phase prior to ionization. This constraint makes thermally labile and nonvolatile compounds

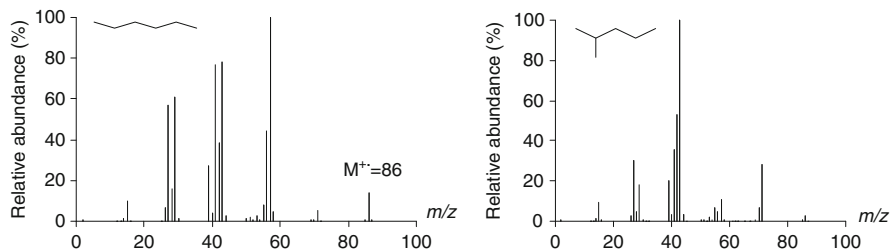


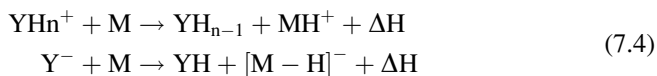
Fig. 7.3 Low-resolution EIMS of two C_6H_{14} (MW 86) isomers

inaccessible to EI, making the determination of the molecular mass challenging. Extensive fragmentation may also make the interpretation of a mass spectrum difficult. Also, there is lack of a causal link between precursor and fragments. A useful mass range for compounds that are amenable to EI is rather low (ca. <1,000 amu).

Alternatively, there are a host of *soft ionization processes* such as chemical ionization and spray ionization techniques that provide an extra approach to obtain MS data. In general, soft ionization results in spectra where the molecular ion dominates [20].

7.3.1.2 Chemical Ionization (CI)

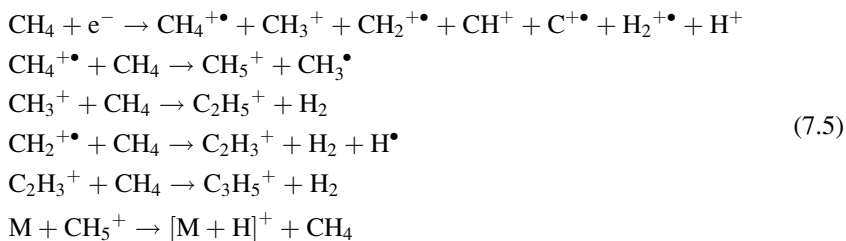
The purpose of CI is to use an *ion-molecule reaction* to maximize the intensity of molecular ions while diminishing that of fragment ions [21]. Relatively high pressures (0.5–1.5 torr) are used, and a substrate is ionized by reaction with the reagent gas (YH) which has been pre-ionized by the electron beam. The ionized reagent gas YH^+ or Y^- can interact with a substrate via proton or charge exchange reactions. Many such reactions are possible, and they are exemplified by those generating positive or negatively charged molecular ions, respectively:



Ion transfer in CI requires a positive ΔH (exothermic reaction). In this context, the ΔH for the reaction that generates the MH^+ is the difference of the proton affinity (PA) of the conjugate base of reagent gas YH minus the PA of the substrate M. In positive CI, the usual choices are ammonia, methane, and hydrogen.

A series of reactions occur to produce the reactive reagent ions. Methane serves as an interesting example because several cation species are formed. The major ones responsible for ion exchange in positive CI are shown in bold below. The process is begun by electron impact reaction with the reagent gas (e.g., CH_4),

followed by a series of ion-molecule reactions according to the following equations:



Clearly, it is important to know what major ions are produced as a function of the reagent gas employed in positive CI. In general, most analytes accessible to EI can be analyzed by CI; however, a major benefit of CI vs. EI is to provide molecular mass information. Another useful feature of CI is selectivity in ionization. The extent of fragmentation can be controlled by the correct choice of a reagent gas. On the other hand, CI has major drawbacks: (a) nonvolatile compounds cannot be studied, and (b) many compounds with polar functional groups are excluded from analysis. The CI data are dependent on experimental conditions, making results from this technique not useful for library-searching of databases. As with EI the mass range for compounds that are amenable to CI is also low (ca. <1,000 amu).

7.3.1.3 Spray Techniques

Spray ionization techniques such as electrospray (ESI), thermospray (TSI), or photospray (APPI) employ the strategy of rapid vaporization [22]. These methods have gained in popularity since 1995 because they are effective for most samples including those unresponsive or unsuited to EI or CI. Currently, ESI is the spray method of choice. Although the concept of electrospray was first conceived by Malcolm Dole in 1968, the development of ESI-MS is attributed to John Fenn, who was awarded the 2002 Nobel Prize in Chemistry for that contribution. The original stimulus for its development was to analyze high molecular weight, nonvolatile materials.

A process analogous to that employed by a perfume atomizer is the basis of spray ionization. A liquid aerosol containing finely dispersed droplets at atmospheric pressure is dispersed from a capillary. During the evaporation of the ionizing solvent by a drying gas such as nitrogen, multiply charged ions are expelled and are extracted by an electric potential difference into the mass analyzer vacuum region of the MS. Thermospray ionization (TSI) was one of the first applications of this process; it is based on passing the droplets through a small heated capillary. The method of ESI involves placing an electric field at the tip of the capillary, which facilitates the process of dispersing charged species from the aerosol. Samples dispersed in aqueous methanolic solution can be directly ionized by ESI, as shown in Fig. 7.4.

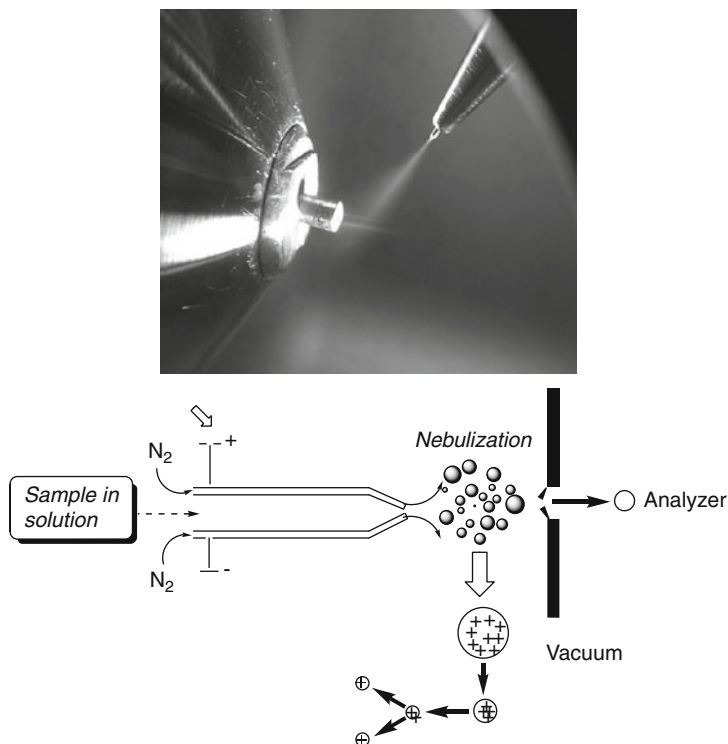


Fig. 7.4 How does electrospray ionization mass spectrometry work?

Electrospray ionization is achieved by passing the sample, in solution, through a metal capillary which is held at a high voltage. As the sample exits the capillary, it is nebulized by a flow of nitrogen gas to produce a fine aerosol of charged droplets. By the use of a flow of nitrogen gas and gentle heating, the droplets evaporate. As the droplets decrease in size, the sample ions in the droplet are forced together until repulsion causes them to be ejected from the surface (ion evaporation followed by a Coulomb explosion). The ions are then extracted through a small orifice into the mass spectrometer vacuum.

An illustration of the type of results obtainable on nonvolatile organic compounds of medium molecular weight is shown in Fig. 7.5a for the HCl salt of the sponge-derived compound manzamine A (**12**) (MW 548). Under positive-ion conditions, an intense $[M + H]^+$ peak occurs at m/z 549.3 for **12**, accompanied by a smaller signal for the $[M + 2H]^{2+}$ peak at m/z 275.2. A singly charged $[M - H]^-$ peak is observed in the negative-ion spectrum of marine-derived steroid **13** at m/z 575.4, as shown in Fig. 7.5b.

It is useful to discuss the strategies for recognizing multiply charged ESI peaks as well as some of the complications that accompany the analysis of high molecular weight substances. A characteristic of some ESI spectra is that clusters of multiply

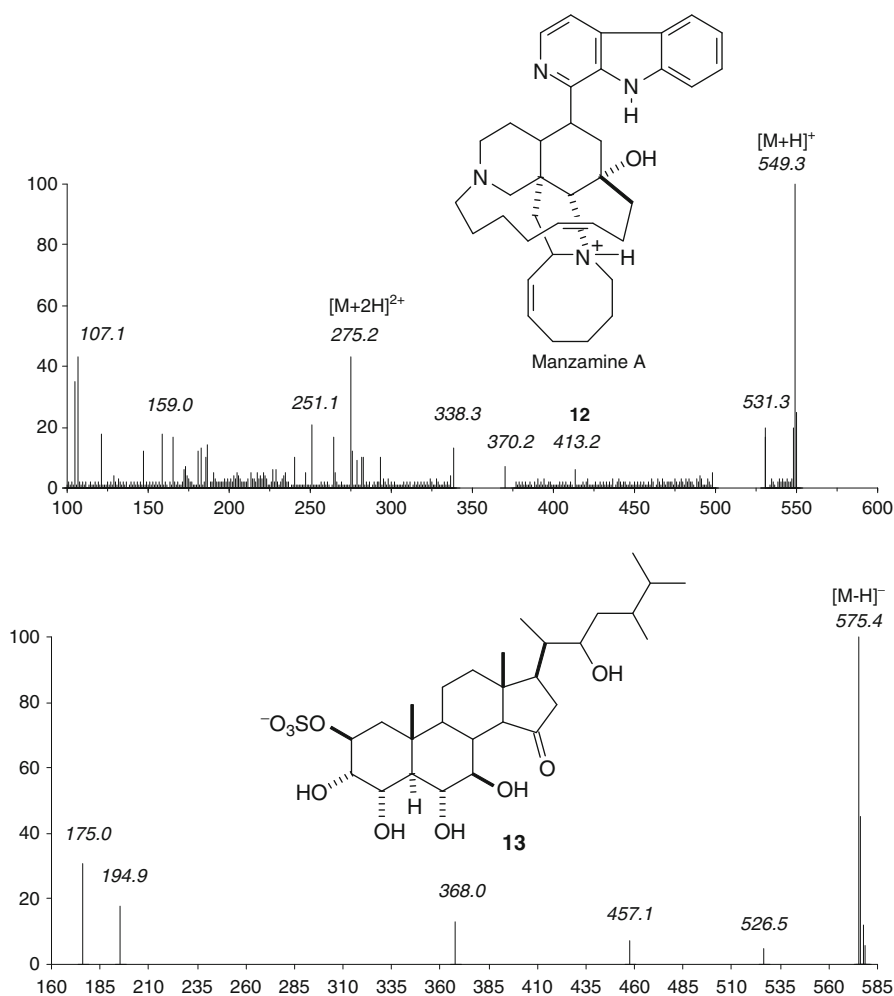


Fig. 7.5 (a) ESI (positive ion) of manzamine A (**12**) ($C_{36}H_{44}N_4O$, MW 548). (b) ESI (negative ion) of a sulfated steroid (**13**) ($C_{28}H_{48}SO_{10}$, MW 576)

charged peaks are observed in either positive mode, $[M + nH]^{n+}$, or negative mode, $[M - nH]^{n-}$, where n may vary from 1 to greater than 15. When a series of multiply charged molecular ion peaks are observed, each peak differs from the neighboring peak by one charge for the positive-ion ESIMS of myoglobin (**14**) (MW 16951.5), as illustrated in Fig. 7.6. A high-resolution scan on any one of the molecular ion peaks of myoglobin will show additional fine structure diagnostic of the number of charges present for that ion.

The isotopic relationships also dictate the appearance of the $[M + 2H]^{2+}$ ion, which has a diagnostic appearance in that the peaks are separated by 0.5 amu; similarly a $[M + 3H]^{3+}$ ion has peaks separated by 0.33 amu. So the actual charge

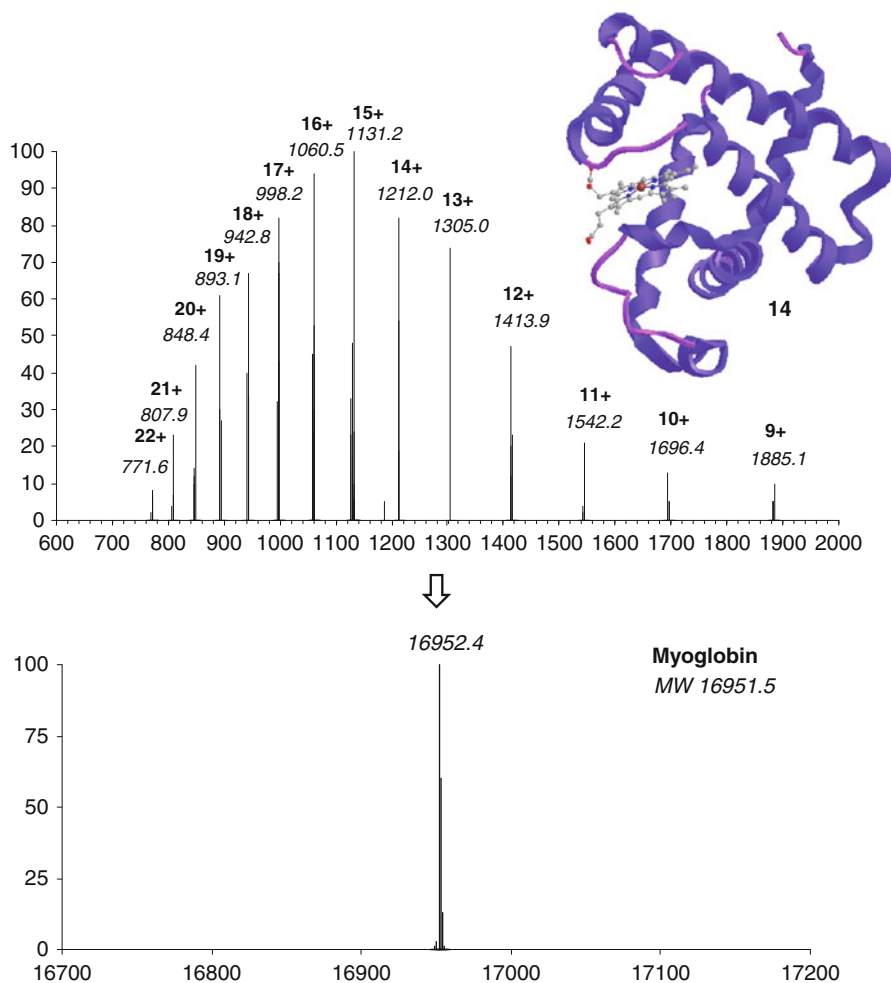


Fig. 7.6 Positive ion ESI spectrum of myoglobin (**14**) (MW 16951.5) in aqueous solution

count can be made by tallying the peaks within a 1 amu region or by using the simple equation: amu distance between peaks = $1/n$, where n equals the charge count. There is deconvolution software where both charge separation, isotope pattern and the m/z base peak of the cluster are taken in consideration in order to easily calculate the MF of an unknown.

7.3.1.4 Atmospheric Pressure Ionization (API)

In atmospheric pressure ionization (API), ions are formed under acidic conditions at ambient pressures followed by introduction into the source region. The sample ions together with solvent vapor and the ambient gas (usually nitrogen) are all held in the

ion source. There are three forms of ionization used in API, which can be applied for either direct insertion of compounds or as a detector for liquid chromatography–MS. These are heated nebulizer with a corona discharge, electrospray ionization (ESI), and thermospray ionization (TSI). The most common form of API consists of the vaporization of solvent and the substrate which is then directed into the ion formation region of the mass spectrometer where chemical ionization at atmospheric pressure (APCI) occurs using the vaporized solvent as the reagent gas. Overall, the technique of APCI is complimentary to ESI. It is used for compounds that do not have appropriate functionality (e.g., alkenes, aromatics) to be easily responsive to ESI.

An important modification of this form of API was introduced in 2005, and it is known as DART (direct analysis in real time) ionization, where the analyte is introduced in an open source. This atmospheric pressure ionization method uses a hot stream of excited-state helium atoms to excite clusters of water molecules in the atmosphere, which in turn transfer protons to the molecules of interest, thus creating the organic ions. Producing a spectrum requires only that the sample be held momentarily in a gas stream. Thin layer chromatography linked to high-resolution mass spectrometry can be carrying out with this innovative methodology [23].

7.3.1.5 Secondary Ion Mass Spectrometry (SIMS) and Fast Atom Bombardment (FAB)

FAB is useful for compounds, especially polar molecules, unresponsive to either EI or CI mass spectrometry. Excellent spectra are obtained with intense molecular ion peaks accompanied by few fragment ion signals. Chronologically, secondary ionization mass spectrometry (SIMS) was the forerunner of the FAB method. In SIMS, the sample is bombarded with a beam of high energy ions, resulting in the formation of secondary ions. A sample is usually placed as a thin monolayer from which the collision of the ion beam of heavy ions radiates secondary ions. Beams of low ion-current density must be employed, resulting in poor yields of ions, making the detection sensitivity a real problem. Also in SIMS, the secondary ion current lasts only for a brief period. Consequently, FAB is a better technique because it overcomes these problems. Fast atom bombardment (FAB) enables both nonvolatile and high molecular weight compounds (up to 20,000 amu) to be analyzed. Reasonably intense parent ions can be observed for both nonpolar and polar compounds including salts. In this technique, a sample is dissolved or dispersed in a polar and relatively nonvolatile liquid matrix, introduced into the source on a copper probe tip. Next, this matrix is bombarded with a beam of atoms of ~ 8 keV energy. FAB uses a beam of neutral gas (Ar or Xe atoms), and both positive- and negative-ion FAB spectra can be obtained. Molecular ions appear as positive-ion $[M + H]^+$ or negative-ion $[M - H]^-$ species (see behavior of compound **15** in Fig. 7.7). Often alkali metal ions, specifically Na^+ and K^+ , substitute for H^+ in the molecular ion, inducing the formation of positive ions like $(M + Na)^+$ or $(M + K)^+$. If the substrate has basic sites, species such as $[M - H + 2Na]^+$ or $[M - H + 2K]^+$ (or $[M - nH + \{(n + 1) \text{Metal}\}]^+$) will be observed.

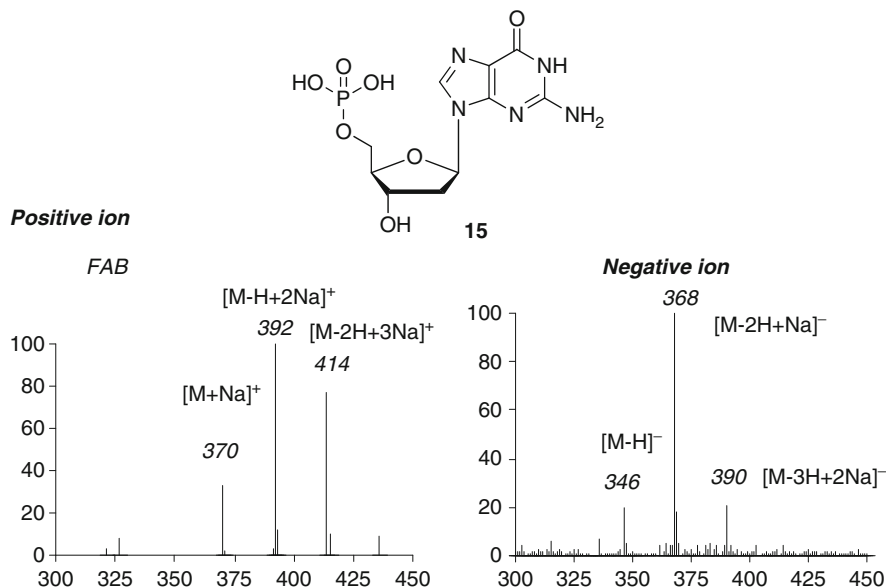


Fig. 7.7 FAB (Xe) spectra of 5'-deoxyguanosine monophosphate (**15**) (MW 347)

It is important to take note of the interfering peaks from the matrix, which must be reasonably viscous, chemically inert, and nonvolatile. In addition, it must possess good solvent and electrolytic properties. Glycerol and α -thioglycerol are two reagents frequently used. Other standard matrices which have been used for many years include the mixture of dithiothreitol and dithioerythritol (5:1) also known as *magic bullet*, 3-nitrobenzyl alcohol (NBA), polyethylene glycol, diethanolamine, and triethanolamine. The proper choice of a liquid matrix is a very crucial step in obtaining a high-quality FAB mass spectrum. For an intense $[M + H]^+$ ion signal, the matrix should be more acidic than the sample molecule, and for good $[M - H]^-$ ion production, the matrix must be more basic.

The molecular mass measurement and structural characterization of a wide range of organic, inorganic, and biochemical compounds (e.g., glycosides, peptides, antibiotics, lipids, carbohydrates, nucleotides, and nucleic acids) are major advantages of FAB. In general, FAB and liquid SIMS will give excellent molecular mass information in the range of m/z 100–2,000. Above this value, the abundance of molecular ions tends to diminish until, in the region of m/z 4,000–5,000, they become either absent or very difficult to discern against the background. It can be useful to collect both positive and negative ion data, as shown by the results of compound **15**.

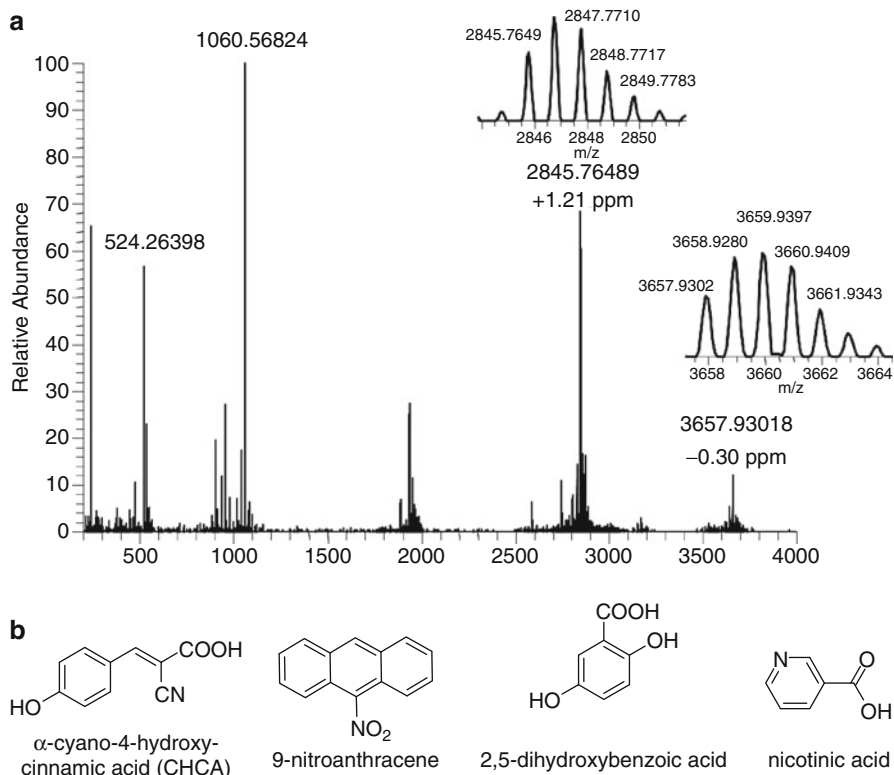


Fig. 7.8 (a) MALDI spectrum of mellitin (amino acid sequence *GIGAVLKVLTITGLPALIS-WIKRRRQQ* (MF $C_{131}H_{230}N_{39}O_{31}$, $[MH]^+$: 2845.761447)). Detected with an LTQ-Orbitrap, provided by Thermo Fisher. (b) Some solid matrices used in MALDI

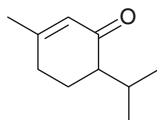
7.3.1.6 Matrix-Assisted Laser Desorption Ionization (MALDI)

Another important method for ion generation by rapid desorption involves irradiation of a sample by a strong laser beam [24]. Compounds of high molecular weight are successfully ionized by this method, called laser desorption ionization (LDI). An important modification of LDI involves using a solid matrix to absorb energy to minimize decomposition of the substrate under analysis. The purpose of the matrix is to absorb the large amount of energy produced by the laser and in a controlled fashion to transfer some of this energy to the substrate. This technique, referred to as MALDI, enables ionization of very large ions of up to m/z 1,000,000. Singly charged ions are produced by MALDI, in contrast to the multiply charged ions commonly observed in ESI, see Fig. 7.8. The obvious disadvantage of MALDI in the analysis of low molecular weight compounds is that some of the matrices used in MALDI completely obscure the region between 100 and 500 amu.

7.3.2 The Search of the Molecular Formula Through Mass Spectrometry

7.3.2.1 Isotopes

Mass spectrometry is based upon the separation of charged ionic species by their m/z ratio. We can calculate the molecular mass of 3-methyl-6-*i*-propylcyclohex-2-ene-1-one (piperitone, **16**) to $152.23 \text{ g mol}^{-1}$ using the average atomic masses of the elements. Since the mass spectrometer does not separate by elements but by isotopic mass, no signal at m/z 152.23 will be observed in the mass spectrum. Instead, a major peak at m/z 152.12 is present accompanied by a minor one at m/z 153.12. In order to fully understand a mass spectrum, we have to know about the different isotopes present for an element, their abundances, and *isotopic patterns*.



16

Chemical Formula: $\text{C}_{10}\text{H}_{16}\text{O}$

Exact Mass: 152.12

Molecular Weight: 152.23

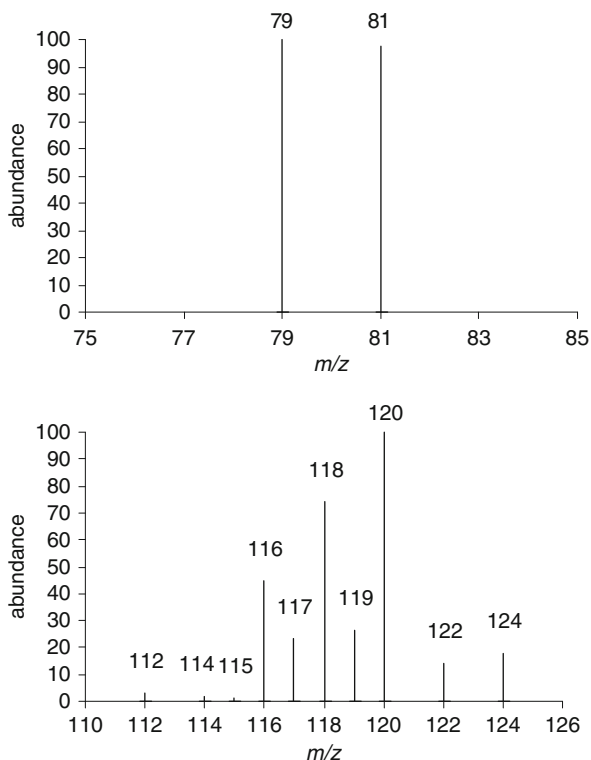
Atoms with nuclei having identical atomic number but differing in the number of neutrons are described as *isotopes*. One differs from another of the same element in that it possesses a different number of neutrons, and therefore a different *mass number*. This number is the sum of the total number of neutrons and protons in an atom, molecule, or ion. The mass number of an isotope is represented by a superscript in the elemental symbol, e.g., ^1H .

Depending upon the number of stable isotopes, elements can be monoisotopic (e.g., ^9Be , ^{19}F , ^{23}Na , ^{27}Al , ^{31}P , or ^{127}I), di-isotopics (e.g., $^1\text{H}/^2\text{H}$, $^6\text{Li}/^7\text{Li}$, $^{10}\text{B}/^{11}\text{B}$, $^{12}\text{C}/^{13}\text{C}$, $^{14}\text{N}/^{15}\text{N}$, $^{35}\text{Cl}/^{37}\text{Cl}$), and polyisotopics (e.g., $^{16}\text{O}/^{17}\text{O}/^{18}\text{O}$, $^{28}\text{Si}/^{29}\text{Si}/^{30}\text{Si}$, $^{32}\text{S}/^{33}\text{S}/^{34}\text{S}/^{36}\text{S}$, or 9 isotopes of Xe). The relative abundance of each isotope of an element must be considered when evaluating the peaks in a mass spectrum. Bar graph representations (histograms) are a great mode to visualize the isotopic composition (see Fig. 7.9), and they depend on the abundance of each isotope.

According to McLafferty's scheme [19b], another type of classification is dividing the elements into three general categories: "*A elements*" with only one natural isotope in abundance; "*A + 1 elements*" those that have two isotopes, the second of which is one mass unit heavier than the most abundant isotope; and "*A + 2 elements*" that have an isotope that is two mass units heavier than the most abundant isotope.

Examples of *A elements* are fluorine, phosphorus, and iodine. Hydrogen can also be included in this class because the abundance of its *A + 1* isotope, deuterium, is very small. Nitrogen and carbon are considered *A + 1 elements* since their second

Fig. 7.9 Isotopic patterns of bromine and tin



isotope is not insignificant and it is one amu higher than the most abundant isotope. $A + 2$ elements are the easiest to distinguish and the first to look for. Oxygen, sulfur, chlorine, and bromine are the most common examples. The presence of these elements in an ion is easily recognized from their isotopic distributions or *cluster*. Chlorine and bromine are very easy to pinpoint by MS. Having two major natural isotopes, they exhibit peaks in a ratio approximately 3:1 and 1:1, respectively.

Since few elements are monoisotopic, it is usually the most abundant species which is considered, especially when evaluating the parent ion M^{+} . For a compound $C_aH_bO_cN_dSi_eS_f$ under analysis, the molecular ion as well as most of the fragment ion peaks would be evaluated by considering only the major isotopes of $^{12}C^{1}H^{16}O^{14}N^{28}Si^{32}S$.

However, the existence of satellite peaks in a mass spectrum has to be considered because they can be useful information in order to deduce the molecular formula of an unknown. These peaks are isotopically shifted lines that emerge at masses one or more units higher than the most important peak M . The satellite peaks, nominated as $M + 1$, $M + 2$, and so on, reproduce the variation in the natural abundances of the isotopes. From the elemental composition of a molecular ion or

fragment ion, the abundances of its satellite peaks (the isotopic pattern or cluster) can be predicted as follows:

E.g., compound MF: $C_aH_bO_cN_dSi_eS_f$;

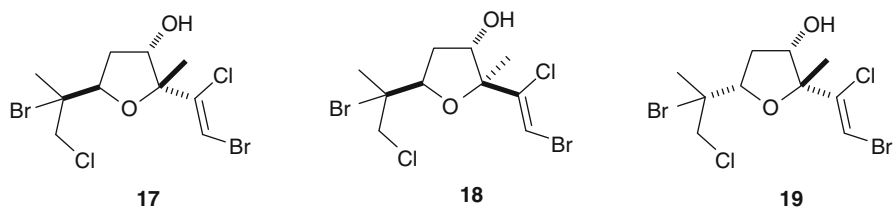
If $[M] = 100\%$, then

$$\%[M + 1] = a(1.08)^* + b(0.011)^* + c(0.038)^* + d(0.369)^* + e(5.0778)^* + f(0.80)^*$$

*Abundances for ^{13}C , 2H , ^{17}O , ^{15}N , ^{29}Si , ^{33}S , respectively

As briefly discussed above, the incidence of $A + 2$ elements is more noticeable for Cl and Br because the $A + 2$ isotopes are highly abundant. The contribution of one chlorine atom to the abundance of the $M + 2$ peak is 31.96%, and that of one bromine atom is 97.28%. In the case that one compound contains one chlorine atom, its $[M + 2]$ will be approximately one-third of $[M]$.

The contribution of more than one $A + 2$ element is calculated from expansion of the binomial $(a + b)^n$, where a is the natural abundance of the light isotope, b that of the heavy isotope, and n the number of atoms of that element present. If two different $A + 2$ elements are present (e.g., Br and Cl), the isotopic pattern is calculated by the expansion of the product given in $(a + b)^n (c + d)^m$, where c and d are natural abundances of the light and heavy isotopes of the second element and m is the number of that element. Using the clusters of peaks (separated by 2 amu) and their intensities as guide enables making a direct count of the number of Br and/or Cl atoms that might be present. Since the contribution of each isotope can be computed by different mathematical approaches, there are several software tools or web pages available to calculate the isotope distribution for an ion of a specific elemental composition and known isotopic abundances [25]. Thus, the structures of the furoplocamioids A-C (17–19), three pantofuranoids isolated from the Antarctic alga *Pantoneura plocamioides*, were determined on the basis of these types of clusters [26].



As we will see in electronic impact mass spectrometry (EIMS), compounds containing C, H, O, and with any type of charge *always* have an even molecular weight, an even number of H atoms, and display an even amu $[M]^{+}$ as an odd electron ion. Compounds having a halogen atom (X) follow the same pattern because the difference in mass between H and X is even. This is a consequence that the most abundant isotope of all elements has either even mass and even

valence, or both are odd, apart from nitrogen, which has even mass but odd valence. This fortunate coincidence leads to what is known as the *nitrogen rule*. Compounds containing a single nitrogen atom are treated by reversing all of the above rules. For example, a $C_nH_mO_yN_1$ compound would have an odd molecular weight, an odd number of H atoms, and possess an odd amu $[M]^{+}$ as an odd electron ion.

For multiple numbers of nitrogen atoms, the preceding rules apply when the total count is odd and they are reversed when the count is even. The only exception is quaternary ammonium salts (R_4N^{+}) which have an even molecular weight and H count. Keep in mind that an obvious possibility for error arises when the molecular ion of a compound without nitrogen is not visible, which makes the largest observed m/z odd due to a fragmentation process.

There are several approaches to calculating a molecular formula once a molecular ion peak has been identified. The M^{+} cluster can be used by comparing either the measured to calculated M^{+} , $[M + 1]^{+}$, and $[M + 2]^{+}$ peak intensities or the candidate molecular formulas obtained from the M^{+} by the *Rule of 13* to the count of C and H obtained by NMR (see next sections). One of the most effective procedures is to use the NMR CH count along with high-resolution M^{+} data.

There is a simple strategy to derive candidate molecular formulas systematically from any m/z peak [8]. It is based on the assumption that C_nH_n and its amu equivalent, 13 for $n = 1$, is present in all molecular and fragment ion formulas. Thus, dividing an M^{+} mass by 13 gives the value of n , and any remainder represents a count of additional hydrogens. As an example, benzene has an $M^{+} = 78$, and its molecular formula is easily derived. The molecular formula of toluene with an $M^{+} = 92$ is similarly obtained taking into account the remainder as hydrogen atom ($92/13 = 7$, $\rightarrow R = 1 \rightarrow C_7H_8$). To consider heteroatoms, the hypothetical C_nH_m formula must first be derived by using the procedure just given. Next the formula is modified by using a series of C_nH_m equivalents deduced by applying the rule of 13 to the mass of such heteroatom. For example, ^{16}O is equivalent to CH_4 , and ^{14}N is equivalent to CH_2 .

<p><i>Any isotope aX</i></p> <p>$a/13 = b \rightarrow R = c;$</p> <p>CH equivalent =</p> <p>C_bH_{b+c}</p>
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Examples

$$^{16}O \quad 16/13 = 1 \rightarrow R = 3; CH + H_3 = CH_4$$

$$^{35}Cl: 35/13 = 2 \rightarrow R = 9, C_2H_{2+9} = C_2H_{11}$$

The procedure for handling heteroatoms is exemplified by the calculation of candidate molecular formulas for anisole with an $M^{+} = 108$: $C_8H_{12} - (CH_4) + O = C_7H_8O$. When an odd amu M^{+} is encountered, the first heteroatom to consider is nitrogen (or odd multiples). Thus, aniline with an $M^{+} = 93$ has candidate molecular formulas ($93/13 = 7$, $R = 2 \rightarrow C_7H_9$; $N = CH_2$; $C_7H_9 - CH_2 + N = C_6H_7N$, $C_7H_9 - 2(CH_2) + 2N = C_5H_5N_2$, $C_7H_9 - 3(CH_2) + 3N = C_4H_3N_3$, $C_7H_9 - (CH_2) - (CH_4) + N + O = C_5H_3NO$, etc.)

7.3.3 Ion Analyzers and Mass Accuracy

In order to calculate the approximate mass of a molecule, we must sum the integer masses of all elements present. For a molecule with formula CH_4 , we calculate what is called the *nominal mass* by adding $12 \text{ amu} + 4 \text{ amu} = 16 \text{ amu}$. The concept is widely used by spectrometrists and is defined as the integer mass of the most abundant naturally occurring stable isotope of an element, and those values represent the low-resolution mass spectrometry (LRMS). This mode in collecting mass spectrometry data is achieved with a single-stage type mass analyzer such as a magnetic or quadrupole sector. In this manner, only integral m/z values are resolved (distinct peaks appear for ions 1 amu apart).

The masses of isotopes can be measured with great accuracy, better than parts per billion, e.g., ^{23}Na : $22.98976928 \pm 0.00000002 \text{ amu}$. This accuracy is reached by the use of mass spectrometers analyzing the ions in the so-called high-resolution mass spectrometry mode (HRMS). In mass spectrometry, the term *mass accuracy* is defined as the difference between experimentally measured mass and calculated exact mass. The mass accuracy can be measured as absolute units of amu (or *milliamu* = mmu) or as relative mass accuracy in ppm.

Good mass accuracy is obtained from adequately sharp and regularly shaped peaks that are well separated from each other. The capability of a mass spectrometer to achieve such separation is called *resolving power*, and it is the function of the *resolution* (R) of such instrument. R is described as the ratio of the mass of interest (m) to the difference in mass (Δm), as defined by the width of a peak at a specific fraction of the peak height.

By definition, it is assumed that two peaks are well separated when the valley separating their maxima has decreased to 10% of their intensity. A larger R means that smaller mass differences can be resolved. Especially useful for spectrometer manufacturers is the definition of FWHM (full width at half maximum) where the peaks separated by a 50% valley are considered as resolved.

The accuracy in mass spectrometry is highly dependent on the type of technique used for analyzing the ions. The separation of ions capitalizes on the inherent differences in the ratio of mass to charge for each ion species. These distinct ions will behave differently in an electric or magnetic field, which provides a convenient way to effect their separation.

An extremely effective way to analyze MS ions after they are formed from electron impact involves passing them through a magnetic field. The radius of curvature for the path of an ion is proportional to m/z . This allows a distinction between heavy ions, which have a less curved trajectory, and the lightest ions, whose trajectory will be more curved.

A relatively simple way to separate ions involves passing them through a quadrupole mass filter [27]. It consists of four parallel rods arranged symmetrically around an ion flight path. Each opposite pair of rods is electrically connected and an electric field is created from a dc voltage overlaid with an RF potential. The ions that pass through the central region are influenced by the dc and RF voltages. Most ions are deflected onto the rods, but those of an

appropriate m/z are modulated in a helical path and enter the detector. Quadrupole detection is very attractive because it is relatively inexpensive and the instruments require less expertise to tune and operate. This analyzer is widely used in GC/MS, LC/MS, and tandem MS instruments.

There is a mass filter which has many features in common with a quadrupole analyzer. In fact, it is popularly known as a *quadrupole ion trap* (QIT), and it was introduced in 1958 by Wolfgang Paul, a contribution that was recognized by the awarding of the 1989 Nobel Prize in Physics [28]. A QIT analyzer consists of three doughnut-shaped central ring electrodes with two end caps. Both an RF and dc potential are applied to generate a stable trajectory for the various ions. The ion trap has a very compact design and, because of its extremely low cost, is widely used as a detector in GC-MS and HPLC-MS applications. Newer instruments merge electrospray ionization with an ion trap analyzer. Additional features too complex to discuss here are incorporated to carry out tandem MS-type experiments. A problem with the ion trap detector is that relatively poor accuracy is achieved at large m/z , but advances in technology are overcoming this limitation. Very recently, *linear ion traps* (LITs) or two-dimensional ion traps have gained interest either as stand alone or as an element of more complex mass analyzers (hybrids). An LIT is similar to a quadrupole formed by four circular or hyperbolic rods placed symmetrically. In a linear ion trap, the ions are confined radially by a two-dimensional RF field.

In a *time-of-flight* (TOF) mass spectrometer analyzer, ions are separated according to their velocities and hence the mass-to-charge ratio. Ions are generated in a short burst and then accelerated. The time taken to traverse a specified path, usually up to 2.5 m, to the detector depends on the mass of the ion; consequently, the velocities of ions are an inverse function of the square root of their m/z values, and therefore, lighter ions travel more rapidly to the detector. TOF mass analyzers can be used in *reflectron mode*, an energy-correcting electrostatic mirror that can minimize undesired effects of initial spatial and energy spreads. With the reflectron, the flight path is increased without changing the physical size of the instrument, resulting in an increase in the mass resolving power.

In FTMS, gas phase ions are introduced into a cubic cell located within the solenoid of a magnet. Contemporary FTMS instruments use high-field superconducting magnets (7T is typical). The phenomenon behind FTMS is that the trapped ions move in a circular path (the cyclotron orbit) at different frequencies due to the strength of B and the mass-to-charge ratio. Detection of the different ions occurs from an RF excitation pulse that accelerates them into a resonant cyclotron orbit. Subsequently, a distinct RF signal is emitted and can be detected as a *time-domain* pattern. This type of signal can be amplified, digitized, and converted by a Fourier transform into the familiar plot of m/z vs. intensity. Overall, the FTMS technique is very different from those described previously. Among its advantages is that the FT approach provides very high resolution and a way to greatly improve signal-to-noise ratio for high mass ions.

An innovative type of mass analyzer, known as the *orbitrap*, has recently been introduced [29]. It works on the principle of an orbital trapping of ions around an axial central electrode with a purely electrostatic field. Since its appearance, the orbitrap mass analyzer has been considered as a potential alternative for FT-ICR because of its high resolution (approximately 150,000 FWHM) and good mass accuracy (better than 3 ppm without internal reference), large space-charge capacity, good sensitivity, and an m/z range up to 6,000.

Ion Mobility: (IM) coupled with mass spectrometry has evolved into a powerful analytical technique for investigating the gas-phase structures of biomolecules [30]. An ion mobility spectrometer uses gas-phase mobility rather than the m/z ratio as a criterion to separate ions. The mobility of ions is measured under the influence of an electrical field gradient and cross-flow of a buffer gas, and depends on ion's collision cross section and net charge. A more accurate mass analysis is obtained when the IMS is coupled to a quadrupole or TOF mass analyzer. Such systems can be engaged for the studies of mixtures of proteins or tryptic digests of peptides and proteins.

Mass spectrometers may be built by combining different types of mass analyzers in a single so-called *hybrid instrument*. The expansion of hybrid instruments started from magnetic sector–quadrupole hybrids, combining the advantageous properties of each mass analyzer. Special nomenclature is used to describe each hybrid spectrometer: symbols Q (quadrupole), q (collision cell–quadrupole), B (magnetic sector), and E (ESA, electrostatic analyzer), along with the previously described terms QIT, LIT, TOF, and ICR are combined to illustrate the different geometries of commercial spectrometers. BqQ, QqQ, Qq-TOF, QIT-TOF, and Q-LIT (or Q-TRAP) are examples that carry the advantage of powerful and affordable machines for tandem MS as will be explained later. Qq-TOF and QqQ systems can be regarded as the commercially most successful hybrids, whereas the next level of performance will be achieved with Qq-FT-ICR spectrometers.

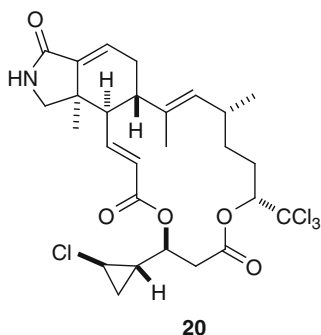
7.3.4 Terms in Mass Spectrometry

7.3.4.1 Exact Mass

Data from HRMS are essential for unambiguous determination of a molecular formula, and its *exact mass* is defined as the mass combination of the most abundant isotopes. HRMS data are obtained at an accuracy better than 0.0001 amu (0.1 mmu), and consequently, this permits a distinction between species of the same unit mass such as $[\text{CO}]^+$ (exact mass: 27.99437 amu) vs. $[\text{C}_2\text{H}_4]^+$ (exact mass: 28.03130 amu).

Care has to be taken when we want to calculate the exact mass of a neutral or charged species, where the mass of an electron ($m_e = 0.000548$ amu) has to be considered. This is the case for muironolide A (**20**), a tetrachloro polyketide isoindolone isolated from the marine sponge *Phorbasp* sp. at the nanomole scale,

when its molecular formula was calculated with high precision by Fourier transformation mass spectrometry [31].



The *exact ionic mass* of a positive ion species produced by the removal of one or more electrons from a molecule is equivalent to its monoisotopic mass minus the mass of the electron. Consequently, for negative ions, the electron mass has to be added.

7.3.4.2 Mass Defect

Comparing the exact mass to the unit (or nominal) mass for each element generates an estimate of the *mass defect* or *mass sufficiency*. Its value can be either positive or negative. For example, notice that ¹H, with nominal mass of 1 amu and exact mass of 1.00783 amu, has a slightly positive mass defect, whereas for ¹⁶O, of nominal mass 16 and exact mass 15.9949, the defect is slightly negative.

Obtaining experimental *m/z* data with a tenth of a mass unit accuracy (or better) can provide the overall estimate of the mass defect for a compound under study. Taking note of the direction of this mass defect can be helpful in many situations. Knowledge about mass defects is essential for correct analysis of low-resolution MS data for compounds of MW near 1,000 Da (or greater), and it can also be helpful in studying unknowns. As an example, low molecular weight compounds with two or more sulfur atoms will have negative mass defects.

7.3.4.3 Hyphenated Mass Spectrometry

Typically, MS is coupled or combined with separation methods such as gas chromatography (GC) or high-pressure liquid chromatography (LC) [32]. For many years GC–MS has been the method of choice in the analysis of complex nonpolar and low MW mixtures, including those from natural product extracts, human body fluids, toxic waste mixtures, industrial processes, and so on. It has been estimated that during the 1980s, about 2,000 papers were published each year in the GC–MS field. In GC–MS, spectra of acceptable quality are obtainable for every component that is separated by gas chromatography, even though the components may be present in nanogram quantities and eluted over periods of only a few seconds. A plot of total ion current vs. time provides a visualization of the retention time and the quantities of individual components eluted from the

GC or LC column. Valuable alternative views of such GC data can be obtained from reconstruction of the GC trace using selected ions such as those characteristic of a particular fragmentation process. Another important tactic involves comparison of the full MS of each GC peak to those within libraries of spectra; this facilitates the rapid identification of known compounds. Thus, GC–MS and LC–MS are widely used as important analytical tools.

7.3.4.4 Tandem Mass Spectrometry (MS–MS)

This technique has grown very rapidly as a tool in biochemical research during the last 5 years [33]. It also has great potential value in organic structure analysis, but it has been somewhat ignored by contemporary researchers engaged in structure elucidation and identification of organic compounds. Tandem mass spectrometry includes several techniques where mass chosen ions are subjected to a second mass spectrometric analysis. MS–MS takes advantage of fragmentations that occur in the field-free regions of magnetic sector instruments or in a collision region of a multiple quadrupole apparatus.

The strategy of collisionally activated decomposition (CAD), also known as collision-induced dissociation (CID), is an important adjunct to the soft ionization techniques discussed. Recall that for soft ionization, the level of fragmentation is relatively low, yielding little or no structural information. The purpose of CAD is to regenerate a fragment ion pattern by subjecting a selected ion to collision with energetically rich species.

As noted above, one method employs collision of the ions with high-energy atoms of an inert gas (e.g., He or Ar) while another uses RF to activate the ions for fragmentation. Triple quadrupole instruments use low-energy (10–100 eV) RF collisions in the central quadrupole to initiate this process. If high energies are desired (~100 eV), then magnetic sector instruments must be used. Two other types of instruments utilizing the concept of MS–MS are ion traps and FT-ICR. Both employ the CAD process, which is then followed by ion detection. In addition, the CAD method has been extended to the analysis of multiply charged ions generated by ESI.

The greatest advantage of MS–MS is that it provides a way to establish an unequivocal relationship between a set of precursor and product ions. With such information in hand, it is possible to prove that a particular fragmentation mechanism is operating, which can be useful in pinpointing substructures or functional groups when diagnostic sets of ions are located. MS–MS can also distinguish between isomeric compounds expected to have different but predictable fragmentation patterns.

Depending on which analyzers are used, four main scan modes for tandem MS–MS can be distinguished (see Fig. 7.10):

- The *product-ion scan* mode is the most familiar mode of MS/MS operation and is very useful for the structure elucidation of an unknown. To obtain this spectrum, the first mass analyzer is set to transmit only the precursor ion chosen, and the second mass spectrometer is scanned over a desired m/z range.

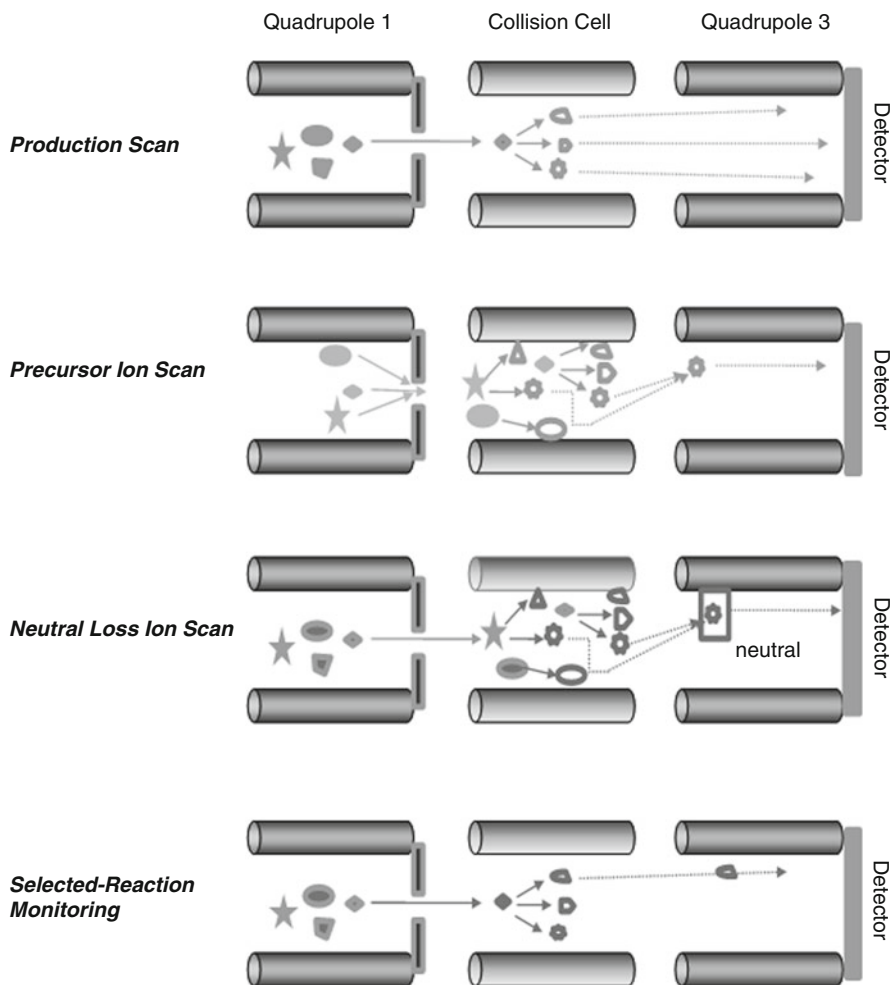


Fig. 7.10 Scan modes in tandem MS-MS

- The *precursor-ion scan* provides in the second analyzer a spectrum of all precursor ions that might fragment to a common, diagnostic product ion. This scan mode is useful for the identification of a closely related class of compounds in a mixture.
- In the *neutral-loss scan*, all precursors that suffer the loss of a particular common neutral fragment are examined. To acquire this information, both mass analyzers are scanned at the same time, but with a mass offset that links with the mass of the specified neutral (e.g., H₂O, CO₂, CO, N₂). This scan mode is similar to the precursor ion scan, being useful in the selective identification of closely related class of compounds in a mixture.
- *Selected reaction monitoring* (SRM) is similar to the product-ion scan. However, instead of scanning the second mass spectrometer in a broad mass range, the two

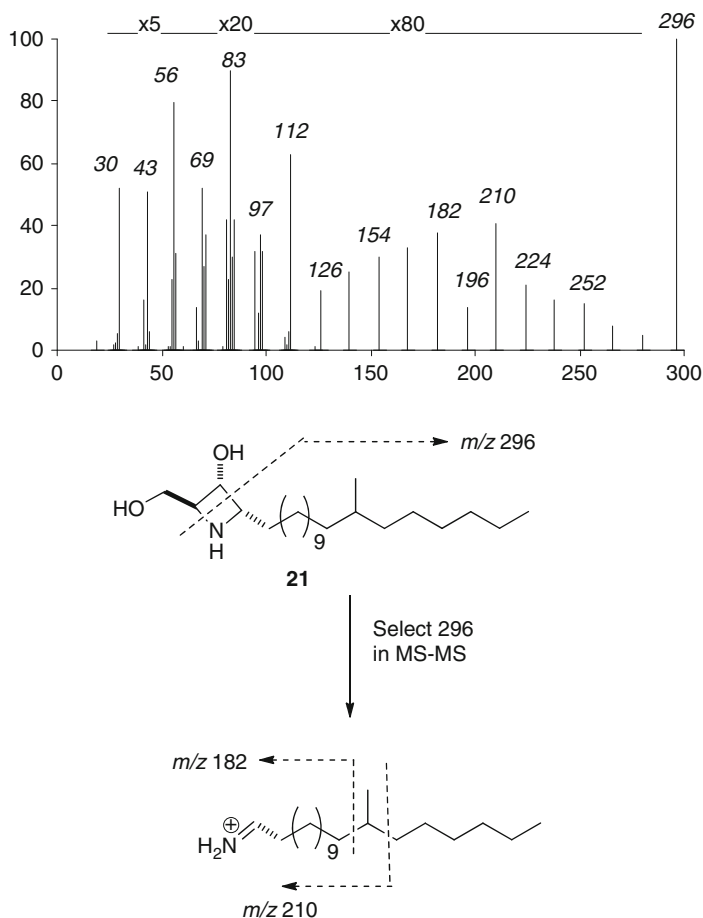


Fig. 7.11 Penazetidine (**21**) (MW 369): assignment of Me side chain by FABMS-MS

mass analyzers are adjusted to monitor one or more chosen precursor–product pairs. This technique is useful in quantitative measurements of analytes present in complex mixtures. When more than one reaction is monitored, the scan mode is termed *multiple reaction monitoring* (MRM).

A good example of product-ion scan mode is the location of the methyl group on the C18 side chain of penazetidine A (**21**) (MW 369) was established by FAB MS–MS data). The lack of dispersion in the 1D and 2D NMR spectrum of **21** meant that NMR data were not useful in addressing this issue. However, MS data were extremely valuable, and the first task was to select the positive fragment ion at m/z 296, not shown but detected by the first mass analyzer. The m/z 296 ion was then subjected to CAD which generated the spectrum shown in Fig. 7.11. This two-step process focuses the fragmentation on that typical of an alkane, so the reduced

intensity of the peak at m/z 196 could be used to specify the location where the methyl group was attached.

One of the most common applications of MS–MS is in the sequencing of peptides [34] which are first ionized by ESI or MALDI. In general, MH^+ species are selected for further CAD to produce a complex pattern of fragment ions.

7.4 Substructures, Working Structures, and Final Structures: Nuclear Magnetic Resonance (NMR)

More information about an unknown compound can be developed by obtaining NMR data for both protons and carbons [35]. Certain isotopes of these nuclei have magnetic properties, which is the characteristic required to generate NMR peaks. It is known that a spinning charge has an associated magnetic field, and much can be learned by briefly reviewing the magnetic characteristics of an electron before looking further at atomic nuclei. Two electrons occupying the same orbital can be distinguished because (by the Pauli exclusion principal) they must be spin paired. A single electron can have two possible spin “orientations”. Magnetic spin properties are further characterized by a fundamental parameter, the spin quantum number I , and its value provides a guide when writing out all possible quantized spin and energy states. The electron has $I = 1/2$, and the labels of $+1/2$ and $-1/2$ designate both its energy and spin states. Like an electron, some atomic nuclei have a spin, but, more importantly, there is a greater range of possible I values. As one example, the two isotopes of hydrogen have different I values. The most important ^1H isotope (protium, 99.98% abundance) has $I = 1/2$, so its magnetic properties, especially spin and energy states, are analogous to those of an electron. The ^2H isotope (deuterium, 0.02% abundance) has $I = 1$, and, as will be discussed later, its properties are somewhat different. Finally, one of the isotopes of carbon, ^{13}C (1.1% natural abundance), also has $I = 1/2$.

There are a large number of nuclides present in natural products which would be of interest for NMR. However, not many meet the strict criterion to be included in our final list of “commonly studied species.” Recall that those having $I = 1/2$ represent the optimal types. Two additional factors are a reasonable natural abundance and a general presence in organic compounds. Only ^1H , ^{13}C , ^{19}F , and ^{31}P meet these requirements, but it is just ^1H and ^{13}C that are common to *all* organic compounds. Consequently, these two nuclides will be the major focus of our attention here. There is a second list of nuclei that are growing in popularity, and this includes ^{15}N , ^2H , ^{11}B , and ^{29}Si . A species of high relative abundance, ^{14}N , that is not on this list also influences the appearance of NMR spectra. Thus, it will be important to consider how each of these nuclides affects the appearance of ^1H and ^{13}C spectra.

In order to get information out of NMR, different parameters can be computed. These include peak areas (integrals), chemical shifts (δ), coupling constants (J), and relaxation effects (especially nuclear Overhauser enhancement, NOE).

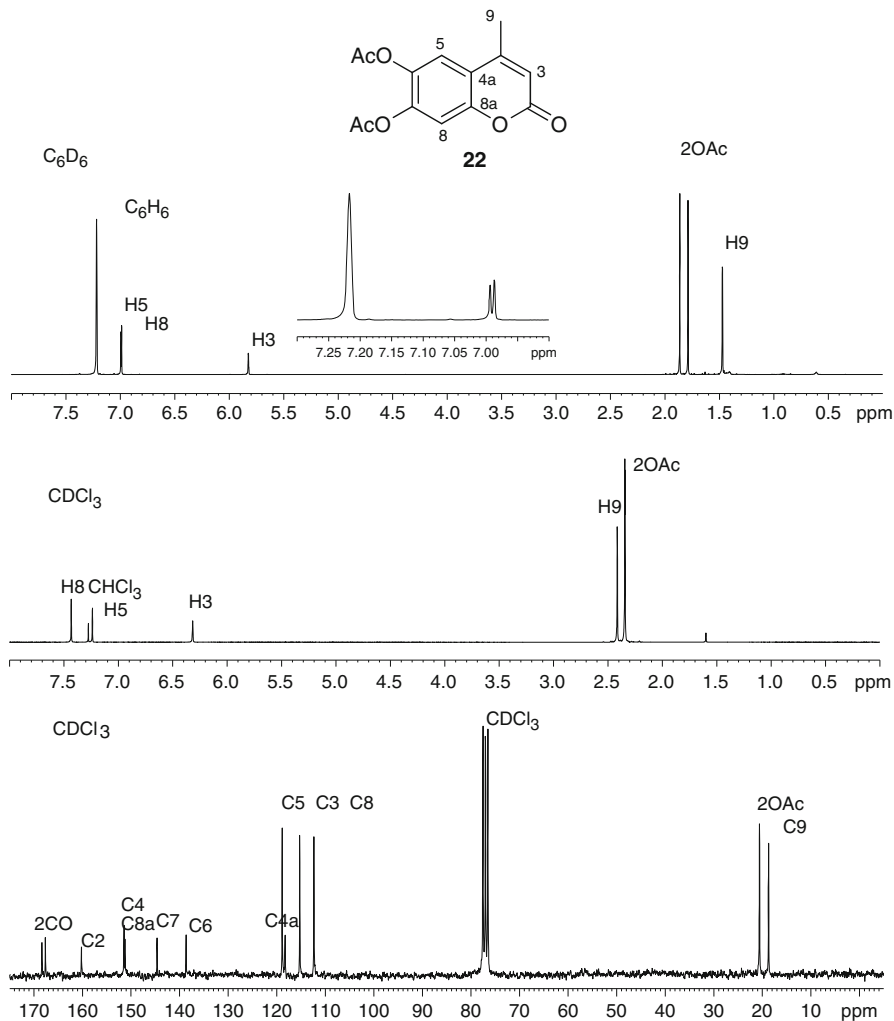


Fig. 7.12 ^1H (500MHz) and ^{13}C (62.3MHz) NMR spectra of 6,7-diacetoxy-4-methylcoumarin (**22**)

7.4.1 Chemical Shifts and Peak Areas

Since chemical shifts and peak areas are some of the first data employed in the analysis of organic structures, it is appropriate to examine briefly how such information is used. Let us inspect the ^{13}C and ^1H NMR spectra of 6,7-diacetoxy-4-methylcoumarin (**22**, $\text{C}_{14}\text{H}_{12}\text{O}_6$) shown in Fig. 7.12. Its ^{13}C NMR spectrum at 125 MHz contains single peaks for each carbon. It was obtained by the procedure of broadband proton decoupling to eliminate all proton J coupling effects. Twelve, rather than fourteen, peaks are observed in the ^{13}C NMR spectrum because

resonances accidentally overlap for the two OAc methyls and for C4a and C8a. At first glance, the ^1H NMR spectrum (500 MHz, CDCl_3 ; the tiny peak at δ 1.6 is due to H_2O) is also a bit confusing – the intense signal at δ 2.36 corresponds to two nonequivalent methyl groups. The ^1H NMR spectrum in benzene- d_6 (500 MHz) is more straightforward (the miniscule H_2O peak at δ 0.6 is closer to TMS) because there are six singlets that are resolved and the peak areas show three methyls, one vinyl H, and two aromatic Hs. Comparison of the ^{13}C NMR carbon count to that in the molecular formula indicates that the molecule is devoid of symmetry. The 11 carbon signals between δ 110 and 170 are due to four double bonds (the ^1H NMR suggests three trisubstituted double bonds) plus three ester groups. Collectively, these features make up seven of the nine unsaturations (calculated from the MF). Also, a tetrasubstituted benzenoid ring is evident from the two protons at δ 7.2–7.5 (CDCl_3); the methyl group δ_{H} 2.2 (CDCl_3) indicates that it is adjacent to an sp^2 center. Notice that the intensities of the ^{13}C NMR resonances in Fig. 7.12 are quite varied. Some peaks with a higher than expected intensity are due to the superposition of two carbons, but there is another factor which explains the low intensity peaks. Quaternary carbons often exhibit smaller peaks, and this can be helpful because it is therefore easier to identify them.

7.4.2 Factors that Determine Chemical Shifts

Early NMR spectrometers operated in a “field sweep” mode in which the magnetic field (B_0) was varied to bring each nucleus into resonance separately [36]. Second generation instruments incorporated a “frequency sweep” design to accomplish this same task, but the pulse Fourier transform technique is now the method of choice. Interestingly, many of the words used to describe relative chemical shifts (δ s) of peaks were derived from the original spectrometer design, and the NMR spectra were plotted with B_0 increasing from left to right. Thus, peaks close to TMS are said to be “upfield,” and those that are far away are “downfield.” Comparing the $^1\text{H}/^{13}\text{C}$ chemical shifts of tetramethylmethane at δ 0.89/ δ 27 to those of tetramethylsilane at δ 0.0/ δ 0.0 illustrates how increased electron density at the proton and carbon in TMS requires a higher B_0 for resonance (hence, “high field”). The greater electron density at the silicon atom of TMS generates a larger induced magnetic field B_0 , resulting in diamagnetic shielding (or an upfield shift) for its attached protons and carbon.

The chemical shifts evident in the NMR spectrum of 6,7-diacetoxy-4-methylcoumarin (Fig. 7.12) arise because the local magnetic fields experienced by protons and carbons in different parts of an organic molecule are not the same. Thus, chemical shifts represent alterations of B_{net} at individual nuclei, so the practice of reporting δ values as differences relative to a standard such as TMS is quite logical [37].

A major factor in ^1H NMR chemical shifts is the effect produced by the circulation of $1s$ hydrogen electrons, as well as the effects created by neighbors with π -orbitals. The effect arising from the electronic shielding of a nucleus

diminishes in proportion to the inverse of the distance between the nucleus and the valence electrons. Electronegativity greatly influences proton chemical shifts and provides a simple way to look at this effect.

The position of ^{13}C shifts is well known to be dominated by effects of electronic asymmetry. This effect increases proportionally to the sum of multiple bond contributions and the number of p -electrons. However, this dominant effect in heavy nuclei decreases proportionally to the average product of the electronic excitation energy, and the cube of the distance r between a p -electron and the nucleus.

7.4.3 Chemical Shift Positions of $^1\text{H}/^{13}\text{C}$ Attached to Common Functional Groups

A summary of the characteristic positions of various proton and carbon types appears in Tables 7.2 and 7.3, respectively. They provide important background information needed to begin to correlate functionality with chemical shift ranges. For example, comparison between the ^1H shifts in Table 7.2 and the ^{13}C shifts in Table 7.3 shows that carbons or hydrogens at sp^3 , sp^2 , or sp hybridized sites have the same relative chemical shift positions. This is also true for a variety of functional groups; alkyl groups attached to an aliphatic chain occur at highest field, whereas those attached to oxygen or halogen are in the middle. The CH resonances at sp^2 centers occur near the center when no heteroatoms are present, but the addition of O or N results in shifts to the left, and the aldehyde and ketone resonances are found to the far left.

It is important to become familiar with the chemical shift regions in both the ^{13}C and ^1H NMR where the most common groups resonate. Also note the differences of ^{13}C vs. ^1H chemical shifts. For example, the ^{13}C shifts of a polyene and a benzene ring occur in nearly the same region, whereas their ^1H shifts are distinctly separated. Aldehydes can be directly observed by ^1H NMR; other carbonyls cannot. As we will see, ^{13}C NMR represents a convenient tool for observing carbonyl groups because many of the various substructures have distinctive shifts.

The overall complexity of a molecular structure will determine the number of distinct chemical shifts observable in an NMR spectrum. Alternatively, there are circumstances where the tally of individual chemical shifts can be difficult to correlate to features of organic structure, especially in an unknown. For example, compounds possessing elements of symmetry or chirality represent one type of challenge. Another troublesome situation occurs for acyclic or cyclic compounds undergoing dynamic processes such as chemical exchange, intramolecular rearrangements associated with tautomeric equilibria, or conformational interconversions. Fundamental insights gained from a brief tour through principles of static and dynamic stereochemistry can be useful and should help in demystifying such situations [15].

There are two elements of symmetry to look for when examining a molecular structure. They are a rotational axis (C_n) and a mirror plane (σ) (a σ is equivalent to

Table 7.2 Proton chemical shifts of different functional groups

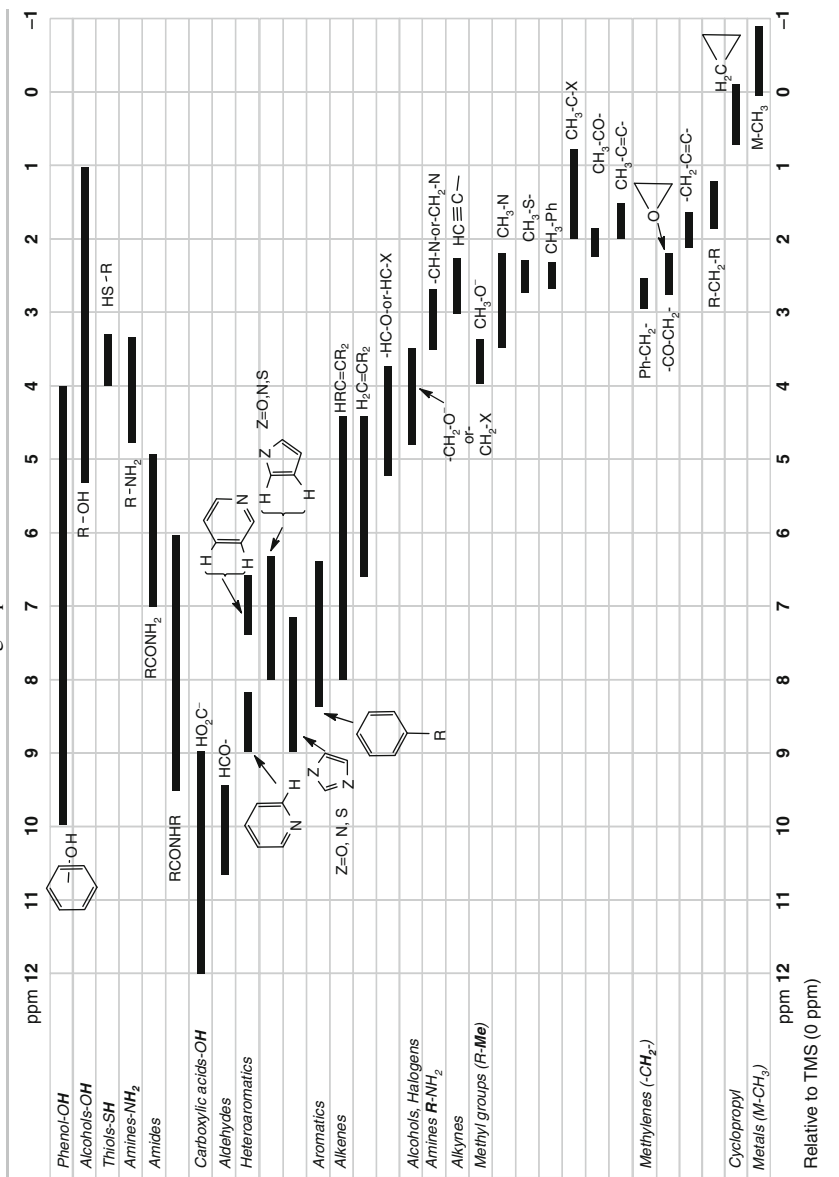
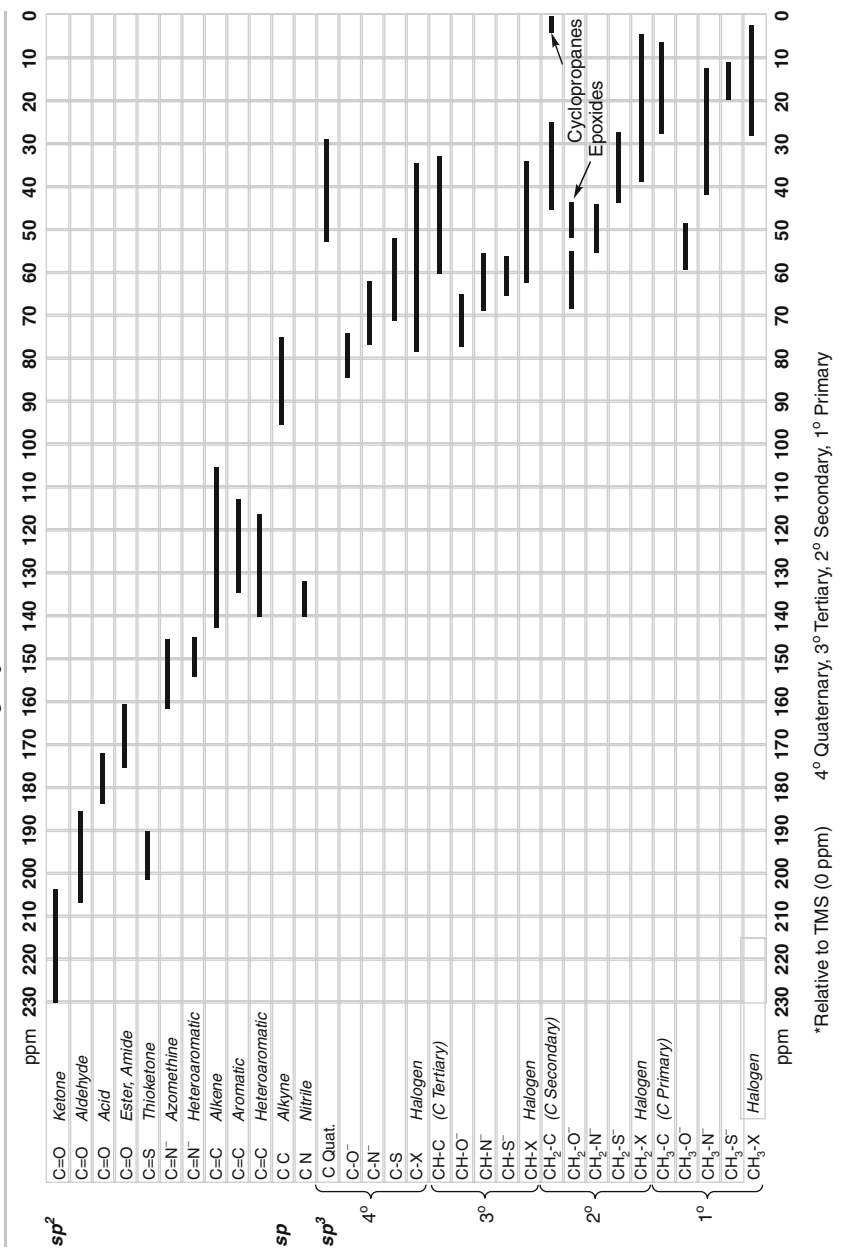


Table 7.3 Carbon chemical shifts of different functional groups

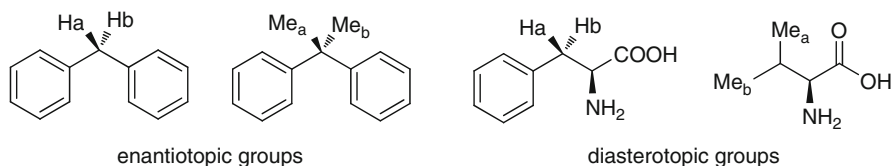
a rotation–reflection axis, S_n). When present, symmetry will allow absolute predictions to be made about the identical (*isochronous*) or nonidentical (*anisochronous*) chemical shifts expected for groups being compared. The best way to identify symmetry in a molecule is to be systematic. First look for a rotational axis (C_n); next search for a mirror plane (σ). The two symmetry elements can be used to relate groups that are either within the same molecule (i.e., an intramolecular comparison) or in different molecules (i.e., an intermolecular comparison).

Several widely used terms ending in “topic,” first coined by Professor Kurt Mislow at Princeton University in the 1960s, describe symmetry relationships between nuclei or groups using the C_n and σ symmetry operations. When two atoms or groups of atoms in the same molecule can be related by a C_n , they are called *homotopic* and will always have identical chemical shifts. Examples of homotopic protons are H_a and H_b in diphenyl methane and homotopic groups Me_a and Me_b in 2,2-diphenylpropane. When two groups can be related only by a σ , they are termed *enantiotopic* and will also have identical chemical shifts in normal solvents. Examples are enantiotopic protons H_a and H_b in benzyl alcohol and enantiotopic groups Me_a and Me_b in 2-phenylpropan-2-ol. Groups in an identical two-dimensional environment (e.g., same connectivity relationships) but not related by either a C_n or σ operation are termed *diastereotopic* and should have nonidentical chemical shifts in normal NMR solvents. Examples of diastereotopic protons and diastereotopic groups: the benzyl substructure bearing a chiral substituent (G^*) or a 2-phenylpropane substituted at C2 with G^* . Be sure that you understand the relationships present in this last example. It should also be apparent that when groups (or protons) being compared are in different structural environments, they should have nonidentical chemical shifts; these are sometimes called *heterotopic*.

Correctly identifying enantiotopic or diastereotopic groups in acyclic molecules can sometimes be troublesome. Also, predicting their NMR behavior in situations of dynamic motion can be difficult. Another point to be mindful of is that very often groups that are nonidentical are observed at the same chemical shift position. This is referred to as *accidental isochrony*, and it can occur in both ^{13}C and ^1H NMR for nuclei or groups that are heterotopic or diastereotopic (or enantiotopic being examined in a chiral solvent). The best way to resolve an inherent shift difference that seemingly cannot be observed is either to change the solvent (Fig. 7.12) or increase the magnetic field strength, or perhaps lower the temperature of the sample to slow down fluxional processes. It is useful to consider further how to identify enantiotopic or diastereotopic groups rapidly as well as recognizing dynamic processes that will unexpectedly simplify an NMR spectrum.

As an important rule of thumb, the presence of a single chiral (or stereogenic center) in either an acyclic or cyclic molecule is all that is needed to generate diastereotopic relationships. This often happens in compounds containing ethyl and isopropyl subunits. At this point, you should be able to recognize the enantiotopic relationships present for the methylene protons of ethanol and for the gem methyl groups of isopropanol. As noted previously, the presence of chiral substituents (G^*)

will make identical geminal groups diastereotopic and will resolve these species as separate NMR signals. The *i*-propyl moiety is considered to be an NMR “chiral reporter group,” and many researchers have used it to examine processes where chirality is created (e.g., by the introduction or presence of chiral centers, axes, or planes).



It is also important to highlight groups that are “symmetrical tops.” The most common are a methyl and a *t*-butyl, and they normally exhibit equivalent NMR signals. The protons of a methyl group and the methyl carbons and protons of a *t*-butyl group are homotopic under all circumstances where rapid rotation can occur. For a methyl in a compound that also contains a chiral center, there are three nonequivalent Hs present in each rotamer, but all three will be averaged to one type (e.g., they become equivalent) when interconversion between rotamers is rapid. The C–C bond rotational barrier is small (about 12 kJ/mol or 3 Kcal/mol), so the room temperature spectra of protons of a methyl *always* appear at the same chemical shift. An identical situation exists for the methyl groups in a *t*-butyl group. Namely, they are equivalent and occur at the same chemical shift in either ¹³C or ¹H NMR, owing to rapid rotamer interconversion. Alternatively, if restricted rotation about the C–C bond to the *t*-butyl quaternary carbon occurs, then three distinct methyl signals would be expected; this has been reported in the literature for some sterically hindered compounds.

7.4.4 Discovering Substructures from NMR: Scalar Coupling

The phenomenon of scalar coupling is prominently represented in most ¹H NMR spectra and often results in a large number of peaks being observed. Nuclei in close proximity with $I \neq 0$ having a small or zero electric quadrupole moment might exhibit the phenomena of “coupling,” which is unique to NMR. It arises from a nuclear spin–spin interaction transmitted by the bonding electrons of proximal atoms.

It is important to be able to distinguish between two different circumstances responsible for the closely spaced ¹H NMR peaks often less than 20 Hz apart. These can arise from spin–spin (*J*) coupled nonequivalent nuclei or isolated nonequivalent nuclei without any direct magnetic interaction. The *coupling constant* is the absolute separation (in Hz) between two or more peaks arising from coupling, and it is reported as a *J* value. The multiplets from $I = 1/2$ nuclei can sometimes be interpreted by the familiar rule: number of peaks = $n + 1$ (*n* is the count of neighbors).

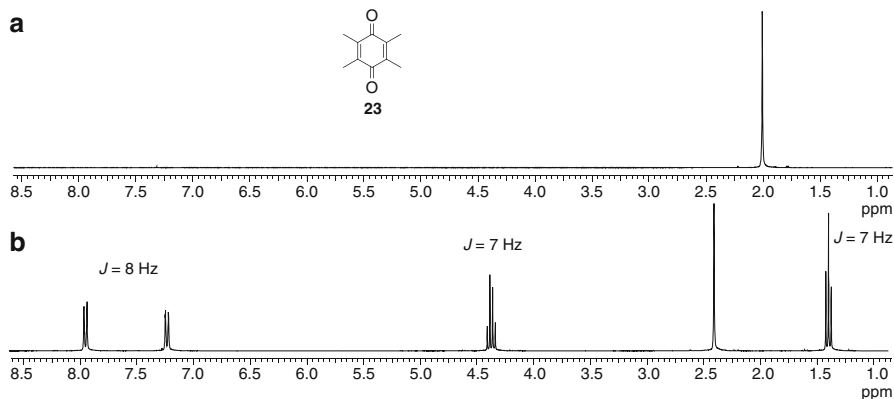


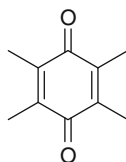
Fig. 7.13 ^1H NMR spectra of $\text{C}_{10}\text{H}_{12}\text{O}_2$ isomers (300MHz, CDCl_3)

It has been argued that the NMR J value is one of the most valuable parameters employed in the analysis of organic compounds. The process of establishing chains of $-\text{CH}_n-\text{CH}_m-$ moieties is greatly simplified by using J value information. Furthermore, having this data assists in the task of defining the conformations of flexible molecules and in establishing relative stereochemistry between pairs of substituents. Other features of the molecular structure can be decided by careful analysis of coupling patterns including carbon hybridization type, number of heteroatoms attached at CH_n , ring size, symmetry relationships, or the presence of dynamic processes.

Proficiency in translating multiplets into substructures and working structure is important in analyzing spectra of organic compounds. A simple example will be presented now to give a sampling of conclusions derived from analyzing multiplet patterns and coupling constant data. Consider the possible structures for two compounds of formula $\text{C}_{10}\text{H}_{12}\text{O}_2$, whose ^1H NMR spectra are shown in Fig. 7.13.

The ^1H NMR spectrum of one isomer (compound **23** in Fig. 7.13) displays just a singlet at δ_{H} 2.0, which is a mixed blessing. Observing multiplets that can be explained by the familiar $n + 1$ rule (recall that n is the number of neighbor protons) is the first step in piecing together carbon-carbon subunits. In general, singlet peaks indicate the lack of nearby protons but little else. In this case, the δ_{H} 2.0 chemical shift of the singlet resonance indicates the presence of sp^3 -type proton(s). In view of the molecular formula, four methyl groups are most likely attached to sp^2 carbons and related by symmetry. The $n + 1$ rule multiplets observable for the second isomer in Fig. 7.13b are informative, but the most important inferences again pertain to the chemical shifts, which can be measured and ascribed to three features as follows. The signals that resemble doublets ($J \approx 8$ Hz) at δ_{H} 7–8 are due to a 1,4-disubstituted benzene ring, the quartet-triplet pattern ($J \approx 7$ Hz) at δ_{H} 4.4 and 1.4 indicates an OCH_2CH_3 group, the singlet at δ_{H} 2.4 is characteristic of a methyl group attached to an sp^2 carbon, and the remaining atoms, from the molecular formula of $\text{C}_{10}\text{H}_{12}\text{O}_2$, must be a carbonyl group. These various subunits can be

straightforwardly combined to define either *p*-methoxyphenyl methyl ketone or ethyl 4-methylbenzoate. Returning to the compound in Fig. 7.13a and after much pondering, we can clearly see that a simple benzenoid ring will not fit the scant data. Once a tetramethyl quinone ring is visualized, then progress can be made, and only one possibility, the 1,4 quinone **23**, can be drawn.

**23**

The take home message illustrated by analysis of the data in Fig. 7.13 is that a worthwhile approach to structure analysis can take place for NMR spectra containing either single lines or many multiplets. Invaluable structural information will be derived by considering complex first-order multiplets, and it will be important to develop strategies to analyze these as well as non-first-order multiplets. We have briefly seen that NMR spectra comprised of mostly singlets can be problematic, and the lack of *J* value data may result in a protracted analysis process. As another complication, even after all of the *J*s have been analyzed, additional data are often needed to distinguish between a set of working structures. In such situations, more advanced NMR experiments are often undertaken to indirectly provide coupling constant data.

7.4.4.1 First-Order Spectra and the $n + 1$ Rule

There are a number of conditions that must be met for a multiplet cluster derived from spin–spin coupling to be considered as a *simple first-order* pattern. The most important is that all coupled spins have a ratio between the chemical shift difference in Hz and the spin coupling magnitude *J* of greater than 6 (expressed as $\Delta\nu/J > 6$) [38]. Another consideration is that when chemically equivalent protons (e.g., homotopic or enantiotopic) are present, they will be magnetically equivalent to one another. The intensities of first-order multiplet peaks will be the greatest at the center of the pattern, and approximately equal intensities should be observed for pairs of peaks equidistant from the midpoint of the multiplet cluster. Finally, peaks observed due to spin–spin coupling should correspond to the expression: $2nI + 1$ (*n* is a total count of neighboring nuclei that have the same *J* to the nucleus under consideration). In contrast to the preceding situation, a *complex first-order* pattern will not have peak intensity and peak counts that fit the relationships just described.

All simple first-order multiplets will have characteristic intensity patterns. The relative peak height will correspond to the coefficients obtained from the polynomial expression $(a + b)^n$. These can also be derived from Pascal's triangle where intensities are calculated by adding the numbers from the top down, as shown for multiplets in Fig. 7.14.

			1							<i>Singlet</i>	(s)						
			1		1					<i>Doublet</i>	(d)						
			1		2		1			<i>Triplet</i>	(t)						
			1		3		3		1	<i>Quartet</i>	(q)						
			1		4		6		4		1	<i>Pentet</i>	(p)				
			1		5		10		10		5		1	<i>Sextet</i>	(sx)		
			1		6		15		20		15		6		1	<i>Septet</i>	(sp)

Fig. 7.14 Intensity profile for basic multiplicities

To be more specific, a first-order multiplet will be observed for two protons coupled by $J = 7$ Hz with a chemical shift difference of greater than 42 Hz at 300 MHz, or 0.14 ppm. The advantage of obtaining proton NMR spectra at high fields is now obvious! At 600 MHz, protons coupled by $J = 7$ Hz need only be separated by 0.07 ppm to give a first-order spectrum, and this will be true for many spin systems.

There are three situations in which simple first-order multiplets will not be observed. The first case involves unequal coupling from two or more neighbors and results in *complex first-order multiplets* [39]. The second circumstance occurs when $\Delta\nu/J \leq 6$, and this produces convoluted patterns called *non-first-order multiplets*. The third situation involves coupling between sets of chemically equivalent (e.g., enantiotopic) but *magnetically nonequivalent nuclei*, and this also produces non-first-order multiplets. It is possible by simple inspection to measure J s in spectra containing complex first-order multiplets. By contrast, very few J s can be easily extracted from non-first-order multiplets. Usually such J s can only be obtained by using spectral simulation computer programs that provide an exact match of an experimental and calculated spectrum when the proper coupling constants and chemical shifts are entered.

7.4.4.2 Using Coupling Constants to Understand the Appearance of Spectra

The task of making ^1H and ^{13}C NMR spectral assignments can be accelerated when insights are applied from J value analysis. It is important to consider another fundamental issue pertaining to measuring J values for magnetically equivalent nuclei. Recall that *no* J multiplets will be seen between two protons having identical chemical shifts, either because of chemical equivalence or accidental isochrony between nonequivalent species.

Measuring proton vicinal couplings or $^3J_{\text{HH}}$ can be very important because useful structural information can be derived from the J value. The major determinants of $^3J_{\text{HH}}$ include the HCCH angle, the HCC angle, the C–C bond length, and the presence of electronegative atoms along the coupling path. When these factors

can be isolated, they provide a powerful application of J values to probe structural features. For example, the well-known Karplus equation (${}^3J_{\text{HH}} = A + B(\cos\Psi) + C(\cos 2\Psi)$) [40] is invaluable in analyzing vicinal couplings in rigid aliphatic systems. The correlation between angle HCCH (obtained from a Newman projection) and J (shown in the left panel of Fig. 7.15), or the relationship between bond order to J (not shown here), is often used to analyze saturated and unsaturated bonds, respectively. Shortly we will consider examples of how ${}^3J_{\text{HH}}$ values can be employed to make relative configuration assignments.

Two other couplings, ${}^3J_{\text{HC}}$ and ${}^2J_{\text{HC}}$, are sensitive to configuration and conformation, and it is often rewarding to measure them. The heteronuclear 3J values follow a Karplus-type pattern (see middle panel of Fig. 7.15) and provide angular relationship information. Obviously the value of ${}^2J_{\text{HC}}$ does not directly depend on a vicinal angular relationship, but there is an important twist. All ${}^2J_{\text{HC}}$ values are sensitive to the dihedral angle between a proton and an electronegative atom three bonds away, as shown in Fig. 7.15 (right panel), and this can be used to extract configuration information.

7.4.4.3 Coupling Constant Values for Different Carbon and Proton Types

Coupling constants can be measured between two nonequivalent ${}^1\text{H}$ s, ${}^{13}\text{C}$ s, or a ${}^1\text{H}$ and a ${}^{13}\text{C}$. In principle J s can be quantified between any other pair of $I \neq 0$ nuclei in close proximity [41]. Such data provide a powerful means to assess functionality, exact connectivity, symmetry, stereochemistry, or other parameters of molecular structure. Unlike chemical shifts, coupling constants are invariant at different magnetic field strengths, and they can be determined to an accuracy of ± 0.1 Hz.

To use J values effectively in organic structure analysis requires an understanding of the factors that influence their magnitudes. Empirical and theoretical work shows that the value of H–H or C–H couplings is influenced by the number of intervening bonds, electron density changes, angular relationships, bond hybridization, or electronegativity of atoms along the coupling path. The J values can be “+” or “–” as a function of alignment of nuclear spins. For a ${}^{13}\text{C}$ – ${}^1\text{H}$, the most stable orientation is both spins parallel to each other, which represents a positive coupling sign. The alternative where the two spins are antiparallel yields a negative coupling sign, but only absolute values are actually measured from an NMR trace. Theory predicts that normally 1J s are “+,” 2J s are “–,” and 3J s are “+,” but a negative magnetic moment (μ) species engaged in coupling will have “–” couplings. Both ${}^{15}\text{N}$ and ${}^{29}\text{Si}$ have a negative μ , so all of the ${}^{15}\text{N}$ – ${}^1\text{H}$ and ${}^{29}\text{Si}$ – ${}^1\text{H}$ J s will be negative.

There are some important problems connected with obtaining coupling constant data. Recall that only first-order or complex first-order spectra can be analyzed by sight to afford J data. Two nuclei can actually be coupled, but this may not be reflected in the spectrum. Keep in mind that different nuclei having the same chemical shift are sometimes referred to as isochronous. Protons with different δ s are referred to as anisochronous and multiplets will always be observed if they are proximate. Nevertheless, nonequivalent nuclei that are accidentally isochronous (same δ) will give singlet peaks!

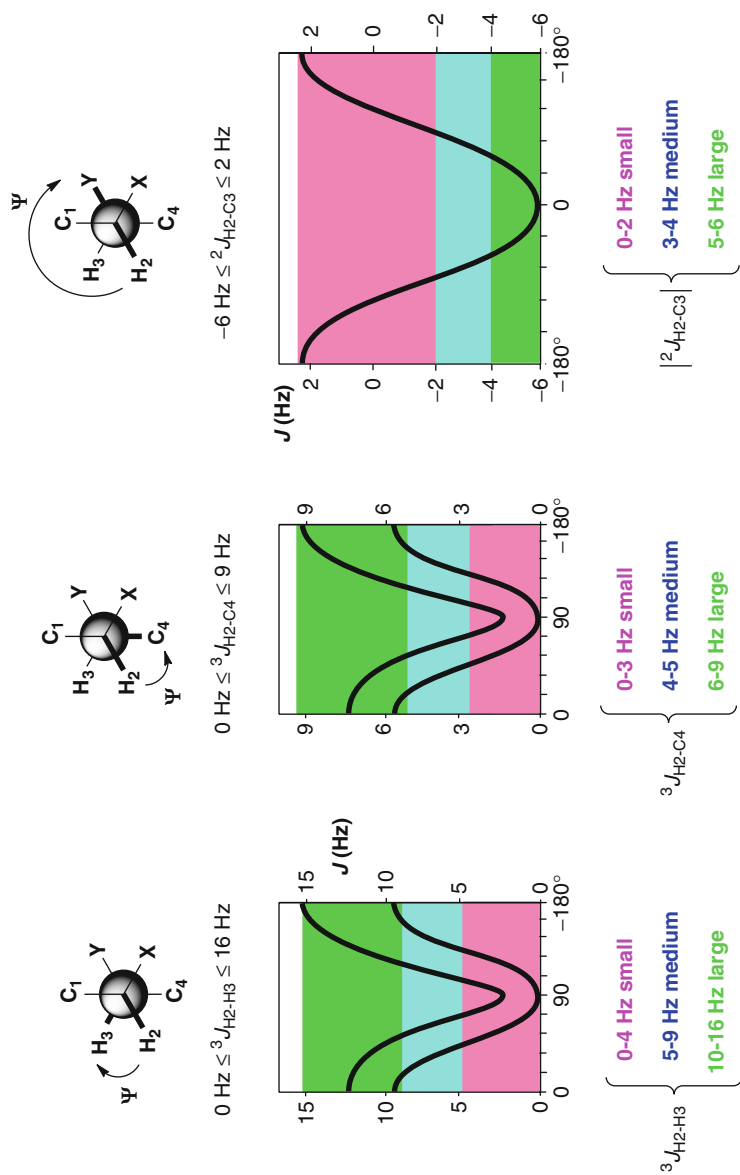
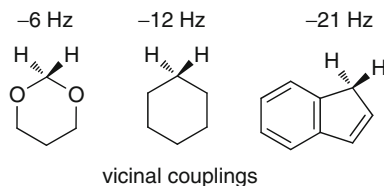


Fig. 7.15 Relationship between coupling constants (${}^3J_{\text{HH}}$, ${}^3J_{\text{HC}}$, ${}^2J_{\text{HC}}$) and dihedral angle (ψ); 3J upper curves – carbon frameworks without heteroatoms, lower curves – carbon frameworks with heteroatoms

One Bond Js. $^1J_{CH}$, $^1J_{CC}$. A linear relationship exists between the percent CH *s* character and the $^1J_{CH}$ magnitude according to the following equation: $\%s = (0.2)(^1J_{CH})$. The $^1J_{CH}$ coupling values range from 125 Hz for aliphatic, sp^3 (25% *s*), 157 Hz for vinyl, sp^2 to 250 Hz for alkyne, sp (50% *s*) carbons. While this correlation is only of minimal diagnostic value, the regular increase in the $^1J_{CH}$ magnitude with increasing electronegativity of substituents is highly useful as illustrated by the $^1J_{CHs}$ in the series CHZ, Z: Li (98 Hz), C (125–129 Hz), NR (131–134 Hz), OR (140 Hz). Typical values for $^1J_{CC}$ are 30–50 Hz, and these are easiest to measure in ^{13}C -labeled compounds.

Two Bond Js. $^2J_{CCH}$, $^2J_{HCH}$, $^2J_{CCC}$. A variety of 2J values can be observed for both homonuclear and heteronuclear interactions. Values of J_{HH} range from +3 Hz for CH_2 to -14 Hz for CH_2 , while the $^2J_{HC}$ vary from -6 Hz for HCC, +5 Hz for $HC=C$, +1–2 for benzenoid $HC=C$, to +50 for $HC\equiv C$; by contrast, the $^2J_{CC} \approx 0$. The large differences observed for $^2J_{HH}$ across an sp^2 vs. an sp^3 carbon are especially noteworthy. Diagnostic changes occur for aliphatic proton *Js* when at least two electronegative substituents are present, or for rigidly oriented adjacent π -bonds. These trends are illustrated by 2J_s in this series: cyclohexane (-12 Hz), 1,3-dioxane (-6 Hz), and indene (-21 Hz). Molecular orbital calculations have been able to simulate the direction rather than the real value of these trends.

The trends in $^2J_{CH}$ range from -5 to +50 Hz, parallel to those observed for $^2J_{HH}$. The orientation of adjacent electronegative groups can increase the coupling magnitude; this has been useful in conformational analysis studies of carbohydrates. Larger values are observed when the coupling path includes an sp^2 carbon, but this does not apply to benzenoid aromatics. This can be seen by comparing the $^2J_{CH}$ data for benzene (1 Hz) to that of furan (5–7 Hz).

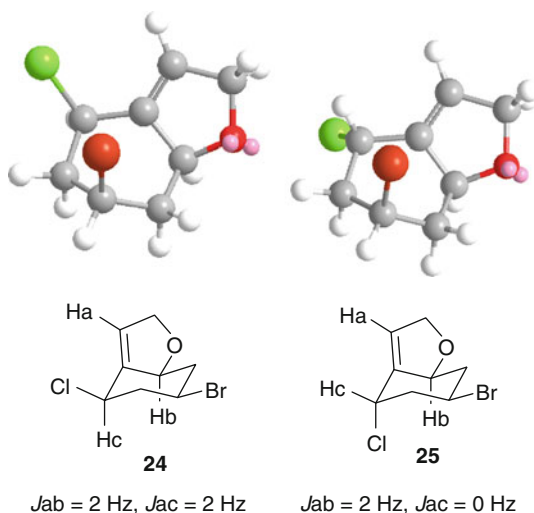


Three Bond Js. $^3J_{HCCH}$, $^3J_{HCCC}$, $^3J_{CCCC}$. Vicinal couplings are routinely employed in structure analysis. Vicinal 3J values for ethane are typified by $^3J_{HH} = +7$ Hz, $^3J_{CH} = +6$ Hz, and $^3J_{CC} = +4$ Hz (propane). A similar trend is observed for this series across double bonds. Collectively these data illustrate that substitution of a proton by a carbon reduces the coupling magnitude by a factor of approximately 0.6–0.8 given by the following relationship: $^3J_{CC} = (a)(^3J_{CH})$ and $^3J_{CH} = (a)(^3J_{HH})$, where $a = 0.6$ –0.8.

Four Bond Js. $^4J_{HCCC}$. Couplings between protons separated by four or more bonds (sometimes called long-range couplings) generally need not be included when applying the $n + 1$ rule. A $^4J_{HH} \approx 0$ is normal when the coupling path consists entirely of sp^3 bonds in an acyclic array. A series of exceptions to this are represented by some cases but are usually 2–3 Hz. An interesting situation is presented by rigid cyclic systems and exceptional among these are bicyclopentane

with a ${}^4J_{\text{HH}} = 18$ Hz and bicyclo (3.1.1) heptane with ${}^4J = 5.5$ Hz. The best opportunity to observe ${}^4J_{\text{HH}}$ is when the coupling path includes one or more sp^2 Cs, and J s from 2–4 Hz often occur. An important example is the benzene ring *meta* coupling of up to 3 Hz.

Both empirical results and theory show ${}^4J_{\text{HH}}$ is maximized when the coupling path atoms are in a “W” coplanar geometry. Only a single 4J from the “W” path is observed for bicyclohexane, even though there are several routes possible for this coupling. Values between 1 and 3 Hz can be observed when the coplanar Cs vary from all sp^3 to all sp^2 . The appearance of a ${}^4J_{\text{HH}}$ can be used to solve stereochemistry problems. For example, the 4J s in the halogenated natural products chondrocole A (**24**) and chondrocole B (**25**) allowed the determination of the stereochemistry of both H_b and H_c by the “W” couplings observed to H_a (build molecular models to verify these relationships).

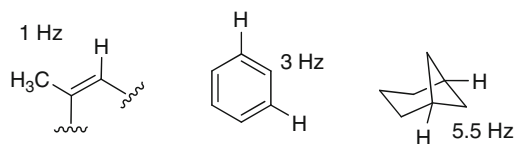


The Karplus relationship, shown previously in Fig. 7.15, is extremely useful because it provides a way to estimate stereochemistry from the J values of aliphatic systems. A graph of its parameters predicts the following correspondence between ${}^3J_{\text{HH}}$ and proton dihedral angle (ψ): $\psi = 0^\circ J = 11.5$; $\psi = 90^\circ J = 0$; $\psi = 180^\circ J = 13$. The subsequent modifications incorporated by the Altona equation [42] provide data for electronegative substituents in the coupling path, and a slight lowering in the magnitude of J is observed. The steep slope of the curve from 180° to 90° is what makes J data so effective in the stereochemical analysis of both acyclic and cyclic C–C chains. Parallel curves are observed for ${}^3J_{\text{CH}}$ and ${}^3J_{\text{CC}}$, and these couplings compared to those of ${}^3J_{\text{HH}}$ will allow you to estimate additional J s.

Assignment of axial or equatorial stereochemistry in a cyclohexane ring is a straightforward example of how to use the J vs. angular relationship in stereochemical analysis. The way ${}^3J_{\text{HH}}$ varies in a cyclohexane ring is illustrated by the appearance of the axial protons. Note that two vicinal diaxial cyclohexane ring Hs with a dihedral angle of 180° have a ${}^3J_{\text{ax-ax}} = 12$ Hz, whereas vicinal

axial–equatorial (or equatorial–equatorial) Hs with a dihedral angle of 60° have a ${}^3J_{\text{ax-eq}} = {}^3J_{\text{eq-eq}} = 4$ Hz.

Obtaining vicinal couplings for vinyl protons can be beneficial. The stereochemistry of a 1,2-disubstituted double bond can be quickly assigned via the angular variation of 3J s. The coupling constants for vinyl protons are *cis* = 11 Hz and *trans* = 17 Hz, and these data can be used to assign double bond geometry. The variation in *J* for an HC = CH with ring size change illustrates the influence of the angle HCC. This angle decreases in going from a cyclopropane to a larger ring while the *J* value increases, but the dihedral angle HCCH is constant and the change in *J* is as follows: cyclopropene (2 Hz), cyclobutene (5 Hz), cyclopentene (6 Hz), cyclohexene (10 Hz), and cycloheptene (11 Hz).



some long range proton-proton couplings

The presence of electronegative groups along the coupling path slightly reduces the magnitude of ${}^3J_{\text{HH}}$. It is reassuring that 3J s are still sensitive to stereochemical changes even when several electronegative groups are present. Be aware that variations of *J*s in accordance with the Karplus equation can also be seen in heterocyclic rings, for example, in the tetrahydropyran rings of carbohydrates.

An evaluation of the ${}^1\text{H}$ NMR spectrum for the marine compound cartilagineal (**26**) $\text{C}_{10}\text{H}_{11}\text{OCl}_3$ shows signals including multiplets for eight individual protons plus an intense methyl singlet. The ${}^{13}\text{C}$ NMR spectrum shown (Fig. 7.16b) has eight intense singlet peaks and two weaker signals. This spectrum was acquired with accompanying broadband proton decoupling to eliminate all J_{CH} multiplets which results in singlet peaks for each carbon.

Before real progress can be made in the assignment of the resonances of cartilagineal (**26**), it is essential to have ${}^{13}\text{C}$ NMR data showing multiplet information from ${}^1J_{\text{CH}}$. Rather than examining such a spectrum now, let us focus just on the results. This important multiplicity information is indicated in Fig. 7.16b by letters above each peak representing the count of attached protons such as S, D, T, and Q to indicate a C (singlet), a CH (doublet), a CH_2 (triplet), or a CH_3 -type residue (quartet), respectively. Observe that one or more of these carbon types are present in cartilagineal and are noted in the spectrum. There are two singlet carbons with the characteristic smaller intensities due to the absence of NOE that arises for a carbon with directly attached protons. Chemical shift differences expected for sp^2 and sp^3 carbons allow assignment of the quaternary signals such as C2 (δ 143.7) and C6 (δ 65). These characteristic chemical shifts plus α -substituent effects enable three of the six doublet carbons to be denoted as: C9 (δ 187), C1 (δ 143.9), and C5 (δ 70). A provisional assignment of C7 (δ 136) could be based on β -additivity effects which leaves C3 and C4 associated with the remaining two doublet carbons (δ 134 and 131). The last two carbons are a triplet C8 (δ 116) and a quartet (δ 24).

Turning now to the ^1H NMR resonances of cartilaginal (26), we find that each one can be definitively assigned. The intense upfield singlet resonance (δ 1.71) is associated with a methyl group, while the intense low field singlet peak (δ 7.05) is due to H1. The lowest field proton H9 (δ 9.04) is a d, $J = 2.0$ Hz, reflecting a 4J coupling by a “W” path to H3 (δ 6.49) a ddd, $J = 15.3, 2.0, 1.0$ Hz. This proton is in turn coupled to H4 (δ 7.05) a dd, $J = 15.3, 8.5$ Hz. In addition, the coupling to this

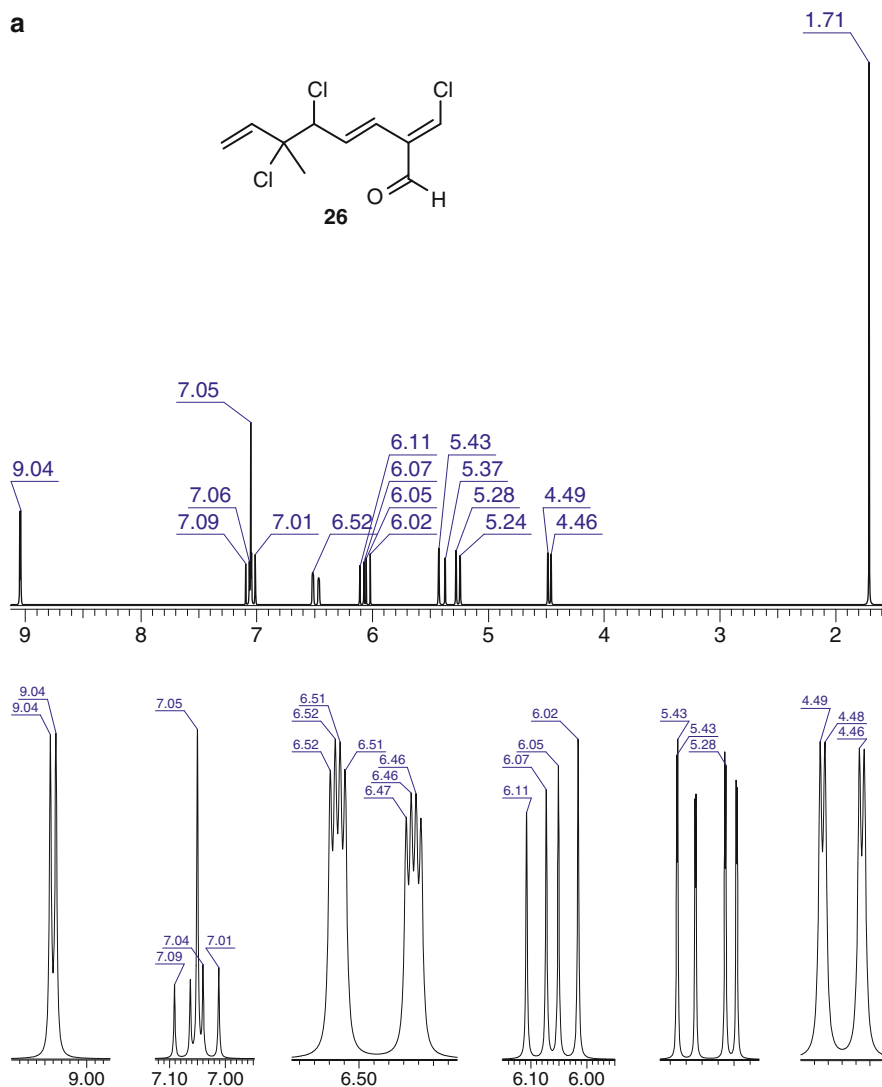


Fig. 7.16 (continued)

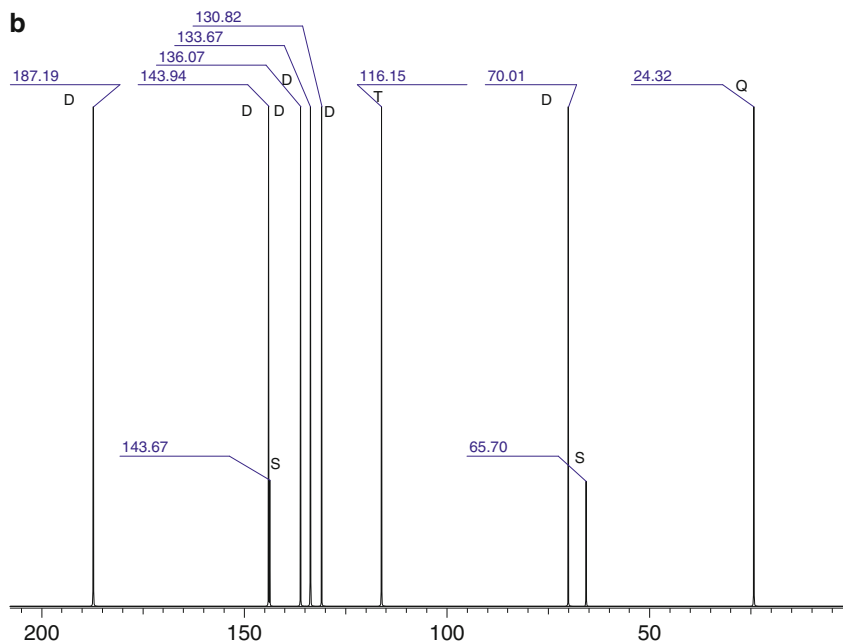


Fig. 7.16 (a) ^1H NMR spectra (CDCl_3 300MHz) of cartilagineal (**26**). (b) ^{13}C NMR spectra (CDCl_3 75MHz) of cartilagineal (**26**)

latter proton allows assignment of H5 (δ 4.47) a dd, $J = 8.5, 1.0$ Hz. The three remaining protons display the characteristic pattern of an isolated vinyl group: H8 (δ 5.26) a dd, $J = 10.5, 1.0$ Hz; H8 (δ 5.40) a dd, $J = 17.0, 1.0$ Hz; and H7 (δ 6.06) a dd, $J = 17.0, 10.5$ Hz.

7.4.4.4 Using Coupling Constants to Make Configurational Assignments

Let us now consider how a J value can be used to define geometrical relationships between substituents on varying molecular frameworks. Our focus will be on adjacent (1,2) or alternate (1,3) configurational centers along a carbon chain. An important element of the process involves cataloging relationships visualized by using Newman projections. Take a moment to revisit how changes in 3J and 2J data depend on dihedral angles (ψ), as indicated in Fig. 7.15. As will be further discussed next, the absolute J values shown are further summarized by a statement about the relative size (small, medium, or large), also defined below as $J_{\text{magnitude}}$.

Take a moment to examine the ^1H NMR spectrum (300 MHz, CDCl_3) of isopulegol (**27**) ($\text{C}_{10}\text{H}_{18}$) shown in Fig. 7.17. Try to assign as many protons as possible to the many multiplets observed. Even though the shapes of the multiplets can be assessed using the $n + 1$ rule, most of them are actually complex first order.

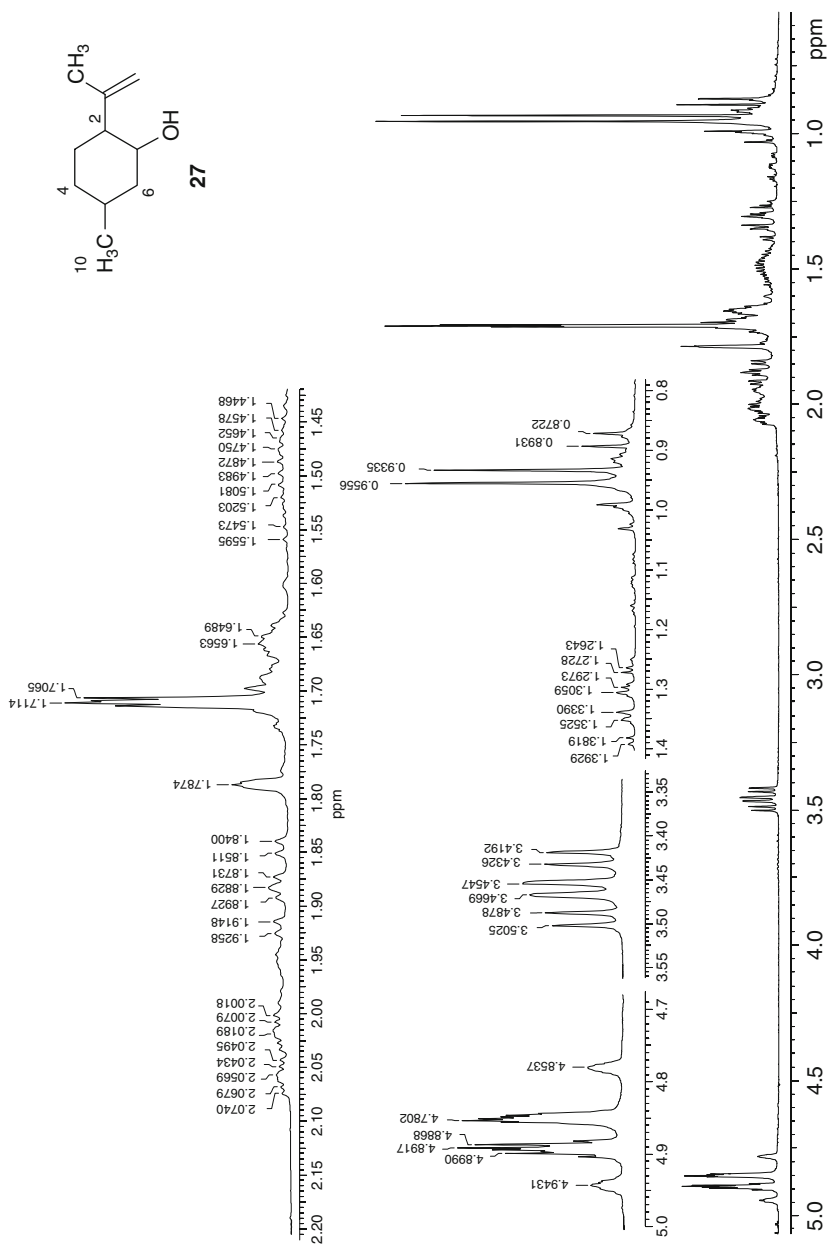


Fig. 7.17 ¹H NMR of isopulegol (CDCl₃, 300 MHz)

With this first inspection completed, it should now be possible to make a list of the J data for the Hs which will provide information to determine the ring conformation of **27** and establish the configuration of its substituents.

The major steps in translating the ^1H NMR data of isopulegol (**27**) into three-dimensional assignments are made using arguments already discussed. The first action, to define the conformation of the ring, is based on locating the J 's diagnostic for Hs at axial or equatorial positions. In this case, a rigid chair form can be confidently proposed for **27** based on observing large J 's diagnostic of bis-axial related protons. For example, the carbinol carbon H1 at δ_{H} 3.45 is a dt $J = 4, 10$ Hz with the large magnitude for the triplet arising from mutual coupling from axial Hs at positions 2 and 6. So the OH group can be concluded to be equatorial, and the propenyl group must also be equatorial. Further confirmation of the latter conclusion comes from looking at the allylic ring proton at position 2. It is expected to be at relatively low field and can be assigned to the ddd multiplet cluster centered at δ_{H} 1.88, $J = 3.3, 9.9, 12.9$ Hz (from two large axial–axial and one smaller axial–equatorial couplings). Clearly H2 is axial verifying that the geminal propenyl group is equatorial. Assessing the geometry at CH_3 10 cannot be decided based on H5, because this proton at δ_{H} 1.49 has a “forest” of peaks. Alternatively evaluating the couplings to axial H6 provides an unambiguous way to set the geometry of this methyl group. However, locating the resonance of axial H6 requires ingenuity because it is obscured by the doublet $J = 6.6$ resonance of CH_3 -10 at δ_{H} 0.94. The H6 axial multiplet appears as a 1:3:3:1 quartet, $J = 12.2$ Hz consisting of the following four transitions at δ_{H} 0.9960, 0.9556, 0.9336, and 0.8931 – but notice that two of these peaks overlap those of CH_3 -10! This quartet pattern is based on one $J_{\text{gem}} = 12.2$ and two $J_{\text{vic}} = 12.2$ Hz couplings. With the assignment completed, the presence of axial–axial coupling between H5 and H6 is now fully documented, making it possible to assign CH_3 -10 as equatorial. No more data analysis is needed to finalize the full configuration assignment of isopulegol (**28**).

Another strategy, which was introduced in 1999 and extends the power of using J s for configurational analysis of polysubstituted acyclic carbon frameworks, is the commonly called the “Murata J -based method” [43]. This is outlined in Fig. 7.18 and involves the evaluation of carbon chain fragment rotamers. The essence of the strategy is to draw Newman projections for the *syn* (threo) or *anti* (erythro) relative configurations of a four-carbon fragment and then use Karplus-type curves to translate the observed dihedral angles into J values. The approach is comprehensive in that it uses three sets of coupling constants: $^3J_{\text{HH}}$, $^3J_{\text{HC}}$, and $^2J_{\text{HC}}$. A series of rotamers drawn for each coupling reflect the three ranges of J s expected (see Fig. 7.18), and these are the basis for the nine rotamers shown in Fig. 7.18. In practice, only the staggered gauche and antirotamers represent NMR-relevant conformations, reducing the total to six. The several important requirements and assumptions connected with the use of the “Murata J -based method” are as follows:

(a) The carbon framework should be conformationally mobile. (b) The $^3J_{\text{HH}}$, $^3J_{\text{HC}}$ values must follow the Karplus relationship and arise from the anti and/or gauche conformations. (c) The substituents are limited to Y, Z = CH_3 , OH, OCH_3 , Cl, or Br. (d) Absolute J values can be used but must be accurately measured

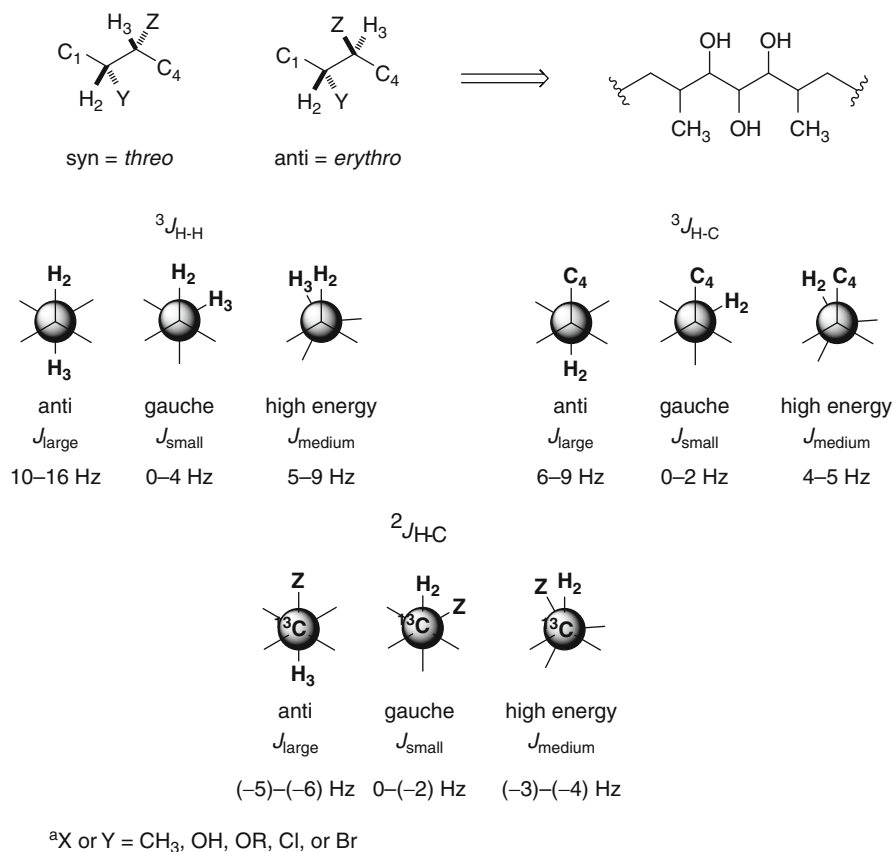


Fig. 7.18 The Murata J -based method to determine relative configurations in acyclic systems

(${}^3J_{\text{HH}}$ to 0.1 Hz; ${}^2J_{\text{HC}}$ and ${}^3J_{\text{HC}}$ to 1 Hz). (e) The conclusion about *syn* vs. *anti* configuration is based on the relative large vs. small J value which varies for each J type, as shown in Fig. 7.19.

The process for implementing the “Murata J -based method” involves obtaining the actual J value followed by substituting these data into a conclusion framework. The analysis is based on a review of six major rotamer forms shown in Fig. 7.18 – three (T1, T2, and T3) for the *threo* (*syn*) configuration, and three (E1, E2, and E3) for the *erythro* (*anti*) configuration. The key $J_{\text{magnitude}}$ results shown are for 42 different possibilities for a chain of four carbons containing the allowed Y and Z substituents. Do not forget that the $J_{\text{magnitudes}}$ indicated by “small” or “large” are relevant as indicated by the data in Fig. 7.19. Be aware that the J -based method cannot be employed when “medium” magnitudes are observed including ${}^3J_{\text{HH}} = 5$ to 9 Hz, ${}^3J_{\text{HC}} = 4$ to 5 Hz, and ${}^2J_{\text{HC}} = (-3)$ to (-4) Hz.

1,2 threo=syn	gauche (T1)	gauche (T2)	anti (T3)
$^3J_{H2-H3}$	small	small	large
$^3J_{H2-C4}$	small	large	small
$^3J_{C1-H3}$	small	large	small
X=Me Y=OR	$^3J_{CY-H3}$ $^2J_{C3-H2}$	large small	small large
X=OR Y=OR	$^2J_{C2-H3}$ $^2J_{C3-H2}$	small small	large large
1,2 erythro=anti	gauche (E1)	gauche (E2)	anti (E3)
$^3J_{H2-H3}$	large	small	small
$^3J_{H2-C4}$	small	large	small
$^3J_{C1-H3}$	small	small	large
X=Me Y=OR	$^3J_{CY-H3}$ $^2J_{C3-H2}$	small large	small small
X=OR Y=OR	$^2J_{C2-H3}$ $^2J_{C3-H2}$	large large	large small

Fig. 7.19 The logic network based on $J_{magnitudes}$ for use in the Murata J -based method to determine relative configurations

7.4.5 The Nuclear Overhauser Effect

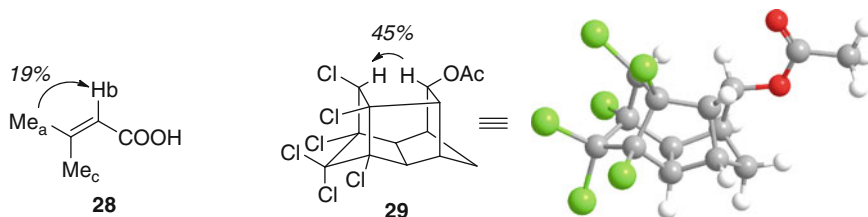
Under certain experimental conditions, unexpected increases or decreases can be observed in the integrated intensities of an NMR absorption. The first application of this phenomenon involved monitoring the intensity of one spin during low-power spin decoupling at a second. This provides what is now commonly called the nuclear Overhauser enhancement (NOE). Currently, there are a variety of situations where NOE data are used, and second generation approaches (often termed nuclear Overhauser effect) do not involve peak integration [44]. A very common application of the NOE is in 1H decoupling routinely used in acquiring ^{13}C NMR spectra. Such decoupling not only generates ^{13}C NMR singlets but it also provides nuclear Overhauser enhancements at carbon of up to 200%. Similarly, in homonuclear 1H NMR, a NOE of up to 50% is possible. The maximum percentage enhancement can

be predicted by the following Eq. 7.6, which is based on ratios of γ' (gyromagnetic ratio).

$$\% \text{ NOE epeak increase} = (100)\gamma'_A/2\gamma'_X \quad (7.6)$$

(A is the peak saturated; X is the peak observed)

In practice, small effects are actually observed in homonuclear ^1H NMR experiments. For example, 3-methyl-2-butenoic acid (**28**) often serves as a standard to ensure a proton NOE experiment is being properly performed. Irradiation of Me_b yields a 19% enhancement in the integrated area of H_a , while irradiation of Me_c results in a 2% decrease in the integrated area of H_a . Even more striking is an NOE observation for the “half-caged” compound **29**, because irradiation of H_a causes a 45% increase in the signal of H_b . Notice in these ^1H NMR examples the use of a concise convention, shown in the drawings of **28** and **29**, in which a curved arrow points from the irradiated proton toward the one experiencing the NOE.



Homonuclear ^1H NOE data are especially useful for making relative stereochemical assignments or in setting distance constraints for molecular modeling calculations. This is possible because the NOE offers an *indirect* measurement of dipolar coupling occurring between nuclei that are in close proximity. Such nuclei can interact by a through-space dipole–dipole relaxation mechanism. A rule of thumb states that the magnitude of an NOE is proportional to the inverse of the sixth power of the distance between two nuclei. However, this relationship must be applied cautiously because the dipole–dipole relaxation pathways that determine NOE magnitudes can be quite varied. Furthermore, molecular motion dynamics which also contribute to an NOE can be both random and variable in different parts of the same molecule. In spite of these potential complications, it is often stated that short, medium, or long-range NOEs are defined as H–H distances of up to 2.8 Å, 3.4 Å, or 4.2 Å, respectively. A further subdivision of the NOE intensities correlated to distance constraints includes [% intensity // distance in Å] strong = 6.1–14%/1.8–2.8 Å; medium = 4.1–6.0%/2.8–3.4 Å; and weak = 1.0–4.0%/3.4–5.0 Å. Finally, it is further assumed that interproton distances of greater than 5–6 Å cannot give a detectable NOE.

It is useful to briefly visit the origin of the nuclear Overhauser effect. Recall that the NOE is the signal intensity change of a first nucleus when the resonance (or transition) of a second nucleus is perturbed. A set of two $I = 1/2$ nuclei whose

distance is less than 5 Å which are interacting by dipole–dipole relaxation (sometimes called coupling) has six pathways for the relaxation mechanism. It is the dominance of one path over another which ultimately influences the type of NOE to be observed: positive, nil, or negative. In this regard, random molecular motions denoted as τ_c (rotational correlation time) occurring within the compound dictate which dipole–dipole relaxation pathway will prevail. Molecular size and molecular shape influences the magnitude of τ_c : Small molecules have short correlation times ($\tau_c \approx 10^{-12}$), and macromolecules have long correlation times ($\tau_c \approx 10^{-8}$). When τ_c is short, then a positive NOE will be observed, and when τ_c is long, then a negative NOE might be observed.

In summary, the technique of NOE difference spectroscopy is widely used and is certainly effective in homonuclear ^1H applications. However, there are two-dimensional methods such as NOESY (*nuclear Overhauser effect spectroscopy*) which are more attractive and are being increasingly applied to obtain NOE data.

7.4.6 Multipulse NMR

Success in using NMR data to assemble partial or total molecular structures depends on the accurate interpretation of just four parameters: chemical shifts, coupling constants, peak areas, and relaxation effects. Up to this point, we have been evaluating one-dimensional (1D) NMR spectra obtained by the “single-pulse” FT NMR method. Often 1D NMR data obtained at the highest available magnetic field do not provide enough information to complete a structure analysis or to assign the resonances in a complex spectrum. Two impediments are common, especially in ^1H NMR. The first involves spectra having many coincident resonances (overlap), and the second includes spectra where mostly proton singlets are observed. In both situations, the obstacle to further progress is the lack of interpretable J and/or δ values.

The only way to obtain accurate J and δ parameters in these cases is by 2D NMR spectroscopy. Some 2D NMR experiments simultaneously reveal all spin–spin couplings. Such data can be used to derive firm conclusions about connectivities between proton–proton, proton–carbon, and carbon–carbon subunits.

A large number of multidimensional NMR methods are available for routine use today. The acronyms for both 1D and 2D NMR techniques seem unusual, for example: COSY, NOESY, HOHAHA, DEPT, INADEQUATE, TOCSY, and HMBC (see [Tables 7.4](#) and [7.5](#) for more information about these and others). In this chapter, we will not consider all of the 1D and 2D NMR methods known. Instead, our focus will be on the principal strategies that provide useful information for molecular structure analysis.

Usually the first types of 2D NMR experiments performed are NMR, ^1H – ^1H COSY and ^1H – ^{13}C correlation spectroscopy (\approx HSQC or HMQC). These are valuable because all spin–spin couplings are simultaneously revealed between magnetically nonequivalent species of the same element (homonuclear) or between different elements (heteronuclear). Most of these techniques are concerned with

Table 7.4 One-dimensional NMR experiments useful for molecular structural studies

Information desired	Experiment	Nucleus	Results
Proton–proton connectivity	Homonuclear decoupling	^1H	^1H multiplets collapse
Proton–proton connectivity	1D-TOCSY	^1H	All protons within a J -coupled spin system appear upon selective excitation of one proton in the spin system
Number of protons attached to a carbon	DEPT	^{13}C	^{13}C – ^1H coupling revealed by positive intensity singlets for CH_3 and CH and negative singlets for CH_2 's with C's nulled DEPT
Spatial relationships	NOE	^1H	Changes in peak intensities that can be measured by difference spectroscopy Modern variant is a selective NOE experiment in which selective excitation of one proton leads to appearance of peaks in spectrum which are close in space
Exchange reaction mechanisms	DNMR	^{13}C , ^1H	Narrow lines at separate δ 's broaden and eventually merge by varying the temperature
Proton–carbon connectivity	SIMBA	^{13}C	Selective excitation at one carbon reveals coupled protons up to three bonds removed


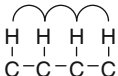

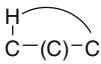
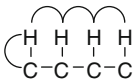
^1H and ^{13}C , but with small modifications, they can also be applied to other $I = 1/2$ nuclei common in organic molecules such as ^{31}P and ^{15}N .

7.4.6.1 One-Dimensional Multipulse NMR Techniques

A useful method to determine the multiplicity type of the carbon you are dealing with is the *distortionless enhancement by polarization transfer* (DEPT) experiment. The DEPT-135 spectrum displays CHs and CH_3 s as positive singlet peaks and CH_2 s as negative singlet peaks with the quaternary Cs nulled (Fig. 7.20). DEPT-45 gives all protonated carbons as positive peaks, while quaternary carbons are nulled. The DEPT-90 gives CH peaks positive with all other carbon peaks nulled. Automated editing (by addition and subtraction) of these three types of DEPT spectra taken can be used to obtain spectra which display only one carbon type. However, in practice, completely “clean” (e.g., CH_3 s only) edited spectra are difficult to obtain. Overall, the DEPT-135 is used most often as it gives the most information because a distinction can be made between CHs and CH_3 s, since peaks at lower chemical shifts ($< \delta$ 20) can be assigned to methyls (except CHs in cyclopropyl rings) and peaks at shifts greater than δ 30 to CHs (except *O*-methyls at δ 60 and *N*-methyls at δ 30–40). The major purpose of this experiment is to provide an unambiguous way to assign carbon types. Taken one step further, this data provides a count of carbons and protons that can be used to determine a partial molecular formula. We will see later how the same information can be obtained from edited ^1H – ^{13}C correlation experiments (edited HSQC).



The development of frequency selective, low power, “shaped” pulses has allowed a large number of new 1D pulse sequences to be developed. These are extremely useful, especially when there is a high degree of overlap in the

Table 7.5 Two Dimensional NMR experiments useful for molecular structural studies

Information desired	Experiment	Nucleus	Results	
Proton–proton couplings (vicinal proton connectivities)		^1H – ^1H COSY	^1H	Auto-correlated spectrum with frequencies along each axis and the diagonal. Off-diagonal contours, those that can be connected by a line perpendicular to the diagonal, show ^1H – ^1H spin-couplings
Long-range proton–proton couplings (all protons in one spin system)		^1H – ^1H TOCSY	^1H	Auto correlated spectrum like ^1H – ^1H COSY, showing geminal, vicinal and longer range couplings simultaneously depending on mixing time used. The intensity of the contour is independent of the coupling between the protons
Direct proton to carbon couplings (proton to carbon connectivities)		HMQC, HSQC	^{13}C , ^1H	Cross-correlated spectrum with proton frequencies along one axis and carbon frequencies along the second axis. Cross-peaks show one bond ^1H – ^{13}C couplings = 140 Hz
Long range proton–carbon couplings via a H–C–C or H–C–C–C coupling pathway		HMBC	^{13}C , ^1H	Cross-correlated spectrum with proton frequencies along one axis and carbon frequencies along the other. Intersection contours show ^1H – ^{13}C long range couplings = 5–10 Hz. Two or three bond correlations across quaternary C or heteroatoms possible
Long range proton–carbon couplings via a H–H–C coupling pathway (proton to carbon connectivities within one spin system)		HMQC-TOCSY, HSQC-TOCSY	^{13}C , ^1H	Cross-correlated spectrum with proton frequencies along one axis and carbon frequencies along the other. Shows direct responses (one bond) and multiple bond correlations (up to seven bonds depending on mixing time) on the same plot. Gives ^1H – ^1H connectivities equivalent to TOCSY spectrum, sorted by carbon chemical shifts Correlations across

(continued)

Table 7.5 (continued)

Information desired	Experiment	Nucleus	Results
Spatial relationships between protons		^1H - ^1H NOESY ^1H - ^1H ROESY	^1H Auto-correlated spectrum with frequencies along each axis and the diagonal. Off-diagonal contours, those that can be connected by a line at 90° to the diagonal, show ^1H - ^1H spin-couplings or NOE's
Carbon-carbon connectivities		INADEQUATE	^{13}C Double quantum spectrum with carbons as pairs of doublets for C-C units connected by a horizontal line ending at the f_2 value corresponding to the carbon chemical shift. The horizontal lines are separated along the f_1 frequency axis

corresponding area of the 1D spectrum. A selective pulse is shaped so that only one resonance in the NMR spectrum is excited, and it is possible to obtain a spectrum of that resonance alone, although this would be of little value in a structure elucidation process. The key is translating the information from the frequency domain (the chemical shift of the resonance to be excited) via an “inverse Fourier transform” into a shaped pulse in the time domain so that no other resonances are excited.

One of the most useful applications of selective pulses is in the selective 1D TOCSY spectrum, which is a one-dimensional variant of the ^1H - ^1H TOCSY. The pulse sequence is extremely simple. The selective (90°)_x pulse centered on the resonance of interest is followed by a spin-lock mixing period which is of variable length. During this period, transfer of magnetization occurs between the excited proton and adjacent protons within the spin system. The nature of the TOCSY mixing process means that protons in the spin system are excited in strict sequence, which makes this a powerful technique to simplify complex overlapping spectra and assign resonances to structural features very quickly as in the antibiotic amikacin (**30**). In this example H2 = 3.53 ppm, H3 = 3.65 ppm, H4 = 3.23 ppm, H5 = 3.88 ppm, and H6/6' = 3.32/3.01 ppm. In modular structures such as saccharides and peptides, exciting the easily identified anomeric protons or α -protons, respectively, permits the rapid assignment of all resonances and relative configurations of some of the chiral carbons (Fig. 7.21).

A second powerful experiment which relies on selective excitation by shaped pulses is the selective 1D NOE experiment in which a single resonance is excited and its through-space coupling partners identified. An example is given in Fig. 7.22

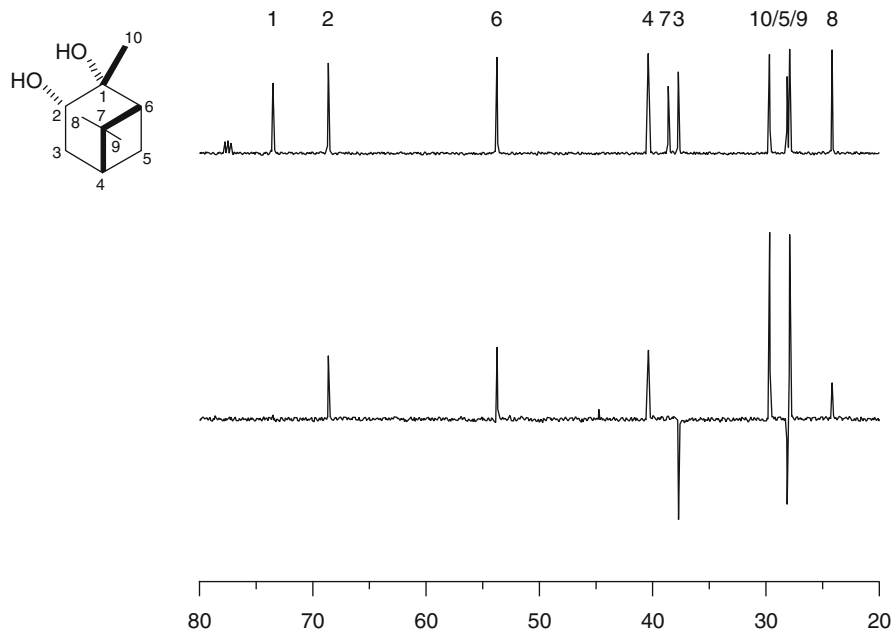


Fig. 7.20 ^{13}C NMR and DEPT-135 of (+)-pinane-1,2-diol (CDCl_3 , 125MHz). Signals have been phased so that CH_3 and CH are up, CH_2 is down, and C is nulled

for 2-chloro-dodec-2,11-dien-1-ol which contains a trisubstituted double bond, and for this reason, the stereochemistry cannot be determined using coupling constants. The *E* and *Z* configurations would give different NOEs for H1 (Fig. 7.22); for *E* we would expect H1–H4 and for *Z* we would expect H1–H3. For the *Z* configuration shown, H1 and H3 are in close proximity, whereas for the *E* geometry, H1 and H4 would be close in space. In this experiment, H1 was selectively excited and an NOE to H3 observed indicating that the *Z* geometry shown is correct. Note that the phase of the NOE peak is opposite to that of the excited peak, and that the spectrum contains very few artifacts compared to a typical NOE difference spectrum. Very weak NOEs can be detected using this pulse sequence, down to 1–2% in magnitude.

7.4.6.2 Two-Dimensional NMR Techniques

The groundwork for two-dimensional NMR experiments can be traced back to theoretical descriptions appearing during the mid-1970s. It took almost a decade of further development before such procedures became routine, work for which Richard Ernst received the Nobel Prize in 1991 [45]. The most important benefit of these methods is that individual chemical shifts and all coupling constants can be measured unequivocally even when multiplets are overlapping. Many 2D

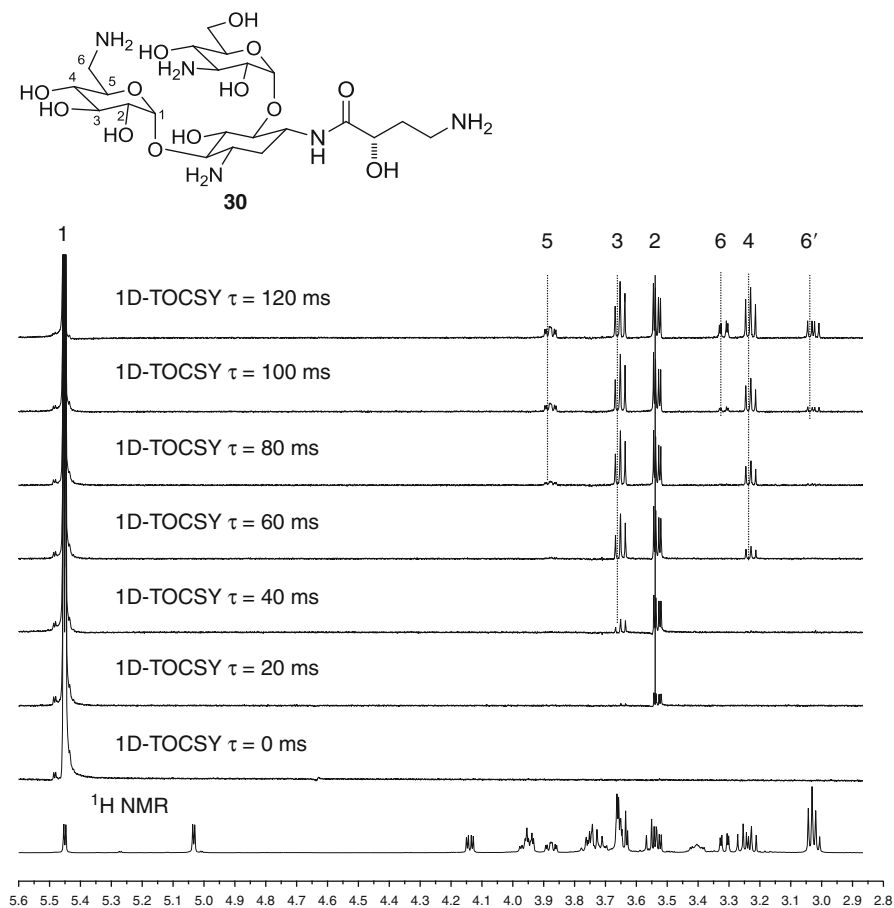


Fig. 7.21 The effect of increasing mixing times in the selective 1D-TOCSY pulse sequence carried out on amikacin (30). Irradiation at 5.45 ppm (H1)

experiments are made up of five basic “building blocks”: spin echo, polarization transfer (DEPT), COSY, TOCSY, and HMQC. Thus, an enormous number of 2D NMR procedures can be conceptualized by combining these building blocks, some of which will be discussed later.

Two-dimensional spectra are obtained by a modification of the approach used to obtain 1D multipulse spectra. The major difference is that the time domain 1D FIDs are further manipulated by incrementing the evolution time t_1 for each successive FID (n “increments”). A second FT converts the time dependence of the evolution into a second frequency, yielding a 2D spectrum where both axes are in frequency units; the f_2 axis is associated with the FID (the normal 1D spectrum), and the new axis f_1 is obtained as a result of the evolution period.

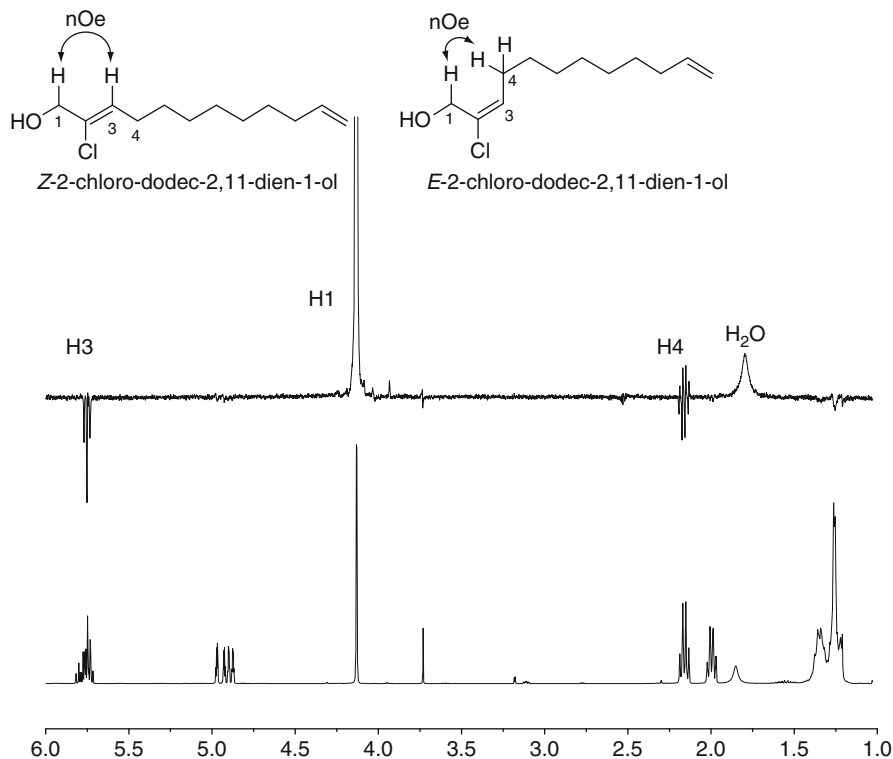


Fig. 7.22 The use of a selective 1D NOE experiment ($\tau = 800$ ms) to determine the stereochemistry of a trisubstituted double bond in 2-chloro-dodec-2,11-dien-1-ol

Most 2D experiments can be divided into auto-correlated or cross-correlated types. Multipulse procedures in which a magnetization (or coherence) transfer occurs within a homonuclear spin system represent auto-correlated experiments, and they produce what are called *off-diagonal* correlation peaks. Two commonly used auto-correlated experiments are the ^1H - ^1H COSY (proton-proton correlated spectroscopy) where homonuclear spin coupling serves to correlate protons along one axis to protons along a second and the 2D NOE (termed NOESY) where correlations between axes occur via homonuclear dipole-dipole interactions. In cross-correlated experiments, the magnetization of one nucleus is modulated by the coupling effects of heteronuclei. The 2D peaks appear at the intersection of f_1 and f_2 ; examples of this technique include ^1H - ^{13}C correlation spectroscopy experiments such as HMQC, HSQC, and HMBC.

Both auto-correlated and cross-correlated experiments are used to obtain data to link different NMR parameters that could not previously be observed easily in the same 1D NMR spectrum. For example, two-dimensional J spectra correlate ^1H chemical shifts on the f_2 axis to ^1H - ^1H spin coupling constants on the f_1 axis

(auto-correlated). Data from an often employed 2D NMR experiment, ^1H - ^1H COSY, have completely changed the approach to identifying protons that are mutually coupled with selective decoupling no longer being very common. Likewise, ^1H - ^{13}C correlation experiments provide invaluable 2D data, since overlapping protons can be resolved by the larger chemical shifts inherent in ^{13}C .

Inverse detection probes are available on most NMR instruments and allow observation of the ^1H FIDs after a pulse sequence has been applied at ^1H and ^{13}C . This approach was developed to deal with limited sample situations where low sensitivity of ^{13}C often gives unacceptable results. This technology takes advantage of the larger γ for ^1H , and it required both a change in probe design as well as the creation of quantum coherences during the experiment. These experiments cannot be described by the vector approach, but extensive explanations of them are in advanced monographs [46]. The key experiments which yield ^1H - ^{13}C correlation information are the HMQC (*heteronuclear multiple quantum coherence*) experiment and its equivalent HSQC (*heteronuclear single quantum coherence*) which give 1-bond H-C correlations and the HMBC (*heteronuclear multiple bond correlation*) experiment which gives 2-3 bond H-C information. In addition to inverse detected NMR methods, a major advance has been the routine application of pulsed field gradients (PFG) to allow the rapid acquisition of nearly artifact-free 2D NMR spectra through coherence pathway selection. Pulsed field gradients form the basis of magnetic resonance imaging, but their application to multidimensional NMR has increased what is possible by a large extent. In previous pulse sequences, "phase cycling" was necessary to remove artifacts, and sometimes these required up to 64 FIDs to be collected for each increment. The application of PFGs on suitable samples permits the acquisition of a single FID per increment, drastically reducing the time needed to acquire 2D NMR spectra. Most NMR instruments now employ PFGs in their pulse sequences to improve performance, and their implementation does not require operator input beyond the initial setting up of the parameters when the pulse sequence is first employed.

7.4.6.3 Strategies for Structure Determination Using 2D NMR

We have considered several multipulse 1D and 2D NMR experiments. These are extremely powerful in solving the connectivities and stereochemistry of the carbon skeleton of a compound under study. Summarized in Table 7.5 are the various proton-proton and proton-carbon connectivities that can be investigated using the most common 2D NMR experiments. A large number of acronyms are used to describe multipulse NMR experiments. These are spread throughout the chemical literature and are in common usage among many NMR spectroscopists. It is useful to review the various types of multipulse NMR spectra that can be employed in solving molecular structure and spectral assignment problems.

Different types of data can be derived from the 2D NMR spectra giving information on C-C (INADEQUATE), C-H (HSQC, HMBC), and H-H (COSY) connectivities. The most unambiguous of these are C-C correlations, but these can also be indirectly obtained from ^{13}C - ^1H and ^1H - ^1H data. Two strategies can be

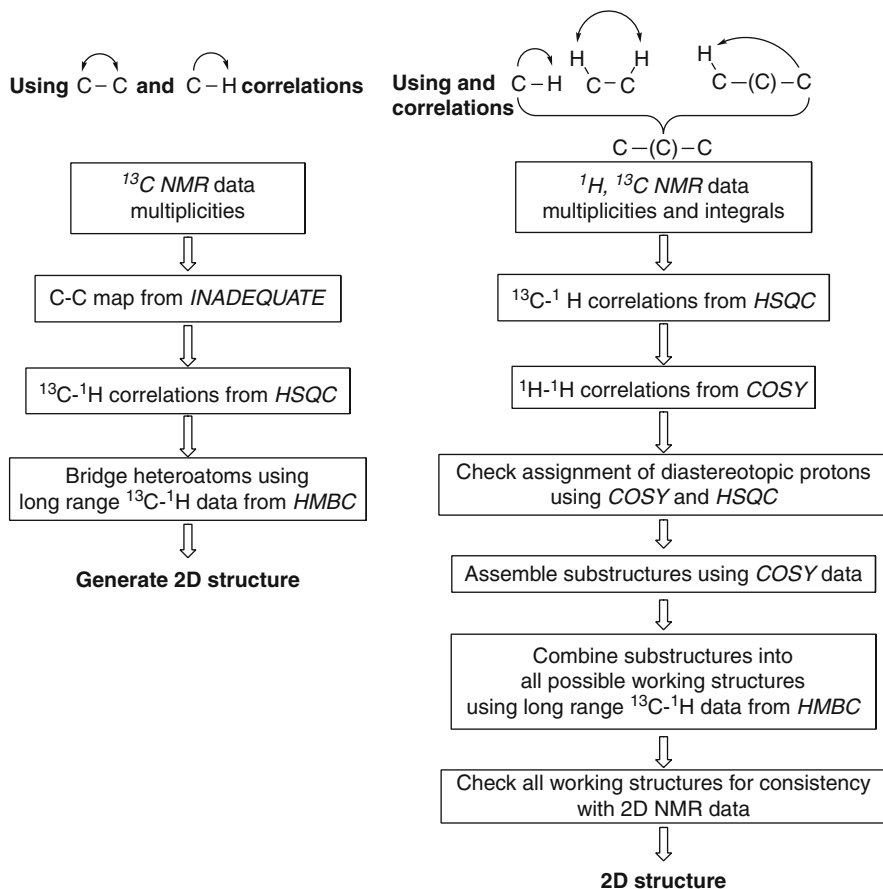


Fig. 7.23 Two possible structure elucidation strategies

envisaged to lead to a 2D structure (Fig. 7.23). The first relies on the use of the INADEQUATE experiment to directly obtain C-C correlations (Table 7.5), and this is complemented by the use of HMQC/HSQC data to obtain direct ^{13}C - ^1H information. This strategy would appear ideal as it gives rise to the carbon skeleton and proton assignments in two steps. For structures whose skeletons are interrupted by heteroatoms, the data have to be supplemented by the use of long-range ^{13}C - ^1H (HMBC) or through-space (NOE) data to bridge the gaps created by the heteroatoms. The alternative and more common strategy is one in which the direct ^{13}C - ^1H (HMQC/HSQC) correlations are used to assign protons to specific carbons, followed by the assembly of substructures using ^1H - ^1H (COSY) data. These substructures are then combined, and quaternary carbons included, using long-range ^{13}C - ^1H (HMBC) data (Fig. 7.23) to give a number of working structures which are confirmed using additional NMR experiments and comparison to literature data. The disadvantage of this strategy is that the HMBC technique gives both C-C-H

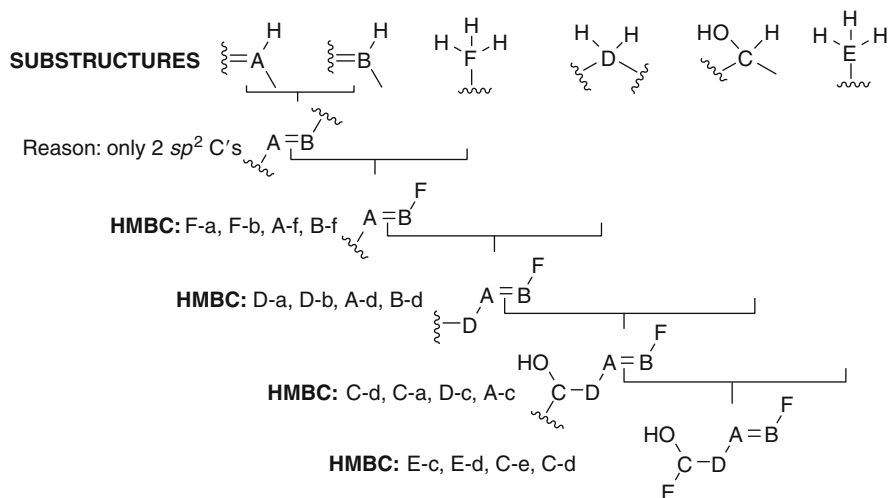


Fig. 7.24 Stepwise use of long-range data to assemble substructures into a secure 2D structure

(2-bond) and C–C–C–H (3-bond) correlations. Specialized pulse sequences such as the 1,1-ADEQUATE can be used to obtain 2-bond correlations only, which may assist in difficult structure determinations.

A simplified example of how such a process is completed using the second strategy is shown in Fig. 7.24. Obvious structural features such as double bonds should be assembled first, followed by the addition of substructures to satisfy the long-range correlations. In principle, two substructures are combined and assessed to determine whether the long-range correlations are satisfied. An iterative process leading to the correct structure then results in each step of the structure elucidation increasing the number of correlations that are satisfied. At the end of the process, the proposed 2D structure must satisfy *all* long-range correlations. The alternative, to assemble all possible structures from the substructures and then assessing these to see if they fit the long-range correlations, would lead to a very large number of possible structures (24 in this case, but far larger numbers for more complex structures) which would be difficult to achieve; hence, the strategy in Fig. 7.24 is inherently more sensible.

Table 7.6 summarizes the sample and time requirements for the two different approaches using standard 5-mm inverse detected probes. A concentrated sample and long acquisition time are necessary to execute the strategy depending on the INADEQUATE sequence. This is a “double quantum” method which involves suppressing the normal carbon singlet signals while enhancing the signals from pairs of adjacent carbons. The use of low volume probes, for mass-limited samples with high solubilities, or cryoprobe technology, means that INADEQUATE data can now be acquired on much smaller samples than previously possible.

Cryoprobes tuned for ^{13}C and ^{15}N are now available to obtain useful data in cases where the previous approach is unsuccessful and can yield a fourfold

Table 7.6 Comparison of typical sample and time requirements for two possible structure elucidation strategies

C–C strategy		C–H strategy	
Experiment	Time	Experiment	Time
^1H NMR	<1 min	^1H NMR	1 min
^{13}C NMR	<1 min	^{13}C NMR	1–4 h
DEPT-135	<1 min	DEPT-135	1–4 h
HSQC $nt = 1, ni = 256$	15 min	HSQC $nt = 4, ni = 256$	1 h
HMBC $nt = 1, ni = 512$	15 min	HMBC $nt = 4, ni = 512$	1 h
NOESY $nt = 4, ni = 256$	1 h	NOESY $nt = 4, ni = 256$	1 h
INADEQUATE	24 h	COSY $nt = 1, ni = 256$	15 min
Total time	~26 h		6–12 h
Sample conc	6 M		10–100 mM

nt number of transients (FIDs for each increment), *ni* number of increments

sensitivity advantage. More recently, parallel recording of different data types (^{13}C , C–C, direct and long-range C–H correlations) in a single experiment using such a probe allowed for the very fast structure determination of a small molecule. These techniques offer the possibility to revolutionize the elucidation of 2D structures, but are still at an early stage of application [47].

7.4.6.4 Use of NOESY and ROESY to Determine Relative Stereochemistry and Conformations

As it has been shown, the nuclear Overhauser enhancement (NOE) is critical in determining a molecule's relative stereochemistry. The two-dimensional equivalents of the NOE difference or selective 1D NOE experiments are the NOESY (*n*uclear *O*verhauser enhancement spectroscopy) and ROESY (*r*otating *O*verhauser enhancement spectroscopy) which are used under different circumstances. The appearance of a NOESY or ROESY spectrum is very similar to a COSY spectrum, but the cross peaks are due to dipole–dipole interactions through space rather than through-bond correlations as is the case for a COSY spectrum. An example of a NOESY spectrum is given in Fig. 7.25. Note that true NOE peaks are the opposite phase to the diagonal, and this fact can be used to differentiate them from artifact peaks (COSY peaks, which are positive). The mixing time is field dependent and should be set to the average T_1 for the protons in the ^1H NMR spectrum. The T_1 values can be determined using the inversion-recovery pulse sequence, but rather than a full calculation, a rule of thumb is to set the mixing time τ to the t_1 which results in a ^1H NMR spectrum with half the peaks pointing up and the other half pointing down.

The size of the NOE effect is proportional to the product of the Larmor frequency (ω_0 , which is proportional to the field strength) and the rotational correlation time τ_c (also known as the tumbling rate). The rotational correlation time is long for large molecules and short for small molecules. Small molecules have a maximum enhancement of 50%, whereas very large molecules have an enhancement of 100% in the opposite direction. However, for mid-sized molecules

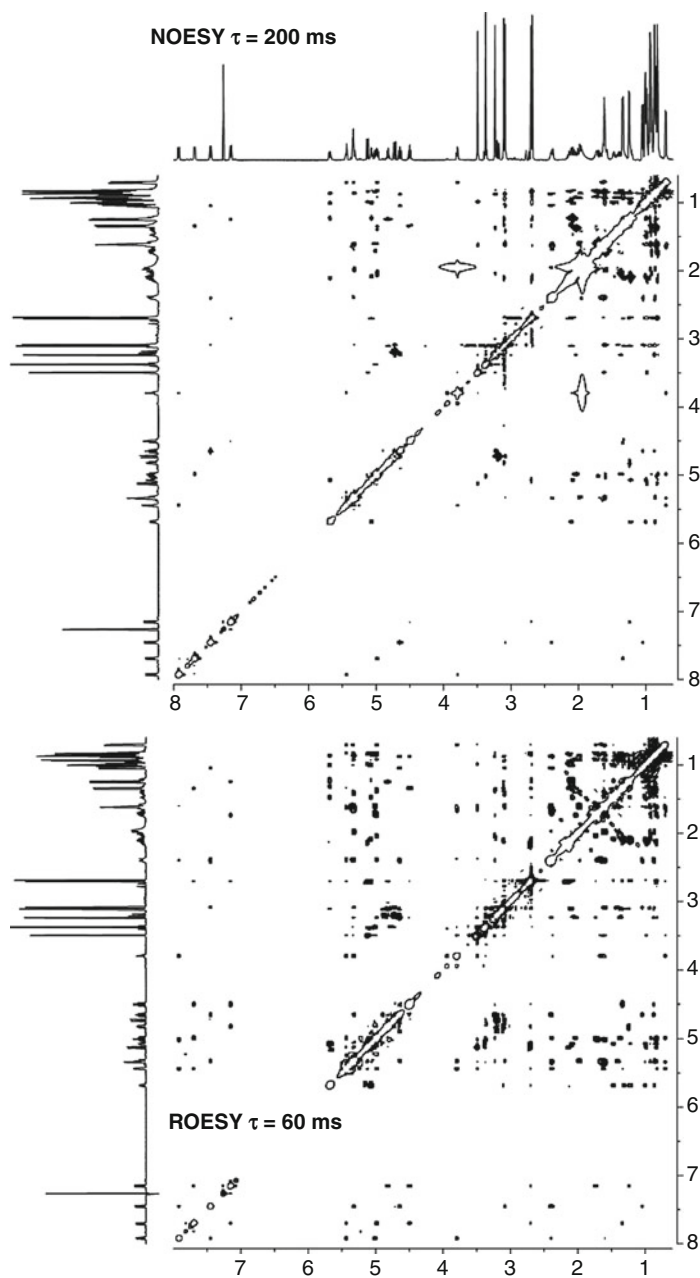


Fig. 7.25 A comparison of the NOESY ($\tau = 200$ ms) and ROESY ($\tau = 60$ ms) of the cyclic undecapeptide immunosuppressant cyclosporine (MW 1202) at 500 MHz. Multiple contours are negative and single contours are positive

(500–1,500 amu depending on their shape) $\omega_0\tau_c = 1$ and the NOE = 0, meaning that it is very difficult to obtain useful NOE data using a standard NOESY pulse sequence. For this size range, the ROESY experiment is ideal as the NOE is always positive and never crosses zero giving useful cross peaks for mid-sized molecules. Artifacts (TOCSY peaks) appear as antiphase peaks. The mixing time for a ROESY should be set to half the average T_1 determined as described above. A comparison of a NOESY and ROESY for a mid-sized molecule (cyclosporine A, MW = 1202) is shown in Fig. 7.25. Despite the longer mixing time in the NOESY, only very weak correlations are visible, whereas the ROESY taken with a short mixing time shows excellent correlations with greater intensity. This greater intensity in the ROESY also means that a larger number of correlations will be visible, and therefore, this is the preferred experiments when a NOESY experiment yields little data (e.g., when the molecular size and field strength multiply to give $\omega_0\tau_c = 1$).

NOE data can be very powerful when applied to solving the relative stereochemistry of complex molecules, particularly in conjunction with coupling constant-derived dihedral angles. It can be used for instance to make diastereotopic assignments or to determine if certain protons are on the same face of the molecule. The use of molecular modeling to determine relative stereochemistry when used together with NOE data can allow you to distinguish between different diastereomers. All possible stereoisomers can be subjected to a conformational search to determine their global energy minimum. Measurement of key distances can then be made to determine if they are consistent with the NOE data, remembering that the maximum possible distance for the NOE effect is 5 Å, but in practice, this is often much less. Be careful as in some cases a small NOE does not necessarily mean the two protons are not close in space as other effects may be involved. The possible structure that satisfies all of the NOE data is then a good candidate for the correct relative stereochemistry of the molecule under study.

7.4.6.5 Specialized Pulse Sequences

There are many 2D NMR pulse sequences that might be applied to solving a chemical structure, and the main ones in everyday use have been discussed in the previous sections and are listed in Table 7.5. There are a number of other more specialized sequences that you will need to be aware of that may be very useful in certain instances to solve complex problems. In addition to this, there are many, many more sequences that you will find in the current NMR literature that will not be discussed here [48].

We will begin with the discussion of a sequence that combines the features of the ^1H – ^{13}C correlation spectrum (HSQC) with the advantages of a DEPT-135. The edited HSQC gives both types of data simultaneously, thus obviating the need to obtain a separate DEPT-135 which saves time and can be a challenging experiment on dilute NMR samples. The use of inverse detected techniques brings with it an inherent sensitivity gain, and this is employed to great advantage here. The 1-bond correlations in the edited HSQC can be easily separated into CH/CH₃ and CH₂ using the phase of the correlation with the former being positive and the latter

negative. As discussed for DEPT, you can use chemical shift information as well as integrals of ^1H peaks to separate CH and CH_3 .

The task of establishing connectivities between protons separated by four or more bonds and between protons and carbons separated by two or more bonds is important. These constitute long-range relationships, and 2D NMR methods provide a way to interrelate such *pairs* of unconnected nuclei. There are three additional 2D techniques that can be used alongside the ^1H - ^1H COSY and HMBC (^1H - ^{13}C correlation, $J = 9$ Hz) to interrelate three or more nuclei at a time. All mutually coupled proton spins can be grouped from the cross peaks present in a TOCSY (*total correlation spectroscopy*) or its near equivalent, a HOHAHA (*homonuclear Hartmann-Hahn*) spectrum. The HMQC-TOCSY or HSQC-TOCSY experiment links together two 2D NMR procedures and provides a way to analyze crowded ^1H NMR spectra because additional resolution is provided along the ^{13}C chemical shifts.

Other sequences exist (e.g., ACCORDION) which allow acquisition of HMBC spectra with ranges of mixing times set from 2 to 25 Hz so that all possible $^{2-3}J_{\text{CH}}$ and some $^4J_{\text{CH}}$ are observed in one spectrum. Other variants of the HMBC sequence (e.g., HSQMBC or *J*-HMBC) are useful to obtain accurate $^{2-3}J_{\text{CH}}$ values to apply Murata's method of configurational analysis.

In many cases, it would be desirable to distinguish between $^2J_{\text{CH}}$ and $^3J_{\text{CH}}$ in an HMBC spectrum to aid the structure elucidation process. One experiment that makes this possible is the 1,1-ADEQUATE which reports only the $^2J_{\text{CH}}$ correlations and by comparison with the HMBC, which gives $^{2-3}J_{\text{CH}}$, allows the $^3J_{\text{CH}}$ to be distinguished. Despite this apparent usefulness, the experiment still requires more time than an HMBC, so it is often not used until a strict distinction between two and three bond C-H correlations is needed. Other variants of this experiment exist, and these are powerful in situations where there are quaternary carbons in a molecule which are more than three bonds from the nearest proton, and hence show no correlations in an HMBC. These experiments, called n,n-ADEQUATE, can give up to six-bond correlations and should be considered when you suspect such a situation may be at hand [49].

The TOCSY (\approx HOHAHA) technique identifies all mutually coupled protons, whereas the HMQC-TOCSY or HSQC-TOCSY method reveals connectivities between a CH and all other protons in the same spin system. The HMQC-TOCSY or HSQC-TOCSY spectrum is regarded as the most powerful among this trio because it can be applied in cases where a proton NMR spectrum is severely congested.

7.4.6.6 Experimental Measurement of $^{2,3}J_{\text{CH}}$ Couplings

Despite yielding valuable structural information, the low sensitivity of ^{13}C has meant that the measurement of heteronuclear coupling constants was very difficult until quite recently. In the last 10 years, spectroscopists have developed a large number of experiments to implement these measurements. There is no generally accepted method, and all have advantages and disadvantages. These experiments can be classified in two groups: HSQC-TOCSY and HMBC type.

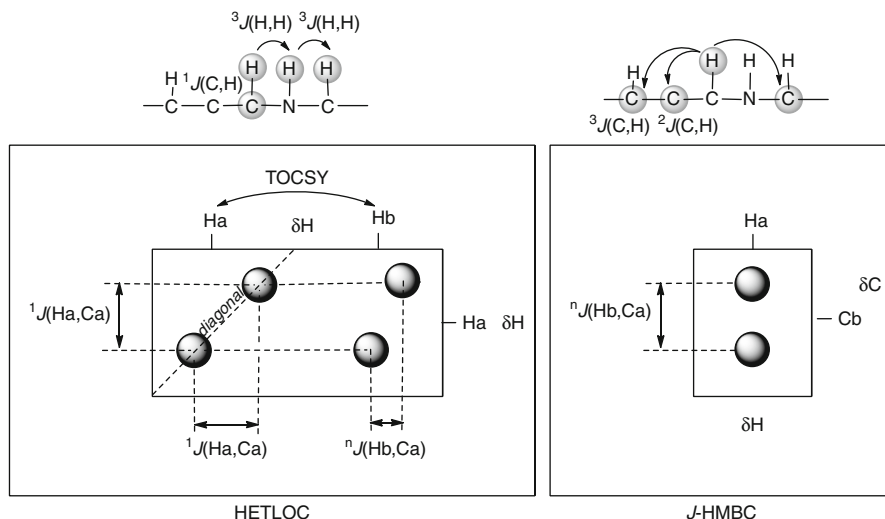


Fig. 7.26 Direct measurement of $^{2,3}J(CH)$ coupling constants through analysis of HETLOC cross peaks and J -HMBC

The original methods used by Murata were called 2D hetero half-filtered TOCSY (HETLOC) and a phase-sensitive heteronuclear multiple bond correlation (PS-HMBC). HETLOC is a two-dimensional homonuclear correlation experiment in which the usual TOCSY-type peaks are complemented in both dimensions by heteronuclear couplings (see Fig. 7.26). In particular, a correlation in the spectrum corresponding to long-range coupling between two protons (Ha and Hb) shows a diagonal displacement due to the heteronuclear direct coupling between Ha and Ca ($^1J_{CaHb}$). These two correlations also display a very valuable splitting in the second dimension due to the heteronuclear long-range coupling between Ha and Cb ($^2J_{CaHb}$ or $^3J_{CaHb}$). The major drawback in the HETLOC method lies in the intrinsic nature of the peaks: the two protons must belong to the same spin system and must exhibit a TOCSY correlation peak. For this reason, it is impossible to use this experiment to measure coupling constants between a proton and a quaternary carbon or a proton and a carbon belonging to a different spin system. To obtain these latter values, methods based on HMBC pulse sequences provide information on long-range couplings between protons and carbons separated by two or three bonds. Among others the J -HMBC experiment can be used to quantitatively analyze the proton-carbon coupling constants by observation of the splitting of HMBC correlations in the ^{13}C dimension. Also, an HMBC-type experiment is the HSQMBC which allows the measurement of long-range heteronuclear coupling constants from protonated carbons to quaternary carbons.

7.4.6.7 Computer-Assisted Structure Elucidation

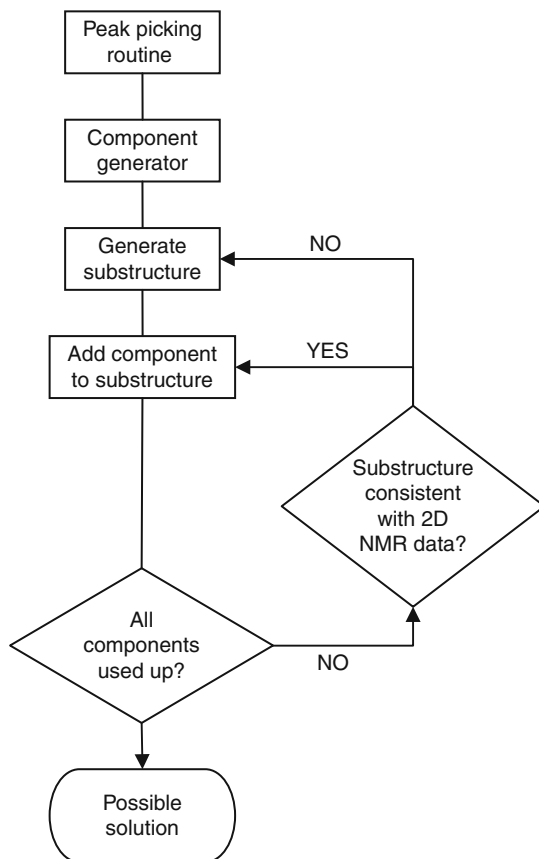
Many of the processes described in this chapter to derive a 2D molecular structure can be automated. Sophisticated computer programs now exist that can analyze 1D and 2D NMR data and, given a molecular formula or accurate mass, propose structures consistent with all the data. This is referred to as computer-assisted structure elucidation (CASE) [50], and their mode of operation is very similar to the human thought process, as depicted in Figs. 7.23 and 7.24. In all cases, a trained human operator is necessary to obtain reliable results from these programs. A simplified flow chart of CASE is shown in Fig. 7.26, and this is similar to the process depicted in Fig. 7.23 for the method using C–H and H–H information. The first step is peak picking which can either be done by the operator, or by the program, but the latter must be checked by the operator to ensure that noise peaks are not assigned as correlations. The use of pulsed-field gradients in 2D NMR pulse sequences means that noise levels are reduced and false peak picking is less likely. Typically the HSQC spectrum is assessed for correlations to protons at the 1D ^{13}C NMR resonance frequencies to give the direct C–H correlations. After this the COSY and HMBC spectra are analyzed for two and three bond correlations producing a number of data tables which are used to generate a number of components. These are then assembled as in Fig. 7.24, and after each stage, the substructure produced is checked to see if it satisfies the long-range correlations. If it does, then an additional component is added and the process repeated. If it does not satisfy the long-range correlation, then the component is removed and another added in its place and the new substructure assessed to see if it fits the long-range correlations. This cycle is repeated until all components are used up giving a possible solution to the problem, which should then be inspected by the human operator to see if it is chemically sensible and to check the ^{13}C NMR shifts against literature values (Fig. 7.27).

7.5 Complementary Spectroscopic Techniques: IR and UV

7.5.1 Confirming Functional Groups: Infrared Spectroscopy

All organic molecules absorb light in the infrared region of the electromagnetic spectrum due to vibrational changes in the chemical bonds between atoms [51]. The collection of vibration responses, called an IR spectrum, is distinct for every organic compound because the frequencies of these absorptions are sensitive to molecular structure. Prior to the widespread use of NMR data, infrared spectroscopy (IR) was considered the most important tool used to characterize an organic compound. Instrumentation for IR is relatively inexpensive and it is commonplace. Collecting an IR spectrum continues to be useful because it can provide invaluable information to identify functional groups. Very often IR spectra are also employed in analyses to compare samples suspected of being identical. A serious limitation is that specific information about atom connectivities or stereochemical features

Fig. 7.27 Simplified flowchart for the decision processes used by computer-assisted structure elucidation (CASE) programs



cannot usually be deduced by this method. As another important development, new generation IR spectrometers are being used in food science and technology applications to detect common organic substances. Such automated analyses provide quantitative estimates of important components of foods and beverages ranging from estimates of sugar compositions to the measurement of alcohol levels and beyond.

The IR wavelengths are typically divided into three subregions. These are the near IR ($4,000\text{--}13,000\text{ cm}^{-1}$, $2.5\text{--}0.8\text{ }\mu\text{m}$), the mid IR ($400\text{--}4,000\text{ cm}^{-1}$, $25\text{--}2.5\text{ }\mu\text{m}$), and the far IR ($400\text{--}40\text{ cm}^{-1}$, $250\text{--}25\text{ }\mu\text{m}$). It must be noted that the units most commonly used in IR spectroscopy are wavenumbers ν' in $\text{cm}^{-1} = 10,000/\mu\text{m}$. Only the mid-IR is of direct use in organic structure analysis because this is where the observed stretching vibrations occur that can be correlated to molecular structural features. Thus, the data sought from an IR trace are absorption band

positions and shapes, as well as semiquantitative peak intensities. Specific functional groups have “characteristic group frequencies,” and these are used to determine the functionality present in the molecule under investigation (see Fig. 7.28). This area of an IR spectrum, from 4,000 to 1,500 cm^{-1} , is usually referred to as the “functional group region.” In all cases an IR spectrum shows many more bands than can be easily correlated to structural features. Often only a few of the bands corresponding to particular functional groups are interpreted, whereas the rest are used only for detailed molecular comparisons. The so-called “fingerprint region” appears on the right hand side of an IR spectrum from 1,500 to 500 cm^{-1} . The peaks seen here arise from very complicated absorptions usually ascribed to all possible mechanisms of bending vibrations.

Introductory organic chemical texts usually point out that IR spectra taken under the same conditions for identical compounds must be the same. Also no two compounds (except enantiomers) will have identical IR “fingerprint” regions. It would therefore seem safe to assume that the IR of two identical samples ought to be identical, but care must be taken to compare data obtained under similar conditions. In fact, slight changes in band positions or shapes can be observed for the same compound in a solution as compared to a neat film or a KBr pellet. Also a spectrum of a compound in the crystalline state may contain more absorptions compared to that of a melt or of a sample in solution. Polymorphic crystals of the same compound can occasionally display nonidentical absorption bands.

The task of deciding which IR peaks confirm the presence or absence of a particular functional group is greatly simplified by the use of correlation charts or tables. The first place to begin this process is to note that Fig. 7.28 summarizes characteristic frequencies for a core group of substructures. Encyclopedic tables and discussions of small variations of frequencies for different functional groups can be found in a specialized text such as that by Socrates [52] or Colthup [53] or in compilations of IR spectra [54]. Be mindful that structural conclusions drawn from IR analysis can be readily correlated to that from ^{13}C NMR data, and this should be done whenever possible.

Using correlation charts does not involve matching each peak to a molecular structural feature. Instead, general regions of an IR spectrum are analyzed, and the three regions which should be initially scrutinized are the Z–H stretch region from 3,100 to 3,700 cm^{-1} , the C–H stretch region from 2,700 to 3,100 cm^{-1} , and the C = O/C = C stretch region from 1,600 to 1,850 cm^{-1} . Relative intensity of peaks should be noted, and a comparison might be considered for a spectrum run on a sample prepared as a mull or in a solvent such as CHCl_3 . Reference to correlation charts, tables, or data memorized from past experience is drawn on to identify the presence or absence of various functional groups.

To summarize, analysis of an IR spectrum will normally consist of the following steps:

- (a) Examine the functional group region to determine the presence or absence of peaks characteristic of common structural features such as: OH, NH, carbon types (sp^3 , sp^2 , sp carbons), C = O, C = C, and $\text{C}\equiv\text{N}$.

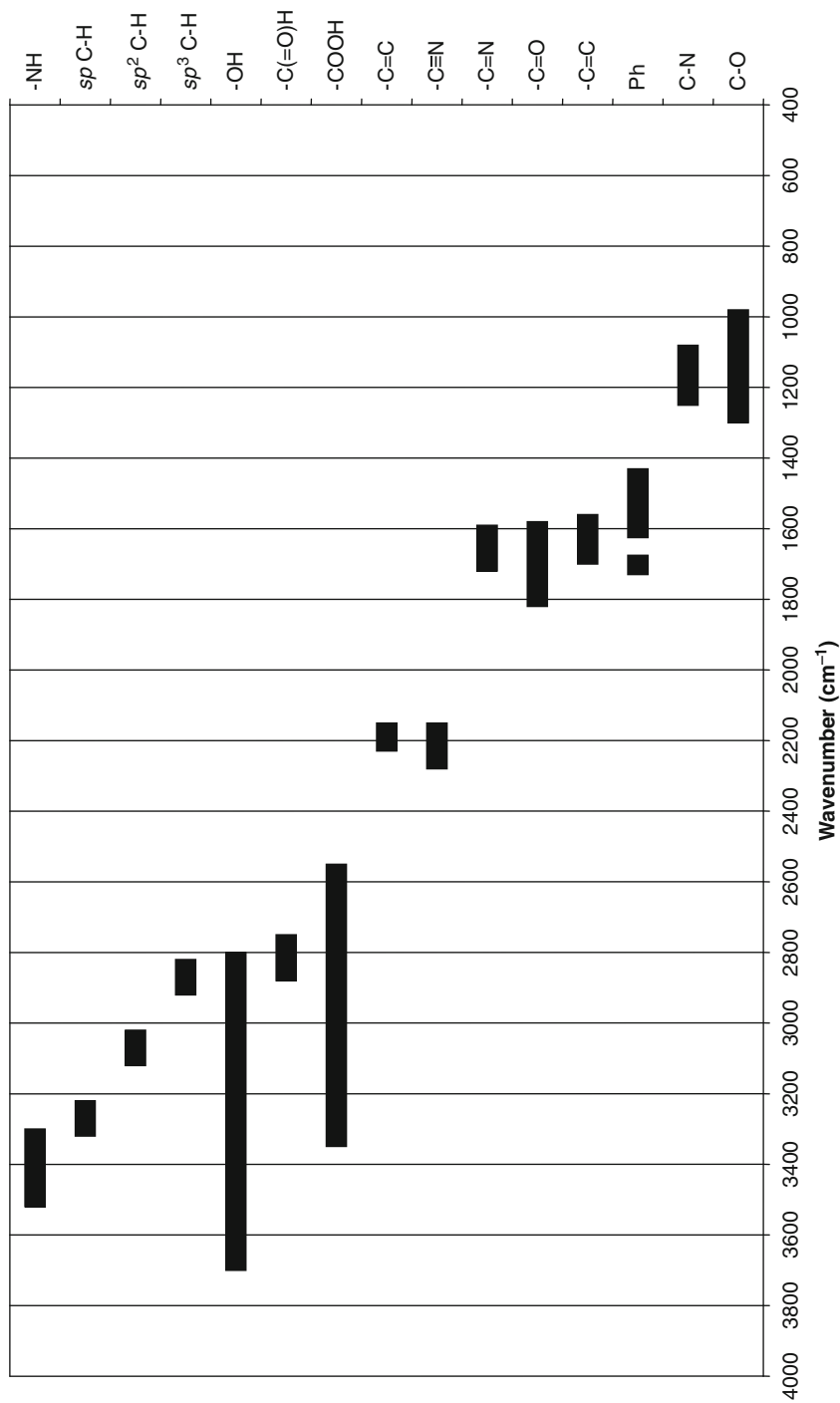


Fig. 7.28 A summary of IR bands for common functional groups

- (b) Confirm the presence of a particular structural feature by searching for bands which are complementary to the major functional group bands. As an example, the C–O stretch at $\approx 1,100\text{ cm}^{-1}$ would be expected to accompany an OH stretch at $3,300\text{ cm}^{-1}$, or an sp^2 C–H stretch at $2,720\text{ cm}^{-1}$ should accompany a C = O stretch at $1,720\text{ cm}^{-1}$ for an aldehyde.
- (c) Use ^{13}C NMR data to confirm inferences about a particular structural feature or to resolve ambiguities of a range of functional groups assignable to a particular band.
- (d) Use the “fingerprint” region to establish a positive identity for a known compound by comparison to spectral libraries. Two obvious difficulties to be expected are that water impurities or C = O overtones might be mistaken for an alcohol group, and many IR spectra are insensitive to stereochemical or isomeric structural variations.

7.5.2 Confirming Functional Groups: UV Spectroscopy

All organic compounds absorb ultraviolet (UV) light. However, the absorption frequencies of the C–C or C–H bonds of an organic molecule, as well as those of isolated functional groups such as a C = C, cannot be observed in the easily accessible region of the UV spectrum. The value of UV is based in examining compounds with groups such as $\text{R}_2\text{C} = \text{O}$, $-\text{O}(\text{R})\text{C} = \text{O}$, $-\text{NH}(\text{R})\text{C} = \text{O}$, or polyunsaturated compounds with conjugated multiple bonds. At one point UV spectroscopy was the only physical method available for the analysis of organic compounds. Nowadays, due to the limitations noted above, few organic chemists rely on UV as a primary tool for structural elucidation.

UV represents a method similar to IR for structure analysis, and like IR, this technique utilizes electromagnetic radiation that can be absorbed by a compound. The light frequencies that are employed span the ultraviolet (200–400 nm) and the visible (400–800 nm) regions of the electromagnetic spectrum. UV wavelengths below 200 nm are strongly absorbed by air (oxygen and carbon dioxide), or solvents commonly used in UV spectroscopy, so vacuum techniques are required to observe transitions in this range. Vacuum UV data in the region between 200 and 10 nm are not often obtained because few commercial instruments are designed to scan these wavelengths.

How much specific structural information can be obtained from a UV λ_{max} value? Inferences about the presence or absence of conjugated multiple bonds can be made from a UV spectrum. Obviously, when no absorptions are observed in a UV spectrum, this indicates the absence of conjugated multiple bonds. It should be emphasized that in most situations, UV data are used to reaffirm a conclusion about the presence or absence of a chromophore previously identified by NMR or IR. The most common situations in which specific conclusions about functionality can be obtained from UV data are summarized in [Table 7.7](#).

Also with recent improvements in theoretical chemistry software and increases in computing power, it is now possible to calculate the UV spectra of

Table 7.7 Summary of UV λ_{\max} and transition types for simple chromophores

Chromophore	Compound	Transition	λ_{\max} (nm)	ϵ
C–H	CH ₄	$\sigma \rightarrow \sigma^*$	122	
C–C	C ₂ H ₆	$\sigma \rightarrow \sigma^*$	135	
C = C	C ₂ H ₄	$\pi \rightarrow \pi^*$	103	15,000
			174	5,500
C = C = C	C ₃ H ₄	$\pi \rightarrow \pi^*$	170	4,000
			227	630
C \equiv C	R–C \equiv C–R'	$\pi \rightarrow \pi^*$	178	10,000
			196	2,000
			223	160
C–O	R–O–R	$n \rightarrow \sigma^*$	180	500
C–O	R–O–R'	$n \rightarrow \sigma^*$	180	3,000
C–N	Amino	$n \rightarrow \sigma^*$	190–200	2,500–4,000
C–S	R–S–H	$n \rightarrow \sigma^*$	195	1,800
C–S	R–S–R	$n \rightarrow \sigma^*$	235	180
C = O	Aldehyde/Ketone	$n \rightarrow \sigma^*$	166	16,000
		$\pi \rightarrow \pi^*$	189	900
		$n \rightarrow \pi^*$	270	10–20
C = O	Carboxylic acid	$n \rightarrow \pi^*$	200	50
C = O	Carboxylate	$n \rightarrow \pi^*$	210	150
C = O	Ester	$n \rightarrow \pi^*$	210	50
C = O	Amide	$n \rightarrow \pi^*$	205	200
C = N	(NH ₂) ₂ C = NH	$n \rightarrow \pi^*$	265	15
C \equiv N	CH ₃ C \equiv N	$\pi \rightarrow \pi^*$	<170	
N = N	Me–N = N–Me	$n \rightarrow \pi^*$	350–370	15
N = O	Me ₃ NO	$n \rightarrow \pi^*$	300	100
			665	120
N = O	Me ₃ NO ₂	$n \rightarrow \pi^*$	276	27
C = C = O	Et ₂ C = C = O	$\pi \rightarrow \pi^*$	227	360
		$n \rightarrow \pi^*$	375	20
C–Cl		$n \rightarrow \sigma^*$	173	200
C–Br		$n \rightarrow \sigma^*$	208	300
C–I		$n \rightarrow \sigma^*$	259	400

small to medium sized molecules, although expert knowledge is required to achieve the best results. For very small molecules such as ethene, which has a gas phase $\lambda_{\max} = 171$ nm, it is possible to calculate the energies and oscillator strengths of electronic excitations using quantum chemical methods based on advanced molecular orbital calculations which can then be converted into absorbance maxima. Using different variations of this approach, the theoretically calculated λ_{\max} is found to range from 162 to 179 nm, the best being a prediction of 172 nm.

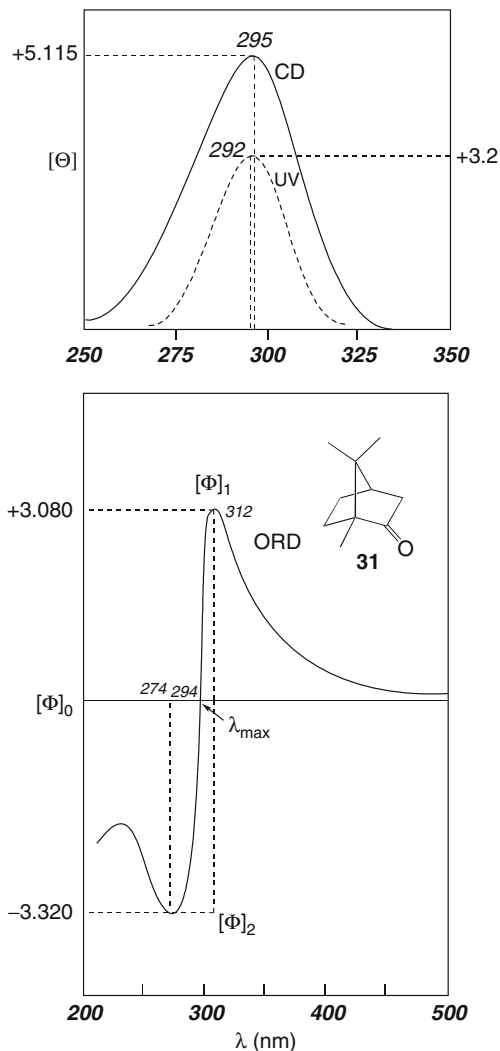
As another consideration, the theoretical approach is computationally very expensive. Most theoretical UV predictions for molecules of a chemically interesting size use electronic structure calculations at the density functional theory (DFT) level to achieve excellent results in a reasonable time. The major limitations are that solvent, concentration, and temperature effects on the λ_{\max} generally cannot easily be incorporated yet, although improvements are constantly being made to allow theory to reliably match with experimental data. In brief, the geometry of the molecule under study is optimized at some suitable level of theory, after which time-dependent DFT (TDDFT) is used to calculate the UV spectrum. The most commonly used form of TDDFT in spectroscopic applications such as calculations of UV/Vis spectra does not involve the calculation of excitation energies directly as differences between the ground state and excited state configurations. Instead, the linear response of the ground state density to an applied electric field is calculated using perturbation theory.

7.5.2.1 The Behavior of Chiral Chromophores ORD–CD

Chiral molecules can rotate the plane of polarized light, and this property is the basis of optical activity. Optical rotation data are reported as a specific rotation, $[\alpha]$, measured at a particular temperature, concentration, and wavelength of light, usually at 589 nm, the sodium D line. The $[\alpha]$ value can be calculated from the experimentally obtained rotation, α : $[\alpha] = 100\alpha/lc$, where c is the concentration of the solute in g/100 ml and l is the path length in decimeters. Molar rotations $[\Phi]$ are also sometimes reported when rotatory power is being compared on a quantitative basis: $[\Phi] = [\alpha] \text{ (MW/100)}$.

A useful approach to stereochemical analysis is the measurement of a series of $[\alpha]$ or $[\Phi]$ values for an enantiomerically pure compound over a range of polarized light wavelengths. The resultant is referred to as an optical rotatory dispersion (ORD) plot [55]. Plane polarized light can be viewed as a superposition of equal quantities of left- and right-handed circularly polarized light. These are differentially absorbed by a chiral compound and yield elliptically polarized light, with molar ellipticity $[\theta]$. The difference between the molar extinction coefficients, $\delta\epsilon$, of the left- and right-handed circularly polarized light can be measured. For small values of $[\theta]$, the molar ellipticity and molar extinction coefficients are related by $[\theta] = 3,300\delta\epsilon$. A plot of $\delta\epsilon$ or $[\theta]$ vs. wavelength is a circular dichroism (CD) plot [56]. The availability of commercial instruments makes it possible to routinely obtain both ORD and CD traces.

Chiral compounds containing a UV chromophore can give anomalous CD or ORD curves, known as the Cotton effect. An ORD spectrum in which the peak is at higher λ than the trough is said to have a positive Cotton effect, and the opposite situation with the peak at lower λ than the trough has a negative Cotton effect. Optically pure enantiomers always display opposite Cotton effect ORD curves of identical magnitude. Another feature of the ORD plot is that the zero crossover point between the peak and trough closely corresponds to the normal UV λ_{\max} .

Fig. 7.29 ORD, CD, and UV of camphor (**31**)

The appearance of CD plots is rather simple in that they are Gaussian rather than S-shaped. The positive or negative nature of the CD curve is given by the sign of $\delta\epsilon$ or $[\theta]$ and corresponds to the sign of the Cotton effect. A comparison of the CD, ORD, and UV spectra of camphor (**31**) is shown in Fig. 7.29. Akin to ORD, CD peaks occur only in the vicinity of a UV absorption band, and the maximum absorption in a CD spectrum occurs at approximately the UV λ_{\max} . In situations where more than one Cotton effect is observed, a CD spectrum with its simpler absorption peaks is often more straightforward to interpret than ORD displaying overlapping S-shaped peaks.

Interpreting Cotton effect curves for carbonyl-containing compounds is the most important application of ORD–CD data in organic structure analysis. In spite of the low ϵ for the $C = O$ $n \rightarrow \pi^*$ transition, occurring at approximately 280 nm, it can easily be observed by ORD–CD on dilute samples (10^{-2} – 10^{-6} M). A set of semiempirical rules has been developed to allow conclusions to be made about $C = O$ location, ring conformational properties, and absolute stereochemistry. Using these rules, either the constitution, conformation, or configuration of a molecule can be determined, provided two such features are known. This involves use of the octant rule to translate the sign of a $C = O$ Cotton effect peak into a conclusion about molecular structure. It was developed from the study of rigid cyclohexanones and has been extended to a large number of compound classes [57].

7.5.2.2 The Exciton Chirality Method

Most circular dichroic spectra are the result of one chromophore per molecule interacting with the electromagnetic field of light. In this case, the interaction with the chromophores in neighboring molecules is negligible. However, if two UV chromophores are present in one molecule, exciton coupling is observed. Simply put, exciton coupling is the delocalization of the excited state between two chromophores, resulting in the splitting of the excited state (exciton coupling or Davydov splitting) [58]. Excitations to the two split energy levels generate Cotton effects of mutually opposite signs. This effect is manifested in the CD spectrum as two bands of opposite sign, and the maximum and minimum are separated by $\Delta\lambda$ (Davydov splitting). The signs of the first (greater λ) and second (smaller λ) Cotton Effect can be used to determine the spatial disposition of the chromophores. Sugars can be derivatized as benzoates, and the absolute sense of the twist between two of these groups can be determined using the exciton chirality rules previously mentioned. This method has been used to determine the absolute stereochemistry of both small natural products as well as large natural products such as brevetoxin B [58].

7.6 Limitations of Spectroscopic Data in Structure Analysis

Even seasoned investigators sometimes experience difficulties in analyzing the structures of organic compounds. At times, problems occur in interpreting NMR, IR, UV–VIS, or MS data, or in applying the strategies outlined in Fig. 7.1, or both. Also, ambiguities can arise if extraneous signals are present from impurities. When this happens, reconsidering the conclusions by an iterative process will sometimes resolve the difficulty. In some cases, additional efforts are needed including obtaining additional data from a simple derivative, examining degradation products, or carrying out total synthesis of the putative structure or a model compound. Success in using spectra for organic structure analysis requires the careful comparison of data and conclusions derived from the four techniques. Of course, whenever possible, two or more arguments based on

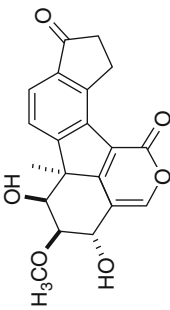
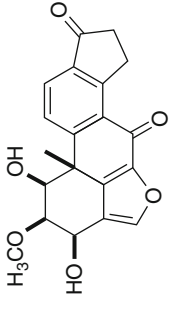
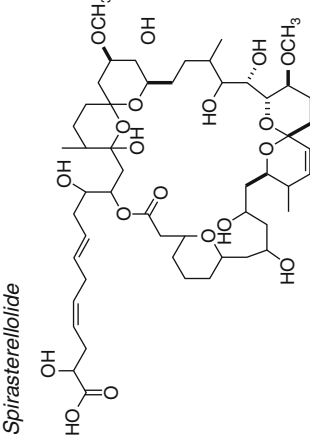
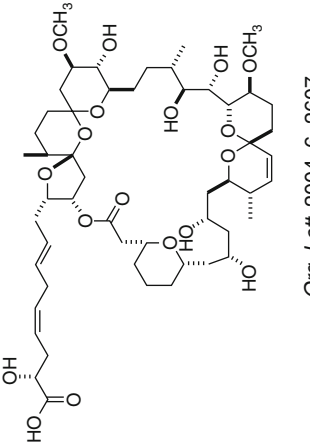
spectroscopic or chemical data should be used to generate a conclusion about a particular structural element. It is important to learn from past success and failures in organic structure analysis. However, what usually attracts much attention is when something goes wrong. There are hundreds of cases in the chemical literature where revisions have been made to a published structure [59]. Some of the most common types of difficulties where a (published) *reasonable 2D or 3D molecular structure* did not endure the test of time are represented in three examples shown in Table 7.8. These compounds are all natural products ranging from terpenoids, polyketides, to alkaloids, and all are in the mass range of 250–1,100 amu in molecular weight. The “original structures” for these compounds were based on a great deal of supporting data within the papers listed by each of these structures. However, the second literature citation accompanying each entry contains another viewpoint based on new experimental information – either from the original investigators or from others – leading to a “revised structure.”

Failure to propose correct functional groups, even when the molecular formula was known, has caused problems. The characterization of the polycyclic polyketide TAEMC161 was sidetracked because not enough possibilities were considered for the substructure containing three fused rings comprised of two six-sided and one five-sided system. The ^{13}C NMR chemical shifts were seemingly in accord with the initial structure. However, further evaluation of the carbon shifts predicted by density functional theory revealed that the structure represented by viridiol provided a better fit. The total synthesis of this structure provided additional data to confirm the revision.

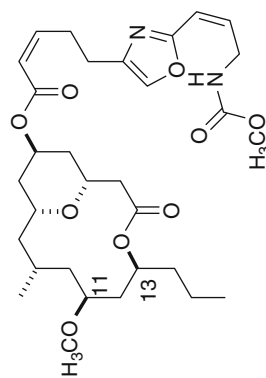
A faux pas in establishing an appropriate molecular formula can be devastating. When this happens, the list of substructures and functional groups will always be incorrectly assembled into a final *2D structure*. It took a surprisingly short time to amend the originally proposed rendering for spirastrellolide. It heads a family of compounds of greater than 1,000 amu having a polyether polyketide framework and possesses 21 chiral centers. Advanced NMR data were used to substantiate the ten units of unsaturation as a carboxylic acid, a macrocyclic lactone, a homoconjugated diene, one dihydropyran ring, and three pyran groups. The myriad of remaining oxygen atoms were considered to be present as 2 OCH_3 and 8 OH residues. Subsequent peracetylation of spirastrellolide methyl ester gave only a pentaacetate product, indicating a serious inconsistency. Reevaluation of the molecular formula by ultrahigh-resolution mass spectrometry indicated a first problem, that the count of hetero atoms was O_{17}Cl and not O_{19} . A substantial additional effort carried out over a 4-year period provided the final corrected structure by isolating analogs, obtaining degradation products, and total synthesis of key fragments.

The complete 3D structure of (+)-neopeltolide was quickly challenged after its publication. In this case, the spectroscopic data of the natural product did not match that of material prepared by enantioselective synthesis. This example provides an unexpected outcome in the process shown in Fig. 7.2 – transforming a *reasonable 3D molecular structure* into a *very secure 3D molecular structure*.

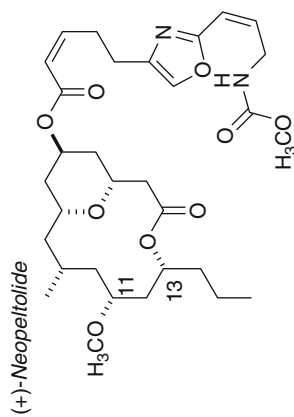
Table 7.8 Some marine organic structure analyses gone bad

Original structure	Revised structure	Features
<p>TAEMC161</p>  <p><i>J. Nat Prod.</i> 2000, 63, 1677</p>	<p>Viriditol</p>  <p><i>J. Nat Prod.</i> 2003, 66, 716</p>	<p>TAEMC161 = Viriditol</p> <p>This cytotoxic compound was isolated from a tunicate. The entire carbon chain structure was revised by automated analysis of the ^{13}C-^{13}C Correlation (2D INADEQUATE)</p>
<p>Spirasterellolide</p>  <p><i>J. Am. Chem. Soc.</i> 2003, 125, 5296</p>	 <p><i>Org. Lett.</i> 2004, 6, 2607</p>	<p>A sponge derived polyketide of isotopic mass = 1026.5. The original MF $\text{C}_{53}\text{H}_{86}\text{O}_{19}$ was corrected to $\text{C}_{53}\text{H}_{83}\text{O}_{17}\text{Cl}$. An inconsistency was the methyl ester formed a pentaacetate. Synthesis of fragments and degradations on other analogs supported the revised structure and absolute stereochemical assignments shown</p>

This deep-water sponge metabolite is a powerful cytotoxin. Extensive use of advanced NMR methods was used to identify parallel features to that of leucascandrolide. The original ^{11}R , ^{13}R assignment was revised to ^{11}S , ^{13}S after examination of the NMR properties of diastereomers



J. Am. Chem. Soc. 2008, 130, 804



J. Nat Prod. 2007, 70, 412

Many additional attempts were undertaken to decipher the stereochemistry at the six chiral centers of neopeltolide. All of them involved the synthesis of other logical diastereomers (e.g., *working stereo structures*). Eventually, a revised structure was published based on a side-by-side comparison of the synthetic isomers to the natural sample.

The preceding discussion, as well as the compilation of [Table 7.8](#), raises an important question. Can the process of organic structure analysis ever produce an *absolutely secure 3D molecular structure*? Some would argue that the answer is – rarely! Recall the steps in establishing a molecular structure discussed earlier in this chapter (e.g., [Fig. 7.1](#)). One important milestone in the process involves pruning a broad list of possible *working 2D structures* to obtain a single candidate which after further analysis can be designated as a *reasonable 3D molecular structure*. Collecting and recollecting data are what it usually takes to substantiate that a *very secure 3D molecular structure* has been proposed. But when does this process stop? Is a combination of spectroscopic data, the results of total synthesis, or even data from X-ray crystallography the minimum needed in support of the designation as a *very secure* or even *absolutely secure 3D molecular structure*? Seldom would a compound be subject to such intense scrutiny. With experience gained in applying the concepts outlined in this chapter along with acquiring skill in solving complex structure elucidation problems, you will be able to formulate a conclusion on this issue. The next step might involve spending month or years solving such problems. We suggest that you now embark on such a journey!

7.7 Study Questions

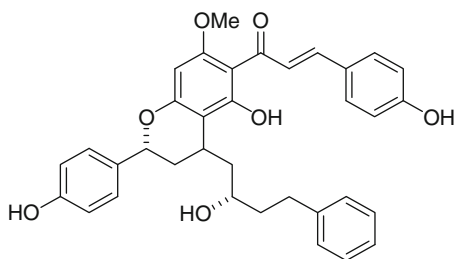
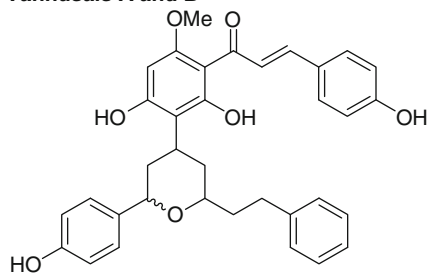
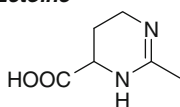
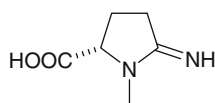
1. The ^{13}C NMR spectrum of CDCl_3 shows a triplet (intensities 1:1:1) separated by 31.9 Hz. Explain.
2. The structure for three marine products was wrongly assigned and later revised based on synthetic models. Propose the structural features which were responsible for these three mistakes!

Originally reported structure	Revised structure
<p>Diversolic acids</p>	

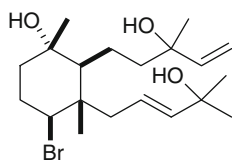
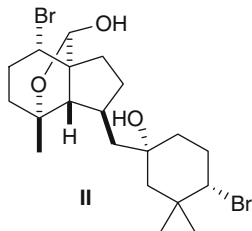
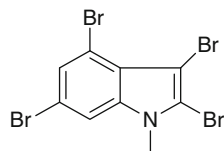
(continued)

Originally reported structure

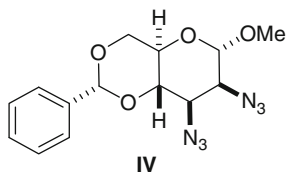
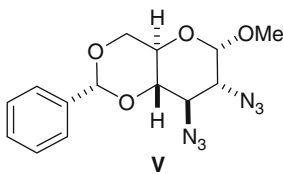
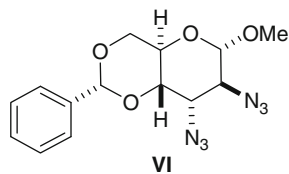
Revised structure

Vannusals A and B**Ectoine****2-imino-1-methylpyrrolidine-5-carboxylic acid.**

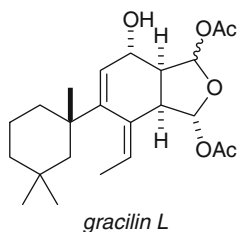
3. Three marine natural compounds isolated from marine red alga *Laurencia decumbens* were analyzed by MS means. Describe the expected cluster patterns for the (+)-ESIMS of **I**, **II** and **III**.

**I****II****III**

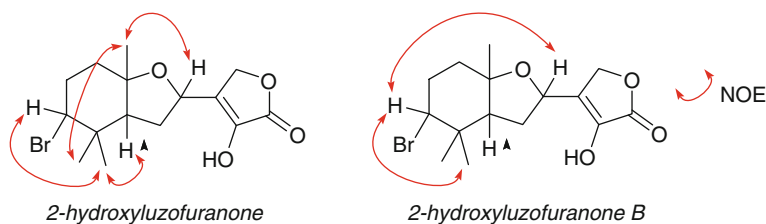
4. Distinguish between the three alternative structures **IV**, **V** and **VI** based on the analysis of the following ^1H NMR data: δ_{H} 7.51 (m, 2H), 7.39 (m, 3H), 5.67 (s, 1H), 4.73 (d, 1H, $J = 1.7\text{Hz}$); 4.29 (dd, 1H, $J = 10.7$ and 15.8Hz); 4.16 (dd, 1H, $J = 3.7$ and 10.3Hz); 4.07 (t, $J = 10.3\text{Hz}$); 3.91 (dd, 1H, $J = 1.5$ and 3.7Hz), 3.85 (m, 2H), 3.42 (s, 3H).

**IV****V****VI**

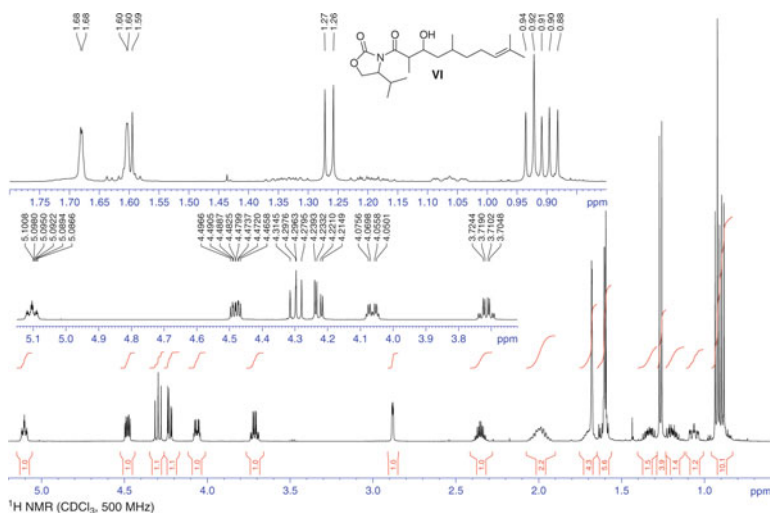
5. It is very helpful to read out the $M + 1/M$ intensities ratio from a mass spectrum to calculate the approximate number of carbon atoms. However, as soon as oxygen, nitrogen, and/or hydrogen are present, care has to be taken because ^{15}N , ^{17}O , or ^2H also contribute to the $M + 1$ intensity. Deduce the expected ratio for the marine compound gracilin L.

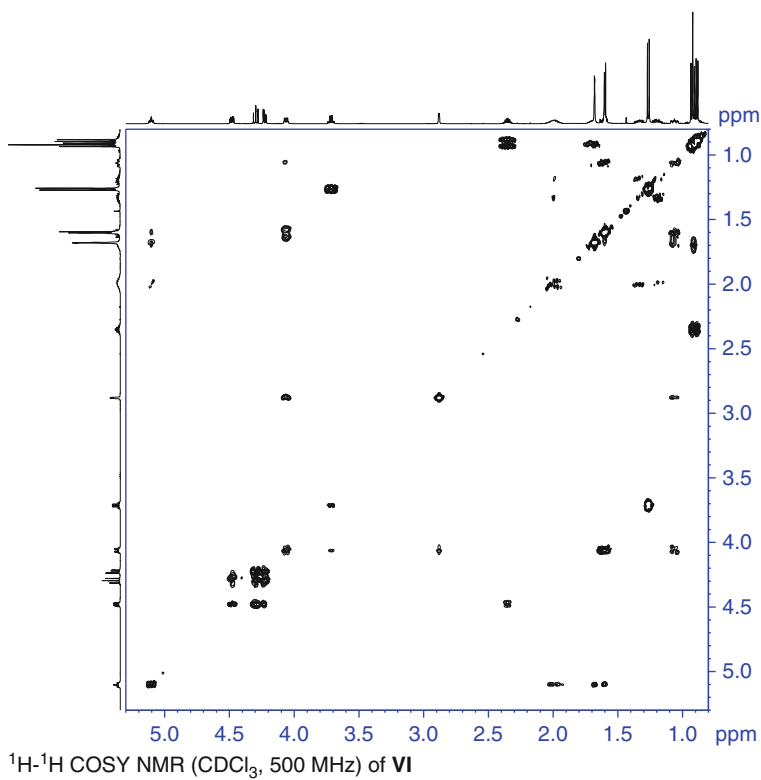
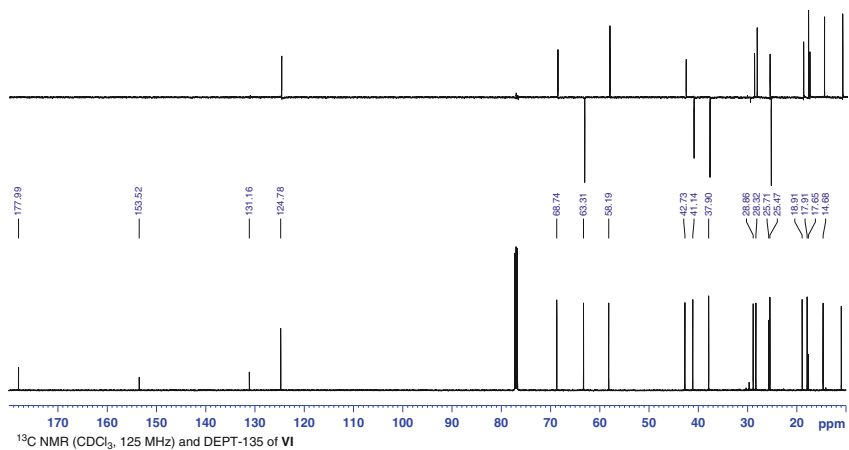


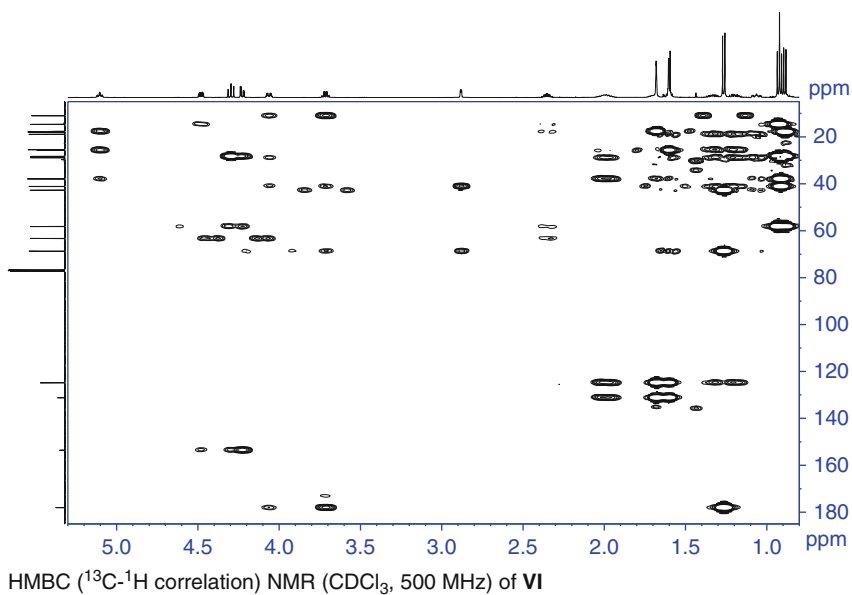
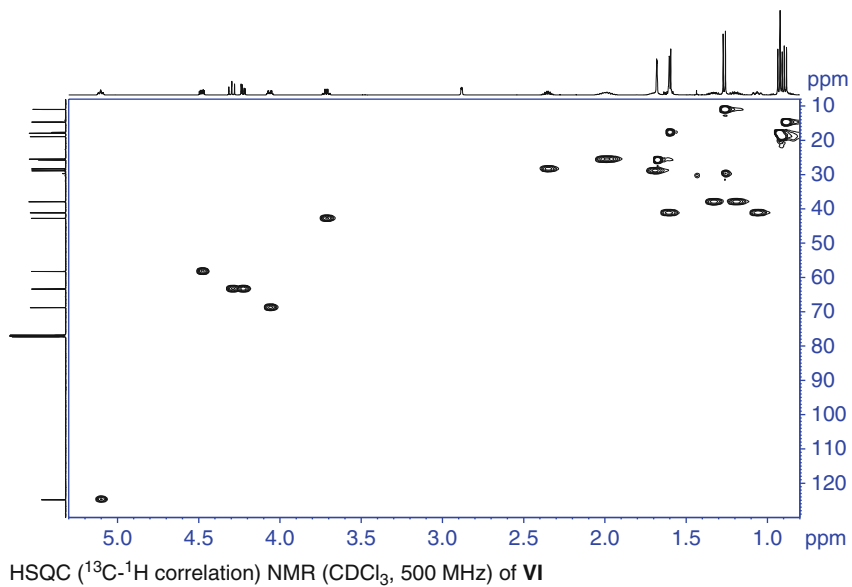
6. Deduce the relative stereochemistry of the 2-hydroxyluzofuranes based on NOESY data.



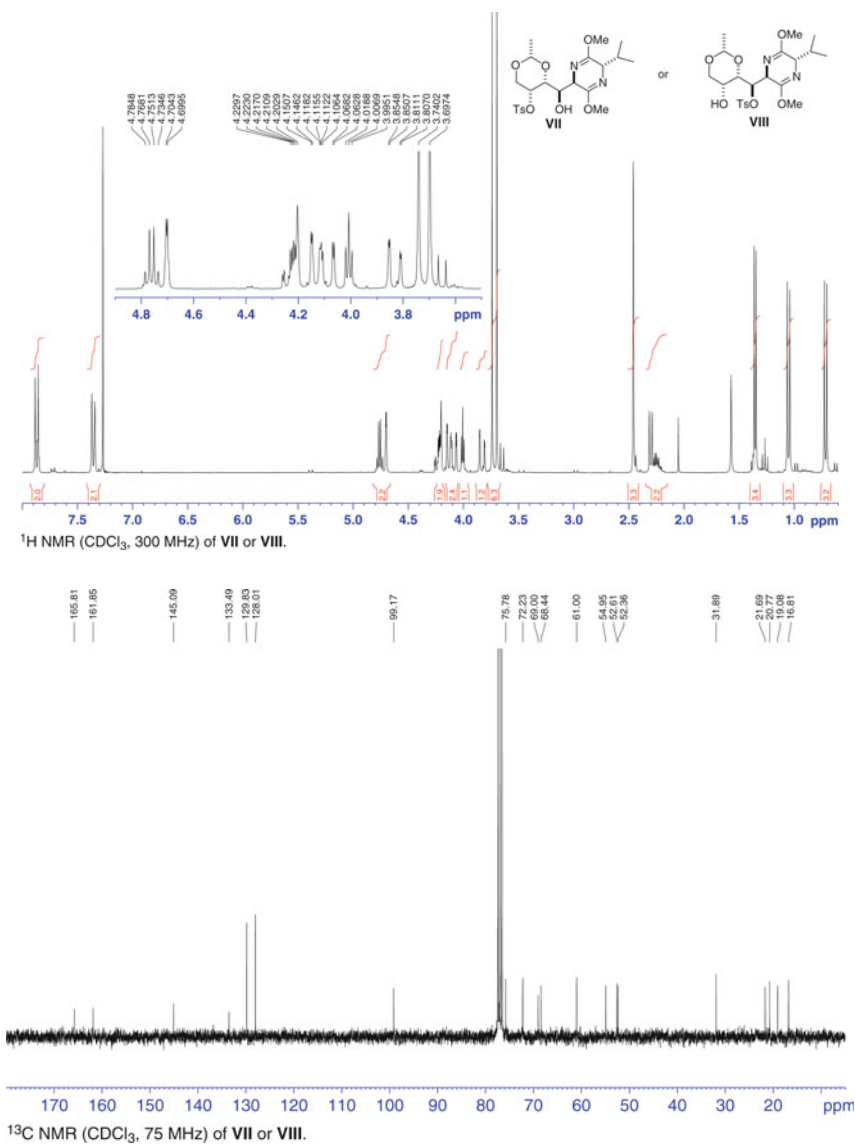
7. An advance synthetic intermediate **VI** of the synthesis of the marine compound tularin A showed the next 1D and 2D NMR data. Use the data to assign all ^1H and ^{13}C chemical shifts to the structure.

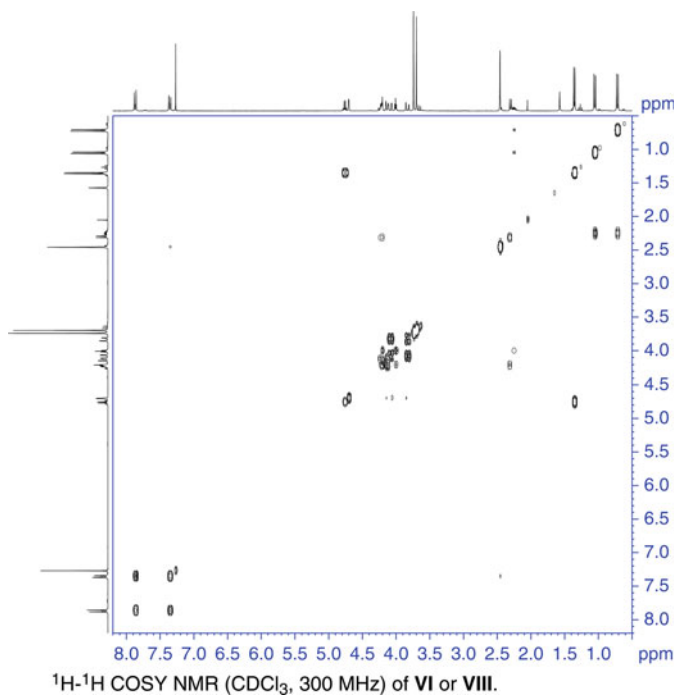
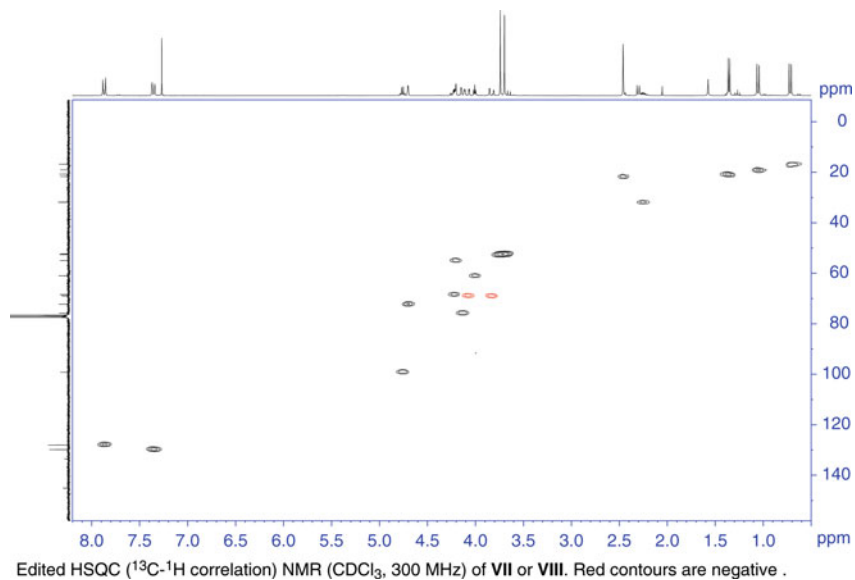


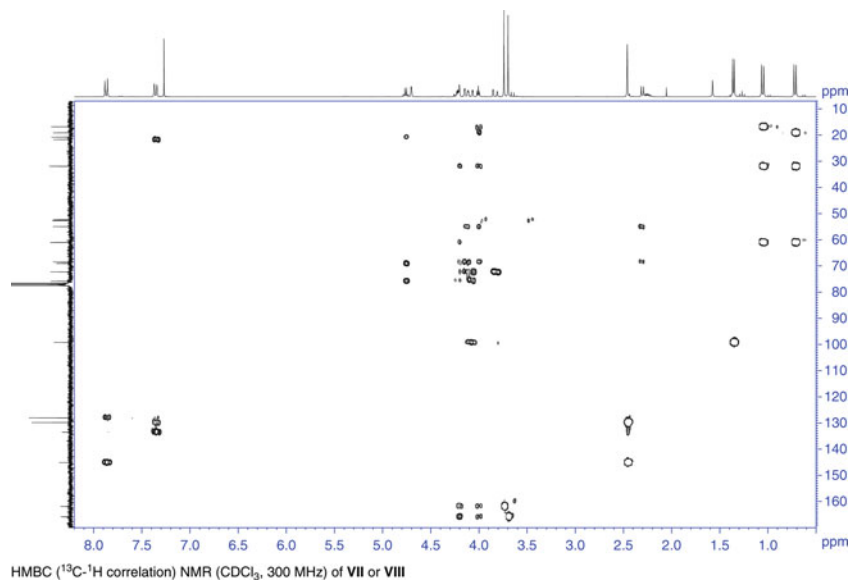




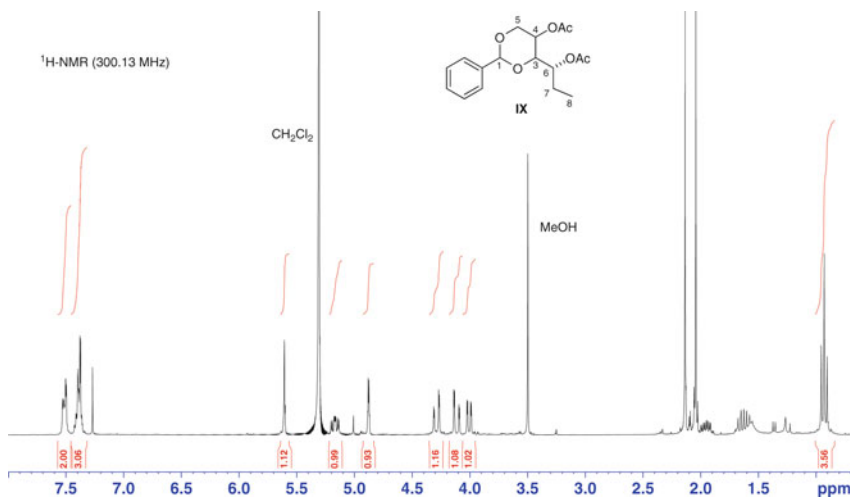
8. The tosylation of a diol gave an intermediate which the NMR data can be assigned to either **VII** or **VIII**. What is it?

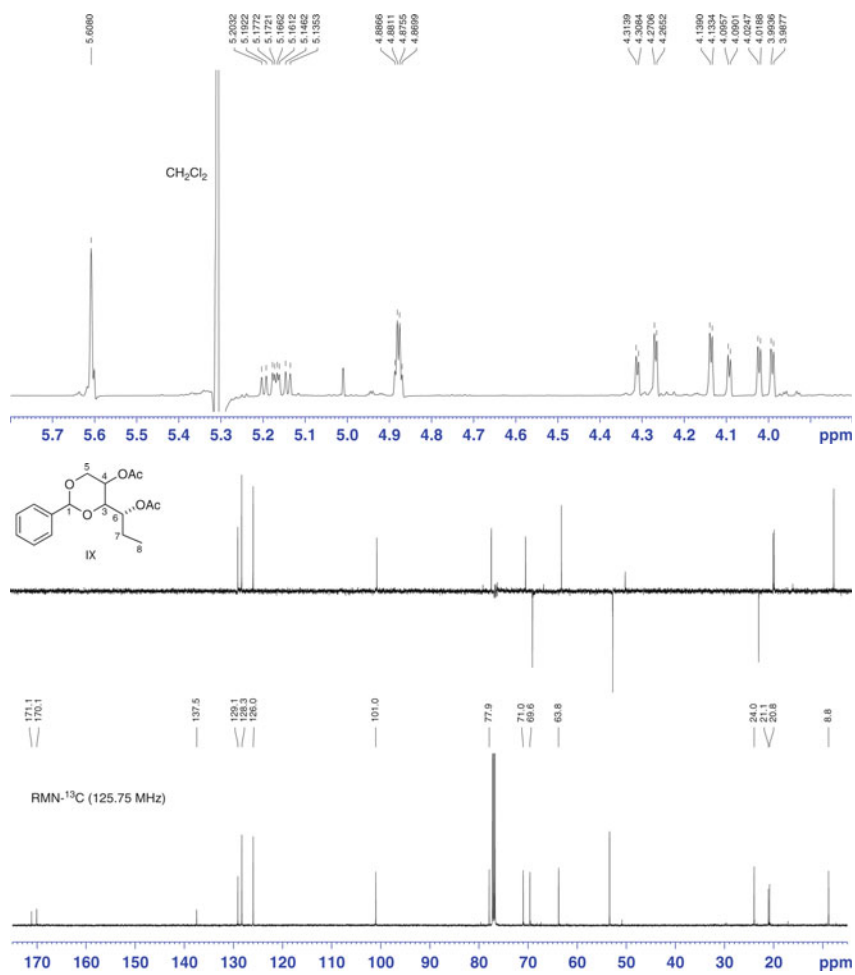


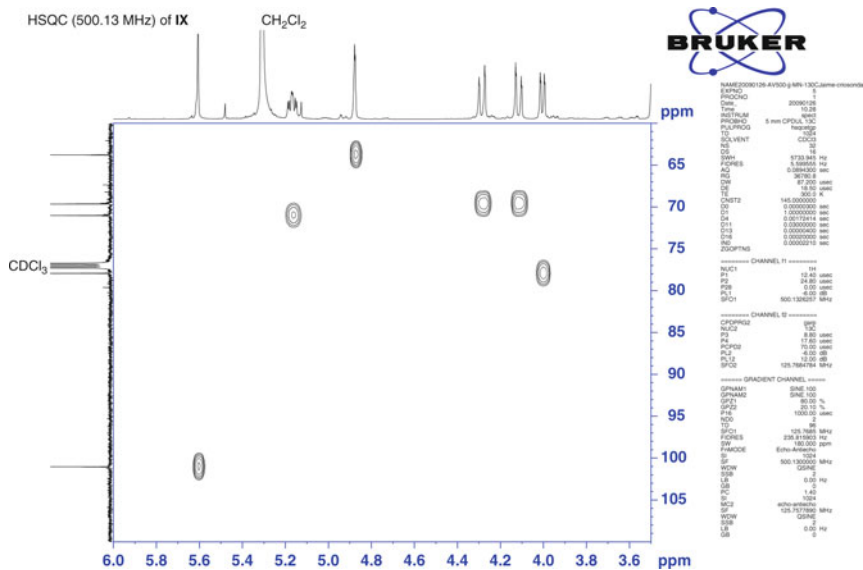
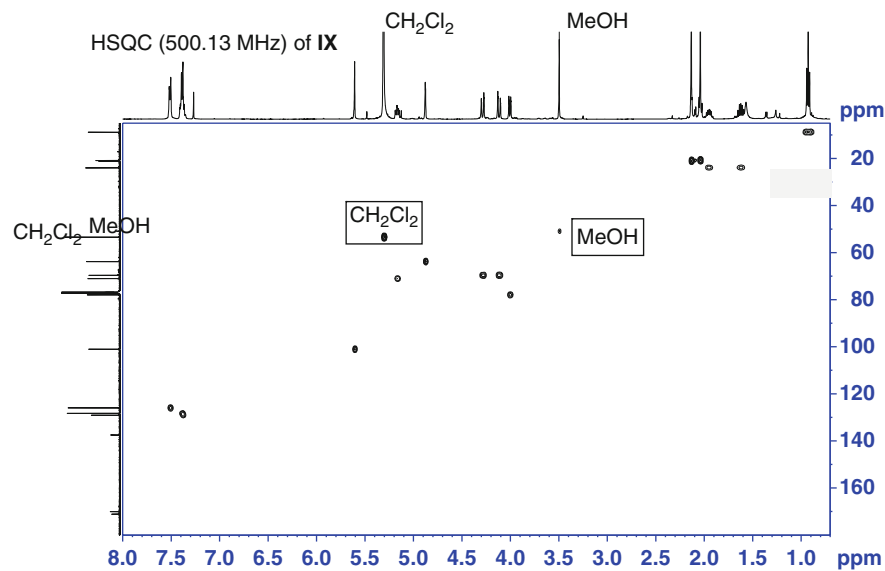


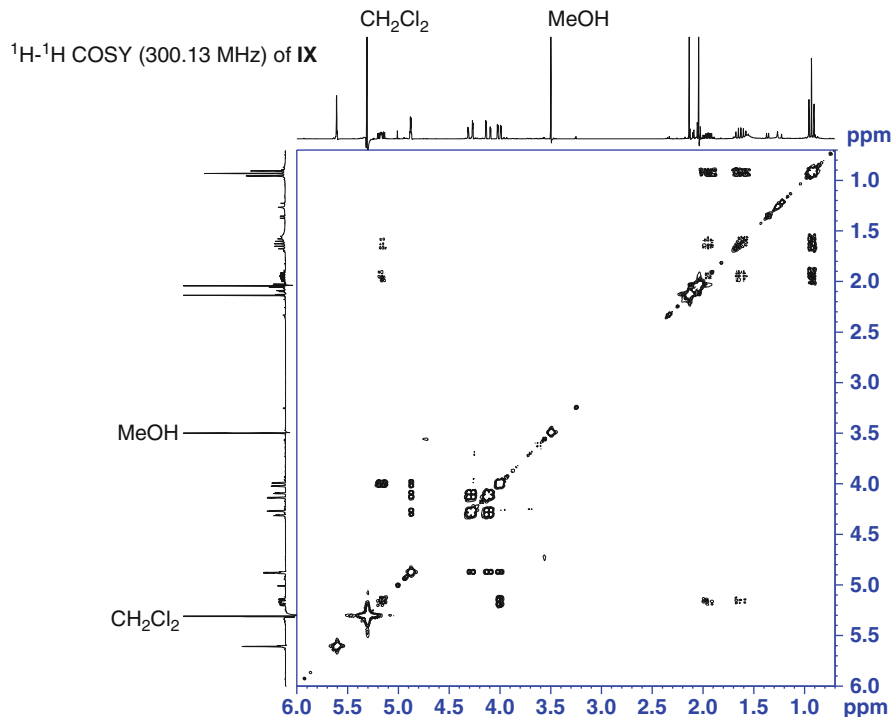


9. **IX** is a key synthetic intermediate in the total synthesis of a marine natural compound. Using NMR data, deduce the stereochemistry at positions 1, 3, and 4.









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Strategies for Structural Assignment of Marine Natural Products Through Advanced NMR-based Techniques

8

Alfonso Mangoni

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Abstract

This chapter surveys the standard 2D NMR techniques (COSY, TOCSY, NOESY and ROESY, HSQC and HMQC, HMBC, and INADEQUATE) including also some suggestion about the most suitable experimental parameters to be utilized in the different cases. In addition, an entire section describes some tricks and techniques that can be used in difficult cases of structural elucidation.

A. Mangoni

Dipartimento di Chimica delle Sostanze Naturali, Università di Napoli Federico II, Via D.

Montesano 49, Naples, Italy

e-mail: mangoni@unina.it

8.1 Introduction

In spite of the increasing interest in the biological activity, ecology, and biogenesis of natural compounds, structure elucidation remains the central part of the study of natural products. Since its introduction in late 1970s, two-dimensional NMR (2D NMR) spectroscopy has represented by far the most valuable technique for the elucidation of the structure of unknown organic compounds. After the molecular formula of an unknown compound has been determined from mass spectrometry, its structure (even a complex one) can be often determined using NMR alone.

The wide availability of highly automated spectrometers has made 2D NMR spectra routinely available to nonspecialists, and most organic chemists are involved in their interpretation on an everyday basis. In most cases, the 1D ^1H and ^{13}C spectra and three standard 2D experiments (COSY, HSQC, and HMBC) lead easily to an unambiguous structure, as far as stereochemistry is not concerned. We assume that the reader has at least some familiarity with these basic 2D experiments. More or less standard strategies for structure elucidation can then be used, which are widely discussed in reviews [1] and textbooks [2]. In more difficult cases, however, less common experiments and/or more sophisticated interpretation strategies are required. Barring exceptionally complex molecules (such as some polyether toxins), complexity itself is seldom the problem. More often, difficulties can arise from:

- Overlapped signals (particularly overlapped coupled protons, i.e., strongly coupled systems)
- Proton-poor molecules or molecular moieties (such as aromatic compounds and heterocycles)
- Unusually large long-range proton–proton couplings (like in bridged polycyclic compounds)
- Molecules experiencing conformational equilibria.

In such cases, additional experiments may be needed, but the choice of the most appropriate experiment to perform among the myriad of pulse sequences available in the literature (and provided by the manufacturers along with any NMR spectrometer) is not trivial. Alternatively, the use of standard sequences with a rational modification of the acquisition parameters or of the experimental conditions (solvent, temperature, sample concentration) may be the easiest way to get to the structure. Finally, spectral simulation can be a useful aid to extract NMR parameters (particularly coupling constants) which cannot be measured directly from strongly coupled or overlapped multiplets.

The present chapter contains a section surveying the standard 2D NMR techniques, with some suggestion about the most suitable experimental parameters, followed by a section describing some tricks and techniques that can be used in difficult cases of structural elucidation. Methods specifically directed to the determination of relative and absolute configurations will not be treated because they are covered by another chapter of this book.

8.2 Basic 2D NMR Experiments

The general goal of all NMR experiments is to make available the NMR parameters of the nuclei present in a molecule, which are then translated into structural information. Chemical shift provides information of the chemical environment of a given nucleus, and dipolar coupling (which is not directly observable in isotropic solution but can be detected indirectly through the nuclear Overhauser effect, NOE, and the rotating-frame Overhauser effect, ROE) provides information on distances between nuclei. Scalar coupling is by far the most informative phenomenon. The *presence* (or absence) of a coupling is essential to determine connectivities between atoms; the *magnitude* of a coupling constant may provide useful information about relative configurations, especially for cyclic or conformationally biased systems, through the well-known Karplus relationship [3] or more sophisticated empirical [4] or quantum-mechanical approaches (► Chap. 10 of this book). In this respect, the work of Murata [5] has recently extended to proton–carbon couplings what had been done for years with proton–proton couplings.

If *all* the chemical shifts and couplings of all the nuclei in a molecule are known, the structure of this molecule is always unequivocally determined (except for stereochemistry). This goal can rarely be achieved completely. The work of the NMR spectroscopist is to find a way to determine as many NMR parameters as possible, and the experiments described below are by far the most useful tools to this end.

8.2.1 ^1H – ^1H Connectivity

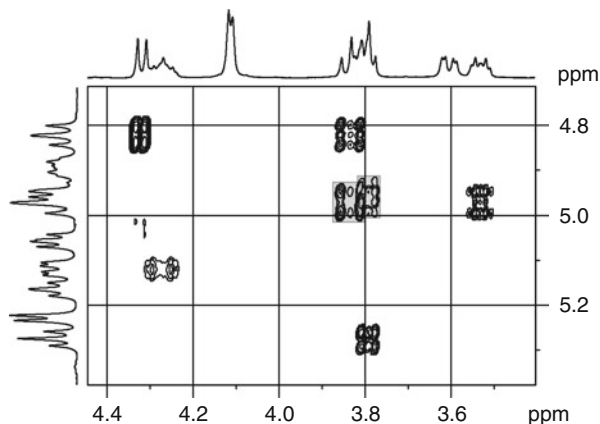
8.2.1.1 COSY

The COSY experiment is the first introduced [6] and most frequently acquired 2D NMR experiment. The simple and sensitive basic COSY sequence (sometimes called COSY-90) can be run even on the oldest spectrometers. Several improved COSY sequences have been proposed which find a significant use in structure elucidation work. Long-range COSY enhances small coupling constants; double-quantum filtered COSY (DQF-COSY) [7] shows less pronounced diagonal peaks, which moreover assume the same phase of cross peaks, allowing phase-sensitive acquisition. E-COSY [8] simplifies the multiplet pattern of COSY cross peaks, making the measurement of coupling constants easier.

In addition, the gradient-enhanced versions of all the above sequences exist. They are slightly less sensitive than their nongradient counterparts, but require shorter phase cycles (even 1 scan per t_1 increment) and therefore shorter acquisition times, and are useful for concentrated samples where sensitivity is not an issue (as it is often the case with the sensitive COSY sequence). For more diluted samples, requiring more than 8 scans per t_1 increment, the nongradient COSY sequences usually produce better spectra.

In spite of all the improved COSY sequences, when dealing with an unknown compound, the original, magnitude-mode COSY-90 sequence (or its

Fig. 8.1 Two partially overlapped peaks (*gray squares*) are easily discerned in a COSY-90 spectrum



gradient-enhanced version for concentrated samples) remains the sequence of choice. In fact, thanks to the clear rectangular shape of the cross peak which is characteristic of this experiment, it is very easy to discern partially overlapped cross peaks and follow the correct connectivity pathway even in very crowded spectra (Fig. 8.1).

To fully exploit this advantage, it is important to acquire an adequately large number of points in the F1 dimension, usually at least 512, corresponding to an F1 acquisition time of about 100 ms for a typical 4,000-Hz spectral width. Such a long F1 acquisition time cannot be replaced by F1 linear prediction, which is not useful for COSY spectra, because the antiphase COSY cross peaks start with zero intensity. While using a relatively long F1 acquisition time, an enhancement of cross peaks arising from small couplings is also observed, limiting the need of a dedicated long-range COSY experiment to very special situations.

It is often argued that the more sophisticated double-quantum filtered COSY (DQF-COSY) experiment should always be preferred to the original COSY sequences. DQF-COSY allows phase correction to give pure-absorption multiplets, so as to distinguish between active (i.e., the one generating the cross peak) and passive couplings in a multiplet. This advantage is rarely exploited in practice, because the active couplings give antiphase components, making phase correction tedious and analysis of fine structure difficult for complex multiplets, and the majority of published COSY spectra are recorded and transformed in magnitude mode. If the spectrum has to be transformed in magnitude mode, then it is better to use the original COSY-90 sequence, which is more sensitive and requires a shorter phase cycle. If, on the other hand, one intends to use DQF-COSY for a detailed analysis of fine structure of cross peaks, then a higher digital resolution is required (typically, F2 acquisition time of at least 500 ms, corresponding to 2,048 complex points for a 4,000-Hz spectral width).

In summary, use COSY-90 and at least 512 points in the F1 dimension. Leave the other parameters to their default values. Do not use F1 linear prediction.

8.2.1.2 TOCSY

In the TOCSY experiment [9], cross peaks are generated between all protons belonging to a coupled spin network (spin system). The inphase coherence transfer occurs during the isotropic mixing, and its extent is related to the duration of the coherence transfer period (mixing time). In case of large spin systems, the coherence transfer is limited to 4–5 couplings when the standard 80–100-ms mixing time is used (see Sect. 8.3.3 below); in addition, the coherence transfer is blocked by very small couplings. As long as the signal of at least one proton of a certain spin system is not overlapped to other signals, all the protons belonging to the spin system can be easily identified (Fig. 8.2). Therefore, TOCSY is typically used for compounds composed of many isolated spin systems, such as peptides and oligosaccharides.

However, TOCSY is by no means limited to these classes of compounds but may find a very general use in structural elucidation of any kind of compounds. The inphase coherence transfer, characteristic of the TOCSY experiment, fully preserves the fine structure of multiplets. When suitable acquisition parameters are used, a trace extracted from a 2D TOCSY spectrum is a subspectrum containing only signals from a particular spin system, with multiplicities as distinct as in a 1D proton spectrum (Fig. 8.3). TOCSY can therefore allow the direct measurement of coupling constants from multiplets even in crowded spectra.

If TOCSY has to be used in this way, some care must be taken in selecting the correct sequence and acquisition parameters. Because the measurement of coupling constants requires a good lineshape, a filtered TOCSY sequence that takes advantage of the zero-quantum filter recently proposed by Thrippleton and Keeler [10] (zTOCSY) should be used. In this filter, zero-quantum coherence is suppressed by applying simultaneously a 180° adiabatic pulse and a gradient, leading to

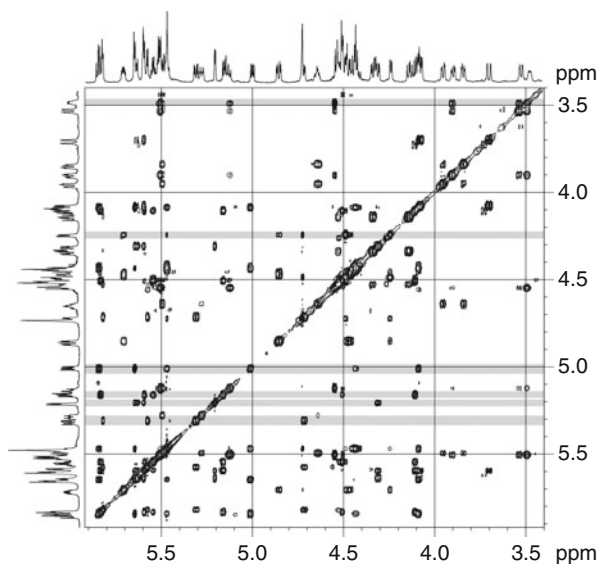


Fig. 8.2 The zTOCSY spectrum of the peracetylated glycosphingolipid vesparioside B, a glycosphingolipid from the marine sponge *Spheciospongia vesparia*. The correlation peaks on each gray line identify protons belonging to the same sugar

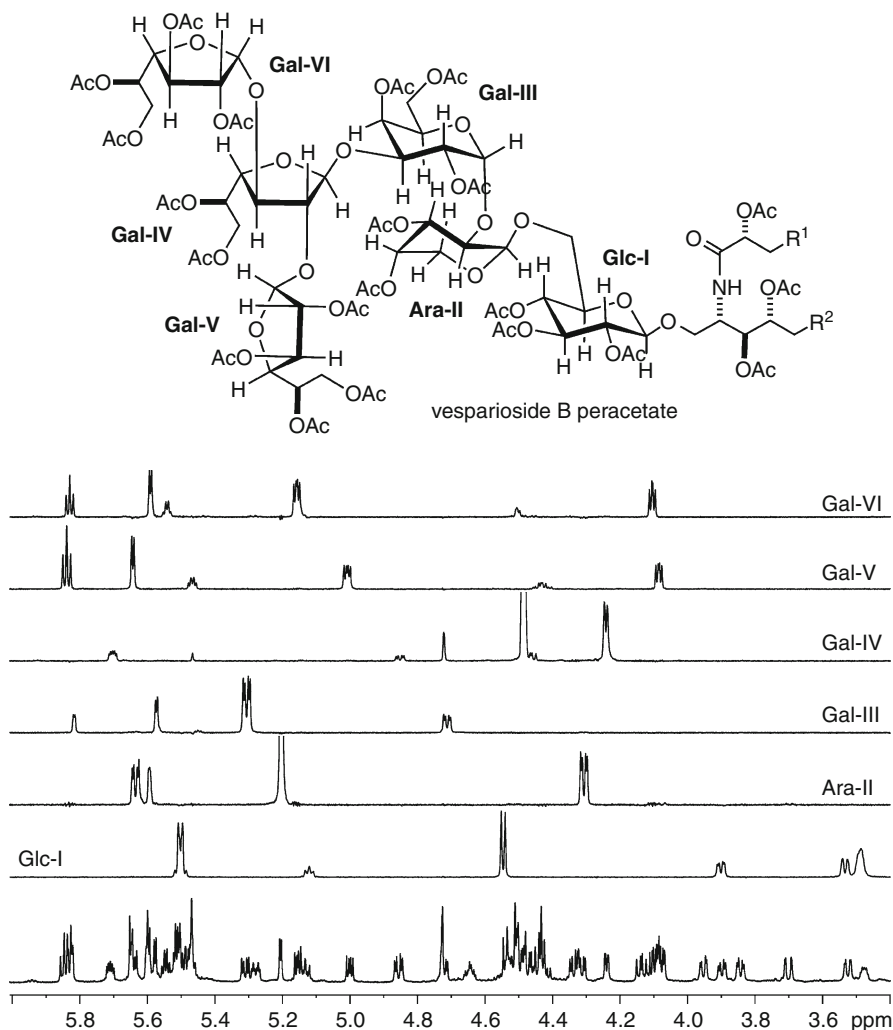
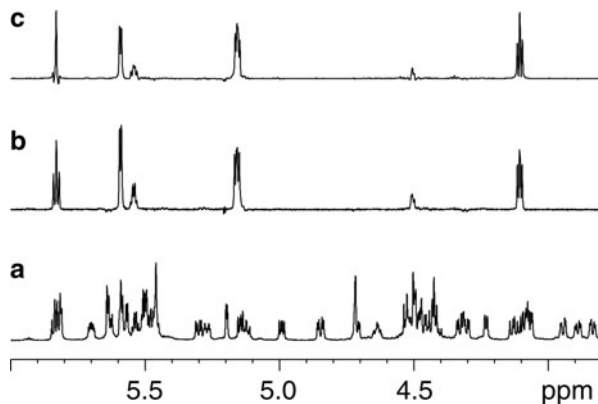


Fig. 8.3 Sections of the zTOCSY spectrum in Fig. 8.2 showing separate subspectra for each of the six sugars of vesparioside B. The spectrum was acquired with 8,192 complex points and transformed at 16,000 points in the direct dimension. Multiplet resolution was comparable with that of the 1D proton spectrum

pure-absorption inphase multiplets. Figure 8.4 compares a trace from the zTOCSY spectrum (a) and the nonfiltered TOCSY spectrum (b) of peracetylated vesparioside B, a glycosphingolipid from the marine sponge *Sphēciospongia vesparia*: [11] in the latter spectrum, lineshape distortion from zero-quantum coherence is apparent. This sequence is available from all the NMR manufacturers and is preinstalled in the most recent spectrometers; if the spectrometer supports it, there is no reason to prefer standard TOCSY over zTOCSY.

Fig. 8.4 (a) The ^1H NMR spectrum of peracetylated vesparioside B. (b) A section of the zTOCSY spectrum. The pure absorption in-phase multiples preserved the lineshape of the proton spectrum. (c) A section of the standard TOCSY experiment. The multiplets are distorted by zero-quantum coherence effects (see in particular the triplet at δ 5.32)



In addition, a long t_2 acquisition time should be selected to achieve an adequate digital resolution, much longer than the usual few hundred microseconds used in 2D experiments. An acquisition time of about 2 s is suggested, corresponding to a 0.5-Hz digital resolution or 8,192 complex points in F2 for a typical spectral width of 4,000 Hz. After such a long acquisition, the relaxation delay can be set to 0 or to a few ms, taking care to disable or delete from the sequence the gradient and/or rf pulses sometimes used to suppress the residual magnetization from the previous scan. During processing, a generous fourfold zero filling in the F2 dimension will allow an easier comprehension of the structure of complex multiplets as well as an accurate measurement of coupling constants.

As for the F1 dimension, 256 t_1 increments are enough if one plans to use the 2D spectrum in the structure elucidation work (linear prediction works fine with TOCSY), while 128 increments may be sufficient if one is only interested in extracting the 1D traces. More t_1 increments can be considered only if correlation peaks from two sharp and very close signals need to be distinguished.

If a molecule contains very extended spin systems (like, e.g., in many polycyclic terpenoids), the TOCSY spectrum may contain many overlapped correlation peaks, nullifying most of the advantages discussed above. It may then be helpful to use a very short mixing time (10–15 ms) so that coherence transfer is limited to one or two couplings. The spectrum is then greatly simplified (it indeed becomes similar to a COSY spectrum), but the multiplets are still inphase and can be easily analyzed.

In summary, use zTOCSY if your hardware supports it, 4,000 or 8,000 points in the F2 dimension (they come at almost no cost and can be cut during processing if not needed), and a 100-ms mixing time. Use F1 linear prediction if needed.

8.2.1.3 NOESY and ROESY

The NOESY [12] and ROESY [13] experiments are mainly used for configurational assignment but are also useful to determine the atom connectivity, especially in proton-poor compounds such as heteroaromatics. While the information they

provide is similar, i.e., spatial proximity between protons, there are some important differences that need to be discussed. The NOESY experiment relies on the conventional nuclear Overhauser effect and therefore on T_1 (longitudinal) relaxation. The sign of NOE depends on the molecular tumbling rate, and fast-tumbling small molecules show positive NOE, which results in cross peaks opposite in sign to diagonal peaks in the 2D NOESY spectrum, while macromolecules show negative NOE. Midsize molecules, like many complex natural products, fall between these two regimes and can show little or no NOE.

In contrast, ROESY relies on rotating-frame NOE, which occurs when magnetization vectors are locked in the transverse plane (spin-lock) either by a continuous low-power rf field or by a suitable pulse train, and rotating-frame relaxation ($T_{1\rho}$ relaxation) develops. The rotating-frame NOE is always positive (cross peaks are opposite in sign to diagonal peaks), irrespective of the size of the molecule, and this is the reason why ROESY is used more often than NOESY in the structure elucidation of natural products.

Interpretation of ROESY is often complicated by the presence in the spectrum of cross peaks arising from TOCSY coherence transfer that also occurs during spin-lock. In ROESY experiments, TOCSY coherence transfer is suppressed, keeping the rf power for spin-lock lower (2,000–4,000 Hz) than in TOCSY experiments; in addition, a spin-lock pulse train has been developed to reduce TOCSY transfers [14]. The experiment using it is called transverse ROESY (abbreviated as tr-ROESY, T-ROESY, or TROESY). Even so, TOCSY-type cross peaks between protons sharing large coupling constants (e.g., geminal protons) are invariably present in ROESY spectra. Actually, the TOCSY-type cross peaks cannot be confused with ROESY cross peaks because they are opposite in sign (TOCSY peaks have the same phase as diagonal peaks), but they can hide potentially useful ROESY peaks between coupled protons. Another source of artifacts in ROESY spectra is zero-quantum coherence: it produces weak cross peaks, which can be easily recognized because they are antiphase peaks, but may hide useful information.

The most important experimental parameter of a ROESY spectrum is the mixing time τ_m , i.e., the duration of the spin-lock, during which the ROESY transfer takes place. The maximum intensity of ROESY cross peaks is observed when τ_m is close to the rotating-frame relaxation time $T_{1\rho}$, which in turn is close to T_1 for small molecules. Because T_1 is different for different protons within the molecule, τ_m will be necessarily a compromise value. As a rule of thumb, mixing times between 200 and 500 ms can be used, with mixing times at the low end of this range for large natural products and at the high end for very small ones. There is no particular requirement regarding digital resolution in ROESY experiments, so even a matrix of 512×256 complex points can be enough in the absence of very close resonances.

If the molecule under study is a small natural product, and is therefore definitely in the positive NOE regime, then the NOESY experiment should be considered, because the TOCSY artifacts are not present in NOESY. In addition, the zero-quantum filter described above [10] for zTOCSY can be applied to the NOESY

sequence. The resulting zNOESY experiment is devoid of the weak antiphase cross peaks which are originated by zero-quantum coherence. The optimal mixing time for NOESY is chosen in the same way as for ROESY. For small natural products, zNOESY can give better results than ROESY because of the clean spectra it produces. Like zTOCSY, zNOESY is preinstalled in recent spectrometers.

ROESY and NOESY spectra can also be used to study chemical exchange processes with a rate constant comparable, or a little faster, than $1/\tau_m$ (faster exchange rates lead to broadening and eventually coalescence of the exchanging signals). Exchange cross peaks can be easily identified because they have the same phase as diagonal peaks and therefore opposite phase compared to ROESY and NOESY cross peaks (however, they can be confused with the TOCSY artifacts present in the ROESY spectra).

In summary, use ROESY with a mixing time of 200–500 ms but beware of TOCSY artifacts. For small natural products, which are certainly in the positive NOE regime, zNOESY is a cleaner alternative.

8.2.2 ^1H – ^{13}C Connectivity

8.2.2.1 HSQC and HMQC

Once considered a demanding experiment, the proton-detected one-bond ^1H – ^{13}C correlation experiment HSQC [15] is now easily performed by any recent spectrometer. It has been constantly improved along the years (phase-sensitive acquisition, gradient selection, echo–antiecho acquisition, DEPT-like multiplicity editing, adiabatic inversion pulses), but these features are mostly transparent to the user, who just need to use the most recent sequence available on the spectrometer. However, because it contains several 180° pulses, the HSQC sequence is quite sensitive to pulse miscalibration. Sometimes the alternative HMQC sequence [16] is used instead of HSQC. It produces very similar results, but it is characterized by a lower ^{13}C resolution and is less suitable to F1 linear prediction, [17] so HSQC is always the experiment of choice.

The most important parameter that may need to be optimized is the evolution delay used to create antiphase proton magnetization. This is usually adjusted for an average $^1J_{\text{CH}}$ of 145 Hz, which is adequate for most compounds. When sensitivity is really an issue, a smaller value should be used for fully aliphatic compounds, reflecting the typical 125-Hz coupling constant between protons and sp^3 carbon atoms, while a larger value is preferable for aromatic and heterocyclic compounds, for which proton–carbon coupling constants are around 160–170 Hz. This optimization is not critical, except for compounds with very large coupling constants, like those observed in terminal alkynes (about 250 Hz) and some heterocycles (e.g., 206 Hz for C-2 of imidazole).

The DEPT-like multiplicity editing (giving cross peaks of CH_2 groups with opposite phase compared to CH and CH_3 groups) is a very useful aid in the interpretation of HSQC spectra. However, the multiplicity-edited HSQC

sequence is much more sensitive than standard HSQC to $^1J_{\text{CH}}$ coupling constants significantly different from that for which the experiment is optimized. Multiplicity editing is the most likely cause of failure in detecting HSQC peaks (particularly those of CH_2 groups) for compounds with a wide spread of $^1J_{\text{CH}}$ values and should not be used for such compounds. Alternatively, two multiplicity-edited HSQC spectra optimized for different coupling constants can be acquired.

The HSQC experiments are more sensitive than the 1D ^{13}C NMR spectrum, and many researchers prefer to determine ^{13}C chemical shift indirectly from HSQC and, for nonprotonated carbons, HMBC experiments. If this is the case, it is advisable to use a higher number of t_1 increments than the default (at least 256, better 512) together with linear prediction to achieve a reasonable accuracy.

The HSQC cross peaks preserve the fine structure of the proton signals and could in principle be used to access the multiplicity of overlapped proton signals in the same way as TOCSY. However, the ^{13}C broadband decoupling used in the HSQC experiment is very demanding for the probe, and therefore HSQC acquisition time is usually limited to 150–200 ms, corresponding to a digital resolution of 5–7 Hz. As a consequence, small couplings are not resolved, and large couplings cannot be measured accurately. In addition, often the sensitivity of the HSQC sequence is high enough to detect the presence of a peak, but not to discern its multiplicity. In spite of these limits, analysis of multiplicity of HSQC correlation peaks can be sometimes useful to detect the gross features of an overlapped multiplet, for example, to distinguish between an axial and an equatorial proton in a six-membered ring (Fig. 8.5).

It is also possible to turn off ^{13}C decoupling and acquire a ^{13}C -coupled HSQC spectrum. In this spectrum, each correlation peak is split by the large coupling constant, making interpretation less easy, but the acquisition time, and therefore the digital resolution, may be as long as desired (in addition, the side bands introduced by the ^{13}C decoupling are not present). An acquisition time around 1 s corresponds to a digital resolution of about 1 Hz, so that even small coupling constants can be measured. The sensitivity of the HSQC experiment, however, is further lowered when long acquisition times are used, and therefore, this technique requires a quite concentrated sample. Another use of the ^{13}C -coupled HSQC spectrum will be discussed later (Sect. 8.3.5).

In summary, use multiplicity-edited HSQC with default parameters and linear prediction. Try not to use multiplicity editing when some correlation peaks appear missing because of anomalous $^1J_{\text{CH}}$ coupling constants. Use ^{13}C -coupled HSQC if a high digital resolution is required.

8.2.2.2 HMBC and Related Experiments

The HMBC experiment [18], which detects couplings between proton and carbons across two or three bonds, is extremely useful in structure elucidation because it may extend the connectivity network across nonprotonated carbon atoms and heteroatoms. It is also one of the most frequent reasons for structural misassignments because of its inherent inability to discern between $^2J_{\text{CH}}$ and $^3J_{\text{CH}}$. Like HSQC, also, the HMBC sequence has been improved over the years,

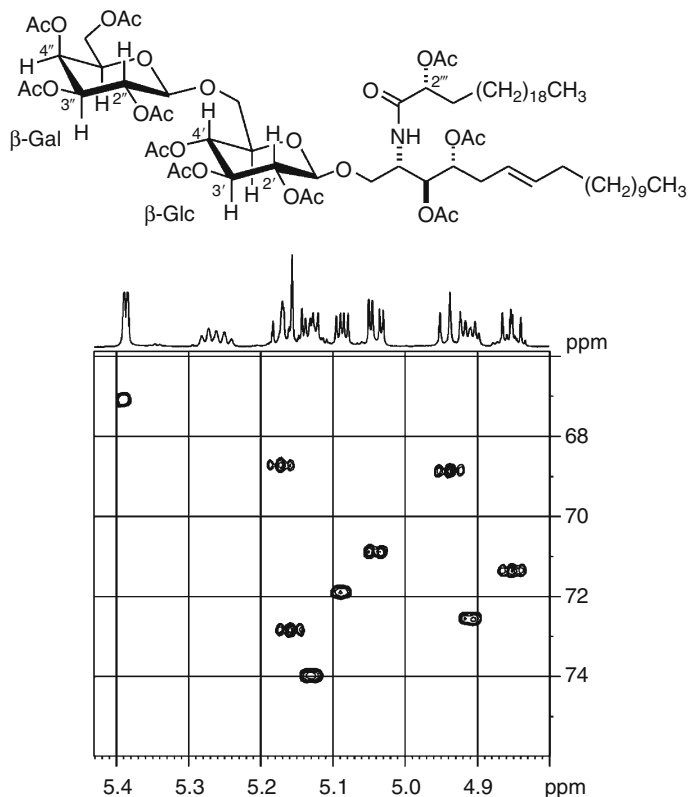


Fig. 8.5 Partial plot of the HSQC spectrum of peracetylated ampicillan B. In spite of the low digital resolution, the two large coupling constants of the two partially overlapped signals at δ 5.16 (the axial proton H-2'') and 5.17 (the axial proton H-3') are apparent. In contrast, resolution is not sufficient to discern the multiplicity of the signal at δ 5.13 (H-2')

with gradient selection, adiabatic carbon pulses, and experiments with pure-absorption lineshape in F1.

Both the $^2J_{\text{CH}}$ and the $^3J_{\text{CH}}$ coupling constants vary over a wide range of values (0–12 Hz), but the experiment can be optimized only for a single value, usually a compromise 7–8 Hz. If the J_{CH} is much smaller than this, the relevant correlation peak may be weak or absent. In addition, *homonuclear* coupling constants also evolve during the evolution delay, and this may also lead to the complete cancellation of a correlation peak. As a result, in most HMBC spectra, not all the theoretical correlation peaks are present, or, in other words, the *absence* of an HMBC peak is not diagnostic. To maximize the number of observed correlation peaks, it is a good idea to acquire a series of two or more HMBC experiments, optimized for different $^2J_{\text{CH}}$ couplings, for example, 8 and 5 Hz.

While the HMBC experiment relies on $^2J_{\text{CH}}$ and $^3J_{\text{CH}}$ couplings, it is not the first-choice experiment when one wishes to measure the value of such coupling

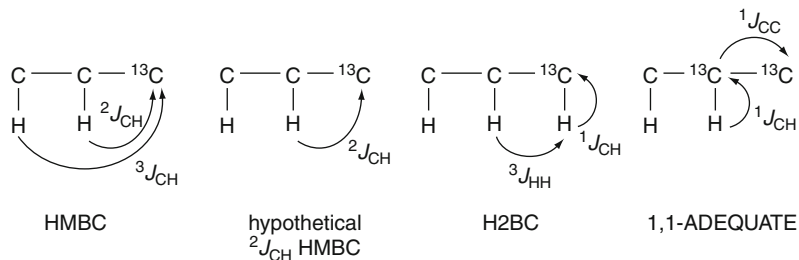


Fig. 8.6 Coherence transfer scheme in HMBC, a hypothetical $^2J_{CH}$ -selective HMBC, H2BC, and 1,1-ADEQUATE experiments

constants (this usually happens when a relative configuration needs to be determined using the Murata method) [5]. In fact, the presence of homonuclear couplings results in phase-modulated cross peaks which are difficult to analyze. Specific experiments (HETLOC, HSQMBC) may be used to this end, which will not be discussed here because they are extensively treated in ► [Chap. 9](#) of this book.

Interpretation of HMBC spectra is hampered by the fact that a correlation peak may mean that the proton is either two bonds or three bonds away from the carbon. An HMBC experiment which can discern between $^2J_{CH}$ and $^3J_{CH}$ would be highly desirable, but this is impossible in principle because the very phenomenon on which HMBC relies, long-range coupling between 1H and ^{13}C , has similar magnitude across two and three bonds. However, several experiments have been proposed providing similar information as a hypothetical $^2J_{CH}$ -selective HMBC but using different coherence transfer schemes ([Fig. 8.6](#)).

The H2BC sequence [19] can be described as an HSQC/COSY experiment, so that correlation peaks rely on $^1J_{CH}$ and $^3J_{HH}$ couplings. Therefore, only correlation peaks across two bonds are present. However, no correlations are observed for nonprotonated carbon atoms, vanishing one of the main advantages of HMBC. This experiment may be useful in complex spectra, where analysis of proton–proton couplings is difficult, and has indeed been used in the analysis of complex carbohydrates [20].

The 1,1-ADEQUATE sequence [21], as well as its improved version ACCORD-ADEQUATE [22], is comparable to an HSQC-INADEQUATE experiment. Proton coherence is transferred first to the directly bound carbon atom through $^1J_{CH}$ and then to the next carbon atom through $^1J_{CC}$. Therefore, the information provided by the experiment is fully equivalent to that of a “true” $^2J_{CH}$ HMBC, with the subtle difference that correlations of protons bound to heteroatoms are missing. An additional advantage is that small $^2J_{CH}$ couplings, causing missing correlations in the standard HMBC experiments, do not affect the 1,1-ADEQUATE spectrum. The main disadvantage of 1,1-ADEQUATE is the low sensitivity (at least for natural abundance samples) that it shares with all the experiments which rely on $^1J_{CC}$ couplings. 1,1-ADEQUATE is at least one order of magnitude less sensitive than HMBC but, being both proton-excited and proton-detected, is still much more

sensitive than the ^{13}C - ^{13}C INADEQUATE experiment (see below). To date, 1,1-ADEQUATE and ACCORD-ADEQUATE have found only occasional use in structure elucidation (see, e.g., Refs. [23, 24]) but, with the increase in sensitivity provided by cryogenic probes and improved instrument design, are expected to become more and more used.

In summary, use standard HMBC optimized for ^{13}C - ^1H coupling of 8 Hz. A second experiment optimized for 5 Hz may show additional correlation peaks. If sensitivity is not a problem, 1,1-ADEQUATE can make structure elucidation much easier.

8.2.3 ^{13}C - ^{13}C Connectivity

8.2.3.1 INADEQUATE

The homonuclear ^{13}C - ^{13}C correlation experiment INADEQUATE [25, 26] is potentially very useful to structure elucidation of natural compounds, allowing a direct access to the carbon skeleton of the molecule even for molecules or molecular portions devoid of protons. In spite of this theoretical advantage, it has only a limited use in practice (see, e.g., Refs. [27, 28]) because of its very low sensitivity when used on natural abundance samples. Only in one molecule out of about 10,000 ^{13}C is present at both ends of a given bond, and this adds up to the inherent lower sensitivity of ^{13}C -detected experiments. When the metabolite of interest is produced by a cultured microorganism, this problem can be strongly alleviated using a ^{13}C -enriched medium to obtain a ^{13}C -enriched sample [29, 30]. It is quite surprising that, in spite of the increasing diffusion of sensitive ^{13}C cold probes, the INADEQUATE experiment is not gaining popularity. A possible reason may be that in most situations, ^1H - ^{13}C correlation experiments are sufficient to solve a structure.

In summary, if enough sample is available, and the other 2D experiments did not solve the structure, INADEQUATE should be definitely tried.

8.3 Real-Life Examples

Structure elucidation based on the experiments described in the previous sections (and, of course, on molecular formula deduced by mass spectrometry) is straightforward for many compounds. There are still situations, however, where NMR data cannot unambiguously solve a structure, especially when only little amounts of sample are available and the less sensitive experiments such as INADEQUATE and 1,1-ADEQUATE are not possible. What do we do in these situations? Before trying to crystallize the compound for X-ray diffraction studies, one should consider that NMR experiments contain, or can provide, more information than is commonly used. The knowledge and the intelligent use of *all* the information NMR can provide can lead to solve structures that appear irresolvable by NMR at first sight. In this section, several examples will be given, mostly taken from my own real-life

structure elucidation work. They have been selected to draw attention to some less common aspects of structural elucidation that are not usually treated in general reviews or textbooks. Emphasis is not placed on theoretical aspects but rather on the nonstandard interpretation of standard experiments or in the use of standard experiments with unusual parameters.

8.3.1 Starting from HMBC

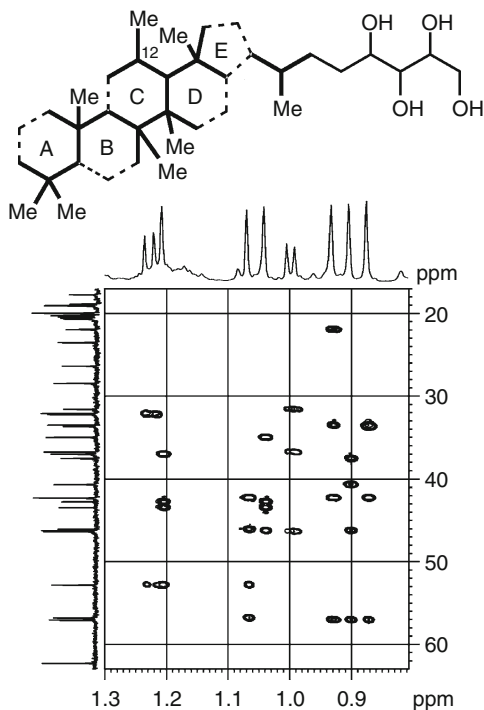
In the classical structure elucidation flow, the HMBC experiment is used to connect partial structures which have been previously determined from the analysis of the COSY, HSQC, and maybe TOCSY experiments. When dealing with some classes of compounds, most typically polycyclic terpenes, this may not be the best strategy because the analysis of COSY spectrum is made difficult by the extensive overlapping between aliphatic proton signals and the significant chance to observe large long-range W couplings. A valuable alternative strategy starts the analysis from the HMBC spectrum and, in particular, from the correlation peaks of the methyl protons.

We have mentioned before that in a typical HMBC spectrum, many expected correlation peaks are missing. This problem is not present when correlations of methyl protons are concerned. The free rotation about the C-CH₃ bonds guarantees that $^2J_{\text{CH}}$ and $^3J_{\text{CH}}$ do not vary much, being around 4.5 and 6 Hz, respectively [31, 32]; homonuclear coupling evolution is absent for methyl singlets, while for methyl doublets, the single 7-Hz homonuclear coupling does not affect much the intensity of the correlation peaks; finally, the methyl resonances are strong and narrow and produce correspondingly strong HMBC correlations peaks.

As a result, *all* the expected HMBC peaks of methyl protons (which are four for a methyl on a quaternary carbon, three for a methyl on a tertiary carbon, and two for an ethyl group) are invariably present in the spectrum. These peaks are still visible when the sample is so diluted that all the other correlation peaks are obscured by noise; if one is only interested in the correlations of methyl protons, the acquisition time for an HMBC experiment can be considerably shorter than that for a good HSQC. In favorable cases, it is possible to assign most skeletal carbon atoms of a polycyclic terpene just looking at the HMBC correlations of methyl groups.

An example of this strategy is found in the structural elucidation of 12-methylbacteriohopanetetrol [33]. The pentacyclic skeleton was devoid of functional groups, and most proton signals were severely overlapping. All the methyl groups (six singlets and two doublets) were well discernible in the spectrum, and each showed all the expected correlation peaks in the HMBC spectrum. In addition, identification of two-bond correlations for the six singlet methyl protons was easy because the relevant carbon atoms were necessarily quaternary carbon atoms. Overall, 27 out of the 31 carbon atoms in the pentacyclic hopane skeleton were assigned unequivocally, and 23 of them were connected into a single framework (Fig. 8.7).

Fig. 8.7 The HMBC spectrum of 12-methylhopanetetrol (only the correlation peaks of methyl groups are visible) and partial structure determined by long-range proton–carbon couplings of methyl protons



Starting from this carbon framework, completion of the structure elucidation was straightforward: the relevant protons were identified using the HSQC spectrum, and the remaining connections were determined from COSY and/or other HMBC correlation peaks.

8.3.2 HMBC and “False HSQC” Peaks

While the HMBC experiment is designed to detect two- and three-bond couplings between protons and carbons, correlation peaks originating from one-bond couplings are also present in the spectrum. These one-bond correlation peaks are easily recognizable: because no ^{13}C decoupling is used in the HMBC experiment, these signals appear as wide doublets in F2 due to the large $^1J_{\text{CH}}$ coupling constant, while the true HMBC peaks are not visibly split by the small two- and three-bond couplings. These signals are generally unwanted and are suppressed by a pulse sequence element called “low pass filter,” but even so, they are occasionally present in the HMBC spectrum.

In some compounds, however, a regular correlation peak (not a doublet), identical to the peak present in the ^{13}C -decoupled HSQC spectrum, can be observed at the chemical shift of directly linked proton and carbon atoms (the peak may appear in the middle of the doublet from one-bond correlation, if the latter is present). These “false HSQC” peaks may appear puzzling at first sight (directly linked

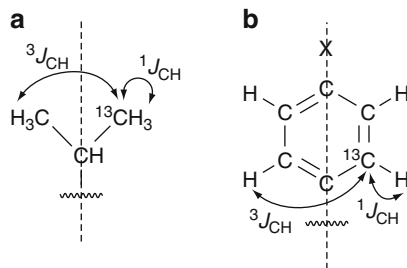


Fig. 8.8 (a) A ^{13}C nucleus in the methyl of an isopropyl group is coupled with the protons of the other methyl. A “false HSQC” correlation between methyl protons and methyl carbons is present in the HMBC spectrum. (b) In a $para$ -substituted benzene, the ^{13}C nucleus is coupled through one and three bonds, respectively, with two protons with the same chemical shift, and a “false HSQC” correlation appears in the HMBC spectrum

protons and carbons appear to be long-range coupled) but are absolutely obvious when the structure is drawn.

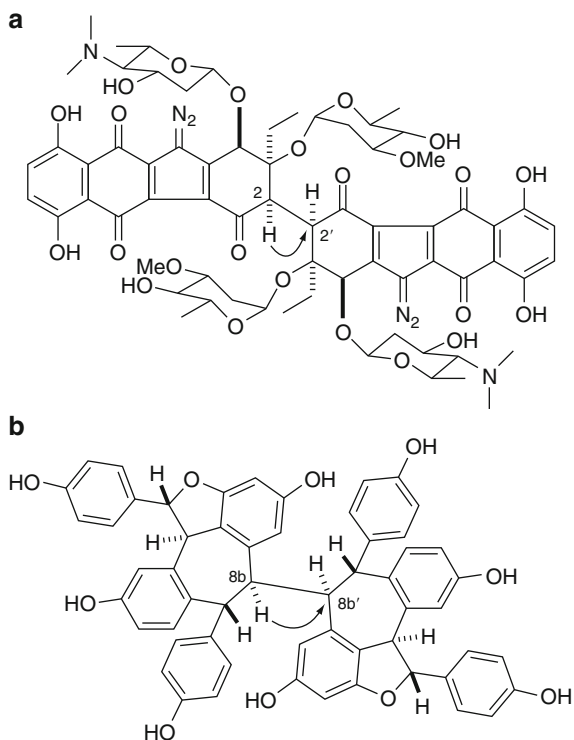
The most common (although not the most useful) example of this is seen in isopropyl groups. A ^{13}C nucleus in the methyl group of an isopropyl is long-range coupled with the protons of the other methyl group, which are equivalent to the protons directly linked to the ^{13}C nucleus (Fig. 8.8a). As a consequence, an HMBC correlation peak will appear between the methyl protons and carbon signals, exactly where the HSQC peak would appear. Similar peaks can be observed in $para$ -disubstituted and monosubstituted benzene rings (Fig. 8.8b).

These “false HSQC” correlation peaks have been used sporadically in structural elucidation of complex molecules, such as lomaiviticin A, an antibiotic from the ascidian *Micromonospora lomaivitiensis*. [34] The connection between the two symmetric halves of lomaiviticin A was demonstrated by the HMBC correlation peak between $\text{H}2/\text{H}2'$ and the relevant carbons $\text{C}2/\text{C}2'$ (Fig. 8.9a). The connection between the two halves of hopeaphenol, a tetrastilbene from the plant *Carex pumila* [35], was demonstrated similarly (Fig. 8.9b). Other than for solving complex structures like the ones shown, the “false HSQC” peaks are indeed very useful in the early steps of structure elucidation because they are only observed in symmetric structures or partial structures and are a clear hint for them.

8.3.3 Dealing with Alkyl Chains

Nonfunctionalized alkyl chains are a common source of problems in NMR-based structure elucidation. In such structures, proton chemical shifts heavily overlap even at high fields, preventing to follow the connectivity pathway using the standard experiment triad COSY/HSQC/HMBC. A means to overcome this problem is the TOCSY experiment, in which the coherence transfer is effective also for protons with coincident chemical shifts. This makes it possible to relate neighboring functional groups connected through alkyl chains.

Fig. 8.9 Structures of lomaiviticin A (**a**) and hopeaphenol (**b**). The linkage between the two couples of equivalent atoms C2/C2' and C8b/C8b' was established from “false HSQC” correlation peaks



A significant example of how the TOCSY spectrum can be used in this context is the determination of location of methyl branches in either of the two alkyl chains of clathroside B (Fig. 8.10), an atypical glycolipid isolated from the marine sponge *Agelas clathrodes* [36]. This required correlation of the terminal methyl groups of the alkyl chains with protons at C-3 or C-3', but the presence of a large number of overlapped methylene signals made a sequential assignment impossible. The only way to correlate these protons was a TOCSY experiment. Coherence had to be transferred through as many as 13 vicinal couplings for the experiment to be successful, which are much more than the 5–6 coherence transfers that occur in the standard 80–120-ms mixing time. A very long mixing time (600 ms) was therefore used, which turned out to be the best compromise between the increased coherence transfer obtained as the mixing time increases and the overall loss of sensitivity due to relaxation during the mixing time. In addition, the 1D version of TOCSY was used to maximize the sensitivity. In a first experiment, selective excitation of the allylic proton H-3a (δ 2.21) was performed, and only the methyl triplet of the unbranched chain (δ 0.88) appeared in the spectrum (Fig. 8.10b); in contrast, when H-3'a (δ 1.65) was excited, only the methyl signals of the antiseo chain appeared in the spectrum (Fig. 8.10c). Therefore, the additional methyl group was in the “southern” chain, i.e., linked to C-13'.

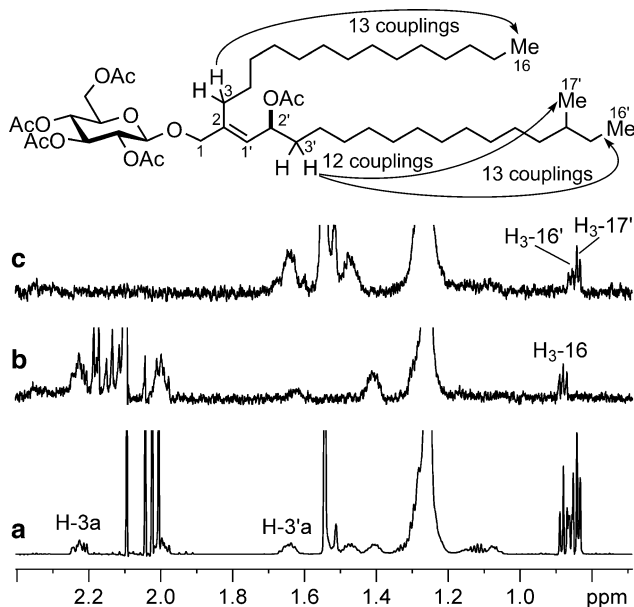


Fig. 8.10 (a) The ^1H NMR spectrum of peracetylated clathroside B. (b) 1D TOCSY, mixing time 600 ms, selective excitation at δ 2.21, H-3a; the terminal methyl triplet of the unbranched chain is clearly visible. (c) 1D TOCSY, mixing time 600 ms, selective excitation at δ 1.65, H-3'a; only the branched chain methyl protons are visible

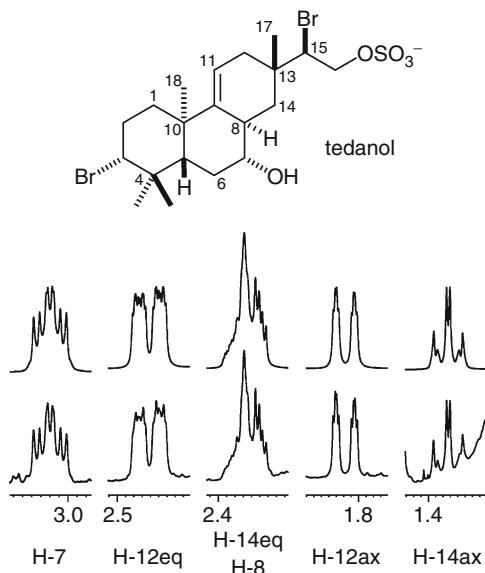
This work also illustrated an important limit of the TOCSY spectrum, i.e., that it does not allow to measure the number of coherence transfer steps which give rise to a correlation peak, or, in other words, how far apart are the protons connected by a TOCSY correlation peak. This information would have made it possible to determine the length of the two alkyl chains of clathrosides, which instead had to be determined by chemical degradation.

8.3.4 Dealing with Non-first-order Multiplets: Spectral Simulation

In a ^1H NMR spectrum, non-first-order multiplets appear when coupled protons have close chemical shifts. Chemically equivalent protons which are not magnetically equivalent may also give rise to non-first-order multiplets. The common approach of the natural product chemist toward non-first-order multiplets is to report them as *m* in the NMR characterization and give up from the beginning any attempt to get information from their lineshape.

As a matter of fact, the theoretical tools to predict the lineshape of a non-first-order multiplet have been known for a long time, and the necessary computational efforts are not a problem for modern computers for spin systems up to 10–12 protons.

Fig. 8.11 Selected signals of the simulated spectrum of the spin system of H-5 through H-14 (*upper trace*) of tedanol compared to the experimental spectrum (*lower trace*). The lineshapes of the non-first-order multiplets of H8/H14eq and H-14ax are accurately reproduced



A comparison of the predicted and experimental lineshapes makes it possible to determine all the NMR parameters of the spin system under examination. Therefore, if spectral simulation is used, even an apparently hopeless bump can provide the same coupling constant information as a clear first-order multiplet.

The reasons why spectral simulation is not as popular as it should be among natural product chemists can be identified in the need to obtain and learn specific software for a technique that is useful only in some particular situations and, in the quite lengthy process, required to extract the NMR parameters. (A very good simulation program, NMR-SIM, is included in the commercial Bruker's TopSpin suite. Unfortunately, no automated fitting procedure is present in this program, so that the optimization has to be performed manually. A free alternative, which also allows some automatic optimization, is Spin Works, <http://www.umanitoba.ca/chemistry/nmr/spinworks/index.html>). This use of spectral simulation first requires an intelligent guess of the initial parameters, followed by their optimization for the best possible fit of experimental and simulated signals. In spite of the lengthy process, whenever the comprehension of the fine structure of a multiplet is important for structure elucidation, spectral simulation represents an important tool to use.

For example, spectral simulation has been used in structure elucidation of the brominated and sulfated diterpene tedanol from the marine sponge *Tedania ignis* [37]. The key connection between H-8 and the two protons at C-14 could not be evinced from the COSY spectrum because the chemical shifts of H-8 and H-14eq were almost identical, leading to non-first-order multiplets. However, this coupling could be demonstrated by spectral simulation. The subspectrum of the 10-proton spin system comprising all protons on rings B and C was calculated (Fig. 8.11), optimizing

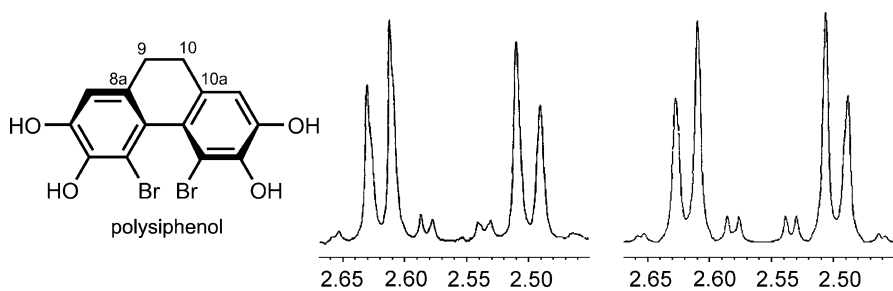


Fig. 8.12 The experimental (*left*) and simulated (*right*) ^1H NMR spectrum of methylene protons of polysiphenol

the unknown NMR parameters until the simulated multiplets reproduced accurately the experimental ones. The simulation also evidenced an otherwise undetectable W coupling (3.1 Hz) between H-12eq and H-14eq.

In an older example [38], the AA'BB' system originating from the methylene protons of polysiphenol, a conformationally blocked 9,10-dihydrophenanthrene, was studied using spectral simulation (Fig. 8.12). The coupling constants determined in this way were used to calculate, by a generalized Karplus equation [4], the torsion angle C8a–C9–C10–C10a; this torsion angle was a necessary information to determine the absolute configuration of the molecule from CD data.

8.3.5 Dealing with Non-first-order Multiplets: ^{13}C -Coupled HSQC

An alternative approach to deal with non-first-order multiplets is to acquire a ^{13}C -coupled HSQC spectrum. Let us consider two coupled protons, H_A and H_B , with very close chemical shifts. In a ^{13}C -coupled HSQC experiment, the correlation peak of H_A is split into two correlation peaks along the ^1H dimension by the large (125–170 Hz) $^1J_{\text{CH}}$ coupling constant with C_A (the two peaks are actually branches of the same multiplet but can be safely considered as separate peaks in the following discussion). These peaks now resonate at a frequency which is no longer overlapped with H_B (the correlation peak only originates from the molecules having a ^{13}C nucleus at C_A ; in these molecules, proton B experiences only a small $^2J_{\text{CH}}$ coupling with C_A , and its resonance frequency is unchanged). Therefore, the two peaks now appear as first-order multiplets along the ^1H dimension, and their coupling constants can be easily measured. Of course, the same applies also to the correlation peak of H_B . While using this method, it is essential to use a long acquisition time, to achieve an enough digital resolution (see Sect. 8.2.2 above) to resolve small couplings.

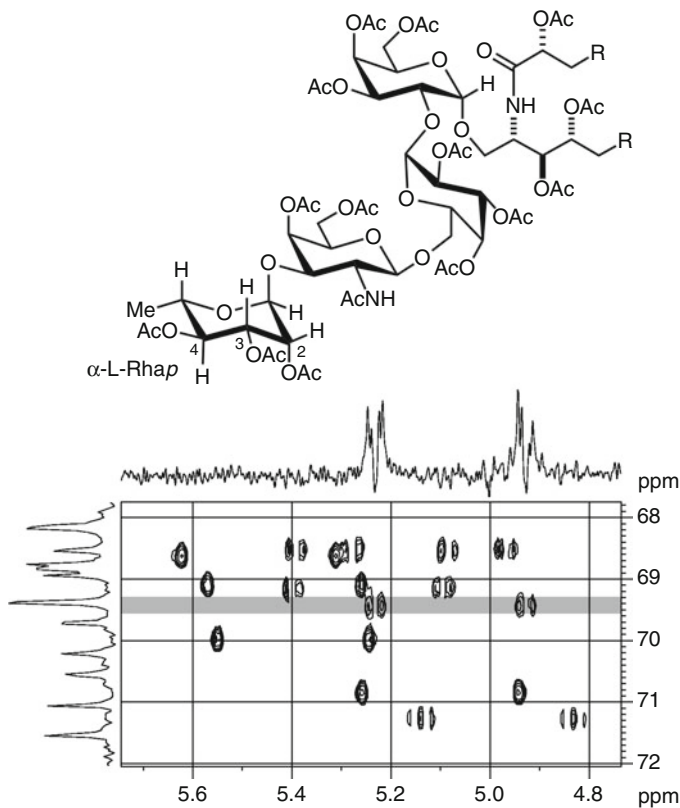


Fig. 8.13 Partial plot of the ^{13}C -coupled HMQC spectrum of clarhamnoside peracetate (**1b**). The top trace is the section of the spectrum at δ 69.4, which was used to measure coupling constants of H-3

This method has been used in the structure elucidation of clarhamnoside, a glycosphingolipid isolated from the marine sponge *Agelas clathrodes* [39]. Coupling constants are routinely used to determine relative configuration of sugars, but for the rhamnose IV of clarhamnoside, the nearly coincident chemical shifts of H-2 and H-3 prevented the measurement of their coupling constants. Instead, in the ^{13}C -coupled HMQC spectrum (in this work, HMQC was used instead of the almost equivalent HSQC), the signal of H-3 appeared as a well-defined first-order multiplet, with only one large axial-axial coupling constant (Fig. 8.13). Because H-4 was known to be axial, the orientation of H-2 was determined as equatorial, and the 6-deoxysugar was established to be a rhamnose.

This approach has also been used to measure coupling constants between equivalent protons, for example, to distinguish between *cis* and *trans* symmetric stilbenes [40].

8.3.6 Coupling Constants and Furanose Sugars

Today, the structure of a pyranose sugar is routinely determined by 2D NMR methods because *J*-coupling analysis provides an easy means for addressing stereochemical issues in a six-membered ring. The successful use of coupling constant information for stereochemical assignment in pyranosides is based on the conformationally rigid six-membered ring they contain. This is not the case for furanosides, where the flexibility of the five-membered ring (leading to the so-called pseudorotation) causes large variations in coupling constants between conformers, which prevent such an easy correlation between coupling constant values and relative configuration of adjacent carbon atoms. Therefore, when the sugar is in the furanose form, proton–proton coupling constants are considered to be of little use.

As a matter of fact, some correlation between vicinal couplings and relative configuration of furanosides is present in the literature. As early as in 1963, in a paper reporting the proton NMR spectra of all methyl pentofuranosides [41], it was clearly recognized that a small vicinal coupling in a furanoside implies that the coupled protons are *trans*-oriented. However, this principle has been used in the subsequent structure elucidation work only sporadically, partly because the threshold below which a coupling constant can be considered “small” had not been defined.

An in-depth computational study of coupling constants of furanosides as a function of the pseudorotation angle of the furanose ring was recently performed [11]. The dependence of the vicinal proton–proton coupling constants on the pseudorotation angle was calculated for each of the eight diastereomeric pentofuranosides (the presence of the additional CH₂OH of hexoses has a negligible influence on the conformation of the five-membered ring) using quantum-mechanical DFT methods (mPW1PW91/6-31G+).

The results (Fig. 8.14) showed that, when for *cis*-oriented pairs of protons, no conformation exists in which the calculated coupling is lower than 2.5 Hz for the H-1/H-2 pair, 4.0 Hz for the H-2/H-3 pair, and 2.5 Hz for the H-3/H-4 pair. Therefore, even allowing for some error in the calculation, whenever a furanoside vicinal coupling constant is <2 Hz (for H-1/H-2 or H-3/H-4) or <3.5 Hz (for H-2/H-3), the relevant protons must be *trans*-oriented. Of course, this rule does not work the other way round, and a coupling above the threshold does not provide any information about the stereochemistry of the coupled protons. This principle was used to define the relative configuration of one furanose sugar of the complex glycosphingolipid vesparioside B. The small coupling constants of the H-1/H-2 and H-2/H-3 pairs demonstrated the *trans* relationship of these pairs of protons (Fig. 8.15).

It must be noted that this is *not* an empirical rule because it does not rely on a particular conformation of the furanoside, but is based on the geometrical behavior of five-membered rings, in which the dihedral angle between the *cis*-oriented pair of protons cannot reach the values close to 90° that would lead to small coupling constants. For the same reason, the rule can most likely be extended to cover five-membered carbocycles.

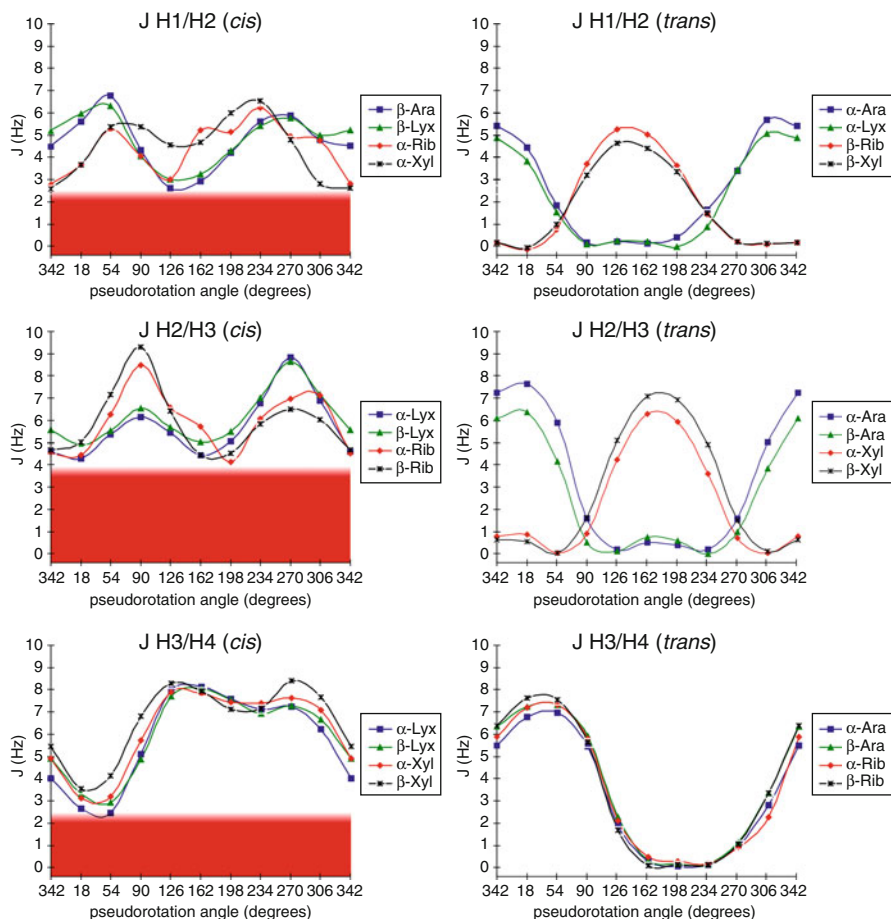
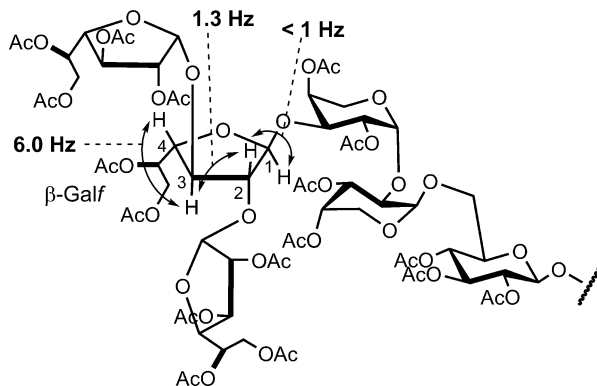


Fig. 8.14 Coupling constant of vicinal proton pairs in the eight pentofuranosides as a function of the pseudorotational angles of the furanose ring. The coupling constants were calculated using quantum-mechanical DFT methods. It is apparent that, in spite of the flexibility of five-membered rings, small coupling constants between *cis* vicinal protons are not possible in any conformation of the furanose ring. Therefore, a small coupling constant points to the *trans* relationship between vicinal protons. The threshold value is higher (3.5 Hz) for the H-2/H-3 pair and lower (2 Hz) for the H-1/H-2 and H-3/H-4 pairs

8.4 Future Perspectives

Structure determination by NMR is a well-established practice that in most cases leads smoothly to the desired results. However, as shown in the previous sections, there are still some unresolved problems and therefore a need for improvements in several areas.

Fig. 8.15 The saccharide chain of peracetylated vesparioside B. In the central galactofuranose, the small coupling constants between H-1 and H-2 and between H-2 and H-3 are a proof of the *trans* relationship of the two pairs of protons. On the contrary, the 6.0-Hz coupling constant between H-3 and H-4 does not provide any information about the relative configuration of C-3 and C-4



Many innovations in structure elucidation have been driven by the technical development of NMR spectrometers, so it is interesting to see what is going on in this respect. The race toward higher magnetic fields has currently come to a stop because the current technology based on niobium wires is close to its limits. The highest field available for NMR magnets was 400 MHz in 1980, 600 MHz in 1990, and 900 MHz in 2000, but only this year, after more than 10 years, a 1000 MHz magnet has become available. Only a drastic change in the superconducting material will allow a significant further increase in magnet fields. Much more significant is the dramatic enhancement of sensitivity (one order of magnitude and more) of NMR spectrometers that occurred in the last 10 years, following the introduction of the new micro and cold probes. This now makes possible structure elucidation of samples available in microgram amounts. Probe design is still susceptible to improvements, and further gains in sensitivity are expected.

A new frontier is the development of spectrometers with multiple receivers for the parallel acquisition of different 2D NMR experiments, which promises a further improvement in the speed of data acquisition. Specific experiments (e.g., PANACEA [42]) that allow to combine without interference the excitation schemes of two or more different homo- and heteronuclear 2D NMR experiments have been proposed, leading to shorter acquisition times and higher consistency between experiments (because the experiments are acquired in parallel, there is no risk of physical changes of the sample or of the instrument). Higher sensitivity and shorter acquisition times are of course extremely useful to the work of natural product chemists, but do not affect significantly the general strategy and the methods used for structure elucidation.

Some efforts are being devoted to the automated structure elucidation from raw spectroscopic data. One program has been proposed at the end of the 1990s [43] and is not being developed anymore, another one is commercially available, [44] but these tools have never come into common practice. While such programs can potentially be valuable for scientists involved in structure elucidation only occasionally, it appears unlikely that in the near future they will be a standard work tool for natural product chemists as they are becoming for protein chemists. On one hand, the amount of data to be handled is much lower, making it easily manageable

on paper; on the other hand, the workflow of structure elucidation of a natural product is much less defined than in protein chemistry, making its implementation into an algorithm more challenging. However, because these programs are not biased by the expectations of the researcher about the “most likely” structure, they could maybe find a role in the validation of new structures and therefore lower the rate of incorrect structures in the literature.

The major issue in structure elucidation remains the determination of stereochemistry, for which no general NMR method exists, particularly when stereocenters are located on conformationally flexible molecules and/or involve nonprotonated carbon atoms. Progress in this respect is coming from quantum-mechanical prediction of chemical shifts and coupling constants combined with conformational analysis of the molecule under study. However, in spite of some interesting attempts on specific targets [45], determination by NMR of the relative configuration of remote stereocenters is still an unsolved problem. Some help could come from the use of residual dipolar couplings [46, 47], especially if simpler methods for inducing molecule alignment will be developed. Although undoubtedly useful, these methods are not expected to be as revolutionary as 2D NMR has been, so it is likely that many unassigned configurations will continue to appear in the literature.

Finally, it must be mentioned that, as most chemists involved in the study of natural products may have experienced, there are many compounds which still elude NMR analysis. They typically show spectra with very broad and unresolved signals and are unsuitable for any 2D technique. They are sometimes polymeric compounds, but there may be many reasons why small molecules may behave this way, including complexation with paramagnetic ions, conformational or tautomeric equilibria, or aggregation phenomena. These intractable compounds are usually simply ignored by natural product chemists who, like anyone else, move along the line of least resistance. However, in a time when dereplication is becoming an increasingly important task for natural product chemists, there is room for some creative efforts toward these compounds.

8.5 Study Questions

1. One of the common artifacts present in the ROESY and NOESY spectra are peaks from zero-quantum coherence (Sect. 8.2.1.3). Look in the literature and NMR textbooks for a definition of zero-quantum coherence and the reason why it can affect cross-relaxation experiments like ROESY and NOESY.
2. ^{13}C decoupling in proton-detected experiments (such as HSQC) is a much more demanding technique than proton decoupling in ^{13}C -detected experiments (such as the 1D ^{13}C and DEPT experiments). Why?
3. Consider a mid-sized molecule, dissolved in CDCl_3 , which shows a very weak NOE because it falls between the positive and negative NOE regimes. What happens to NOE if the same compound is dissolved in a high-viscosity solvent such as DMSO?

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Abstract

Various NMR techniques have been developed that allow assignment of the relative and absolute configuration of many of the stereogenic carbons that occur in marine natural products. The application of chiral anisotropic reagents in conjunction with NMR analyses has been particularly useful for determining the absolute configuration of secondary alcohols, α -substituted primary amines, and α -substituted carboxylic acids. Derivatization of these functional groups with appropriate chiral reagents (e.g., MTPA) provides diastereomeric products that have diagnostic differences in their ^1H chemical shifts. A recently developed technique known as *J*-based configurational analysis uses proton–proton couplings and 2- and 3-bond carbon–proton couplings ($^{2,3}J_{\text{CH}}$) to assign the relative configuration of adjacent (1, 2) stereogenic carbons in conformationally flexible molecules. The *J*-based method involves comparing experimentally measured scalar couplings and NOE interactions with those predicted from this model to assign the relative configuration of the chiral methines. This technique is also applicable to oxygenated systems since there is a dihedral angle dependence for $^2J_{\text{CH}}$ couplings between a proton and an adjacent carbon that bears an

K.R. Gustafson

Molecular Targets Laboratory, Center for Cancer Research, National Cancer Institute-Frederick, Frederick, MD, USA

e-mail: gustafki@mail.nih.gov

electronegative oxygen substituent. Strategies have also been developed to utilize *J*-based configurational analysis when there is a methylene separating the two stereogenic methine carbons, and even when conformational interconversion results in the coexistence of two major conformers.

9.1 Assignment of Absolute Configuration Using Chiral Anisotropic Reagents

Marine natural products are often comprised of complex molecular architectures that incorporate one or more stereogenic carbon atom. Assignment of the absolute configuration of these chiral carbons is crucial to define the three-dimensional structure of a molecule, and this can be a significant challenge in the structural elucidation of new metabolites. A variety of chemical and spectroscopic methodologies (e.g., X-ray crystallography, circular dichroism) have been developed to address questions concerning absolute stereochemistry, but each technique has quite specific requirements and limitations that can restrict their utility. While there are no universal approaches for assigning absolute configuration that are applicable to all compounds of interest, NMR techniques based on chiral anisotropic reagents have been widely used in the structural determination of new marine natural products.

These NMR-based methods are useful for characterizing chiral secondary alcohols, α -substituted primary amines, and α -substituted carboxylic acids, and they are based on the shielding effect of a benzene ring (or other aryl group) in a chiral auxiliary that is appended to the molecule of interest. This methodology generally entails derivatization of the natural product with the two enantiomers of a chiral anisotropic reagent and comparison of the ^1H NMR chemical shifts of the resulting diastereomers. Characteristic changes in the chemical shifts of protons in the two diastereomeric derivatives can be explained by the ring current effect of an aryl group that occurs in the applied magnetic field of an NMR spectrometer. When π -electrons circulate at right angles to an applied magnetic field, they induce their own secondary magnetic field that can perturb nearby nuclei. Protons that reside where the magnetic lines of force for the induced magnetic field oppose the applied field experience a shielding effect, while protons situated where the induced magnetic field complements the applied field are deshielded. For a benzene ring, protons located directly above or below the center of the ring are shielded and shifted upfield, while protons lateral to the ring are deshielded and shifted downfield (Fig. 9.1). This kind of spatial variation of magnetic field is referred to as diamagnetic anisotropy.

In 1973, the Mosher laboratory in Stanford described an empirical correlation between the configuration of a chiral alcohol and the NMR chemical shifts of the diastereomeric products that result from reaction with specific chiral esterification reagents [1, 2]. All of these reagents contained an aryl substituent that caused characteristic changes in the chemical shifts of neighboring protons due to the anisotropic effect of the aromatic ring current. The most useful diastereomers for these NMR studies were the α -methoxy- α -trifluoromethylphenylacetic acid

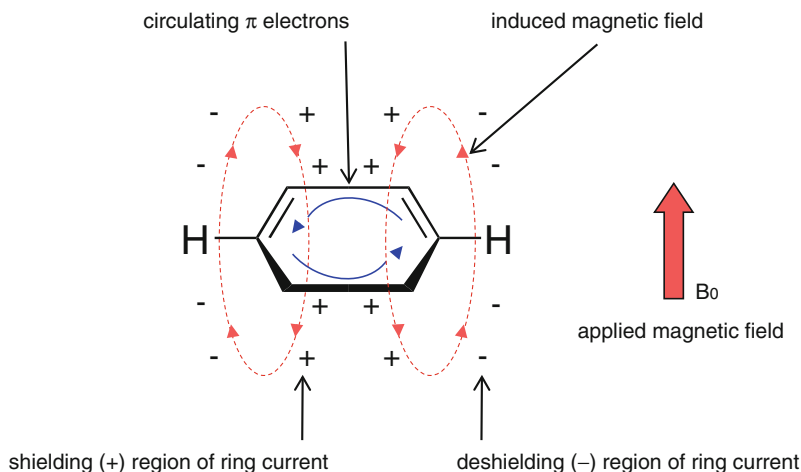


Fig. 9.1 Diamagnetic shielding and deshielding effects of the benzene ring current

(MTPA) ester derivatives of the chiral alcohols. A model was developed to rationalize the correlation between NMR chemical shift changes and the configuration of the stereogenic carbinol carbon. The model proposed that MTPA ester derivatives adopt a predominant conformation in which the original carbinol proton, the ester carbonyl, and the trifluoromethyl group all lie in the same plane (Fig. 9.2). This conformational hypothesis has been supported by X-ray crystal studies and computational analyses, and the plane defined by these three substituents is commonly referred to as the MTPA plane.

As illustrated in Fig. 9.2, R_1 and R_2 represent the substituents or faces of the original secondary alcohol that are located on opposite sides of the MTPA plane. When viewed in this manner, R_1 is oriented behind or to the right of the MTPA plane, while R_2 is in front of or to the left of the plane. In the case of the (*S*)-MTPA ester, R_1 is on the same side of the plane as the MTPA methoxy group, while in the (*R*)-MTPA ester, it is on the same side of the plane as the MTPA phenyl ring. The most significant diamagnetic impact of this phenyl substituent on neighboring protons in spatial proximity to its ring current is a shielding effect. It therefore stands to reason that proton resonances for R_1 in the (*S*)-MTPA ester, which do not experience this shielding, will be downfield relative to the corresponding R_1 protons in the (*R*)-MPTA ester.

This correlation between NMR shifts and the configuration of the MTPA ester was later refined and elaborated into the advanced Mosher's method [3, 4], which took advantage of more recent advances in high field NMR that allowed assignment of virtually all of the proton resonances in complex molecules. In this modified method, the difference in chemical shift between the (*S*)- and (*R*)-MPTA esters was experimentally determined for all of the proton signals that could be resolved and assigned. This increased the reliability of the methodology because it utilized numerous data points that could be analyzed for their internal consistency and

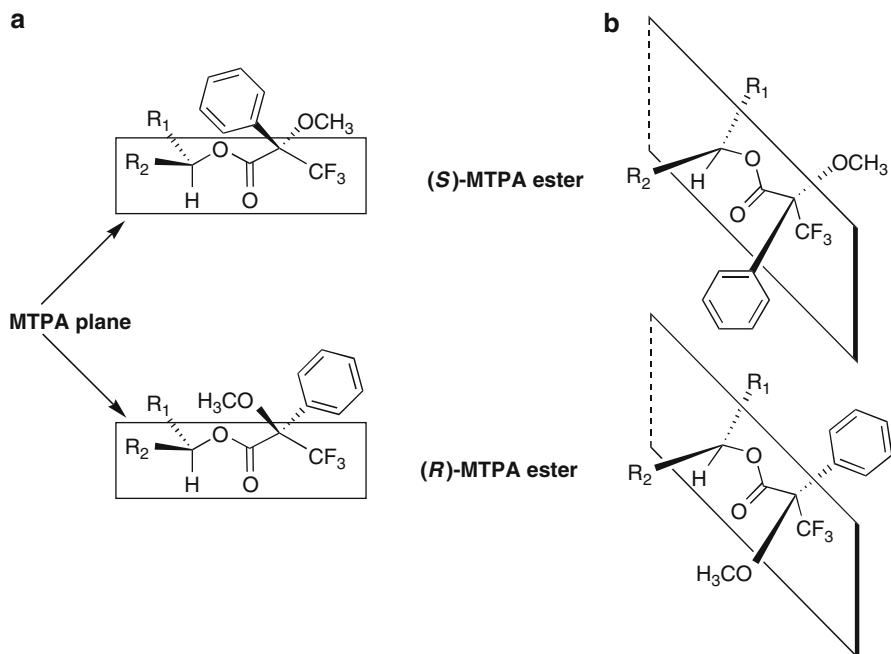


Fig. 9.2 Two alternative views, (a) and (b), of the ideal conformation of the MTPA ester and the resulting MTPA plane

regularity of distribution. The advanced Mosher's method has proven to be a reliable, effective, and easy to implement procedure for assigning the absolute configuration of secondary alcohols, and it has been successfully applied to a wide variety of marine natural products.

Assignments are made by preparing both the (*S*)- and (*R*)-MPTA ester derivatives of a natural product which contains a chiral secondary alcohol, and then determining the precise NMR chemical shifts of all of the protons that are in spatial proximity to the stereogenic carbon. The chemical shift of each proton in the (*R*)-MPTA ester (δ_R) is then subtracted from the chemical shift of its counterpart in the (*S*)-MPTA ester (δ_S) to give the difference in chemical shift ($\Delta\delta$) for that position in the molecule ($\Delta\delta^{S-R} = \delta_S - \delta_R$). There should be a systematic distribution of positive and negative $\Delta\delta$ values on either side of the MTPA plane. When the chiral carbon is viewed in the same plane as the β and β' carbons, and with the -OMTPA group and the carbinyl proton oriented as illustrated in Fig. 9.3, then the $\Delta\delta^{S-R}$ values for protons on substituent R_1 will be positive and those on R_2 will be negative.

The absolute magnitude of the $\Delta\delta^{S-R}$ values are inversely proportional to the distance between the proton and the MTPA group, and protons with $\Delta\delta^{S-R} = 0$ are either too far from the MTPA moiety to experience the anisotropic effect of the aryl ring or they lie on the MTPA plane. The value of $\Delta\delta^{S-R}$ for the carbinyl proton should be zero in the ideal conformation; however, deviation of the MTPA ester

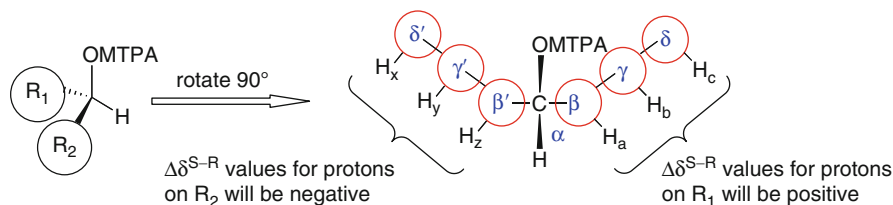


Fig. 9.3 Application of the modified Mosher's method. When the MTPA ester is viewed as illustrated, protons with $\Delta\delta^{S-R}$ values > 0 are assigned to R_1 , and those with $\Delta\delta^{S-R}$ values < 0 are assigned to R_2 . If there is a consistent pattern of positive and negative $\Delta\delta^{S-R}$ values about the MTPA plane, then the absolute configuration can be assigned

from the ideal conformation can cause $\Delta\delta^{S-R}$ for this proton to be non-zero. Anisotropic effects of the nearby ester carbonyl can also impact the carbinyl proton so $\Delta\delta^{S-R}$ values at this position are unreliable and should not be considered when making a configurational assignment. In certain instances, steric factors can cause the -OMTPA group to adopt a conformation that deviates significantly from the MTPA model. In these instances, the $\Delta\delta$ values of the MTPA derivatives will have an irregular distribution that deviates from the rules. If the $\Delta\delta$ values are irregularly arranged across the MTPA plane rather than systematically distributed as predicted, then the modified Mosher's method cannot be used for that particular configurational assignment. Another instance where this technique is inadequate for making an unambiguous assignment is when $\Delta\delta$ values can only be determined for protons on one of the substituents but not the other. This situation can occur when extensive signal overlap in the NMR spectrum prevents precise measurement of the pertinent proton resonances or when one of the substituents has no protons in the vicinity of the original secondary alcohol group [5].

It should be noted that the literature covering the use of chiral anisotropic reagents can be somewhat confusing. The original work by Mosher utilized $\Delta\delta^{R-S}$ values in which $\Delta\delta = \delta^R - \delta^S$, and an extensive body of work with chiral anisotropic reagents from the Riguera laboratory adopted this same convention [6, 7]. However, the advanced Mosher's method employed $\Delta\delta^{S-R}$ values in which $\Delta\delta = \Delta\delta^S - \Delta\delta^R$. There was no inconsistency with regard to the stereochemical conclusions that resulted from using these two contrasting definitions of $\Delta\delta$ because different models were used for placement of the substituents with positive $\Delta\delta$ values versus substituents with negative $\Delta\delta$ values (R_1 and R_2 in Fig. 9.3). When the configuration of an unknown is being determined, it is imperative that the configurational model used to make the assignment is consistent with how $\Delta\delta$ is calculated. Most of the literature data on MTPA derivatives of marine natural products utilizes the $\Delta\delta^{S-R}$ convention, so that is the format used in this chapter.

The most common approach for preparing MTPA esters is to treat the natural product containing a secondary alcohol with MTPA chloride in the presence of a mild base, such as triethylamine or pyridine. An acylation catalyst such as 4-dimethylaminopyridine can also be used to speed the reaction. Both the (*R*)- and (*S*)-MTPA chlorides are commercially available. However, it is important to note

that due to IUPAC rules for nomenclature and functional group priorities, (*R*)-MTPA chloride will produce the (*S*)-MTPA ester, while (*S*)-MTPA chloride will generate the (*R*)-MTPA ester. MTPA ester formation is generally performed at room temperature for 1–15 h. The course of the esterification reaction can be monitored by TLC, and it should be worked up when the starting material is gone or decomposition becomes apparent. HPLC purification of the MTPA esters is usually required to facilitate unambiguous NMR analyses. Use of aromatic NMR solvents such as benzene-*d*₆ and pyridine-*d*₅ for analyzing the MTPA esters should be avoided due to the potential for spurious results. The concentration of the (*S*)- and (*R*)-MTPA esters for NMR analyses should be the same and each spectra should be carefully referenced to an internal standard such as the residual deuterated solvent signal. The data from a combination of ¹H NMR, COSY (or TOCSY), and HSQC experiments is generally sufficient to make all of the necessary proton assignments and chemical shift measurements for the MTPA esters. These are relatively sensitive NMR experiments, so complete MTPA ester characterizations have routinely been accomplished on sub-milligram samples using NMR spectrometers equipped with conventional room temperature probes and on samples weighing 10–100 μg with cryogenically cooled probes. An application of the Mosher's ester methodology is illustrated below (Fig. 9.4) for assignment of the absolute configuration of a secondary alcohol in enigmazole A (**1**), a marine sponge-derived phosphomacrolide [8].

If the chemical shift differences of the diastereomeric MTPA esters are so small that they are within experimental error, then a variety of other chiral anisotropic reagents are available that have been reported to produce larger proton NMR shift differences [9–11]. Use of methoxyphenylacetic acid (MPA) as a chiral auxiliary has been recommended by the Riguera laboratory for a variety of reasons [5–7], including the fact that $\Delta\delta$ values for diastereomeric MPA esters can be increased simply by acquiring their ¹H NMR spectra at lower temperature (Fig. 9.5).

The modified Mosher's method is also applicable to chiral methine carbons bearing a primary amine group. In this case, diastereomeric (*S*)- and (*R*)-MTPA amides are prepared and analyzed by NMR in a manner directly analogous to MTPA esters. NMR data for the pair of amide derivatives is collected and analyzed, and $\Delta\delta^{S-R}$ values are calculated and assigned to R₁ and R₂ as illustrated in Fig. 9.6. MTPA amides generally produce larger $\Delta\delta$ values than MTPA esters.

Chiral anisotropic reagents such as phenylglycine methyl ester (PGME) are also available for elucidating the configuration of stereogenic methine carbons that are α to a carboxylic acid [12]. In this case, the (*R*)- and (*S*)-enantiomers of PGME are condensed with the carboxylic acid to generate a pair of diastereomeric PGME amides. The ¹H NMR spectra of these amides are assigned, $\Delta\delta^{S-R}$ values are calculated, and the R₁ and R₂ substituents are defined as illustrated in Fig. 9.7. The ideal conformation of the PGME amide has the original stereogenic carbon, the new amide carbonyl, and the nitrogen, α -carbon, and carbonyl carbon of PGME all coplanar. In this conformation, the PGME phenyl group exerts a diamagnetic shielding effect on protons in R₁ and R₂ similar to that seen with MTPA esters. Thus, protons on R₁ have $\Delta\delta^{S-R}$ values > 0, while protons on R₂ have $\Delta\delta^{S-R}$ values < 0.

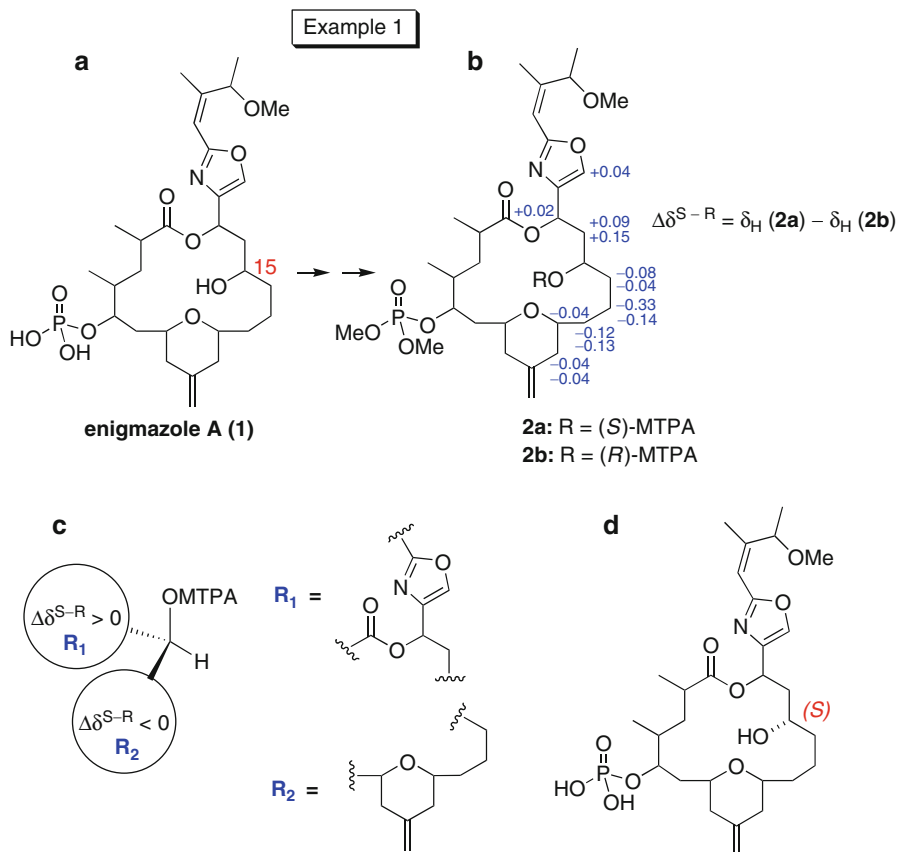


Fig. 9.4 Example 1: Assignment of the absolute configuration at C-15 of enigmazole A. (a) The phosphate group was protected by methylation, and then treatment with (*R*)- or (*S*)-MTPA chloride provided the (*S*)- and (*R*)-MTPA esters, respectively. (b) The $\Delta\delta$ values were calculated, and they showed a systematic distribution of positive and negative values. (c) When the MTPA ester was modeled as shown above, the R_1 and R_2 substructures could be identified. This established the absolute configuration at C-15 as *S*. (d) The structure of enigmazole A with *S*-configuration at C-15

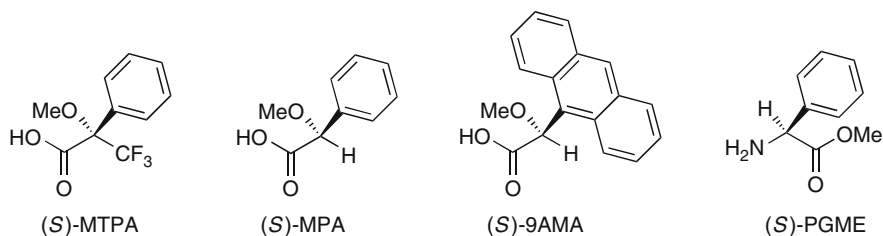


Fig. 9.5 Structures of some of the more commonly utilized chiral anisotropic reagents: MTPA (methoxytrifluoromethylphenylacetic acid), MPA (methoxyphenylacetic acid), 9-AMA (9-anthrylmethoxyacetic acid), and PGME (phenylglycine methyl ester)

Fig. 9.6 Distribution of $\Delta\delta^{S-R}$ values when the MTPA amide is viewed as illustrated

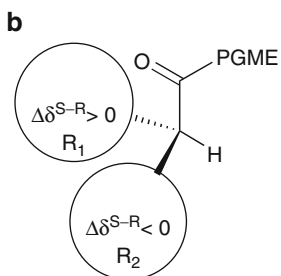
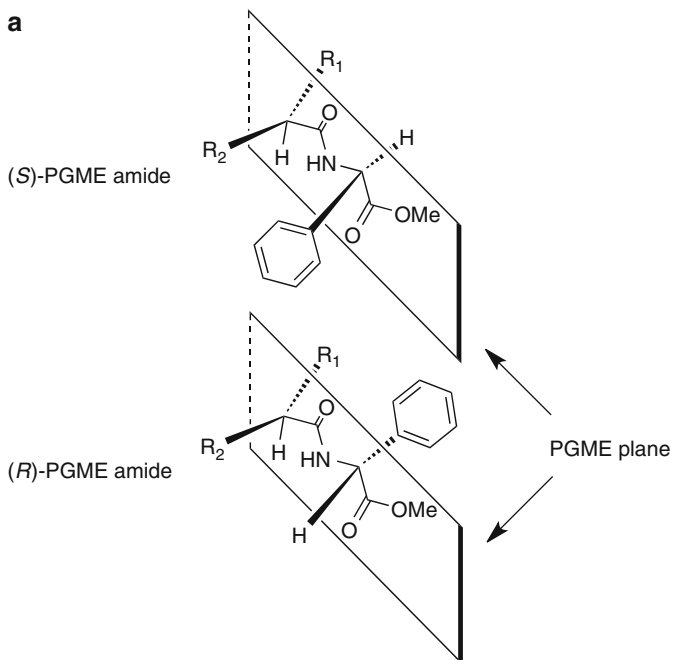
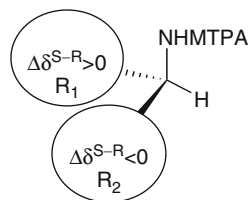


Fig. 9.7 Conformation of the PGME amide (**a**) and distribution of the $\Delta\delta^{S-R}$ values for assigning the absolute configuration (**b**)

In practice, PGME is condensed with the carboxylic acid in the presence of base (triethylamine), a peptide coupling reagent (PyBOP[®]), and a racemization suppressor (HOBt) at room temperature for 1–4 h. Both enantiomers of PGME are commercially available, and this reagent has been successfully used with a variety of structurally complex natural products. Phenylglycine dimethylamide (PGDA) and a variety of other chiral auxiliary reagents have also been used to determine the configuration of α -chiral carboxylic acids [12, 13]. The use of PGME to assign the absolute configuration at C-2 of enigmazole A (**1**) is illustrated in Fig. 9.8 [10]. In this case, the macrocyclic ester functionality in compound **1** was hydrolyzed to generate a linear carboxylic acid-containing product, which could then be derivatized with PGME to give the desired diastereomeric PGME amides.

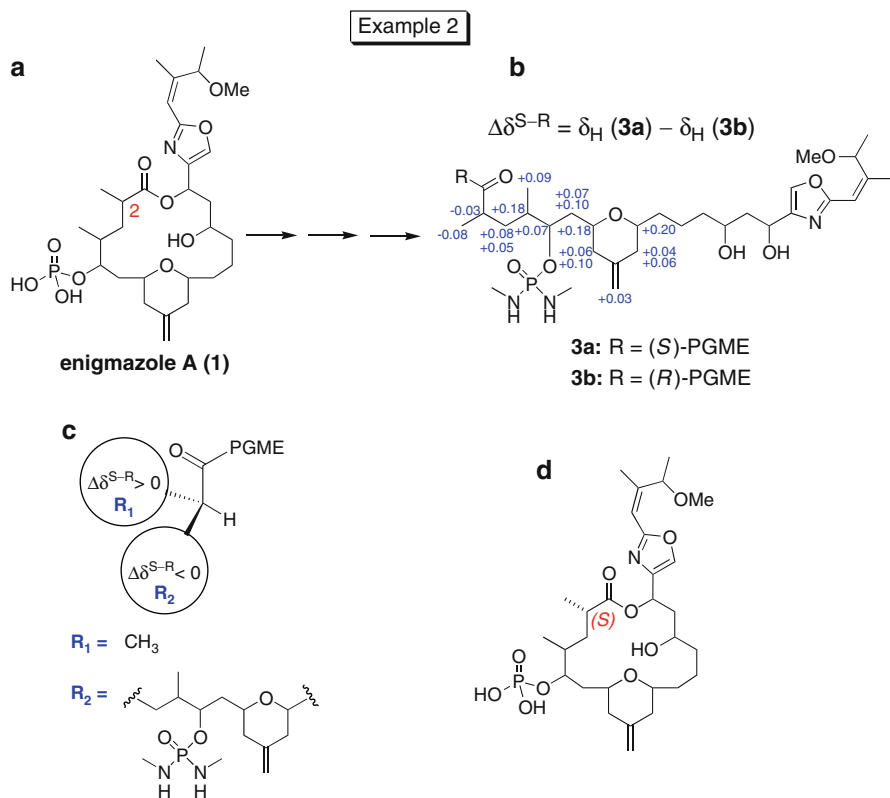


Fig. 9.8 Example 2: Assignment of the absolute configuration at C-2 of enigmazole A. (a) The phosphate group was protected as an *N,N*-dimethylphosphorodiamidate, and then the macrocyclic ring was hydrolyzed. The linear, carboxylic acid-containing product was condensed with (*S*)- or (*R*)-PGME to give the (*S*)- and (*R*)-PGME amides, respectively. (b) The $\Delta\delta$ values were calculated, and they showed a systematic distribution of positive and negative values. (c) The \mathbf{R}_1 and \mathbf{R}_2 substituents were assigned based on the PGME amide model. This established the absolute configuration at C-2 as *S*. (d) The structure of enigmazole A with *S*-configuration at C-15

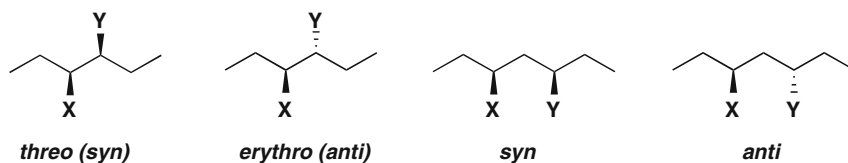


Fig. 9.9 Relative configuration of 1,2-methine diastereomers and 1,3-methine diastereomers

9.2 *J*-Based Determination of Relative Configurations

A seminal paper by Murata and coworkers in 1999 described a method to assign the relative configuration of stereogenic methine carbons based on analysis of long-range (2- and 3-bond) carbon–proton coupling constants, 3-bond proton–proton coupling constants, and nuclear Overhauser effect (NOE or ROE) interactions [14]. This technique is often referred to as *J*-based configurational analysis or as the Murata method, and it can be applied to acyclic compounds and to larger macrocyclic structures that are conformationally flexible. Advances in NMR hardware, probe design, and pulse sequences have made measurement of $^{2,3}J_{\text{CH}}$ coupling constants feasible for mass-limited samples, and this has greatly facilitated further development and application of this method. The utility of *J*-based configurational analysis for making stereochemical assignments has now been demonstrated in a large number of structurally diverse marine natural products.

Before describing details of the Murata method, it is useful to clarify some of the terms used to define stereochemical arrangements. The relative configuration of two adjacent chiral methine carbons can be described as *threo* or *erythro*. This nomenclature is derived from Fischer projections used in carbohydrate chemistry, but in the present discussion, it is most useful to look at its application with structures drawn in an extended zigzag projection (staggered formation). The main carbon chain defines a plane, and the substituents project behind the plane or in front of the plane. When two chiral centers are adjacent, if the two substituents with highest priority are on the same side of the plane, then the relative stereochemistry is *threo* or *syn*. If they are on opposite sides of the plane, then the diastereomer is *erythro* or *anti*. When chiral centers are not adjacent, the *syn* and *anti* nomenclature should be used to describe the relative configuration (Fig. 9.9).

For acyclic structures and other flexible systems, the relative conformation of adjacent stereogenic centers can be represented by six staggered rotamers. Newman projections for the three possible *threo* rotamers and the three *erythro* rotamers of a 1,2-methine system are shown in Fig. 9.10. For each configuration, the chiral methine protons have an *anti* orientation in one rotamer and *gauche* orientations in the other two rotamers.

If this system adopts one main conformer (> 85% of the total), then analysis of selected homonuclear and heteronuclear coupling constants associated with the methine protons can be informative. The magnitude of vicinal ^1H – ^1H couplings ($^3J_{\text{HH}}$) and vicinal ^1H – ^{13}C couplings ($^3J_{\text{CH}}$) are dihedral angle dependent, and they

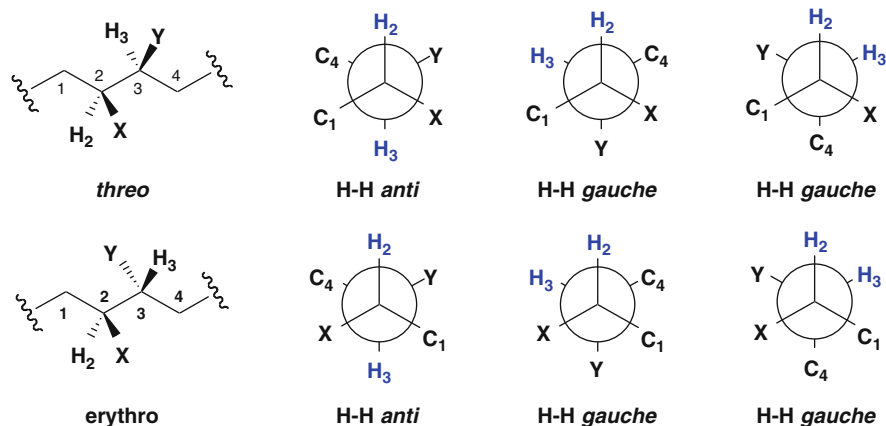


Fig. 9.10 Staggered rotamers of *threo* and *erythro* diastereomers

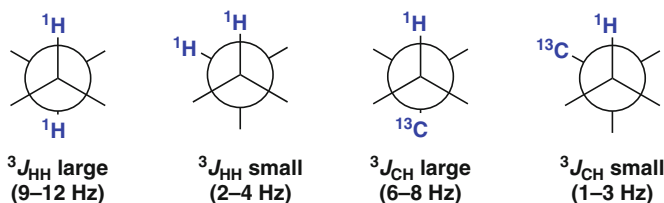


Fig. 9.11 Vicinal (3J) ${}^1\text{H}$ – ${}^1\text{H}$ and ${}^1\text{H}$ – ${}^{13}\text{C}$ coupling constants. J values adapted from Matsumori et al. [14]

can be described by the Karplus equation [15]. The range of expected 3-bond coupling values for *anti* (180° dihedral angle) and *gauche* (60° dihedral angle) orientations are shown in Fig. 9.11.

The J -based configurational method involves conceptually breaking a larger, more complex molecule into a series of adjacent (1,2) or alternating (1,3) asymmetric centers, and then assigning the relative configuration of the two chiral carbons in that structural fragment. All of the relevant ${}^1\text{H}$ – ${}^1\text{H}$ and ${}^1\text{H}$ – ${}^{13}\text{C}$ scalar coupling constants are experimentally determined, and then these values are compared with the predicted values (large or small) for the three staggered rotamers that arise from each diastereomer. Theoretical coupling values for a 1,2-methine fragment are illustrated in Fig. 9.12. It can be seen that there is a unique distribution of large and small coupling values for each of the four rotamers where H_2 and H_3 are *gauche*. So when the methine protons in the dominant conformer are *gauche*, it should be possible to identify the rotamer that best fits the experimental coupling data, and thus assign the relative configuration as *threo* or *erythro*. The two rotamers in which H_2 and H_3 are *anti* have identical distributions of large and

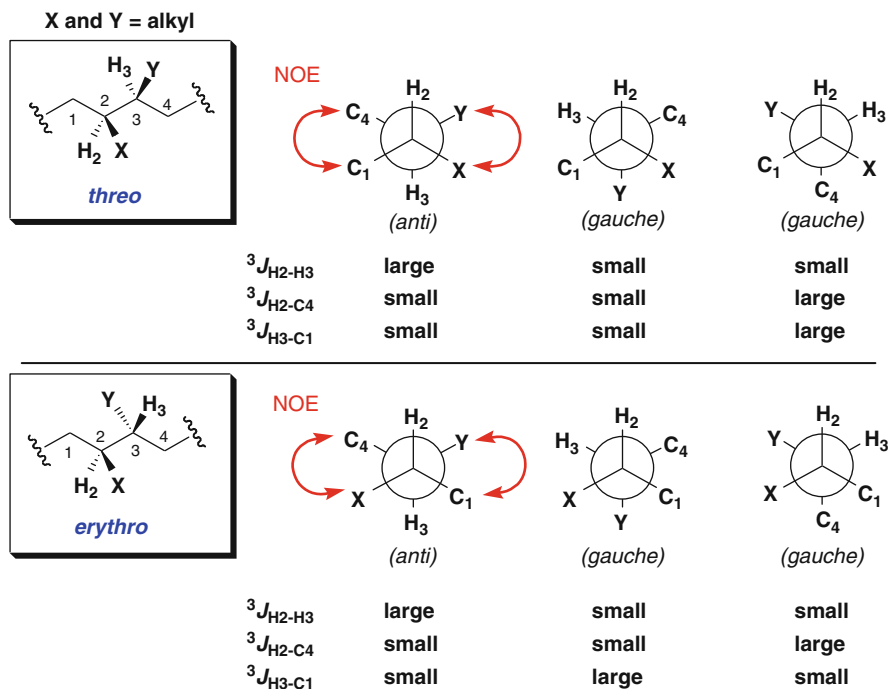


Fig. 9.12 ${}^3J_{\text{HH}}$ and ${}^3J_{\text{CH}}$ coupling values for the rotamers of a 1,2-methine system when substituents X and Y = alkyl

small couplings, and thus they cannot be distinguished by this type of analysis alone. However, when the chiral methine protons are *anti*, then C₁ and C₄ are *gauche* in the *threo* diastereomer, and NOE interactions between their respective protons (H₁ and H₄) should be possible. For the *erythro* diastereomer, when H₂ and H₃ are *anti*, then C₁ and C₄ are also *anti*, and no NOE interactions between H₁ and H₄ are possible. In this case, if substituents X or Y are protonated, then H₁–H_Y or H₄–H_X NOE interactions might be observable. Diagnostic NOE interactions can often be used to distinguish between the two different *anti* rotamers, and they can also help verify the identity of *gauche* rotamers that were assigned on the basis of coupling constant analyses (Fig. 9.12).

When X or Y is an electronegative substituent such as oxygen (OH or OR), then geminal C–H couplings (${}^2J_{\text{CH}}$) can also be diagnostic. Unlike ${}^3J_{\text{CH}}$ values which are positive, the sign of these 2-bond couplings is generally negative. While ${}^2J_{\text{CH}}$ values do not show a direct C–H dihedral angle dependence (the carbon and proton do not constitute a dihedral angle), they are related to the dihedral angle between the proton and the electronegative substituent bound to the coupled carbon (Fig. 9.13). When an oxygenated functionality is oriented *anti* to the neighboring methine proton, then the absolute value of the 2-bond heteronuclear coupling between that proton and the oxygen-bearing carbon is small. Conversely, when the oxygen substituent is *gauche*, the geminal C–H coupling is large.

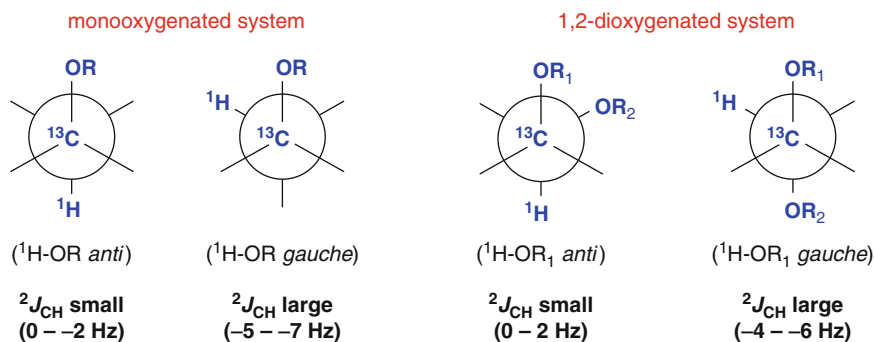


Fig. 9.13 Dihedral angle dependence for $^2J_{\text{CH}}$ coupling between a proton and an adjacent coupled carbon that bears an electronegative substituent such as oxygen (R = H or alkyl)

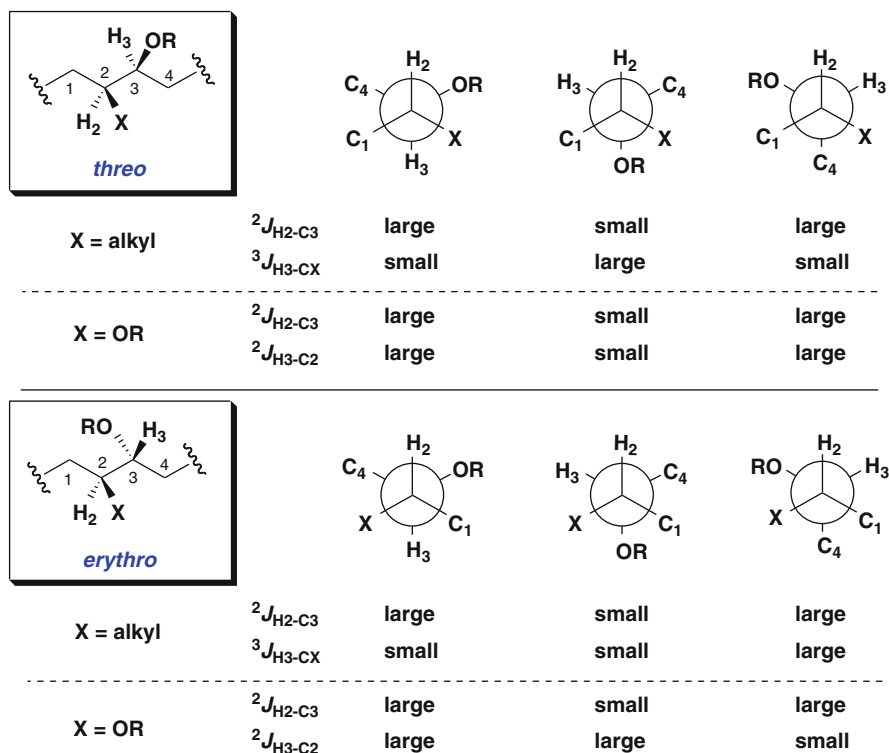


Fig. 9.14 $^2J_{\text{CH}}$ coupling patterns for the rotamers of oxygenated 1,2-methines

When assigning the relative configuration of 1,2-monoxygenated or 1,2-dioxygenated chiral fragments, the $^2J_{\text{CH}}$ values show a diagnostic pattern and they can be used in conjunction with 3J homonuclear and heteronuclear couplings. It should be noted that the distribution of large and small $^3J_{\text{HH}}$ and $^3J_{\text{CH}}$ couplings in

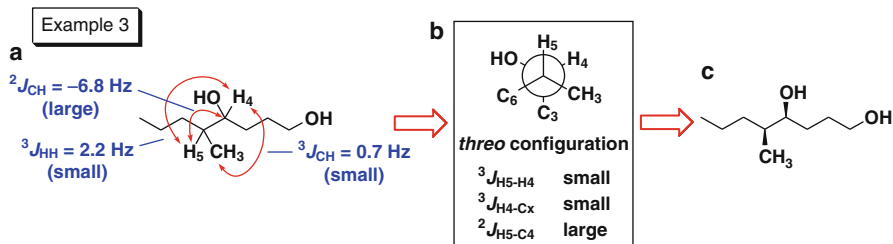


Fig. 9.15 Example 3: Assignment of the relative configuration of 4-hydroxy-5-methyloctanol. (a) Experimentally measured J values are classified as large or small in accordance with the scheme in Fig. 9.3. (b) H_4 and H_5 must be *gauche* due to their small vicinal coupling. Similarly, H_4 and the CH_3 group (C_x) have a small vicinal coupling, and they must also be *gauche*. H_5 has a large geminal coupling to C_4 , which requires a *gauche* orientation with the hydroxyl group. Comparison of the distribution of large and small couplings observed for the compound under study with the coupling patterns for the six possible staggered rotamers in Fig. 9.6 confirms that the configuration at C_4 and C_5 is *threo*. (c) The relative configuration of 4-hydroxy-5-methyloctanol illustrated in an extended (zigzag) structure. (Note: The J values used in this exercise are for illustrative purposes only; they do not represent actual measured values)

these oxygenated systems is the same as those for alkyl-substituted 1,2-methines. However, the magnitude of these 3-bond vicinal couplings can be somewhat reduced [14, 16]. The characteristic distribution of ${}^2J_{\text{CH}}$ values for mono- and dioxygenated systems, which can help define the configuration of adjacent methines, are illustrated in Fig. 9.14. Even with these additional 2-bond couplings, the *threo* and *erythro* diastereomers cannot be distinguished by J measurements alone when H_2 and H_3 are *anti*. In this case, additional NOE experiments are needed to assign the relative configuration.

The characteristic influence of oxygen substitution on ${}^2J_{\text{CH}}$ values is also observed with other electronegative substituents, such as nitrogen or halogens. These elements also result in ${}^2J_{\text{CH}}$ couplings that are dependent on the dihedral angle between the proton in question and the electronegative substituent bound to the coupled carbon. While the overall pattern of large and small J_{CH} values that is observed with these other substituents is identical to the distribution described for oxygen, the range of J_{CH} couplings can vary. Experimentally determined ranges of large and small J_{CH} values for various electronegative substituents have been described, and these should be consulted when J -based configurational analysis is done with these systems [16, 17] (Fig. 9.15).

When two diastereomeric methines are separated by a methylene, both methylene protons must be assigned in a stereospecific manner with respect to the adjacent methines. This requires that the methylene protons resonate at sufficiently different chemical shifts that accurate coupling constant measurements can be made. This type of 1,3-methine system can conceptually be broken into two overlapping two-carbon fragments which are separately analyzed. First, the methylene protons are stereospecifically assigned relative to the first methine based on the unique pattern of ${}^3J_{\text{H,H}}$ and ${}^{2,3}J_{\text{C,H}}$ values for the six possible rotamers (Fig. 9.16). Once this stereospecific relationship is established, the methylene

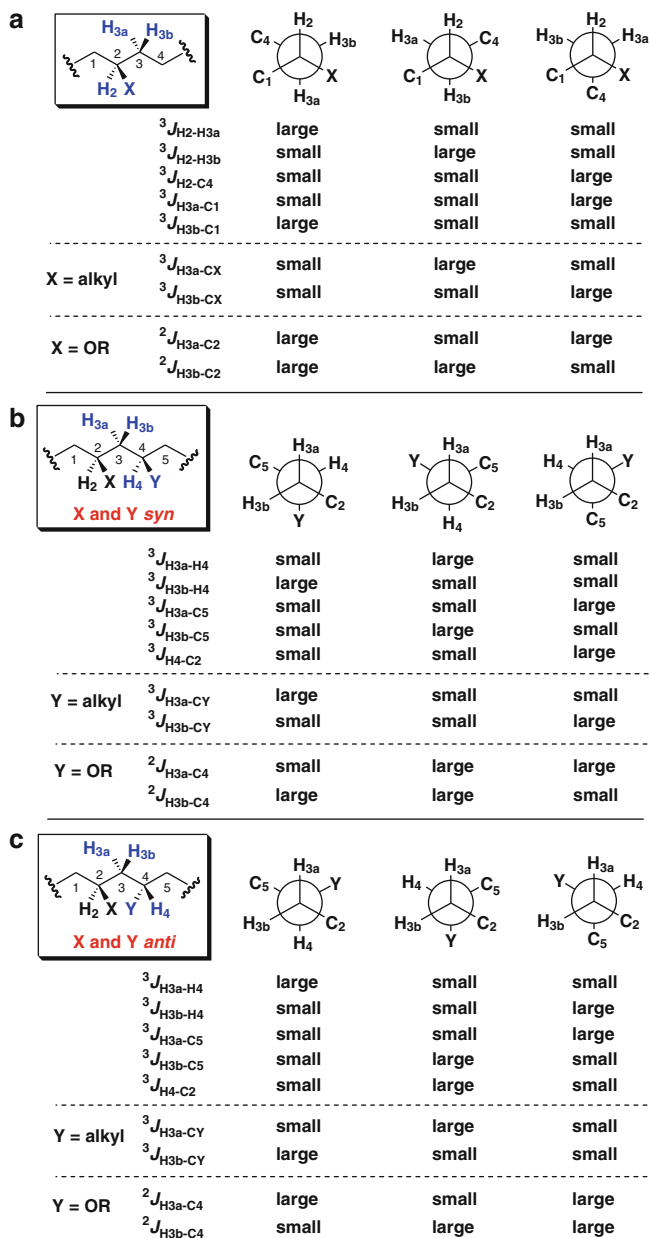


Fig. 9.16 Configurational analysis of 1,3-methine systems when X = alkyl or -OR, and Y = alkyl. (a) The *erythro* or *threo* orientation, relative to H₂, of the diastereotopic methylene protons H_{3a} and H_{3b} can be assigned based on the pattern of their respective *J* values. (b and c) Next, the configuration of H₄ relative to H_{3a} and H_{3b} can be established in a similar manner. This process correlates the stereochemical orientation of both H₂ and H₄ with the two diastereotopic methylene protons, and thus the relative configuration at C₂ and C₄ can be assigned as *syn* or *anti*

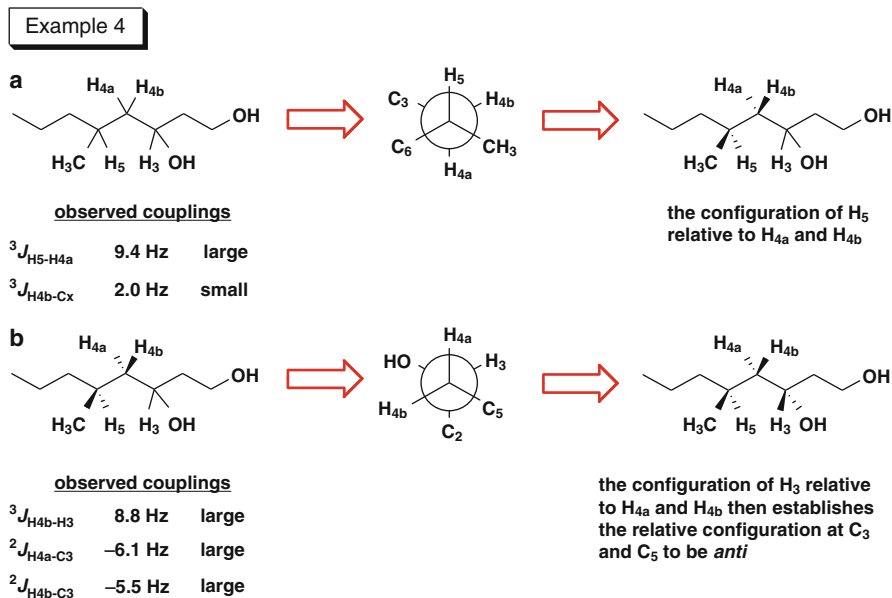


Fig. 9.17 Example 4: Assignment of the relative configuration of 3-hydroxy-5-methyloctanol. (a) The configuration of H₅ relative to the diastereotopic methylene protons H_{4a} and H_{4b} is established by selecting the appropriate rotamer that fits the experimental *J* values. In this case, two key couplings were sufficient. The large vicinal coupling between H₅ and H_{4a} defines an *anti* orientation for these two protons, while the small vicinal coupling between H_{4b} and the CH₃ group (C_x) requires a *gauche* orientation for these two substituents. Thus, H_{4a} has a *threo* relationship to H₅, and H_{4b} is *erythro*. (b) Once the stereospecific orientation of H_{4a} and H_{4b} has been defined, their configuration relative to H₃ can be established. H₃ and H_{4b} must be *anti* due to the large vicinal coupling. Large geminal couplings for H_{4a} and H_{4b} with C₃ require them both to be *gauche* to the hydroxyl group, which then defines the appropriate rotamer. This establishes an *erythro* relationship between H_{4a} and H₃, which means the relative configuration of C₃ and C₅ is *anti*. Note: The *J* values used in this example are for illustrative purposes only; they do not represent actual measured values

protons are correlated with the second methine using the same *J*-based analysis. In this manner, the configurational relationship of the 1,3-methines can be unambiguously assigned via the intervening diastereotopic methylene protons. The configuration of two methines separated by two intervening methylenes can be correlated in a similar fashion, if all the resonances of the diastereotopic methylene protons are sufficiently resolved (Fig. 9.17).

For some acyclic or highly flexible molecules, conformational interconversion results in the coexistence of two or three different rotamers. When multiple conformers do exist, if any one conformer accounts for over 85% of the population, then *J*-based configurational analysis of only the dominant conformer is still valid. However, if ${}^3J_{\text{HH}}$ couplings have intermediate values between those expected for either the H-H *anti* or *gauche* rotamers, then the presence of two major conformers needs to be considered. It is often valid to view these systems as two interconverting

staggered rotamers. In these instances, the ^1H - ^1H and ^1H - ^{13}C couplings represent a weighted average of the values for each conformer, and the observed coupling values can be large (when two large couplings are averaged), small (when two small couplings are averaged), or medium (when a large and a small coupling are averaged). For a 1,2-methine system, there are four possible pairs of rotamers where one alternating conformer has H-H *anti* and the other has H-H *gauche*. These pairs of alternating rotamers can be distinguished based on their unique distribution of $^3J_{\text{HH}}$ and $^{2,3}J_{\text{CH}}$ values, and thus the configuration can be assigned as illustrated in Fig. 9.18. When both interconverting conformers have H-H *gauche*, then analysis of coupling values alone is not sufficient to assign the relative configuration. *J*-based analysis also breaks down when there are significant contributions from three different rotamers since this causes all of the *J* values to be averaged. When multiple conformers exist, it may be possible to reduce conformational interconversion and enhance the percentage of a single conformer by acquiring the NMR data at low temperature.

9.3 Measurement of *J* Values

The ability to accurately determine both ^1H - ^1H and ^1H - ^{13}C coupling constants is crucial for successfully employing *J*-based configurational analysis in structure elucidation studies. Vicinal ^1H - ^1H couplings can often be measured directly from standard ^1H NMR spectra when the resonances are adequately resolved. For overlapped resonances, selective pulse sequences such as 1D TOCSY, 1D NOESY, or 1D ROESY may eliminate the other overlapping signals and allow direct measurement of ^1H - ^1H coupling constants [18, 19]. Phase-sensitive 2D COSY experiments such as DQF-COSY and E-COSY [20] can often be effective for overlapped or extensively coupled resonances. While the determination of ^1H - ^1H coupling values is relatively straightforward, there are inherent problems associated with the measurement of long-range ^1H - ^{13}C couplings, such as low signal-to-noise and digital resolution limitations. A variety of 2D NMR experiments have been described for determining $^{2,3}J_{\text{CH}}$ coupling constants, but they all have some practical limitations or experimental challenges associated with their routine use [21]. Three of the more common pulse sequences that have been successfully applied in natural products studies are the HETLOC [22], *J*-HMBC [23], and HSQMBC [24] experiments. HETLOC (hetero half-filtered TOCSY) is similar to a ^1H - ^1H TOCSY experiment except the correlations have E-COSY-type splitting patterns, with 1-bond $^1J_{\text{CH}}$ coupling in F_1 and the long-range $^{2,3}J_{\text{CH}}$ coupling as an offset in F_2 . Heteronuclear coupling values can be read directly from the HETLOC spectrum, but this experiment relies on TOCSY-like correlations so its application is limited to protonated carbons within a given proton-proton spin system. J_{CH} couplings cannot be measured for quaternary carbons or for protonated carbons outside of the ^1H spin system. The *J*-HMBC pulse sequence provides spectra similar to HMBC, but the correlation peaks are split in the F_1 dimension by a multiple of the heteronuclear coupling constant and a *J*-scaling

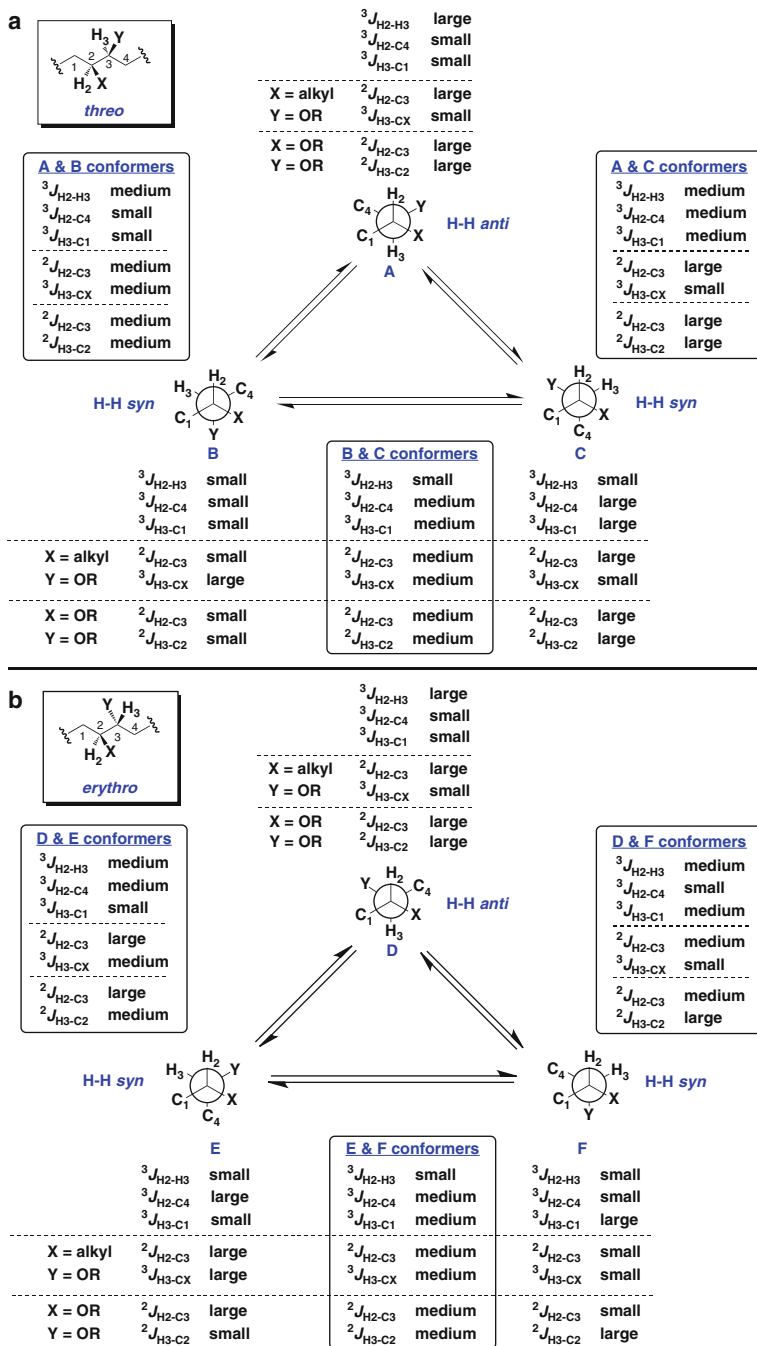


Fig. 9.18 (continued)

factor (observed F_1 splitting = $^{2,3}J_{\text{CH}}$ x J -scaling factor). The J -scaling factor can be controlled by changing the variable delay periods in the pulse sequence. The actual $^{2,3}J_{\text{CH}}$ values in a J -HMBC data set are obtained by applying a mathematical correction to the measured F_1 splittings. Low signal-to-noise due to the length of the pulse sequence can be an inherent problem with J -HMBC, but this experiment can provide heteronuclear coupling constants for quaternary carbons and for couplings that encompass components from different ^1H spin systems. The HSQMBC experiment employs a modified HSQC-type pulse sequence for the evolution of long-range ^1H - ^{13}C couplings. It does not rely on ^1H - ^1H coupling, so it can be used to measure long-range couplings with quaternary carbons or couplings between systems that are separated by a heteroatom or quaternary carbon. Extraction of $^{2,3}J_{\text{CH}}$ coupling constants from HSQMBC data is relatively straightforward for systems with simple ^1H - ^1H coupling patterns, but it can be more challenging for systems with complex ^1H - ^1H couplings. When there are complex ^1H multiplets, a peak-fitting protocol may be required to match the 1D ^1H resonance with the dispersive coupling pattern of a 1D slice through its HSQMBC correlation peak. This latter process can be complicated by nonuniform phase effects in the data.

It is anticipated that the continued evolution and improvement of these and other NMR pulse sequences will enhance our ability to accurately determine $^{2,3}J_{\text{CH}}$ coupling constants, and thus expand the utility of the J -based methods for making configurational assignments. In addition to these experimental NMR approaches for measuring long-range heteronuclear couplings, computational methods have recently been developed to predict homonuclear and heteronuclear spin-spin couplings [16, 25]. Quantum mechanical density functional theory calculations of J -coupling values can now be exploited to predict coupling constants for all of the staggered rotamers and compare these computed values with the experimentally determined ones. This computational approach has already been employed in the structural assignment of natural products, and its utility and application is likely to increase in the future.

9.4 Concluding Remarks

The utilization of NMR methods to successfully make both relative and absolute configurational assignments has significantly increased the utility of this



Fig. 9.18 Interconverting pairs of rotamers for *threo* (a) and *erythro* (b) configurations. The averaged J values for the alternating conformers have a unique distribution when there is interconversion between H-H *anti* and H-H *gauche* rotamers. Thus, the *threo* conformer pairs A and B and A and C can be distinguished from their *erythro* counterparts, D and E and D and F, and the configuration can be unambiguously assigned when any of these conformer pairs coexist. The averaged J values for an equilibrium mixture of the *threo* conformers B and C (both H-H *gauche*) cannot be distinguished from the corresponding mixture of conformers (E and F) for the *erythro* configuration, so a stereochemical assignment is not possible for these conformer pairs

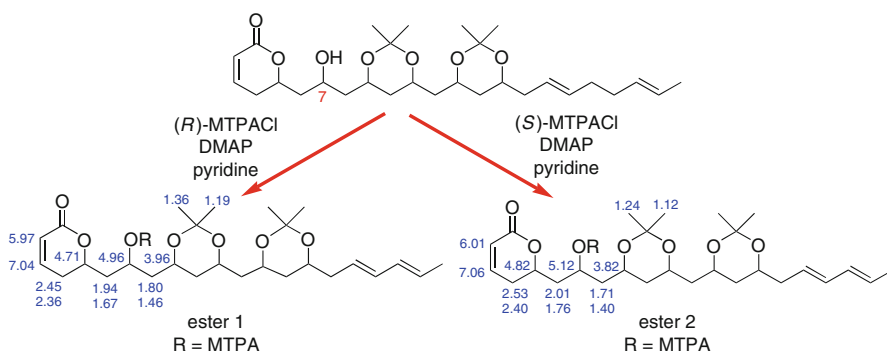
spectroscopic technique in the structural elucidation of natural products. While NMR has long been paramount in determining the planar structures of new metabolites, its utility for establishing stereochemical features of complex organic compounds was often quite limited. The development and validation of new NMR methodologies such as those employing chiral anisotropic reagents, or the *J*-based configurational approach illustrate the continuing evolution and expansion of NMR applications. These advancements have been possible due to a multitude of factors, including improvements in both NMR hardware and pulse sequences. The availability of NMR spectrometers with higher magnet field strengths has increased both the sensitivity and resolution of individual resonances, while the advent of cryogenically cooled probes provided dramatic signal-to-noise improvements. The development and refinement of new pulse sequences now allow the fairly “routine” measurement of long-range ${}^{2,3}J_{\text{CH}}$ coupling constants and ${}^1\text{H}$ - ${}^1\text{H}$ couplings of heavily overlapped proton resonances. While these pulse sequences are now available from the pulse sequence libraries NMR vendors provide with their current software, care must be taken in selecting appropriate experimental parameters. Unambiguous interpretation of the coupling data can also be problematic at times, so it is highly recommended that these types of experiments be performed initially on standards with known coupling values. One should be wary of using these experiments with unknowns until the coupling data has been successfully acquired and analyzed for a standard compound.

Improvements in NMR technologies themselves have only set the stage for the current and future applications of NMR to solve stereochemical challenges. The real credit goes to those individuals who have observed reproducible patterns in the NMR data they acquired with chiral compounds, and then conceptually developed the models to explain these patterns. These were the fundamental contributions that allowed the NMR techniques to develop. Recognition of the potential of chiral anisotropic reagents and *J*-based analysis in the stereochemical elucidation of new natural product structures was also essential for the now widespread use of these techniques. The continued refinement of these current approaches, and the development of new NMR methods for configurational analysis, will undoubtedly continue in the future. It is imperative that those involved in contemporary natural products structural studies develop confidence and expertise in the application of these experiments.

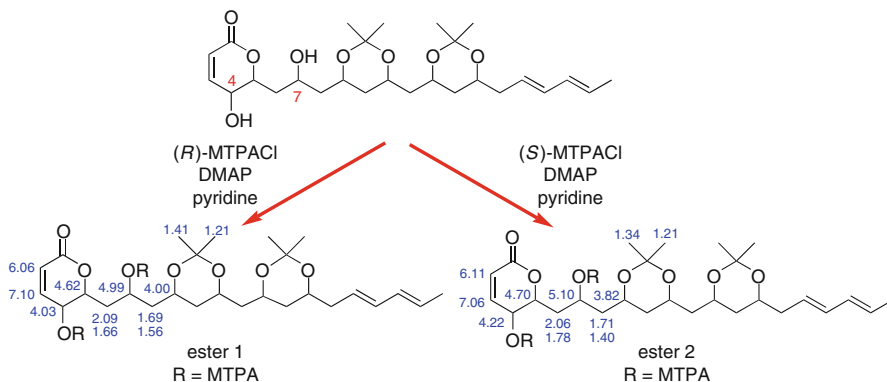
9.5 Study Questions

1. The bis-acetonide derivative of a polyol natural product was treated with MTPA-Cl, and ${}^1\text{H}$ NMR data for the two resulting MTPA esters is shown

below. From this data, determine the absolute configuration of the hydroxy methine carbon at C-7

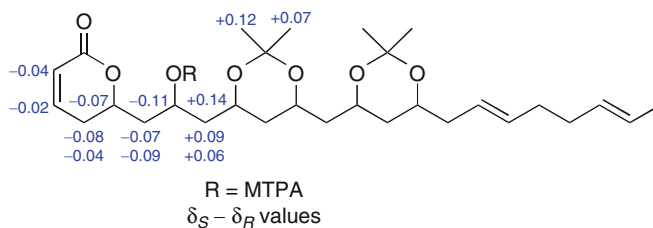


2. A hydroxylated analogue was also treated with MTPA-Cl, and NMR data for the bis-MTPA esters was acquired. From this data, can the Mosher's method be used to assign the configuration of the C-4 and C-7 hydroxy methine carbons? If so, what is the absolute configuration at C-4 and at C-7?

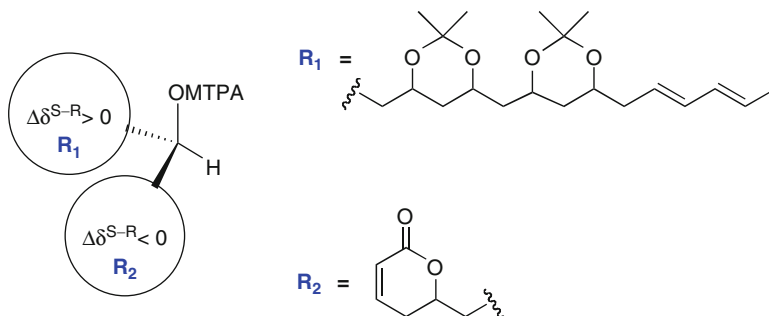


Answer 1

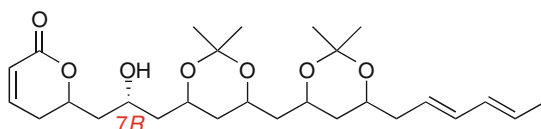
Calculate the $\delta_S - \delta_R$ values.



There is a consistent distribution pattern of $\Delta\delta^{S-R}$ values, so the Mosher's method is applicable in this case. Model the MTPA ester as shown, and assign R_1 and R_2 .

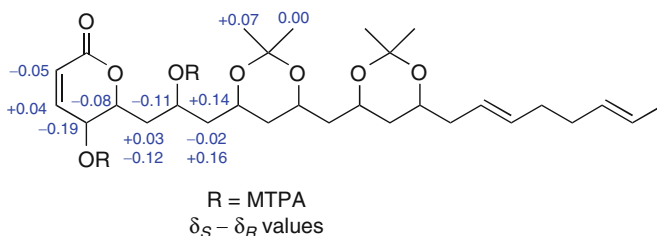


When R_1 and R_2 have been assigned, use the Cahn–Ingold–Prelog priority rules to establish the absolute configuration of the hydroxy methine carbon in the natural product.



Answer 2

Calculate the $\delta_S - \delta_R$ values.



The sum of the shielding and deshielding effects of two MTPA esters in close proximity resulted in a random distribution of positive and negative $\Delta\delta^{S-R}$ values. Assignment of the absolute configuration at C-4 and C-7 by the Mosher's method is not possible in this case.

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Quantum Chemical Calculation of Chemical Shifts in the Stereochemical Determination of Organic Compounds: A Practical Approach

10

Simone Di Micco, Maria Giovanna Chini, Raffaele Riccio, and Giuseppe Bifulco

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Abstract

In this chapter, we report an integrated approach of NMR and quantum mechanical calculation for the determination of the relative configuration of natural products. The entire protocol is described starting from building the investigated compound to the calculation of NMR properties at quantum theory level and the interpretation of the results. Each step of the protocol is described, and the main applied methods are reported. We report, as case studies, the determination of the relative configuration of two natural products: bonannione B isolated from *Bonannia graeca*, and callipeltin A isolated from the sponges *Callipelta* sp. and *Latrunculia* sp. Through the analysis of these natural products, we show the use of ¹³C chemical shift and homo and hetero *J* coupling constants, respectively, as

S. Di Micco • M.G. Chini • R. Riccio (✉) • G. Bifulco (✉)
Department of Pharmaceutical and Biomedical Sciences, University of Salerno, Via Ponte Don Melillo, Fisciano (Salerno), Italy
e-mail: sdimicco@unisa.it, mchini@unisa.it, riccio@unisa.it, bifulco@unisa.it

an important tool in the interpretation of the experimental data for the determination of the relative configuration of organic compounds.

10.1 Introduction

In the last decade, quantum chemical approaches have shown their potential in solving chemical problems. This has been mostly due to the ever increasing computational capabilities at a relatively affordable cost and to a parallel development of user-friendly software. While many aspects of molecular structure and dynamics may be solved with the use of classical methods based on empirical force fields, quantum chemistry allows the comprehension of many problems related to the electronic density distribution. In particular, quantum chemistry methods can be applied for calculating the spectroscopic properties of molecules, and the efficient prediction of UV, IR, CD, and NMR spectra have been extensively reported in the last 15 years. NMR chemical shift calculation by quantum mechanical methods has attracted the interest not only of the theoretical chemists but also of the experimental NMR spectroscopists. In fact, this kind of approach has been used by our and other research groups as a contribution to the structure elucidation of natural products. We have presented two original methodologies, based on GIAO (gauge including atomic orbitals) quantum mechanical ^{13}C chemical shift calculations, that have been efficiently employed as a support in the analysis of the NMR data of organic molecules. The first methodology regards the structure validation of natural products by means of GIAO ^{13}C chemical shift calculations, while the second one, based on the same methodology, has been directed to the determination of the relative configuration of flexible compounds. For the interested readers, the most significant applications of quantum chemical calculations of NMR parameters in the resolution of stereochemical problems have been recently reported by us in two reviews. On the other hand, the scope of this chapter is to present a step-by-step guide for the NMR parameter calculation of organic compounds in the determination of their relative configuration.

10.2 Calculation Protocol for Molecular Frameworks

Different experimental approaches have been proposed for the determination of the configuration of organic compounds [1, 2]. One of the most used is the total synthesis, which is highly demanding in terms of human and economical resources. On the other side, there are analytical methods, such as nuclear magnetic resonance (NMR), X-ray crystallography, circular dichroism (CD), and mass spectrometry, which allow also to preserve the investigated compound. For the stereostructural determination of natural products, it is possible to apply a protocol based on the calculation of ^1H and/or ^{13}C of chemical shifts as a support in the experimental data analysis (Fig. 10.1) [3, 4]. Such a protocol consists of up to six fundamental steps: (a) building the molecules by dedicated software; (b) conformational search at the empirical theory level [5, 6], generally through molecular dynamics (MD) or by Monte Carlo multiple minimum

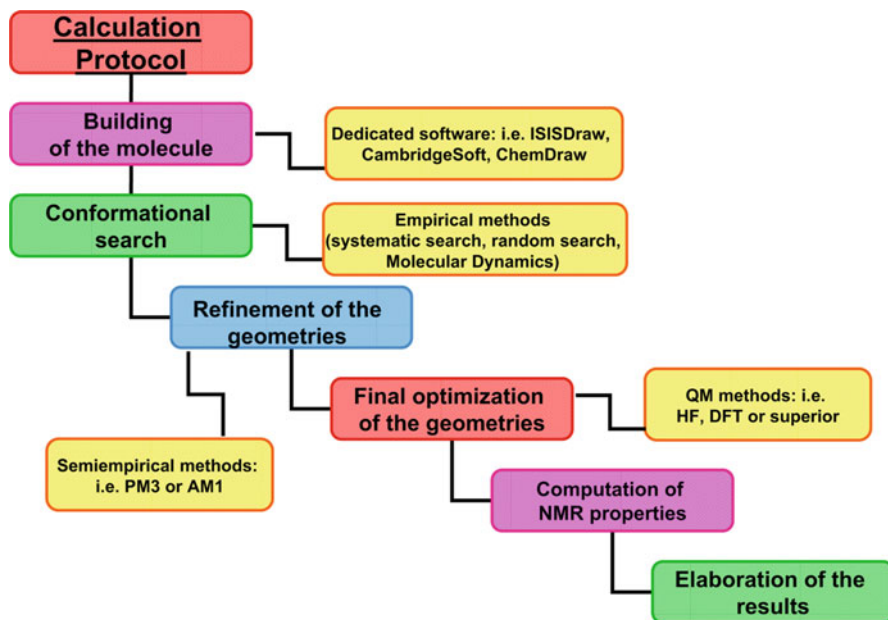


Fig. 10.1 General protocol used for the determination of the relative configuration of organic compounds

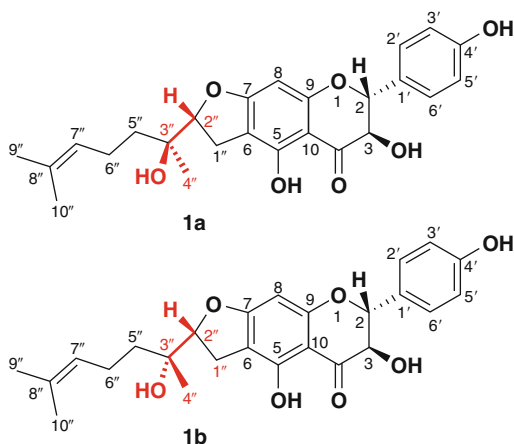
methods (MCMM) [7]; (c) preliminary geometry optimization at semiempirical level (e.g., AM1 [8], PM3 [9]) of all the significantly populated conformers of each stereoisomer; (d) final geometry optimization of all the species at the quantum mechanical (QM) level; (e) GIAO (gauge including atomic orbital) ^{13}C and/or ^1H NMR calculations of all the structures obtained by the optimization at QM level of all diastereomers, taking into account the Boltzmann distribution; and (f) elaboration of the results comparing the Boltzmann-averaged NMR parameters calculated for each stereoisomer with those experimentally measured for the compound under examination. In order to facilitate the understanding of the protocol, we will show an application of the QM/NMR methodology to a real case: the assignment of the relative configuration of the bonannione B (**1**, Fig. 10.2), a flavanone isolated as minor compounds from the aerial parts of *Bonannia graeca* (*Umbelliferae*) [10].

The example of the flavonoid bonannione B (**1**, Fig. 10.2) represents a straightforward application of ^{13}C NMR chemical shift calculation, since the configuration of stereopair (C-2'' and C-3'') under investigation could not be deduced by simple analysis of the 2D ROESY spectra, and the small amount of the isolated compound was not sufficient to apply Mosher's method [11].

10.2.1 First Step: Building the Molecules

The generation of the molecule model represents the starting point for any computational chemistry study. The tridimensional model (3D) defines the relative

Fig. 10.2 Molecular structure of two possible diastereoisomers of bonannione B (**1a** and **1b**)



position of the atoms in the space through a set of Cartesian coordinates obtained from several sources. The X-ray crystallographic database [12], the building from a preexisting fragment library, the conversion of 2D structural data (e.g., .cdx, .skc, .sk2, and smiles files) into 3D form (e.g., .mol, .pdb, .mol2, .mae, and .gjf files) with a dedicated software – ACD/ChemSketch [13], ISISDraw [14], and ChemDraw [15] – represent some examples for the achievement of the model. In the illustrated case of bonannione B (Fig. 10.3), it is possible to build the 2D structure with a molecular editor software, for example, by using the ChemOffice package, and then converting it into a file containing the Cartesian coordinates (Fig. 10.4).

The choice of method to adopt depends on the case and the resources of the user, but in any case, a reasonable and reliable initial geometry is essential for the quality of the following investigation.

10.2.2 Second Step: Conformational Search

The QM calculation of properties belonging to the investigated compound, such as energy, UV, NMR parameters, must be performed on models that better represent the real conformations of the molecule: the minima of the potential energy surface. In fact, differently from rigid molecular systems, flexible molecules may exist in more than a single conformation. The changing among the conformers, derived from the variation of dihedral angles around single bonds, corresponds to different points in the potential energy surface. The diverse energy points, coinciding with local minima, may represent the different conformations adopted at the thermal equilibrium by the molecule. As the spectroscopic properties strictly depend on the compound geometry, their calculation needs to take into account all the possible representative local minima in equilibrium because each conformer will have a specific weight in the global spectroscopic properties. (These concepts can be better understood analyzing the different conformation of ethane and n-butane.

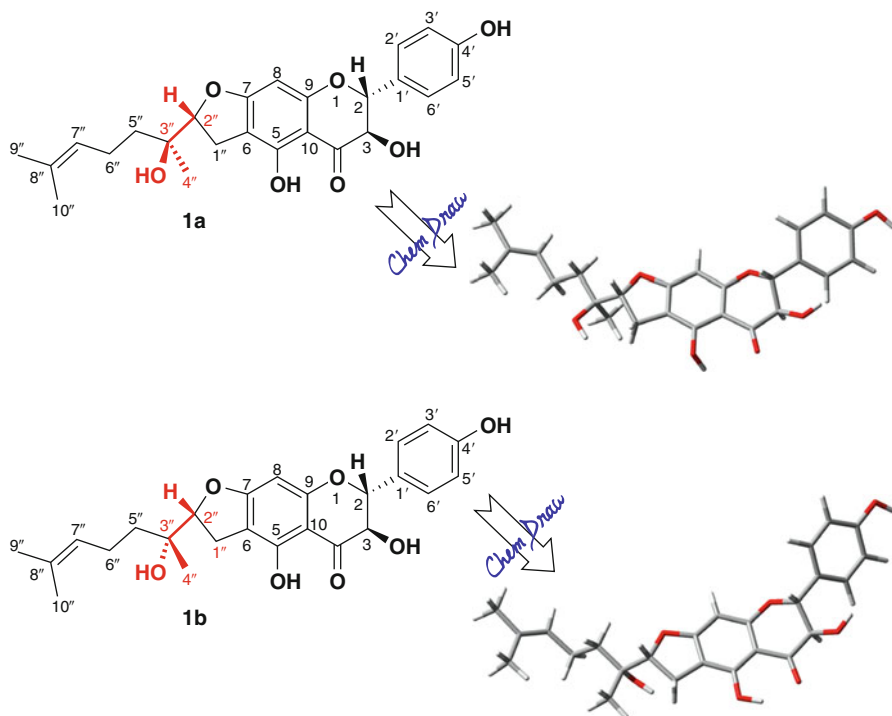


Fig. 10.3 Conversion of 2D structure into a 3D model of bonannione B

Increments of 60° for torsion angle around the C–C bond in ethane translate in two extreme cases: three eclipsed conformations at 0° , 120° , and 240° (global maxima), and three staggered conformations at 60° , 180° , and 300° (global minima), and so for the study of its physical and chemical properties, only the staggered arrangements must be considered (Fig. 10.5). Even if the rotation around carbon–carbon bond is not completely free owing to the energy difference between the two conformer families, in the case of ethane, the difference of 2.8 kcal/mol is small enough to be overcome, and thus, the conformers are interconvertible at room temperature. In the case of n-butane, increments of 60° for torsion angle around the bond C2–C3 give rise to one maximum global at 0° (eclipsed form), two local minima at 60° and 300° (*gauche* form), two local maxima at 120° and 240° , and one global minimum at 180° (*anti* form). At room temperature, the *gauche* and *anti* rotamers (energy difference of 0.9 kcal/mol) are in conformational equilibrium accounting for a 30:70 ratio, respectively, and so, both the conformations must be considered when the physical and chemical properties are studied.)

```

                                Cartesian Coordinates
                                ┌───────────────────┐
COMPND  bonannione.PDB
ATOM    1  C          0    -0.313  0.595  1.218  C
ATOM    2  C          0    -0.200 -0.052  2.477  C
ATOM    3  C          0     1.067 -0.513  2.927  C
ATOM    4  C          0     2.219 -0.326  2.118  C
ATOM   21  O          0    -1.655  0.986  0.966  O
ATOM   23  C          0    -1.532 -0.153  3.151  C
ATOM   31  C          0    -3.398 -1.214  1.128  C
ATOM   32  O          0    -4.363 -0.075  3.074  O
ATOM   33  H          0     0.750  1.275 -0.570  H
CONNECT  1    2    6    21
CONNECT  2    1    3    23
CONNECT  3    2    4    19
CONNECT  4    3    5    7
ENDMDL
END
                                └───────────────────┘
                                Connection between atoms
  
```

} Atom types

Fig. 10.4 The PDB file representation of the bonannione B

Consequently, the conformational search and the analysis of relative stability of different conformers are mandatory to obtain significative results after the QM calculation of NMR parameters.

This fundamental step for the search of the most representative rotamers can be performed in several ways (systematic search or grid search, random search or Monte Carlo methods, and molecular dynamics) by different dedicated softwares (Discover [16], Insight Package [17, 18], Gromacs [19, 20], Spartan [21], Macromodel [22], etc.).

10.2.2.1 Conformational Analysis Methods

The systematic search (grid search) consists in the step-by-step changes for the all possible dihedral angles of the entire and/or a part of molecule for all 360° , taking in account all the possible combinations between them. Each generated conformation must be subsequently minimized. One simple example of this conformational search through this algorithm can be the analysis of the poly-L-alanine peptide (Fig. 10.6).

Considering planar and in *trans* conformation the amide bonds, and the bonds' angles and distances fixed, the only two variables that regulate the different conformations are represented by φ and ψ angles (Fig. 10.6). The systematic increments of $15\text{--}30^\circ$ for both the dihedral angles in the region between 180° and -180° result in changes of the conformation and energy of the peptide. The variation of the energy as function of φ and ψ , in fact, can be visualized in the Ramachandran plot (Fig. 10.7), where the systematic angle changes are equivalent to examine all the significant points of a grid.

In the case of poly-L-alanine peptide, in the grid, few minima points are identifiable and so the most of conformations, after a minimization step, often converge toward the same rotamer. The main inconvenience of the systematic

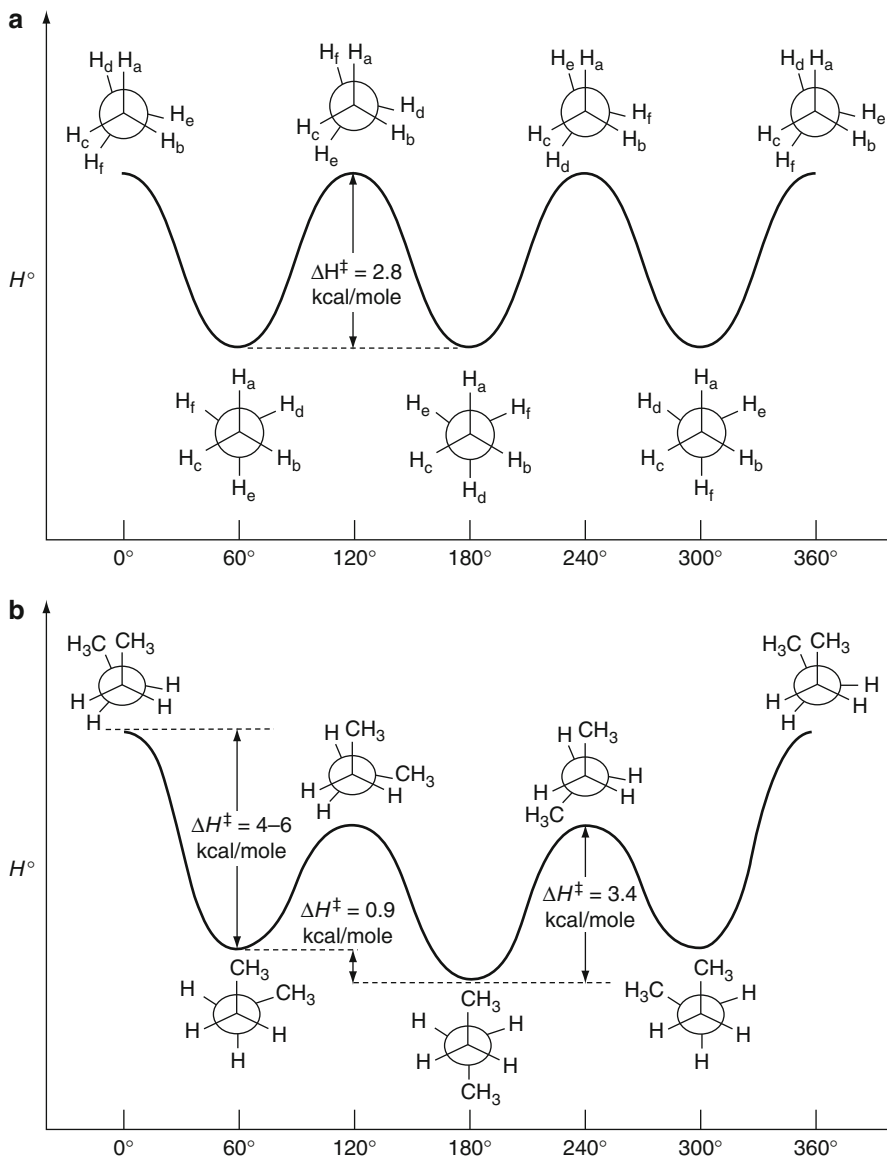


Fig. 10.5 Variation of energy for ethane (a) and n-butane (b) as function of dihedral angle

search is represented by the number of the generated conformations that exponentially increase with the number of rotatable bonds. This method is also difficult to apply to cyclic compounds where the dihedral angles are not independent between each other. On the other hand, the application of the grid search provides a comprehensive exploration of the conformational space, differently from the methods that will be discussed further.

Fig. 10.6 Molecular structure of poly-L-alanine peptide

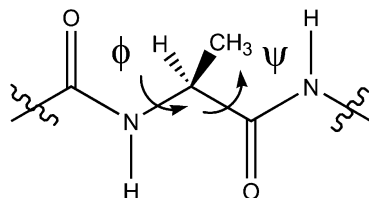
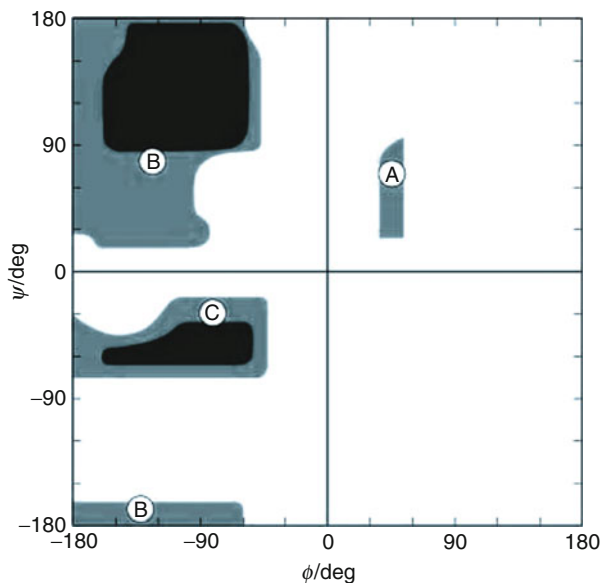


Fig. 10.7 A Ramachandran plot for poly-L-alanine peptide. The *black-and-gray* areas (numbered **a–c**) represent the allowed conformations; the white regions represent the forbidden rotamers



Differently from the systematic search described above, by the Monte Carlo method, the conformational space is explored in a random mode. The conformations are achieved by varying randomly the torsional angles, and then minimizing the so-obtained casual conformations. In particular, the new conformation is generated in two possible ways: varying or the Cartesian coordinates of each atom, or the dihedral angles of random amount. The resulting conformation is minimized, and its energy is compared against those of all structures previously found, and, if unique, it is stored (criterion based on an energy cut off). After this cycle, another conformation is chosen, and the proceeding is resumed. In order to compensate intrinsic limits of the random search, it is appropriate to perform several parallel runs starting from diverse rotamers. In addition to the casual choice, different approaches exist to select the starting structure, and one of these methods consists in using the local minimum found for each search. The main advantage for the Monte Carlo method is the possibility to sample cyclic systems that are difficult to treat by systematic methods. Another advantage is the potential treatment of molecular systems of any size, even though very large and flexible molecules may not provide converging results due to their wide conformational space.

The molecular dynamics (MD) represents another efficient method for the exploration of the molecular conformational space. It may be used for linear compounds with multiple torsions, when both the systematic and the random search are unadvisable, or for cyclic compounds, when the conformational analysis by the random search is complicated by the required computational time. The fundamental aim of the MD is the reproduction of the real behavior of the molecule, mimicking the time-dependent motions of the atoms. The generation of the new structure represents the principal difference of this approach with respect to the other two described above because the molecular dynamics is a deterministic approach, where the new generated structure is causally determined by previous conformer. In particular, given a set of initial coordinates and velocities with a force (F_i), the evolution of the system, all atoms will be moved to new positions following the Newton's second law (Eq. 10.1)

$$F_i(t) = m_i a_i(t) \quad (10.1)$$

where F is the force on atom i at time t , m_i is the mass of atom i , and a_i is the acceleration of atom i at time t . The so obtained conformation will be used as starting point for a new step, the cycle will be repeated for a predefined number of times, and the conformers will be collected (conformational ensemble). In particular, since significant conformational changes do not always happen at room temperature, especially when more atoms are involved, the MD simulations are performed at different increasing temperatures for supplying a sufficient kinetic energy to overcome the energetic barriers between the possible rotamers. During the MD simulations, in order to increase the probability to explore the entire conformational space, it is convenient to vary some fundamental parameters during the calculation as for example the simulation temperature, the time step, the equilibration, and the simulation time. However, if converged results are desired, different parallel MD simulations must be performed starting from different conformations, at diverse temperature – it is preferable to use a gradient of temperature from 450 to 650/700 K – and long time simulations should be used. Thanks to the kinetic energy of molecules it is possible that some collected conformers represent the local and/or global maximum points, and so, after the MD simulation, a minimization process of this ensemble of rotamers is always necessary.

A particular MD simulation is represented by simulated annealing. This methodology consists in a molecular dynamics at high temperature where temperature is gradually decreased to 0 K. During the simulation at high temperature, the molecules are able to explore conformations very different among each other, and thanks to the temperature dropping the molecule may converge in a local minimum. In order to obtain a collection of low energy conformations, the cycle will be repeated several times. The main advantage of simulated annealing with respect to the classic MD approach is represented by the possibility to avoid the minimization step since the resulting structures represent energy minima.

For all the above considerations, the choice of the method is exclusively dictated by the molecule under study, e.g., if it is linear, or cyclic, how many torsions are

present, if some experimental data are available, etc. In conclusion, it should be kept in mind that each method has its advantages and/or limitations.

In addition to the exploration method, the efficiency of the conformational search depends on a series of other factors such as the force fields and the algorithms of minimization.

In the molecular mechanics, the calculation of the energy is obtained through the force fields, functions that approximate the electronic potential surface using the specific parameters and mathematical equations of classic physics. The most simple force field equation is described in Eq. 10.2:

$$E_{\text{total}} = E_{\text{tors}} + E_{\text{vdw}} + E_{\text{elec}} + E_{\text{Hbond}} + E_{\text{oop}} \dots \quad (10.2)$$

where the total energy (E_{total}) of the molecule is obtained by the sum of energy terms associated with the internal coordinates. E_{vdw} , for example, represents the energy related to the van der Waals interactions between atoms, and it is described by the Leonard–Jones equation (Eq. 10.3):

$$E_{\text{vdw}} = \varepsilon \left[(r_0/r)^{12} - 2(r_0/r)^6 \right] \quad (10.3)$$

The electrostatic term (E_{elec}) is calculated by Coulomb's law; E_{tors} is a cosine periodic function (Eq. 10.4), etc.

$$E_{\text{tors}} = k\omega(1 - \cos 3\omega) \quad (10.4)$$

The parameter sets of the force field, e.g., the length and angles of the bonds, the hybridization of the atoms, the charges of the atoms, derive from the experimental data, and so the different force fields are tailored for a particular molecular system and are not able to describe all types of structures under investigation. For example, MM2 [23] is parameterized for the organic molecules, MM3 [24] for conjugated systems, AMBER [25, 26] for the peptides and nucleic acids, and OPLS* [27, 28] for peptides.

In this context, it is clear that the obtained geometries by specific method of conformational search must be minimized. Also in this step, different methods exist for the minimization process, but the most used algorithms are the steepest descent, conjugate gradient, and Newton–Raphson. These utilize the first and second derivative values of energy function in order to choose the direction to undertake. The steepest descent algorithm uses the first derivative value to move the atoms toward the local minimum; this algorithm works very well with conformation far from the equilibrium, but it is less efficient in the conformations close to the energy minimum. The steepest descent direction is also considered in the conjugate gradient algorithm, but in this case, the new direction is dependent from the previous; this permits a dramatic improvement of the efficiency of the method in proximity to the local minima points. The Newton–Raphson algorithm is able to discern between the minima and the maxima points, considering also the value of the second derivative.

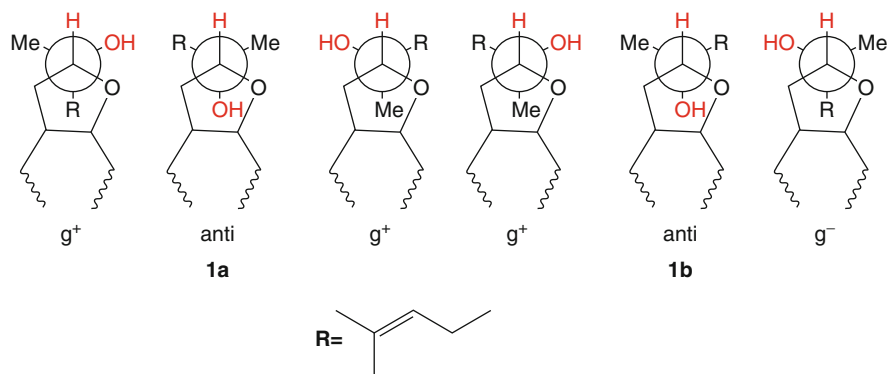


Fig. 10.8 The gauche (g^+ and g^-) and anti rotamers around C-2''–C-3'' for compounds **1a** and **1b**. The gauche and anti positions are referred to the –OH group

Moreover, in addition to the gradient, the curvature of the function allows to identify the search direction. The only disadvantage of this method is represented by the computational resource required (N^2 for N internal coordinates), but it is efficient enough in the conformation close to the minima points. On consequence, for small/medium molecules far from the minimum, it is preferable to apply as first the steepest descent and then the Newton–Raphson method; on the other hand, for biggest molecules, the Newton–Raphson method can be replaced by the conjugate gradient.

Taking into account the above-reported arguments, in the real illustrated example of bonannione B (**1a** and **1b**, Fig. 10.2), the several free molecular dynamics calculations are performed using the MMFFs [29] force field at different temperatures (between 400 K and 650 K) for 10 ns (simulation time), with a time step and an equilibration time of 1.5 fs and 1.0 ps, respectively (MacroModel software package) [22]. All the structures so obtained (numbering 100) are minimized by using the Polak–Ribier conjugate gradient algorithm [30] (PRCG, 1,000 steps, maximum derivative less than 0.05 kcal/mol). This approach leads to the selection of the lowest energy minimum rotamers (g^+ , *anti* and g^-) around the C-2''/C-3'' bond for each diastereoisomers (Fig. 10.8) that can be submitted to the next step: the final energy and geometry optimization.

10.2.3 Final Energy and Geometry Optimization

Following the scheme of the protocol reported in Fig. 10.1, after the conformational search and the preliminary geometry optimization of all found conformers, a further refinement of the three-dimensional coordinates is performed by using a more sophisticated theoretical level. As described above, the force fields are based on classical mechanics laws, and they include, in the description of a given chemical system, parameters derived from experiments or from quantum mechanical calculations. Molecular mechanics methods do not explicitly model the electrons in the

description of a molecular system, but the electrons are treated in the force field by parameterization. This approximation renders the molecular mechanics approaches faster than other more sophisticated theories and allows its application to very large systems. For a well-parameterized general force field, many molecular properties, such as geometry and relative conformational energies, can be calculated with high accuracy for a broad chemical space. Otherwise, where a force field is not able to describe well certain chemical species, the use of more sophisticated theories, such as quantum mechanics, is needed. It is noteworthy that the prediction of molecular properties, where the electron effects are predominant, such as transition state, the formation or breaking of a bond, and spectroscopic parameters, cannot be afforded by molecular mechanics. The quantum mechanics explicitly model the electron system of a molecule, and thus it can be used to study chemical issues.

The geometry optimization is a crucial step to study chemical problems, such as transition state, or to predict spectroscopic properties, such as NMR parameters, IR, and so on. In our case, the aim is to predict chemical shifts or coupling constants for the relative configuration assignment of organic compounds [1, 2, 31]. Moreover, the treatment of the investigated structure by quantum mechanical theory allows to get more accurate energy values for each considered conformers. These energy values are useful to calculate the Boltzmann distribution, which is a function of the energy (Eq. 10.11, see below). Taking into account the Boltzmann distribution is important to forecast molecular properties of flexible chemical systems because the predicted values result from the energy-weighted contribution of each conformer in solution.

Following the general protocol, the conformers' geometry obtained and optimized by using molecular mechanics force fields should be refined through semiempirical methods [32] before the application of quantum theory. The semiempirical methods differ from molecular mechanics because their theory combines the Schrödinger equation and some experimental derived parameters to simplify the computation. The most popular methods applied to organic compounds are AM1 [8] and PM3 [9]. The semiempirical methods present the advantage of being faster than quantum chemical methods, but it is not always that they can correctly predict a molecular property. This is due to the fact that the experimental derived parameters are not representative of all chemical systems. Compared to the quantum mechanical calculation of NMR parameters, the geometry optimization is more time-consuming. Thus, the aim to run a geometry optimization by semiempirical methods is to speed up the following computation at more time-consuming quantum mechanical theory level. Nowadays, thanks to the development of more potent computers this step is not necessary. Indeed, also by a desktop computer, it is possible to optimize the geometry with a modest theoretical level in a reasonable time.

The quantum mechanics is not based on classical mechanics laws and on the use of experimental parameters; indeed, the molecular properties are calculated by solving the Schrödinger equation:

$$\hat{H}\Psi = \hat{H}E \quad (10.5)$$

where \hat{H} is the Hamiltonian operator, Ψ is the wave function, and E is the energy. The wave function Ψ is a mathematical function of the electron and nuclear positions, and it represents a probabilistic description of electron behavior. In details, it can describe the probability of electrons being in certain locations, but it cannot predict exactly where electrons are located. As the quantum mechanics can describe mathematically the correct behavior of the electrons, it is possible to predict chemical properties of molecular systems, by applying relative mathematical operator corresponding to a particular chemical physical observable. For example, in Eq. 10.5, the Hamiltonian operator allows to calculate the energy of the electron, whereas the application of the spin-Hamiltonian can predict NMR parameters. (In order to obtain a physically relevant solution of the Schrödinger equation, the wave function must be continuous, single-valued, normalizable, and antisymmetric with respect to the interchange of electrons.

The Hamiltonian operator \hat{H} is, in general,

$$\hat{H} = - \sum_i^{\text{particles}} \frac{\nabla_i^2}{2m_i} + \sum_{i<j}^{\text{particles}} \sum \frac{q_i q_j}{r_{ij}} \quad (10.6)$$

where ∇_i^2 is the Laplacian operator acting on particle i . Particles indicate electrons and nuclei. The symbols m_i and q_i are the mass and charge of particle i , and r_{ij} is the distance between particles. The first term represents the kinetic energy of the particle, and the second term is the energy due to Coulomb interactions of particles. This formulation is the time-independent, nonrelativistic Schrödinger equation. Additional terms can appear in the Hamiltonian when relativity or interactions with electromagnetic radiation or fields are taken into account.)

Only in few simple cases the Schrödinger equation can be exactly solved, such as particle in the box, harmonic oscillator. The solution of this fundamental equation requires the use of mathematical approximations, and different quantum theories have been developed to this aim. The starting point of all quantum mechanical methods is the Born–Oppenheimer approximation (Eq. 10.6). This approximation treats the electrons and nuclei motions as separated and considers the nuclei fixed, thus neglecting the kinetic contribution of the nuclei.

$$\hat{H} = - \sum_i^{\text{electrons}} \frac{\nabla_i^2}{2} - \sum_i^{\text{nuclei}} \sum_j^{\text{electrons}} \frac{Z_i}{r_{ij}} + \sum_{i>j}^{\text{electrons}} \sum \frac{1}{r_{ij}} \quad (10.7)$$

Here, the first term is the kinetic energy of the electrons only, the second one is the attraction of electrons to nuclei, and the third term is the repulsion between electrons called correlation. The repulsion between nuclei is added onto the energy at the end of the calculation. The motion of nuclei can be described by considering this entire formulation to be a potential energy surface on which nuclei move.

One of the most applied theories is the Hartree–Fock (HF) [32], which is based on the central field approximation. It considers the Coulomb repulsion between two electrons by integrating the repulsion term. This approximation does not give

the exact effect of the electrons repulsion (correlation) but only an average of this repulsive interaction, and it represents an important limitation of HF application. This effect is important because including correlation generally improves the accuracy of computed energies and molecular geometries, as well as NMR parameters [1, 2, 31]. The wave function results from a linear combination of atomic orbitals, which are described by a set of functions called basis set.

One of the most used post-HF methods is the Møller–Plesset [33], which accounts the correlation by adding to the Hartree–Fock wave function the perturbation term. Different Møller–Plesset methods have been developed and the mostly used is the second order (MP2) [34]. Compared to HF theory, the Møller–Plesset methods are more accurate but very computationally expensive; thus, their application is limited to small molecular systems.

In the last years, the density functional theory (DFT) [35, 36] has been gaining a great success due to the lower demanding computational costs but with results accuracy similar to the post-HF methods, such as Møller–Plesset. DFT considers that the energy of a molecule can be determined from the electron density instead of the wave function. The electron density is expressed as a linear combination of basis functions similar in mathematical form to HF orbitals. In particular, a determinant is then formed from these functions, obtaining the Kohn–Sham orbitals. From the electron density of these orbitals, the energy is calculated applying a density functional. Different functionals [37, 38] have been developed, and between them, the most used is B3LYP in the geometry optimization of investigated compounds. The MPW1PW91 [35, 36] has shown to produce adequate structural geometry, and many application of this functional are reported in literature [1, 2, 31]. Recently, new promising functionals have been introduced: M05 [39] and M05-2X [40, 41]. The DFT takes into account the electron correlation, giving better results than the HF-based methods [1, 2, 31].

It is noteworthy that independently from the QM theory applied, the choice of the basis set is important in the prediction of the molecular properties. The basis set should be large enough, for example, to take into account the electron correlation effects or to describe the molecular charge distribution. At the same time, the basis set should be small enough to be applied to the investigated molecule, especially for larger chemical systems. In our contribution, where different methods have been compared in the prediction of chemical shift of organic compounds, we observed that the 6–31 G with DFT is the right trade-off between accuracy and rapidity of calculation [31].

Different softwares dedicated to the quantum mechanical (QM) calculation of molecular properties are available: Gaussian [42], HyperChem [43], Jaguar [44], and Spartan [21]. These softwares allow the application of different theoretical methods to carry out the forecast of different molecular properties.

Let us continue with the case study of the determination of the relative configuration of bonannione B (**1**), to show the application of QM approach for geometry refinement and the prediction of ^{13}C NMR chemical shift (Sect. 10.2.4). From the conformational search, three main conformers are found for two considered stereostructural hypothesis, and all of them have to be treated by the software

Gaussian 03 [45]. For all six staggered rotamers, six input files are prepared. Each file contains the coordinates derived from molecular mechanics level and the instruction for the optimization of the geometry.

In this case, the geometry refinement is performed by applying the DFT theory, the B3LYP as functional, and 6–31 G(d) basis set. After the calculation, a new geometry for each staggered rotamer of **1a** and **1b** is obtained, and it is used for the calculation of the chemical shifts (Sect. 10.2.4). Besides the new spatial arrangements of the conformers, associated energy values are achieved by the computation. This value is expressed in Hartree, and it can be converted in kJ: one Hartree is 2625.5 kJ mol⁻¹.

10.2.4 ¹³C NMR Chemical Shifts Calculation

The nuclear magnetic resonance (NMR) has been playing a crucial role in solving molecular structural aspects thanks to the ability of some NMR parameters (coupling constant, chemical shift) to provide fundamental information on the configurational and conformational arrangement of organic molecules. The configuration of cyclic compounds with three- to six-membered rings, and of compounds with predictable conformational behavior, can be easily determined by analyzing NMR parameters, such as proton–proton *J* coupling values, chemical shifts, and/or nuclear Overhauser effect intensities. The relative configurational assignment of flexible systems, such as polysubstituted open chains and macrocycles, is more difficult to study, due to geometrical uncertainty associated with these types of molecules.

In the last years, great advances have been made in developing quantum mechanical (QM) methods of chemical interest able to predict molecular properties [1, 2, 32]. In particular, quantum mechanical calculation of NMR parameters has been used as an emerging strategy for the assignment of the relative configuration of flexible organic molecules on the basis of the high accuracy in the reproduction of the experimental NMR properties also achieved at a low level of theory [1, 2, 31, 46].

The final step of the protocol described in this chapter is the calculation of an NMR parameter: ¹H, ¹³C, ^{2,3}J_{H-H}, and ^{2,3}J_{C-H}.

Different approaches have been devised to calculate the chemical shift, such as IGLO [47], LORG [48], and CSGT [49], but the most popular is GIAO (gauge including atomic orbital) [50, 51], which is based on the perturbation theory, resulting suitable for HF or DFT theories. In particular, GIAO has shown to provide more reliable results compared with other methods at the same basis set [1, 2, 31, 32, 50, 51]. The electron correlation effect is not negligible in the chemical shift calculation, especially for ¹³C; in fact, DFT or MP theories have shown to give more accurate results than HF approach [31, 52]. In this field, DFT is successfully emerging due to its accuracy in NMR properties prediction and its ability to handle large molecular systems not easily treatable by post-HF methods [1, 2, 52]. For this reason, DFT is widely used in the calculation of NMR parameters

[1, 2]. The most popular functionals applied in the calculations of NMR parameters are B3LYP, MPW1PW91, and PBE1PBE [53, 54].

It is also important that sufficiently large basis sets are used [31]. Of course, the choice of the basis set to use is based on the accuracy and on the size of the molecule under study. The 6-31 G (d) basis set should be considered the absolute minimum for reliable results, but better outcomes are obtained by using 6-31 G(d,p) [31]. The choice of the basis set, thus, depends both on the accuracy and on the size of the molecule and also on the number of the chemical species to take into account.

Continuing with the reported case study, all conformers for both the diastereoisomers under investigation have been optimized by using DFT/B3LYP approach. The new coordinates, derived by quantum mechanical optimization, are now used to calculate the ^{13}C chemical shifts by GIAO method. Thus, six input files are set up, indicating the instruction for the chemical shift calculation. The theory level to apply is the same of that one used in the geometry optimization (DFT/B3LYP), but the basis set is 6-31 G(d,p).

In particular, the quantum mechanical methods calculate the shielding tensor and not directly the chemical shift. One of the mostly used methods to obtain the chemical shift is to subtract the isotropic shielding value of TMS from the shielding tensor of the conformer. This can be easily done by collecting the data in a spreadsheet and subtracting the isotropic shielding tensors of the conformer and TMS in absolute value. Of course, the shielding tensor of TMS has to be calculated at the chosen theoretical level for the investigated compound. We observed for sp^3 carbons referenced to TMS a good fitting between experimental and calculated, whereas for the sp^2 carbons, this agreement is lower [31]. For this reason, the sp^2 carbons could not be considered in the comparison with the experimental chemical shifts. Recently, the multi-standard approach (MSTD) has been reported [55] which is demonstrated to perform better than the application of TMS as reference compound. The MSTD consists on the use of two different reference compounds and calculates the chemical shift through the following equation:

$$\delta_{\text{calc}}^i = \sigma_{\text{ref}} + \sigma_i + \delta_{\text{exp}}^{\text{ref}} \quad (10.8)$$

where σ_{ref} and σ_i are the shielding tensors of atom i and the reference compound, respectively, and the $\delta_{\text{exp}}^{\text{ref}}$ is the experimental value of the reference. In particular, the calculation of sp^3 carbon atoms is referenced to methanol, whereas the chemical shifts of sp^2 and sp carbon are calculated from benzene.

Another method is based on linear regression analysis. In particular, calculated chemical shift of a collection of organic compounds is plotted against their experimental values. The intercept and the slope of the obtained straight line can be used to scale the calculated values:

$$\delta_{\text{scaled}} = \frac{\delta_{\text{calc}} - \text{intercept}}{\text{slope}} \quad (10.9)$$

In the reported case study, the chemical shifts are referenced to TMS. It is important to keep in mind that the experimental chemical shift is a weighted value from the contribution of conformers in equilibrium among them:

$$\delta_{\text{exp}} = \delta_i p_i + \delta_j p_j + \dots \quad (10.10)$$

where p_i is the population fraction of N_i molecules in a determined conformation and δ_i the associated chemical shift. The same is for the number of molecules j and all other conformers in solution. The number of molecules in a specific three-dimensional arrangement depends on the energy of that conformation. The ratio of the number of conformers N_i with energy E_i , to the number of molecules in state j is given by the Boltzmann distribution:

$$\frac{N_i}{N_j} = e^{-(E_i - E_j)/k_B T} \quad (10.11)$$

where k_B is the Boltzmann constant (1.38066×10^{-23} J/K) and T the temperature. Following the Eq. 10.11, two conformers differing for 3 kcal/mol (≈ 10 kJ/mol) in energy present a ratio of 99:1. Thus, each conformation differing from the global minimum by \geq of 3 kcal/mol does not effectively contribute to the averaged chemical shift and can be neglected in the calculation. From the computed energy values for each conformer at quantum theory level, it is possible to calculate the population fractions contributing to the weighted chemical shift, by using the following equation:

$$\delta = \sum_i \left[\delta_i \exp(-E_i/RT) / \sum_i \exp(-E_i/RT) \right] \quad (10.12)$$

where δ_i is the chemical shift of conformer i , R is the molar gas constant (8.3145 J K^{-1} mol^{-1}), T is the temperature (298 K), and E_i is the calculated energy of conformer i relative to the energy of the global minimum.

In the output file, along with isotropic shielding tensors, an energy value at the basis set 6-31 G(d,p) is obtained and is taken into account in the Boltzmann distribution calculation.

From the calculated energies, it is obtained for isomer **1a** that the *anti* and g^+ conformers represent 70% and 28% of the total population, respectively, due to the hydrogen bond between the OH group and the oxygen atom of the ring for both these rotamers. The remaining 2% is attributed to the g^- conformer. A similar trend of the energies and the population distribution is observed for **1b**, where the *anti* rotamer accounts for 71% and the g^+ rotamer for 28%, and 1% is represented by the rotamer g^- (Table 10.1)

The calculated chemical shifts, according to the Boltzmann distribution, are compared with the experimental ones in order to find which of the two considered diastereoisomers (**1a** and **1b**) presents the best fitting with the experimental set of

Table 10.1 Comparison of calculated for stereoisomers **1a** and **1b** vs. experimental ^{13}C NMR chemical shifts in CDCl_3

^{13}C Chemical shifts			
Carbons	1a	1b	Experimental
2	81.4	81.5	79.0
3	46.2	46.1	42.7
4	187.5	187.5	196.3
5	155.4	155.4	158.3
6	103.2	103.2	105.8
7	161.7	161.7	169.5
8	86.3	86.4	90.5
9	158.4	158.4	163.6
10	101.9	101.9	103.1
1'	127.2	127.2	129.6
2'	122.4	122.5	127.6
3'	107.4	107.4	115.8
4'	150.5	150.5	156.8
5'	111.0	110.9	115.8
6'	123.2	123.3	127.6
1''	29.1	29.5	25.9
2''	94.0	94.0	91.3
3''	73.9	73.9	73.8
4''	23.1	19.7	22.4
5''	37.3	40.6	36.6
6''	24.8	25.0	21.8
7''	122.1	122.5	123.7
8''	128.7	128.0	132.0
9''	26.5	26.4	25.4
10''	17.5	17.6	17.5

resonances. The comparison is made, calculating the difference between the predicted and experimental values (Table 10.1). Other parameters could be taken into consideration to understand which hypothesized structure best reproduce the experimental. The mean absolute error is a statistical parameter obtained from the following equation:

$$\text{MAE} = \sum [|(\delta_{\text{exp}} - \delta_{\text{calcd}})|] / n \quad (10.13)$$

where $\delta_{\text{exp}} - \delta_{\text{calcd}}$ are respectively the experimental and calculated chemical shifts, and n is the total number of considered resonances. A variant of the MAE is the corrected mean absolute error (CMAE), where the calculated values are scaled with the experimental chemical shifts. In detail, the predicted set of resonances are plotted in function of the experimental values, and the intercept and the slope obtained by linear regression are used to correct the forecast chemical shifts, by using Eq. 10.9. From the scaled values, the MAE is calculated obtaining the CMAE.

$$\text{CMAE} = \sum [|(\delta_{\text{exp}} - \delta_{\text{scaled}})|] / n \quad (10.14)$$

The correlation coefficient, r , is also used as parameter to compare calculated and experimental chemical shifts. Recently, Smith and Goodman have introduced the DP4 probability which performs better than the mean absolute error and correlation coefficient [56].

It is possible to observe that the resonances of almost all carbon atoms for both diastereoisomers (**1a** and **1b**) are very similar to the experimental chemical shift, differing by a maximum of 0.2 ppm. Large differences are found around the couple of stereocenters under study, in particular, for the C-4'' and C-5'', which are bound to C-3'' (Table 10.1). The predicted values of C-4'' are 23.1 ppm and 19.7 ppm for **1a** and **1b**, respectively. Concerning the C-5'', the **1a** resonance is predicted at $\delta = 37.3$ ppm and at $\delta = 40.6$ ppm for **1b** (Table 10.1). Isomer **1a** shows a variation from the experimental of 0.7 ppm for C-4'' and C-5'', whereas for **1b** larger $\Delta\delta$ values are found: 2.7 ppm and 4.0 ppm for C-4'' and C-5'', respectively. It is noteworthy that the obtained discrepancies reflect the different magnetic environment of the methyl group in the 4''-position and the methylene group in the 5''-position in **1a** and **1b** due to the different configuration of C-3''. Thus, the ^{13}C chemical shift calculation is a useful tool to probe the different 3D spatial arrangement of stereogenic carbon substituents, suggesting the correct relative configuration of the investigated compound. The relative configuration of bonannione B can be assigned as **1a**.

10.2.5 J Coupling Constants Calculation

In the previous section, it has been shown that ^{13}C NMR chemical shifts have been predicted by quantum mechanics method to assign the relative configuration of the compound under study. The chemical shift is not the only NMR parameter that can be calculated by QM approach and used in the stereostructure analysis. Homo and heteronuclear coupling constants can be predicted, and they could be integrated with experimental values to shed light on the relative configuration. The relative configuration assignment of the natural product callipeltin A (**2**, Fig. 10.9), isolated from the sponges *Callipelta* sp. and *Latrunculia* sp. [57], is reported here as an example. In particular, the compound is a peptide (Fig. 10.9) constituted by nine amino acids, but only the following portion has been determined by QM- J method: the two units (named AGDHE_{2,3} and AGDHE_{3,4}) contained in the AGDHE fragment, the two threonine residues (named D- α Thr1 and D- α Thr2), and the β -OMeTyr amino acid.

Behind the use of J coupling constants to assign the relative configuration, through this case study, it is shown how to afford the analysis of large molecule presenting more than one couple of stereocenters. In detail, the strategy consists in dividing the entire molecule in small C_2 fragments, following a rational building: at least two heavy groups (carbon, oxygen atoms) substitute the main chain, and every branched chain is replaced by at least one heavy atom [58]. For each C_2 fragment,

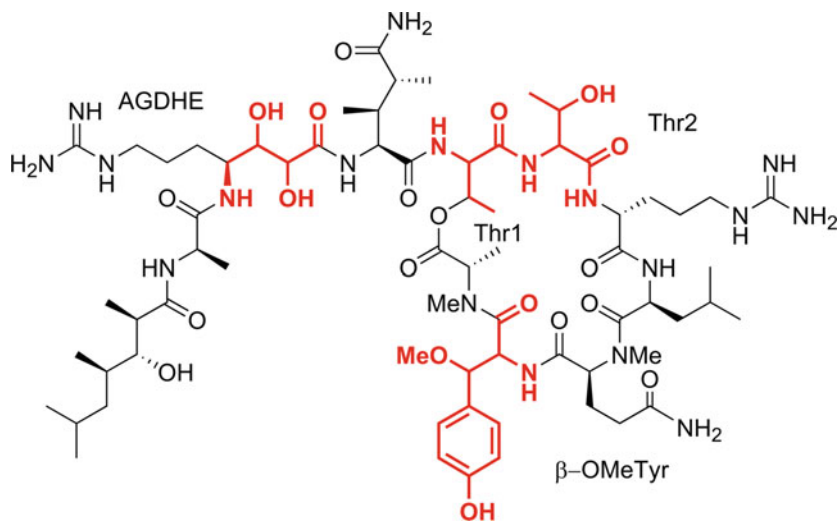


Fig. 10.9 Callipeltin A (2) with amino acid residues still stereochemically undetermined represented in red

the *erythro* and *threo* configuration are considered, and for each diastereoisomer, three main staggered rotamers are built (*anti*, g^+ and g^-) (Fig. 10.10).

As the analysis is based on simple molecular fragments derived from the whole molecule, directly the main three staggered rotamers are built and considered in the calculations. The basic idea to simplify the entire structure with more than one couple of stereocenters is to limit the number of conformers to analyze at the quantum mechanical level. Indeed, the number of combinations of all staggered conformers from C_2 arrangements is $N_r = 6^n$, where n is the number of pairs of stereocenters [58]. The simplification is possible because local atomic environment mainly affects the coupling constants. Usually, further than two atoms away from the nuclei involved in the scalar coupling, the effects are negligible [58].

Let us apply this strategy to the callipeltin A. The following C_2 fragments are built and investigated (Fig. 10.11):

For sake of simplicity, only the analysis of D-aThr1 fragment is described, but the approach is repeated for all the investigated simplified systems. The *anti* and two *gauche* rotamers are built for *erythro* and *threo*, and the geometry optimization is performed at DFT theory level by using the functional MPW1PW91 and the basis set 6-31 G(d). The calculations are performed by taking into account the contributions of the following interactions: Fermi contact (FC), paramagnetic spin-orbit (PSO), diamagnetic spin-orbit (DSO), and spin-dipole (SD). As made for the bonannione B (see previous section), on the optimized geometry at quantum mechanics level, the calculation of the NMR parameter is performed. In this case, the prediction concerns the $^{2,3}J_{C-H}$ and $^{2,3}J_{H-H}$ through the same functional of the optimization step (MPW1PW91) and by the 6-31 G(d,p) basis set. Both the quantum mechanical calculation steps (optimization and NMR property prediction)

Fig. 10.10 Main staggered rotamers (*anti*, g^+ , and g^-) for each relative stereochemical arrangement *erythro* and *threo*

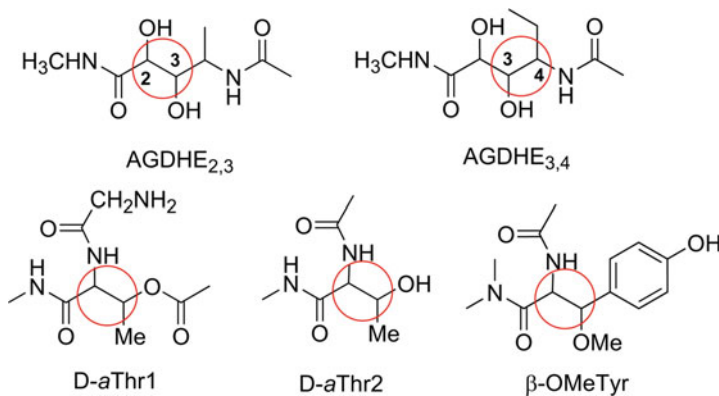
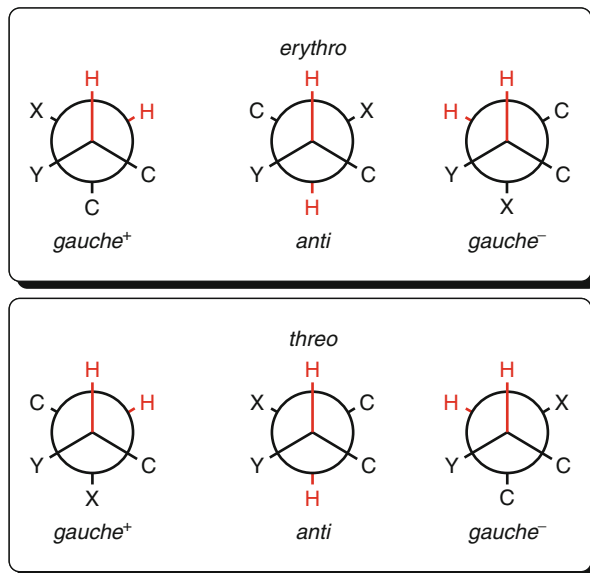


Fig. 10.11 Molecular structures of C_2 fragments from callipeltin A, considered in the QM calculations. The couples of the investigated stereocenters are indicated by red circles

are made by using the IEF-PCM solvent continuum model, to mimic the presence of the methanol. The choice to use the solvent is due to the presence of hydrogen donors and acceptors, which influence the conformational arrangement in absence of the solvent and could cause misleading information for the assignment of relative configuration.

The set of calculated coupling constants for all staggered rotamers of *erythro* and *threo* is compared with the experimental one (Table 10.2). The comparison is made through the total absolute deviation (TAD) values: $\sum |J_{\text{calc}} - J_{\text{expl}}|$. The conformer

Table 10.2 Calculated J values for the six conformational arrangements belonging to *erythro* and *threo* series of C_2 fragments from callipeltin A, in comparison with the experimental data: single deviations and TAD ($\sum |J_{\text{calc}} - J_{\text{exp}}|$) values are reported

	Calc						Exp
	<i>Erythro</i>			<i>Threo</i>			
	g^+	<i>Anti</i>	g^-	g^+	<i>Anti</i>	g^-	
D-aThr1							
$^3J_{\text{H2-H3}}$	3.7	8.6	2.6	4.5	9.2	1.3	2.8
$^2J_{\text{H2-C3}}$	0.9	-4.4	-4.9	-4.5	-4.2	0.6	-5.7
$^3J_{\text{H2-Me}}$	0.7	2.3	4.0	0.3	2.7	1.9	5.0
$^2J_{\text{H3-C2}}$	-1.4	-2.2	0.3	-0.6	-1.8	0.6	-1.4
$^3J_{\text{H3-C=O}}$	7.2	2.4	1.4	7.4	1.0	2.1	2.0
TAD	17.0	11.0	4.3	13.8	11.6	13.0	
AGDHE_{2,3}							
$^3J_{\text{H2-H3}}$	4.6	8.0	3.2	1.8	5.9	6.6	9.0
$^2J_{\text{H2-C3}}$	-3.0	-3.7	-0.3	2.2	-2.7	-3.0	-4.0
$^3J_{\text{H2-C4}}$	6.7	2.3	0.3	0.4	4.6	5.3	2.6
$^2J_{\text{H3-C2}}$	1.9	-0.8	-1.3	3.8	0.3	-2.4	-3.5
$^3J_{\text{H3-C=O}}$	0.1	1.8	6.6	0.2	4.0	7.1	1.2
TAD	16.0	4.9	19.4	23.9	13	13.1	
AGDHE_{3,4}							
$^3J_{\text{H3-H4}}$	3.3	8.7	3.1	4.0	5.0	0.9	1.7
$^3J_{\text{H3-C5}}$	0.4	1.5	4.9	3.8	0.0	2.6	1.7
$^2J_{\text{H4-C3}}$	-4.3	-4.4	0.5	-3.9	-5.3	0.7	1.2
$^3J_{\text{H4-C2}}$	6.2	4.0	0.6	5.9	0.1	2.5	1.2
TAD	13.4	15.6	5.9	14.2	12.6	3.5	
D-aThr2							
$^3J_{\text{H2-H3}}$	3.7	8.6	2.8	4.6	7.7	1.7	3.5
$^2J_{\text{H2-C3}}$	-0.4	-4.9	-4.9	-4.2	-3.6	-1.5	-4.1
$^3J_{\text{H2-Me}}$	0.5	1.9	4.1	4.3	4.4	1.6	1.1
$^2J_{\text{H3-C2}}$	-1.6	-0.3	2.4	-1.2	1.1	0.9	-2.8
$^3J_{\text{H3-C=O}}$	7.3	3.2	0.7	7.0	1.5	2.0	7.3
TAD	5.7	13.2	16.2	6.2	17.6	13.8	
β-OMeTyr							
$^3J_{\text{H2-H3}}$	1.5	8.7	3.9	8.3	10.7	3.7	9.1
$^2J_{\text{H2-C3}}$	-5.4	-3.2	0.0	-3.4	-4.3	-3.4	-3.9
$^3J_{\text{H2-Ph}}$	3.8	2.5	0.7	5.6	1.8	1.1	1.3
$^2J_{\text{H3-C2}}$	-0.8	-2.6	-2.7	-1.2	-2.3	0.4	-3.2
$^3J_{\text{H3-C=O}}$	1.4	2.0	6.4	6.6	1.6	1.5	1.7
TAD	14.3	3.2	14.9	12.5	3.5	9.1	

showing the lowest difference with the experimental values represents the right relative configuration. Concerning the D-aThr1 residue, the lowest sum of absolute errors (4.3 Hz) is observed for g^- *erythro* arrangement, whereas the TAD for all other conformers ranges between 11 and 17 Hz (Table 10.2).

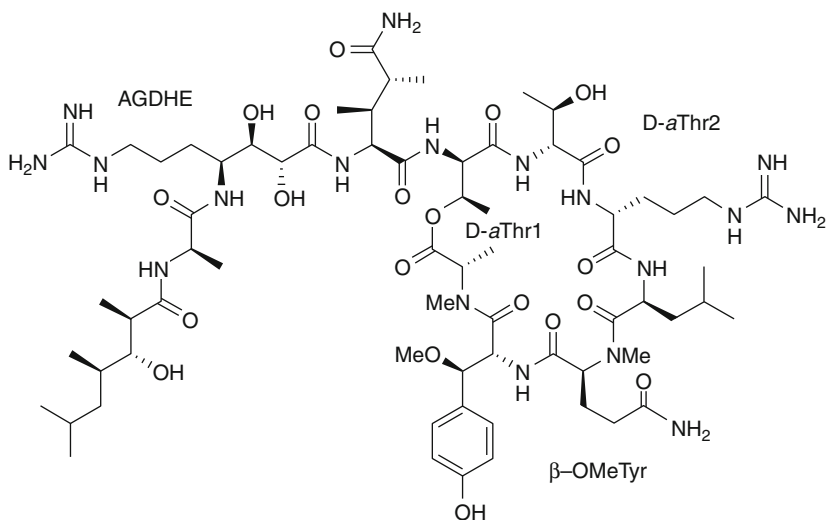


Fig. 10.12 Molecular structure of callipeltin A, with all residues stereostructurally determined

The same analysis is made for the other considered C_2 fragments. In particular, for the residue AGDHE_{3,4}, the best agreement between calculated and experimental is found for the g^- *threo* arrangement, characterized by a total deviation of only 3.5 Hz (compared to TAD values of 5.9–15.6 Hz for the reminder conformers). Also, for the AGDHE_{2,3} fragment, the *anti erythro* model displays the lowest TAD value of 4.9 Hz, much below the other deviations (13.0–23.9 Hz). The analysis of D-aThr2 and β-OMeTyr residues is more complicated because two possible conformers present similar TAD values. For the D-aThr2, the g^+ of *erythro* presents a deviation of 5.7 vs. 6.2 Hz of g^+ of *threo*. For the β-OMeTyr residue, the *anti* arrangements of *erythro* and *threo* show comparable TAD values: 3.2 and 3.5 Hz, respectively. Thus, for these residues, the investigation is integrated by an analysis of ROESY spectra, which confirms the QM-based results. In details, a strong ROE effect between the H-2 proton and the methyl group confirms the g^+ *erythro* arrangement for the D-aThr2. This observation is also consistent with the small $^3J_{H-2,Me}$ value and, consequently, with a *gauche* relationship between these groups. Concerning the β-OMeTyr residue, the observed ROE cross-peak between the aromatic and amide protons suggests the *erythro* configuration as representative arrangement. By using the presented strategy, the fully stereostructural determination of callipeltin A has been carried out (Fig. 10.12).

10.2.6 Solvent Effects

Many of the organic compounds are soluble in nonpolar solvents, and the prediction of NMR parameters can be fairly well conducted in vacuum [1–4, 31, 41]. However, NMR parameters are very sensitive to the surrounding environment. Thus, solvents

are not negligible in the calculations, especially for the polar ones [59]. The solvation affects the solute geometry and the electronic structure, which along with solute–solvent interactions induces variation in the NMR properties [60–62].

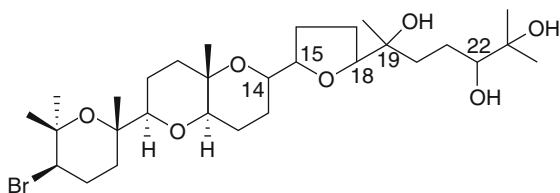
In general, the methods to model the solvent fall in two main categories: the implicit and explicit solvent models. The first model represents the solvent as continuous medium with a uniform dielectric constant, surrounding the solute molecular cavity. The most commonly used methods are the polarized continuum model (PCM) [63], the conductor-like screening model (COSMO) [64], and the generalized born surface area (GBSA) [65]. The explicit model treats the solvent molecules as discrete entities, and it is mostly applied in molecular dynamics. Both methods present advantages and shortcomings, but they could improve the prediction of NMR parameters where solvent effects are not negligible. As reported in literature [60–62], the solvent effects limited to conformational changes of the investigated chemical system are well described by using continuum models. Where the solute–solvent interactions play a crucial role, the use of explicit solvent molecules give better predictions. One strategy to model the discrete solvent molecules around the solute is to run molecular dynamics or Monte Carlo simulations, in order to obtain different configurations of the investigated compound and the surrounding solvent molecules. On the obtained arrangements, the NMR calculation at quantum mechanical levels is performed. However, it is not trivial to model the orientation and the number of solvent molecules around solute counterparts and not always perform well in prediction of NMR properties. This method, based on molecular mechanics to model compound embedded by the solvent, is not feasible for the configurational assignment due to the large number of chemical systems to treat at quantum mechanical level. To date, there is not a well-defined strategy to account the effects of the solute–solvent interactions in the stereostructural studies.

10.3 Conclusions

The protocol described in this chapter shows how the calculation of NMR parameters at the QM theoretical level is a useful tool for conformational and configurational analysis of natural products. The great success of QM prediction of molecular properties is due to its ability to reproduce the experimental data at affordable computational expense.

In particular, two case studies have been reported regarding the determination of the relative configuration of two natural products: bonannione B isolated from *Bonannia graeca*, and callipeltin A isolated from the sponges *Callipelta* sp. and *Latrunculia* sp. With these two examples, we respectively show the use of ^{13}C , $^{2,3}J_{\text{H-H}}$, and $^{2,3}J_{\text{C-H}}$ values calculation as a tool for the determination of the relative configuration of organic molecules. It is noteworthy that both calculated NMR properties at QM theory level can be combined for the stereostructural investigation depending on the organic compound under examination. Moreover, besides the use of QM calculation of NMR parameters in the conformational and

Fig. 10.13 Molecular structure of aplysiol B



configuration analysis, the fast and convenient quantum chemical approach can be applied to lead the total synthesis of complex natural compounds toward the correct stereoisomers, saving time and resources.

It should be highlighted that QM methods have been shown to accurately reproduce experimental molecular properties in vacuum, especially in cases where non-polar solvents are used for acquiring the experimental spectra. On the other hand, solvent effects limited to conformational changes of the solute can be taken into account by continuum solvent models; in cases where the solute–solvent interactions have a significant weight, an explicit solvent treatment should be applied.

10.4 Study Questions

1. What are the molecular features to be considered in the choice of the force field for the conformational search?
2. Why are quantum mechanical methods required to study chemical problems, such as transition state, or to predict spectroscopic properties?
3. Why DFT or MP may be more accurate than HF in the prediction of NMR parameters?
4. In which cases is DFT approach preferred to MP methods?
5. Try to establish a protocol to determine the relative configuration of the stereocenters C-14, C-15, C-18, C-19, and C-22 of aplysiol B isolated from *Aplysia dactylomela* [66] (Fig. 10.13).
6. What are the main features of implicit and explicit solvent models?
7. What are the criteria to select the appropriate solvent model?
8. Why is it important to get an accurate energy value for each conformer?
9. What is a basis set?

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V.L. Wilde • A.J. Phillips (✉)

Department of Chemistry, Yale University, New Haven, CT, USA

e-mail: Victoria.wilde@yale.edu, andrew.phillips@yale.edu

J.C. Morris

School of Chemistry, University of New South Wales, Sydney, Australia

e-mail: jonathan.morris@unsw.edu.au

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Abstract

Synthetic chemistry has played a significant role in the development of natural products chemistry, and the histories of the two fields are inextricably intertwined. Biology, isolation, structure elucidation, and synthesis are central to marine natural products chemistry and many advancements in the past 40 years have come in response to the challenges presented by compounds from the oceans. In this chapter we present an overview of marine natural products synthesis through a looking glass that focuses on some selected total syntheses from the past 40 odd years. In this light we can only provide a snapshot of where the field currently stands and the road that has led here. The vectors that define the size of the field and the constraints of this forum unfortunately do not cross, and as such it is not possible to be comprehensive. We direct the reader to recent reviews that cover the field in greater detail.

11.1 Some Beginnings: *Cypridina hilgendorffii* Luciferin and Tetrodotoxin

Synthetic chemistry has played a significant role in the development of natural products chemistry, and the histories of the two fields are inextricably intertwined [1]. Biology, isolation, structure elucidation, and synthesis are central to marine natural products chemistry, and many advancements in the past 40 years have come in response to the challenges presented by compounds from the oceans. This chapter presents an overview of marine natural products synthesis through a looking glass that focuses on some selected total syntheses from the past 40 odd years. In this light we can only provide a snapshot of where the field currently stands and the road that has led here. The vectors that define the size of the field and the constraints of this forum unfortunately do not cross, and as such it is not possible to be comprehensive. We direct the reader to recent reviews that cover the field in greater detail [2].

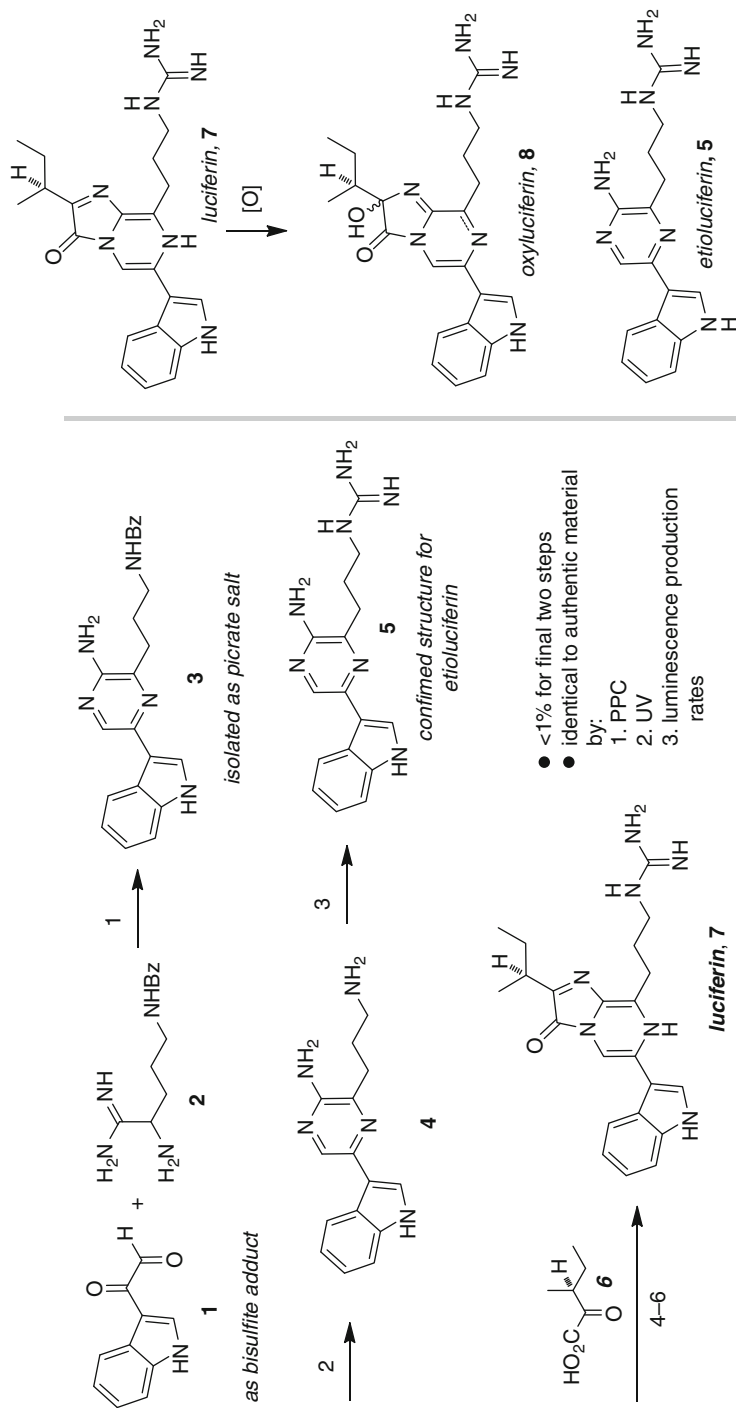
The papers that founded the science of marine natural products chemistry are difficult to identify, although there is little doubt that contemporaneous efforts by scientists in the United States and Japan in the period of 1955–1965 were responsible for the birth of the field. Notable research in this light includes early work by Paul Scheuer at the University of Hawaii into the causative agent of ciguatera poisoning [3], which later led to the structure of palytoxin [4], and by Yoshimasa Hirata at Nagoya University into the structure of the luciferin from the sea firefly *Cypridina hilgendorffii* (now *Vargula hilgendorffii*). It is instructive to consider some of the early work from Nagoya as it provides an illustration of the challenges in structure elucidation at the time and historical significance of total synthesis in structure confirmation.

Heroic efforts to secure crystalline luciferin from *Cypridina hilgendorfi* by Osamu Shinomura (Nobel Laureate in 2008 for the discovery of green fluorescent protein) (see ► [Chap. 24](#)) in the laboratory of Yoshimasa Hirata in the period of 1955–1960 produced material [5] that ultimately culminated in a structure proposal that was published in 1966 as part of a series of three papers [6]. The structure elucidation, which was predicated on careful degradative studies and comparisons to known compounds, suggested luciferin to be **7** ([Scheme 11.1](#)). Oxidation would lead to oxyluciferin, **8**, which was known to be degraded to etioluciferin and α -keto- β -methylglutaric acid by acid hydrolysis. In an accompanying paper, Yoshito Kishi confirmed the structure by total synthesis ([Scheme 11.2](#)) and ushered in the beginnings of an important role for synthesis in marine natural products chemistry: structure confirmation when limited amounts of natural material were available [6, 7].

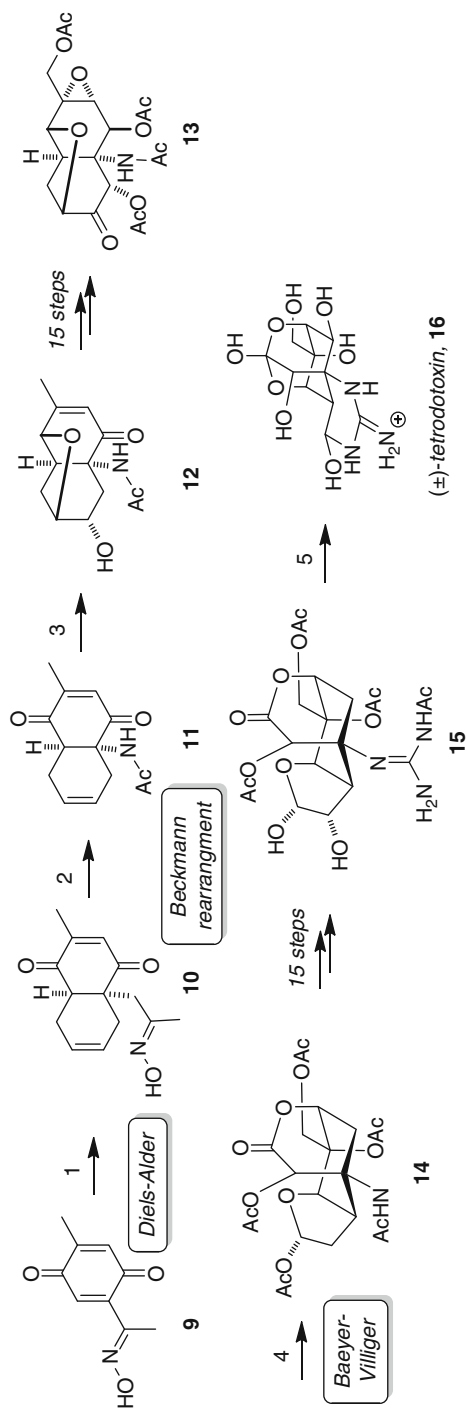
The structure of tetrodotoxin was arrived at almost simultaneously by three groups – Hirata-Goto, Tsuda, and Woodward – and involved an extensive process of degradation and painstaking spectroscopic analysis [8, 9]. The absolute stereochemistry was secured in 1972 by X-ray analysis, and was followed only 2 years later by Kishi's remarkable total synthesis. The Kishi synthesis commenced with oxime-substituted *p*-benzoquinone **9**, which could be subjected to a sequence of SnCl₄-catalyzed Diels–Alder reaction with butadiene and Beckmann rearrangement to give **11**. Selective reduction of the C5 ketone with sodium borohydride and epoxidation of the di-substituted olefin led to tricycle **12**. A sequence of 15 steps transformed enone **12** into tetraacetate **13**. Baeyer–Villiger oxidation broke open the decalin ring system and formed bridged tricycle **14**. A series of modifications installed the remaining oxidation functionalities to give diol **15**. Diol cleavage with periodic acid followed by treatment with base closed the final two rings to give tetrodotoxin, **16**.

Almost 30 years after Kishi's synthesis of racemic tetrodotoxin [10], the first asymmetric syntheses of this molecule were reported by the groups of Isobe [11] and Du Bois [12]. The intervening three decades had provided a wealth of new methods that could be brought to bear on the synthesis problems posed by tetrodotoxin and both syntheses leveraged these advances. However, in a similar vein to the Kishi work, strategic aspects of the two syntheses were also focused on the functionalization of the cyclohexane core of the molecule.

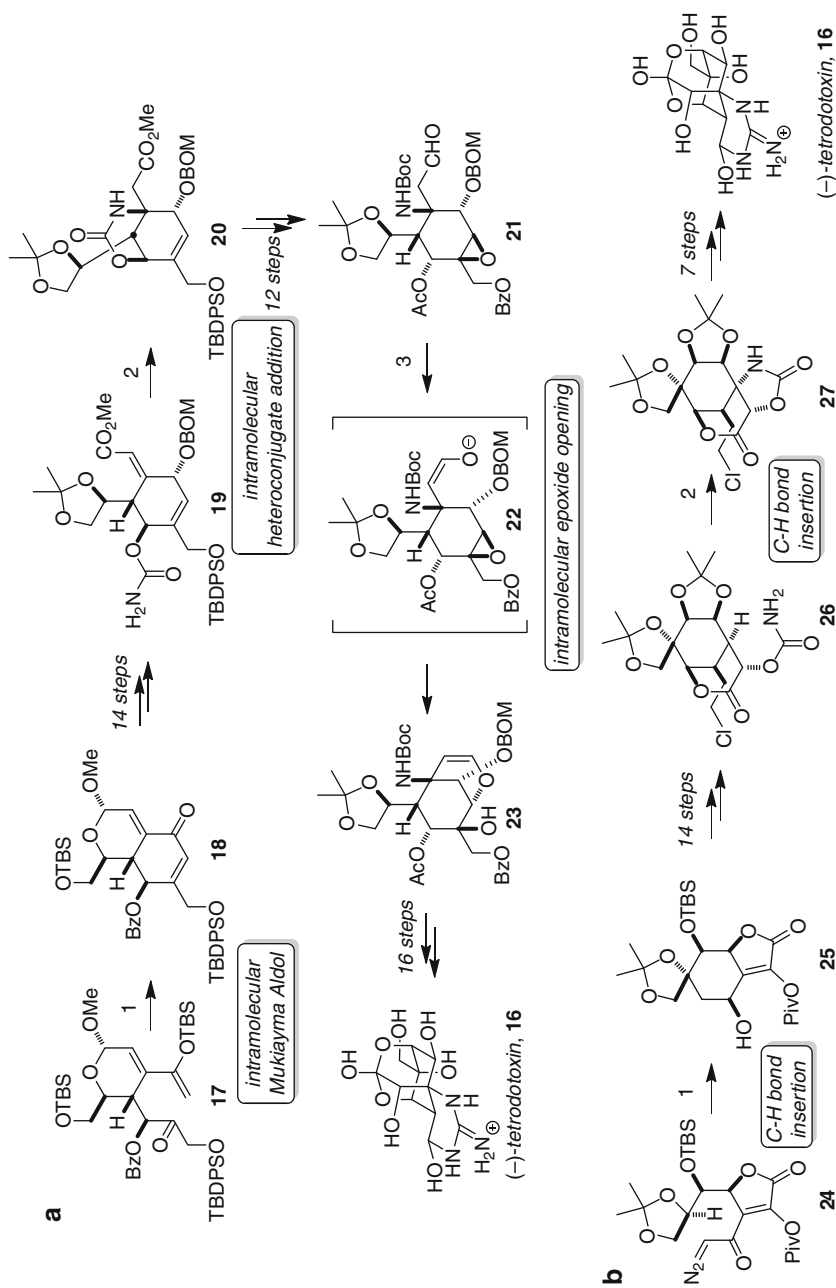
Key steps for the functionalization of the cyclohexane core of tetrodotoxin from Isobe's synthesis are shown in [Scheme 11.3a](#). Silyl enol ether **17** (derived from 2-acetoxy-tri-*O*-acetyl-D-glucal in 23 steps) was subjected to an intramolecular aldol reaction mediated by TBAF, and subsequent elimination with trichloroacetylchloride-pyridine provided enone **18** in >70% yield. Further manipulations advanced **18** to **19**, and upon treatment with potassium *tert*-butoxide in THF, the primary carbamate underwent heteroconjugate addition to produce oxazolidinone **20** in 90% yield. The final key functionalization of the cyclohexane was achieved by an interesting intramolecular *O*-alkylation of enolate **22** by the epoxide to give **23**. With **23** in hand, the first asymmetric synthesis of tetrodotoxin (**16**) was completed by a 15-step sequence consisting of largely straightforward transformations.



Scheme 11.1 Reagents and conditions: (1) KOH, H₂; (2) KOH, MeOH, reflux; (3) 5-methylisothiourea, H₂O; (4) **6**, H₂O; (5) PtO₂, H₂; (6) DCC, 5 °C



Scheme 11.2 Reagents and conditions: (1) butadiene, SnCl_4 ; (2) (a) MsCl , Et_3N ; (b) H_2O , heat, 50% (three steps); (3) (a) NaBH_4 ; (b) *m*CPBA, CSA, 72% (two steps); (4) (a) *m*CPBA; (b) KOAc, HOAc, 98% (two steps); (5) (a) HIO_4 ; (b) NH_4OH , $\text{MeOH}/\text{H}_2\text{O}$, 15% (two steps)



Scheme 11.3 (continued)

In a distinctly different approach, Du Bois and Hinman relied on their newly developed CH bond insertion reaction methodology [13] as the cornerstone of their efforts to functionalize the central cyclohexane ring (Scheme 11.3b). Treatment of diazoketone **24** (available in nine steps from D-isoascorbic acid) with 1.5 mol% $\text{Rh}_2(\text{HNCOCPh}_3)_4$ in CCl_4 results in a CH insertion reaction to give a cyclohexanone that is subsequently reduced with $\text{NH}_3\cdot\text{BH}_3$ to give alcohol **25** in 75% yield over the two steps. Advancement of **25** to carbamate **26** was achieved by a 14-step sequence, and set the stage for the second CH bond insertion. Subjecting this carbamate to conditions related to earlier methods developed in the Du Bois laboratories resulted in CH bond insertion of the carbamate to form oxazolidinone **27** in 77% yield. Given the structural complexity of the substrate, the yield for this reaction is truly remarkable, and nicely underscores the utility of this reaction in a target-oriented setting. A sequence of seven steps led to tetrodotoxin (**16**).

The challenges to synthesis presented by tetrodotoxin's structure were met by employing distinctly different strategies over the course of three decades. The Kishi synthesis employed a classic Diels–Alder reaction with substrate-based stereocontrol for reactions that further functionalized the core of the molecule. Isobe's synthesis relied on an intramolecular aldol reaction and conjugate addition to form two key bonds on a highly functionalized intermediate and the Du Bois synthesis showcases strategic avenues opened by advances in CH insertion reactions on highly functionalized compounds (Fig. 11.1).

11.2 The Continuing Role of Synthesis in Structure Elucidation, Confirmation, and Correction: Palmerolide A, Diazonamide A, Azaspiracid-1, and Palau'amine

The rise of modern spectroscopic methods such as NMR that began in the 1960s resulted in significant numbers of new structures being determined each year, and with increasing ease. Indeed, a survey of the structures recorded in MarinLit by the decade of their initial description shows that the 1960s produced 12 structures; the 1970s, 310 structures; the 1980s, 873; the 1990s, 1,459; and the period 2000–2009 produced 4,781 new structures [14]. In this section we consider a number of contemporary examples where synthesis has played roles in structure elucidation, structure confirmation, or structure corrections. Synthesis remains particularly important in the context of questions of stereochemistry, especially when the amounts of material isolated are small enough to permit connectivity to be established.



Scheme 11.3 (a) Key cyclohexane functionalization reactions from Isobe's synthesis of (-)-tetrodotoxin. Reagents and conditions: (1) TBAF, THF- H_2O then Cl_3CCOCl , DMAP, pyridine, >70%; (2) *t*-BuOK, THF, 90%; (3) DBU, *o*-dichlorobenzene, 130°C, >68%. (b) Du Bois's synthesis of (-)-tetrodotoxin. Reagents and conditions: (1) (a) 1.5 mol% $\text{Rh}_2(\text{HNCOCPh}_3)_4$, CCl_4 , (b) $\text{NH}_3\cdot\text{BH}_3$, CH_2Cl_2 -MeOH, 75% (two steps); (2) 10 mol% $\text{Rh}_2(\text{HNCOCF}_3)_4$, $\text{PhI}(\text{OAc})_2$, MgO, PhH, 65°C, 77%

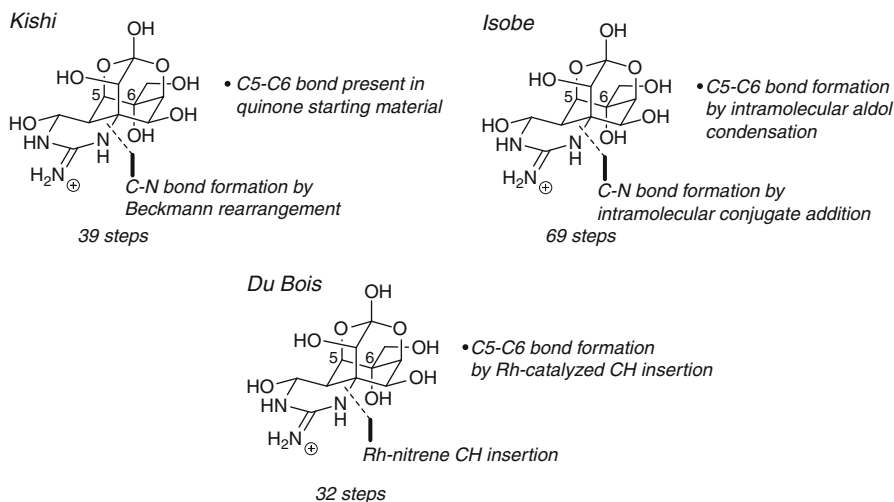
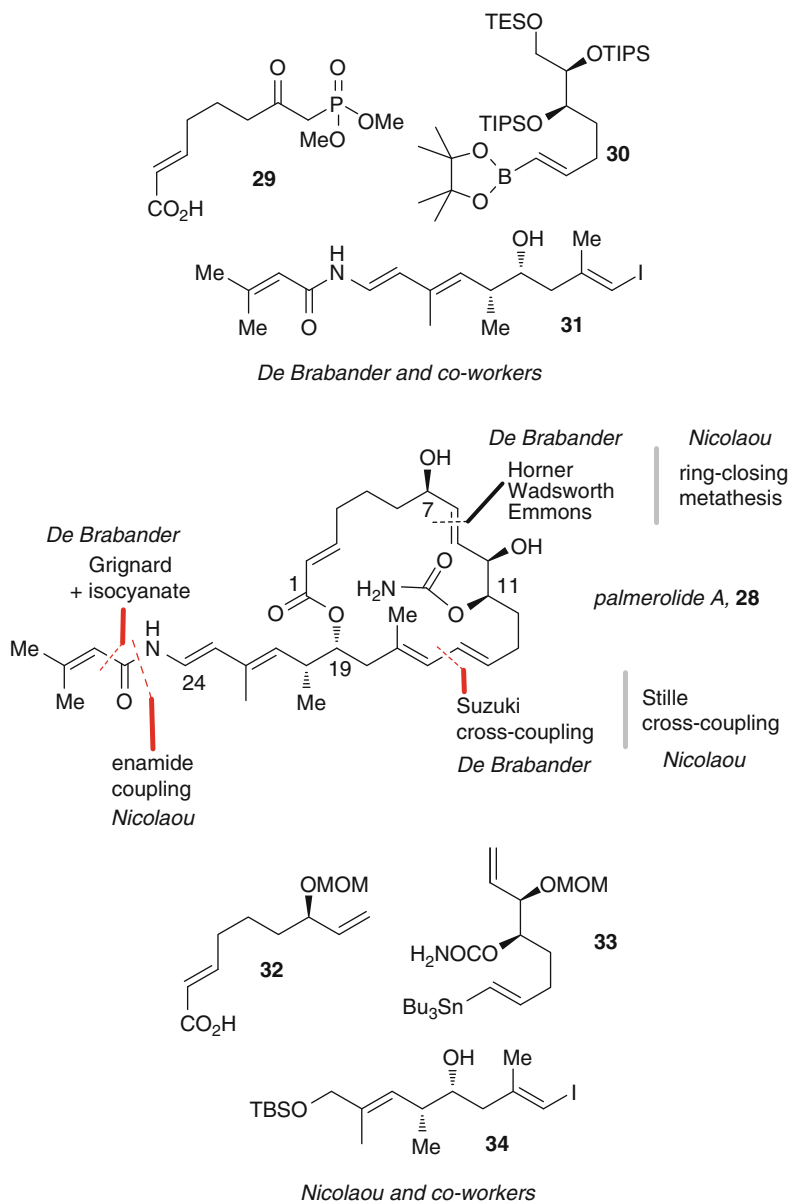


Fig. 11.1 A comparison of key reactions in the Kishi, Isobe, and Du Bois tetradotoxin syntheses

11.2.1 Palmerolide A

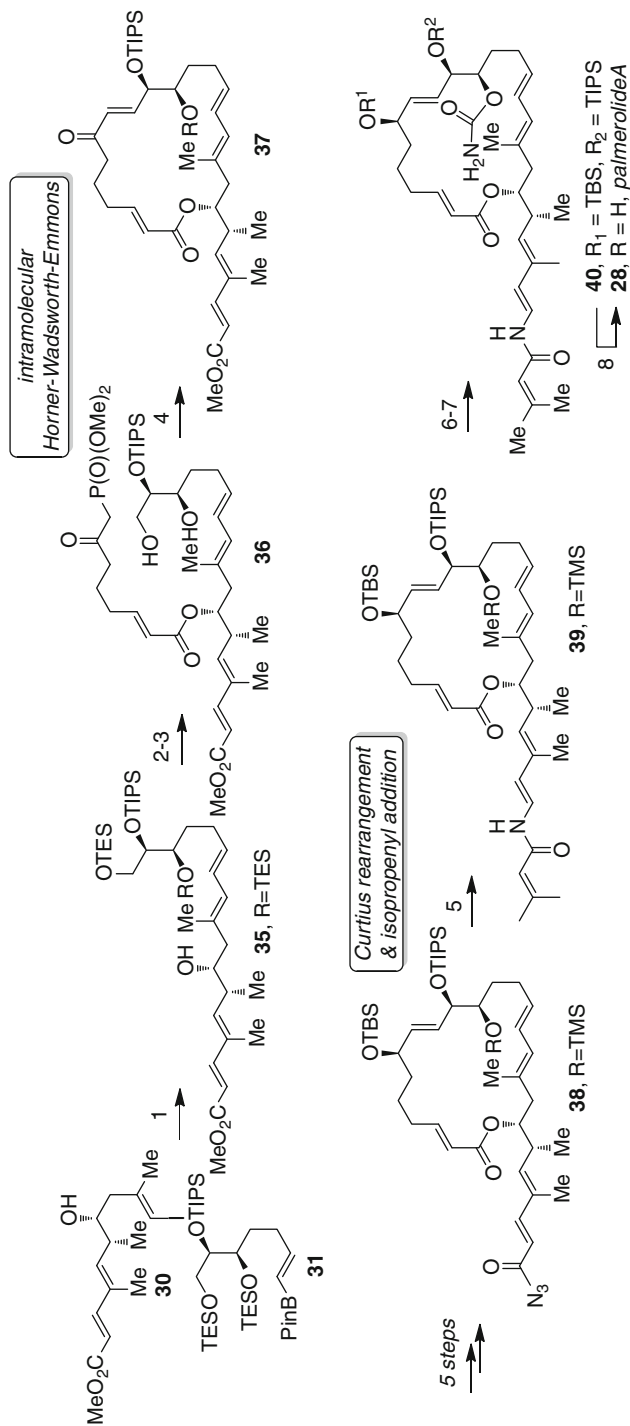
Palmerolide A (**28**) is a complex 20-membered macrolide isolated from an Antarctic tunicate *Synoicum adareanum* [15]. The original structure was described in 2006, and underpinned by the reported potent and selective cytotoxicity toward melanoma cells (UACC-62 LC₅₀ = 18 nM), there was an immediate flurry of activity that resulted in the first total syntheses by the De Brabander [16] and Nicolaou [17] groups (Scheme 11.4). These two total syntheses are instructive because they illustrate (1) the balance of new methods and well-used reactions in the context of a complex macrolide synthesis, (2) the speed with which contemporary total synthesis can provide structural information, and (3) the application of retrosynthetic analysis in the context of macrolide synthesis.

A key step in the De Brabander synthesis was a Suzuki cross coupling of vinyl iodide **31** with pinacolboronate **30**, which proceeded smoothly in the presence of Pd(PPh₃)₄ with Ti₂CO₃ as base to yield **35** (79%) (Scheme 11.5). Acylation of the alcohol with **29** using Yamaguchi conditions (69%), followed by removal of the TES ethers with PPTS in MeOH, led to **36** in 95% yield. The key Horner–Wadsworth–Emmons macrocyclization was achieved by a two-step protocol consisting of selective primary alcohol oxidation with PhI(OAc)₂/TEMPO to yield the aldehyde, and subsequent treatment with K₂CO₃ and 18-crown-6 in toluene at room temperature to provide **37** in 70% yield over these two steps. Enone **37** was then converted to acyl azide **38** in five steps (92%). Upon heating under reflux in benzene, Curtius rearrangement occurred to give an intermediate isocyanate that was intercepted with 2-methyl-1-propenylmagnesium bromide at –78°C to install the *N*-acyl enamine and give **39** in 76% yield over these two steps. Removal of the

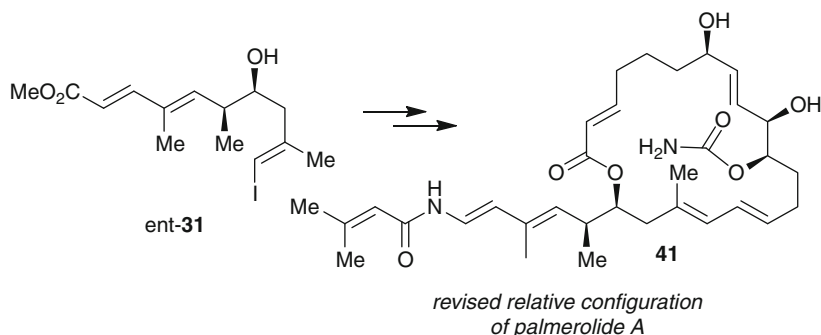


Scheme 11.4 Palmerolide A; a comparison of strategies

TMS ether with HF•pyr buffered with pyridine (95%) and introduction of the carbamate with $\text{Cl}_3\text{CC}(\text{O})\text{NCO}$ gave **40** (95%) and all that was required at this juncture to complete the synthesis was removal of the TBS and TIPS ethers. This was achieved with TBAF in THF at 0°C to give palmerolide A (**28**) in 41% yield.



Scheme 11.5 De Brabander's synthesis of palmerolide A. Reagents and conditions: (1) cat. Pd(PPh₃)₄, TiCl₄, THF, H₂O, rt, 79%; (2) 2,4,6-trichlorobenzoyl chloride, Et₃N, DMAP, PhMe, rt, 69%; (3) PPTS, MeOH, 0°C, 95%; (4) (a) PhI(OAc)₂, TEMPO, CH₂Cl₂, H₂O, room temp; (b) K₂CO₃, 18-C-6, PhMe, 60°C, 70% (two steps); (5) PhH, reflux then 2-methyl-1-propenylmagnesium bromide, -78°C, 76% (two steps); (6) HF-pyr, pyr, THF, rt, 95%; (7) Cl₃CC(O)NCO, CH₂Cl₂, 0°C, Al₂O₃, room temp, 95%; (8) TBAF, THF, 0°C, 41%



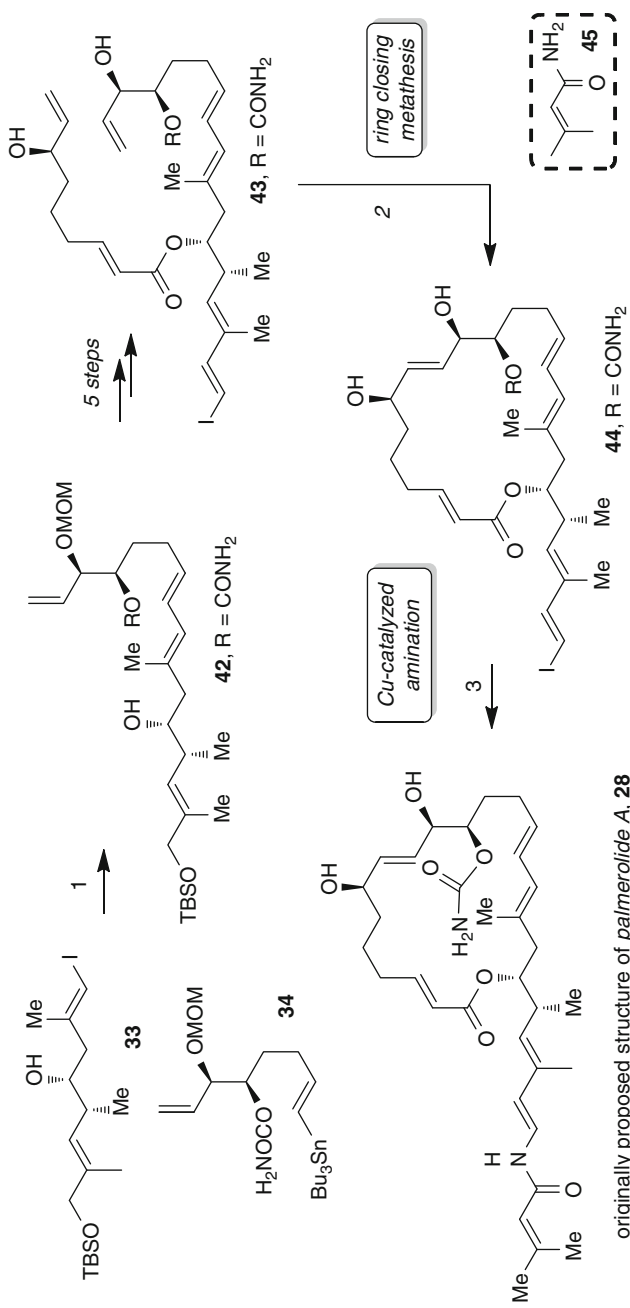
Scheme 11.6 Structure revision of palmerolide by synthesis

Unfortunately, the spectroscopic data for synthetic palmerolide A (**28**) was not consistent with that reported for the natural product, and after careful analysis of both the stereochemical assignments for the synthetic material and the natural product, De Brabander and coworkers concluded that the C19 and C20 stereochemistry was likely enantiomeric to that originally proposed by Baker. Synthesis of the proposed structure was achieved from *ent*-**31** (Scheme 11.6), and this provided material **41** that was identical to palmerolide A with the exception of the sign of optical rotation. As such the structure of palmerolide A was reassigned by synthesis to be the enantiomer of **41**. Contemporaneous with the work, the Baker group also published a reassignment based on degradative studies [18].

The Nicolaou synthesis of the originally proposed structure for palmerolide A involved Stille cross-coupling of **33** and **34** to produce **42** in 67% yield. Acylation with the mixed anhydride derived from **42** under Yamaguchi conditions followed by a four-step sequence gave the ring-closing metathesis precursor **43** [19], which was then treated with 20 mol% of the second generation Grubbs catalyst, and smooth cyclization at room temperature occurred to give **44** in 76% yield. The synthesis was completed by Pd-catalyzed amidation [20] of the vinyl iodide **44** with **45** to yield **28**. As was the case in the De Brabander studies, Nicolaou and co-workers concluded that the correct structure was **41**, and a synthesis of this compound was also completed by the same strategy as delineated in Scheme 11.7. The Nicolaou group has continued to study palmerolide A's chemistry and biology, and palmerolide A also continues to stimulate substantial synthesis activity from other groups [21].

11.2.2 Diazonamide A

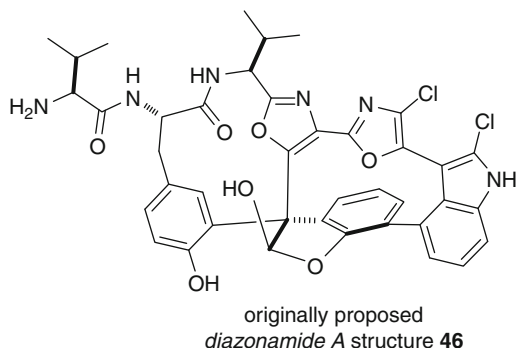
The intricate architecture of diazonamide A **46**, isolated from *Diazona angulata*, was first described by Lindquist, Fenical, and Clardy in 1991 (Fig. 11.2) [22]. The initial structure was secured by X-ray crystallography of the related diazonamide B, and synthesis efforts, driven in part by interest in the impressive anti-mitotic activity, quickly followed [23].



originally proposed structure of palmerolide A, 28

Scheme 11.7 Nicolaou's synthesis of the originally proposed structure for palmerolide A. Reagents and conditions: (1) 25 mol% Pd(dba)₂ Ph₃As, LiCl, NMP, 23°C, 67%; (2) 20 mol% Grubbs II cat., CH₂Cl₂, 23°C, 76%; (3) 45, CuI, Cs₂CO₃, *N,N'*-dimethylethylenediamine, DMF, 23°C, 44% based on 36% recovered starting material

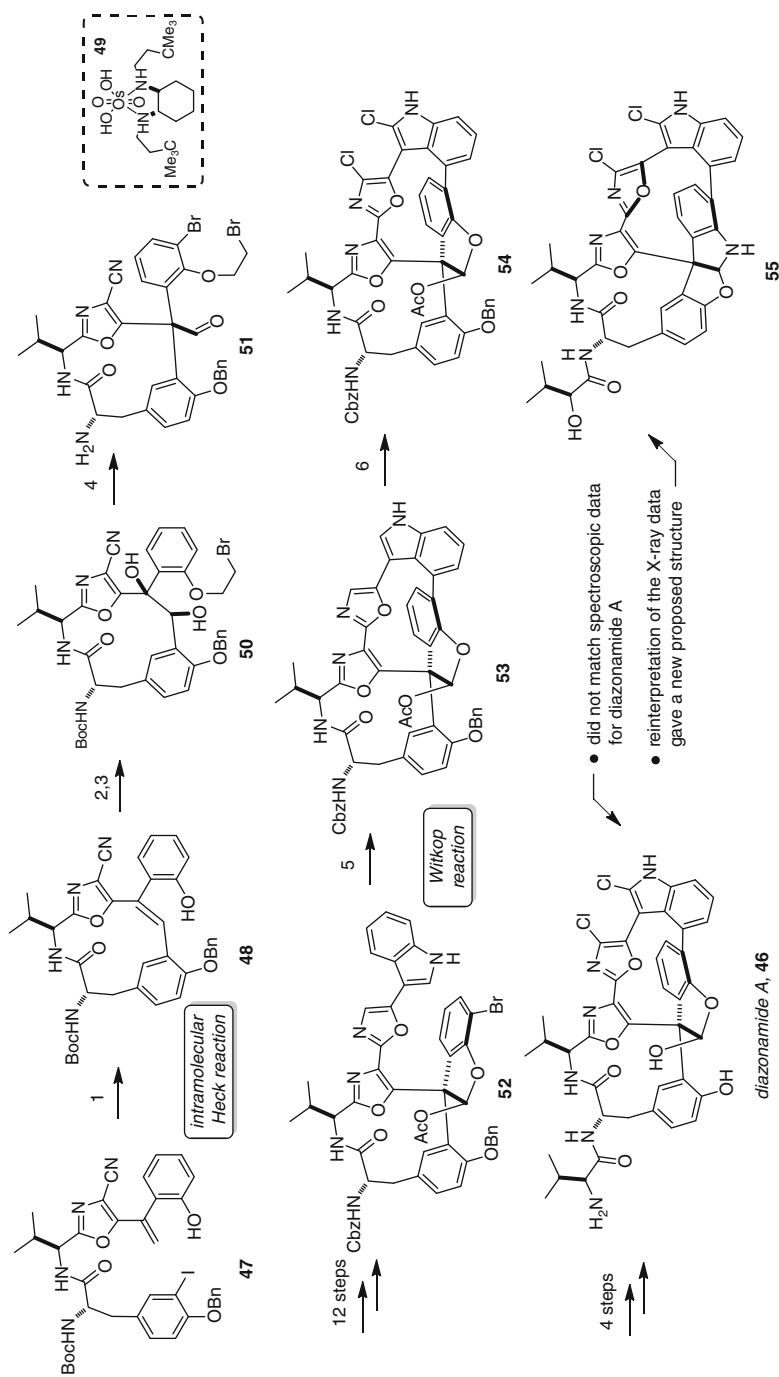
Fig. 11.2 The originally proposed diazonamide A structure



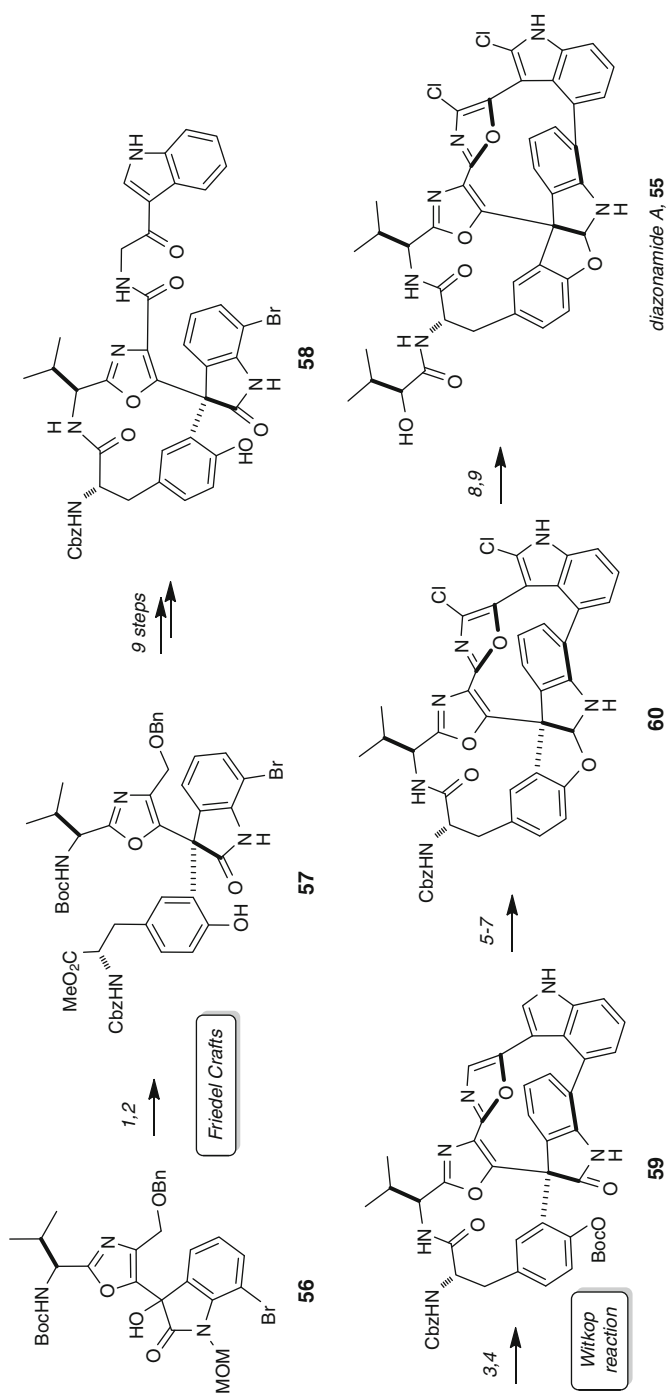
A landmark paper by the Harran group disclosed the synthesis of diazonamide A in 2001 [24]. The synthesis, shown in Scheme 11.8, involved an initial macrocyclization of iodide **47** by Heck reaction to produce **48**. Protection of the phenol and stoichiometric dihydroxylation using **49** gave diol **50**, which underwent pinacol rearrangement upon exposure to *p*-TsOH to produce aldehyde **51** as a single diastereomer. A 12-step sequence led to **52**, and the second macrocycle was formed by a photochemical Witkop reaction to yield **53** as a single atropisomer. Chlorination of the indole and the proximal oxazole produced **54**, and a further four steps led to diazonamide A (**46**). At this juncture it became immediately apparent that the synthesized structure was not the same as natural diazonamide A, especially by comparison of ^1H NMR data. On the basis of synthetic work and reinterpretation of the X-ray crystallographic data, Harran proposed that the structure of diazonamide A be revised to **55**.

The newly revised structure of diazonamide A, **55**, was ratified by total synthesis in the Nicolaou laboratories only 1 year later (Scheme 11.9) [25]. The synthesis commenced with a Friedel–Crafts alkylation of Cbz-tyrosine methyl ester with **56** to give **57** (after reintroduction of the Boc carbamate). A nine-step sequence led to macrocycle **58**, which was then exposed to Gabriel–Robinson cyclodehydration conditions and radical cyclization to give macrocycle **59**. Installation of the chlorines followed by selective BOC deprotection and DIBAL-H- initiated ring closure led to intermediate **60**. Hydrogenolysis of the Cbz- protecting group and installation of the peptide side chain completed the synthesis of diazonamide A, **55**.

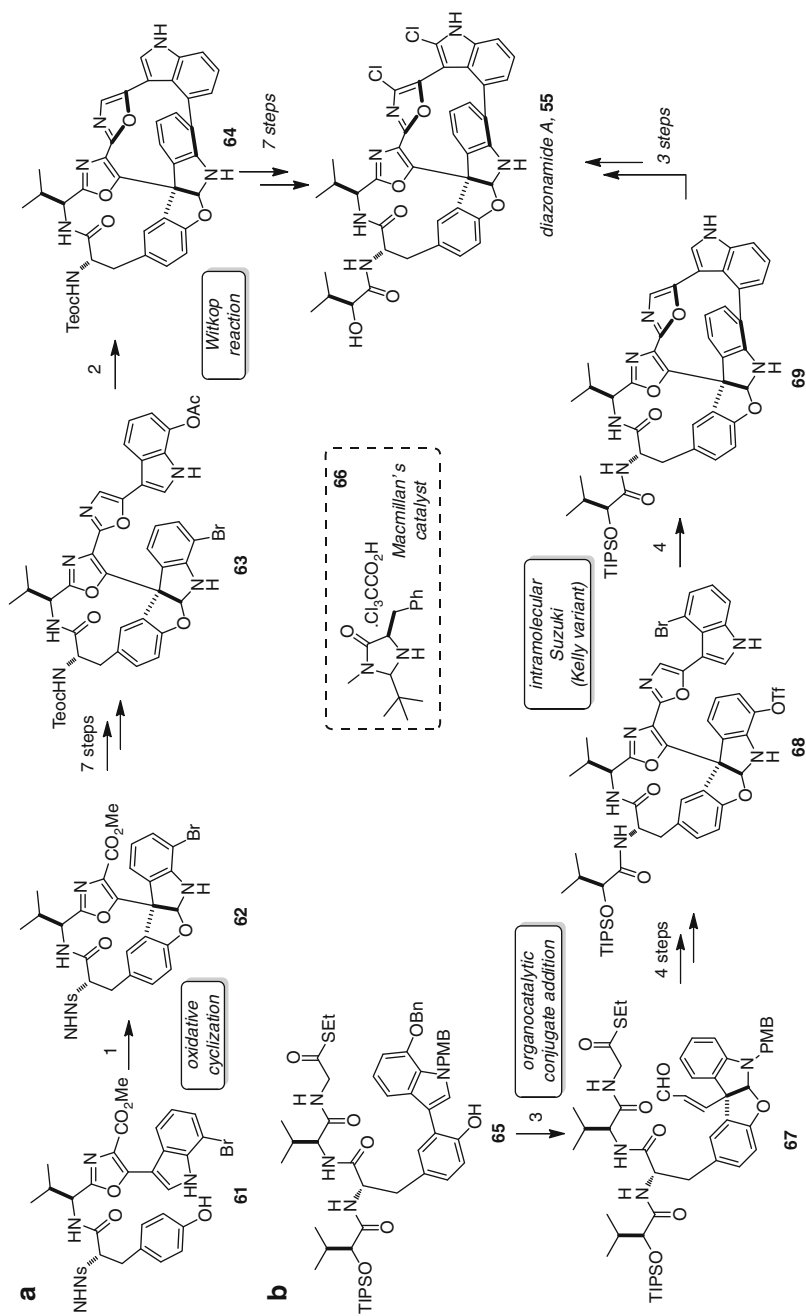
With the structure of diazonamide A secured by the combined efforts of Harran in pursuit of the originally proposed connectivity and Nicolaou in providing the confirmation of structure by synthesis, more recent efforts have focused on diazonamide as a vehicle for methods development and investigations of the underlying biology. Four further total, or formal, syntheses, have been completed. Key elements of the Harran total synthesis of diazonamide A are shown in Scheme 11.10 [26]. Oxidative cyclization produced **62** in a very direct fashion from compound **61**, which was transformed, via a seven-step sequence, to macrocycle **63**. The second macrocycle was then formed via Witkop reaction



Scheme 11.8 Harran's synthesis of the original structure proposed for diazoniamide A. Reagents and conditions: (1) $Pd_2(dba)_3$ (3 mol%), 2-(di-*tert*-butylphosphanyl)biphenyl (6 mol%), Ag_3PO_4 , THF, 75°C, 82%; (2) *t*-BuOK, THF, 2-bromoethyltriflate, (3) 49, toluene, -78°C to -25°C, 68% (two steps); (4) TsOH, toluene, 95°C, >54%; (5) 4 steps; (6) NCS, THF, 32-40%; (6) NCS, THF, 32°C, 60%



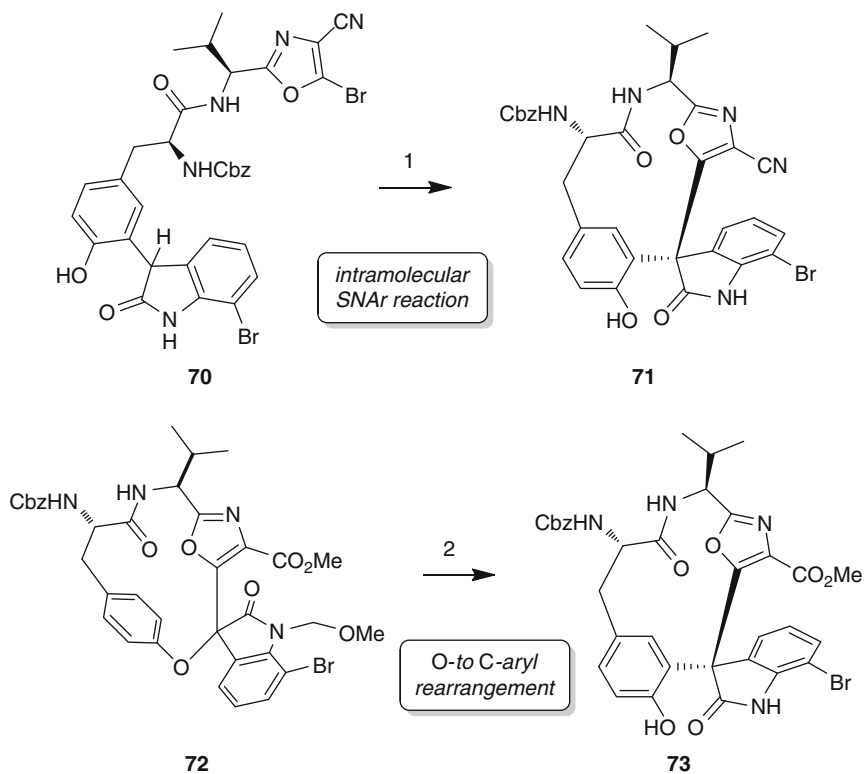
Scheme 11.9 Nicolaou's synthesis of diazoniamide A. Reagents and conditions: (1) CbzTyrOMe, *p*-TsOH, 1,2-DCE; (2) (Boc)₂O, aqueous NaHCO₃/dioxane, 21% (two steps); (3) POCl₃, pyridine; (4) hv, epichlorohydrin, LiOAc, MeCN/H₂O, 16% (two steps); (5) NCS, CCl₄/THF; (6) TFA; (7) DIBAL-H, THF, 29% (three steps); (8) H₂, Pd(OH)₂/C, EtOH, (9) EDC, HOBT, NaHCO₃, DMF, 82% (two steps)



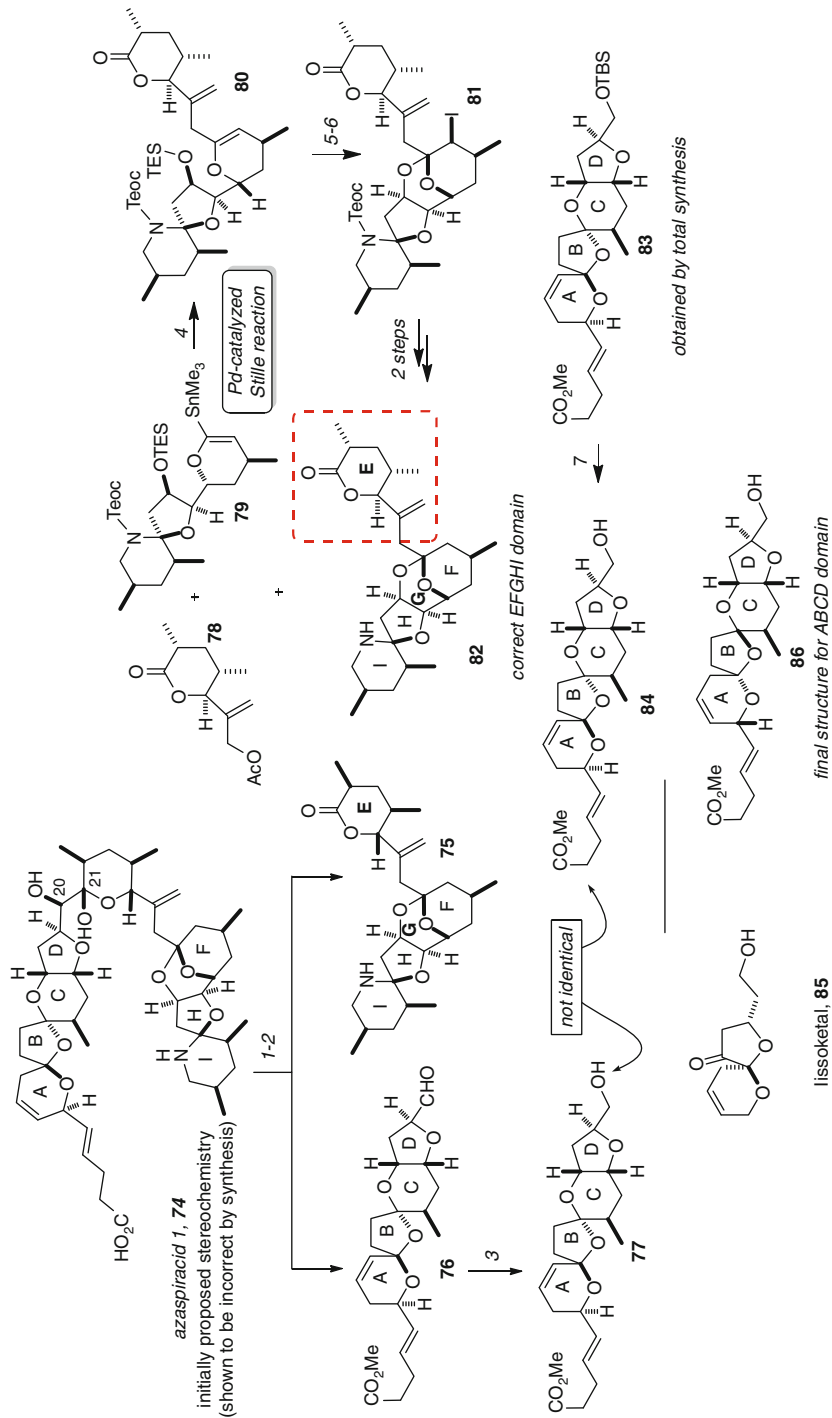
Scheme 11.10 (a) Harran's synthesis of diazonamide A, and (b) The MacMillan synthesis of diazonamide A. Reagents and conditions: (1) $\text{PhI}(\text{OAc})_2$, LiOAc , 2,2,2-trifluoroethanol, 25%; (2) $h\nu$ (300 nm), CH_3CN , H_2O , LiOH ; (3) propynal, 85%, >20:1 dr; (4) $\text{Pd}(\text{PPh}_3)_4$, $(\text{BPin})_2$, KF , MW, 50%

to give bis-macrocyclic **64** which was then taken on to diazonamide A via a seven-step sequence. MacMillan completed a total synthesis of diazonamide A in 2011 via use of an organocatalytic conjugate addition of thioester **65** with catalyst **66** to give enal **67** [27]. Enal **67** was then taken through a four-step sequence to give macrocycle **68**, which underwent a Kelly-type intramolecular Suzuki coupling to give bis-macrocyclic **69**. The total synthesis was then completed via addition of the chlorine residues and deprotection to afford diazonamide A.

Both Sammakia and Magnus have completed formal total syntheses that employ interesting and elegant approaches to the C10 quaternary center (Scheme 11.11) [28]. In the case of the Sammakia synthesis, an intramolecular nucleophilic aromatic substitution reaction was used to form the quaternary center at the same time as closing one of the macrocycles (**70** \rightarrow **71**). In light of strategic considerations that balance the importance of formation of the macrocycles against the challenges inherent in the diastereoselective formation of the C10 center, this is the most direct solution to date. The Magnus synthesis was highlighted by the rearrangement of **72**–**73**, a process that is formally a Friedel–Crafts reaction.



Scheme 11.11 The Sammakia and Magnus syntheses of the quaternary center. Reagents and conditions: (1) Na₂CO₃, DMF, 65°C, 20 h, 56%; (2) CHCl₃, reflux, 70%



Scheme 11.12 (continued)

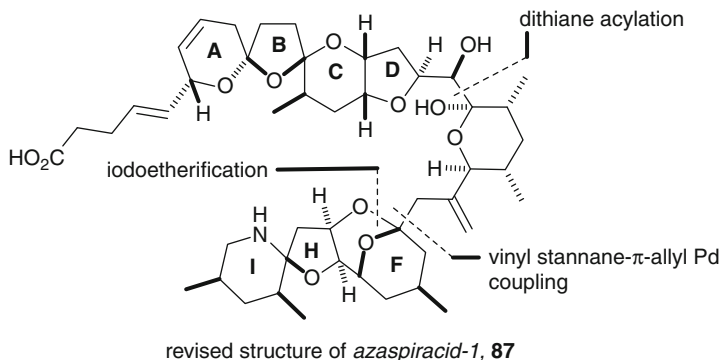


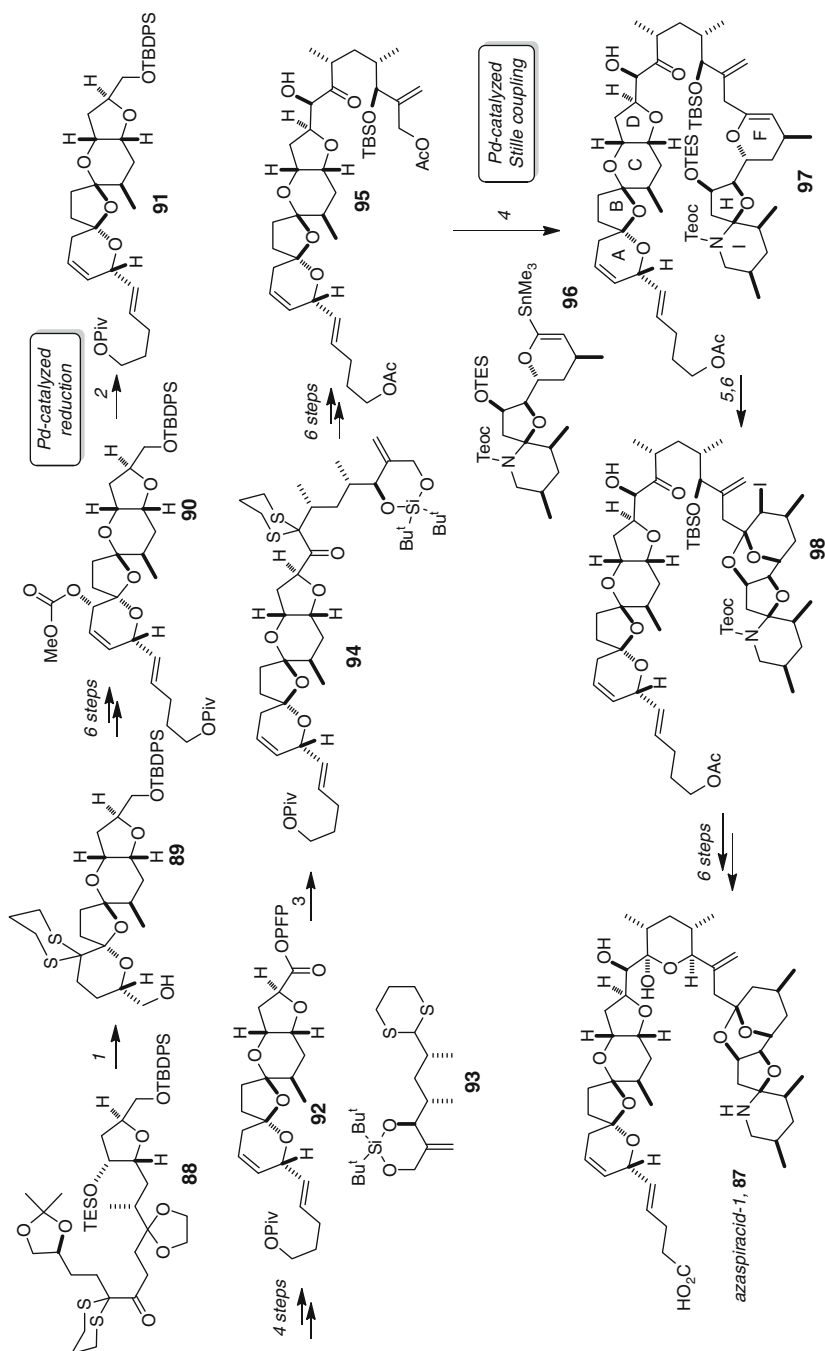
Fig. 11.3 Key carbon–carbon bond forming reactions in the Nicolaou azaspiracid-1 synthesis

11.2.3 Azaspiracid-1

A more complex example of the role of total synthesis in structure correction comes from Nicolaou's synthesis of azaspiracid-1, a complex alkaloidal polyether first described in 1998 by Takeshi Yasumoto and coworkers [29]. In 2003, Nicolaou and co-workers established by total synthesis [30, 31] that the initially proposed structure for azaspiracid-1 was incorrect (**74**, Scheme 11.12). Subsequent degradative studies and synthesis were required to revise the structure of azaspiracid-1 [32]. In work described in 2003, upon realizing that there were structural questions remaining to be resolved, the first path was to degrade natural azaspiracid-1 to smaller fragments and then locate the positions of error by synthesis. This approach was also expected to allow the determination of the relative stereochemistry between the ABCDE and FGHI domains. To this end, an authentic sample of azaspiracid was reacted with TMSCHN₂ and the methyl ester obtained was treated with NaIO₄, which resulted in cleavage of the C20–C21 bond. This provided lactone **75** and aldehyde **76**, which were subjected to short sequences of common transformations to yield alcohol **77** (the stereochemistry shown for this compound corresponds to that originally proposed).

Synthetic materials for comparison with structures **76** → **77** were prepared by coupling of **78** and **79** by a Pd(0)-mediated Stille coupling to give dihydropyran **80**. Removal of the TES ether with HF-pyridine, followed by treatment with *N*-iodosuccinimide to induce iodoetherification, produced iodoether **81** in 38%

Scheme 11.12 Chemical degradation and derivatization of azaspiracid-1 (originally proposed structure) to C1–C20 alcohol **77** and C21–C40 lactone **75**. Reagents and conditions: (1) TMSCHN₂, MeOH, 25°C; (2) NaIO₄, MeOH/H₂O (4:1), 25°C, ~100% over two steps; (3) NaBH₄, MeOH, 25°C, ~90%; (4) **78**, 90 mol% [Pd₂dba₃], LiCl, AsPh₃, DIPEA, syringe pump addition of stannane; (5) HF-pyr, THF-pyr; (6) NIS, NaHCO₃, THF, 38% (three steps); (7) TBAF, THF, 88%



Scheme 11.13 (continued)

yield (for the three steps). Two further steps gave **82** and comparison of the spectral data for this compound with compound **75** showed them to be the same. This established that the structure of the compound obtained by degradation is in fact diastereomeric in terms of the stereochemistry around the E ring to that which was originally proposed. A synthesis of the compound in which the FGH I rings were enantiomeric was also completed by this route, but it did not match the data for **83**. These, and related, synthetic studies established the absolute stereochemistry for this domain. The availability of synthetic materials also allowed questions regarding the connectivity and stereochemistry of the ABCD ring-containing domain to be answered. Desilylation of previously synthesized compound **83** to give **84** allowed for a comparison with degradation product **77**. The spectroscopic data for these two samples differed substantially, particularly in the A ring. Progress towards a corrected structure was assisted by comparison of NMR data with a related compound, lissoketal (**85**) [33]. Based on this comparison, a new structure for **77** in which the A-ring double bond has been relocated was proposed; however, final resolution of the problem did not come until the synthesis of several closely related structures had been completed. Based on this work, the stereochemistry and connectivity shown in compound **86** was secured as being correct.

Armed with the information gleaned from these studies, and the earlier synthesis, plans could be laid to complete a total synthesis of the revised structure **87**, by employing the key couplings shown in Fig. 11.3.

Key steps of the synthesis are shown in Scheme 11.13. Malic acid-derived tetrahydrofuran **88** was treated with TMSOTf in CH₂Cl₂ at low temperature to induce the desired deprotection–spirocyclization sequence to give **89** in 89% yield as a single stereoisomer. A sequence of six steps led to allylic carbonate **90**, and deoxygenation of this compound to give **91** was achieved by employing a modification of an earlier-described Pd-catalyzed method [34] which produced the desired compound in 82% yield (with 7:1 selectivity for the $\Delta^{7,8}$ olefin). After advancement to pentafluorophenyl ester **92**, introduction of the C21–C27 domain involved acylation of the dithiane anion derived from **93** to give **94** in 50% yield. Six further steps provided compound **95** which served as the key precursor to the A → E domain for the final steps of the synthesis. The crucial coupling of the ABCD and FHI subunits occurred by Pd-mediated Stille-type reaction between allylic acetate **95** and dihydropyranyl stannane **96** to give **97** in 55% yield. Removal of the C34 TES ether (TBAF, 80%) and iodoetherification with N-iodosuccinimide produced **98** in an impressive 62% yield given the complexity of the substrate. The synthesis was then completed by a short sequence of six steps that consisted of redox chemistry and protecting group manipulations. Material obtained by this route matched all characterization data for the natural product.



Scheme 11.13 Synthesis of the revised structure of azaspiracid-1 **87**. Reagents and conditions: (1) **93**, *n*-BuLi-*n*-Bu₂Mg, THF, 0°C → 25°C; then –90°C; then **92**, 50%; (2) **95**, 30 mol% Pd₂dba₃, 30 mol% AsPh₃, LiCl, DIPEA; then **96**, NMP, 40°C, 55%; (3) TBAF, THF, 0°C, 80%; (4) NIS, NaHCO₃, THF, 0°C, 62%

11.2.4 Palau'amine

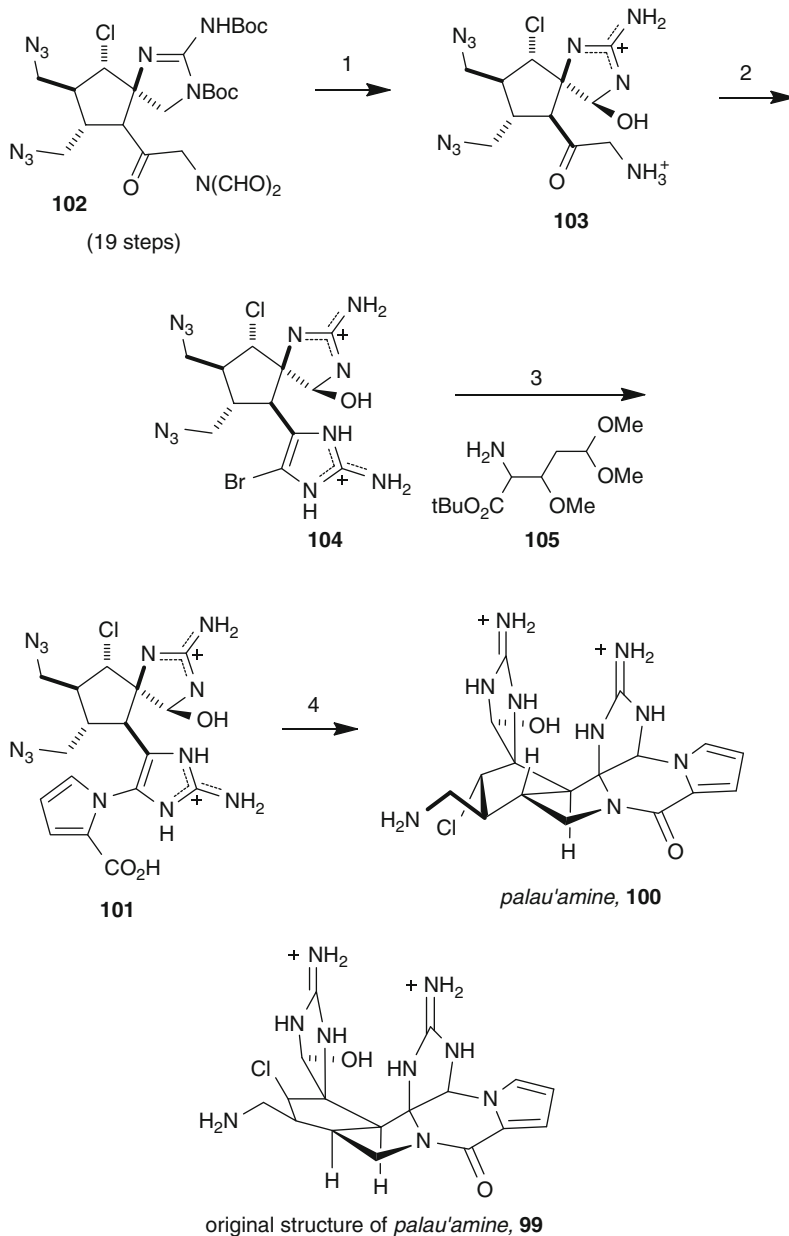
The complex hexacyclic architecture of palau'amine (**99**) has long stood as one of the major challenges of organic synthesis [35]. In 2007, the geometry of the azabicyclo [3.3.0] octane core was determined to be *trans* **100**, rather than the proposed *cis* [36]. Using this information, Baran and coworkers were able to successfully complete a total synthesis of palau'amine [37]. The synthetic strategy was based on the premise that a “macro palau'amine” could be generated from **101** and an irreversible transannular cyclization would yield the desired target (Scheme 11.14). To prepare **101**, Baran converted the cyclopentane core **102** (available in 19 steps) to the hemiaminal **103** in 64% yield, using a selective silver(II)-oxidation protocol. Conversion to the 2-aminoimidazole was achieved by reaction of **103** with cyanamide, and this compound was brominated (Br₂, TFA, TFAA) to afford the bromide **104** in 35% yield for the two steps. After initial efforts to introduce an intact pyrrole failed, the key pyrrole **101** was prepared in 44% yield by reacting bromide **104** with amino ester **105** (AcOH, THF), then heating in TFA. Reduction of the azide groups was achieved by reaction with hydrogen gas and palladium acetate, and this was then followed by reaction with EDC to form the macrocycle. Without isolating the material, TFA was added and the solution heated at 70°C to trigger the critical transannular cyclization and generate palau'amine **100** in 17% yield (from **101**).

A comprehensive coverage of other examples of the role of synthesis in structure reassignment is not possible here, but some further examples are highlighted in Fig. 11.4. The reader is directed to an excellent review by Snyder and Nicolaou that covers in detail this topic [38].

11.3 In Pursuit of Nature's Perfection: Biosynthetic Principles and the Synthesis of Hemibrevetoxin B, Methyl Sarcophytoate, Longithorone, and 11,11'-Dideoxyverticillin

11.3.1 Hemibrevetoxin B

Much has been made of the proposed biosynthesis of the ladder polyether class via cascade epoxide cyclizations (for a review that also details the alternative Townsend oxidative cyclization process see: [39]), as exemplified for brevetoxin B (**113**) below in Scheme 11.15. Early work in the field of polyethers took guidance from these ideas, and Nicolaou provided a solution to the problem of the preference for so-called 5-exo vs. 6-endo cyclization manifolds for the cyclization of hydroxy epoxides by incorporation of a proximal alkene (Scheme 11.16a, **114** → **115**) [40]. This approach has seen broad application, however more recent results from Jamison have demonstrated the possibility for direct cyclization of hydroxy-poly epoxides **121** and **122** to tris-pyran **123** and tetra-pyran **124** (Scheme 11.16b). These reactions are uniquely possible in H₂O as solvent [41].



Scheme 11.14 The final stages of Baran's palau'amine synthesis. Reagents and conditions: (1) 50% TFA/H₂O then 10% TFA, silver(II)-picolinate, H₂O, 64%; (2) (a) H₂NCN, brine; (b) TFAA/TFA; Br₂, 35% (two steps); (3) **105**.AcOH, THF; TFA/CH₂Cl₂, 44%; (4) Pd(OAc)₂, H₂, TFA/H₂O then EDCI, HOBt, DMF; TFA, 17%

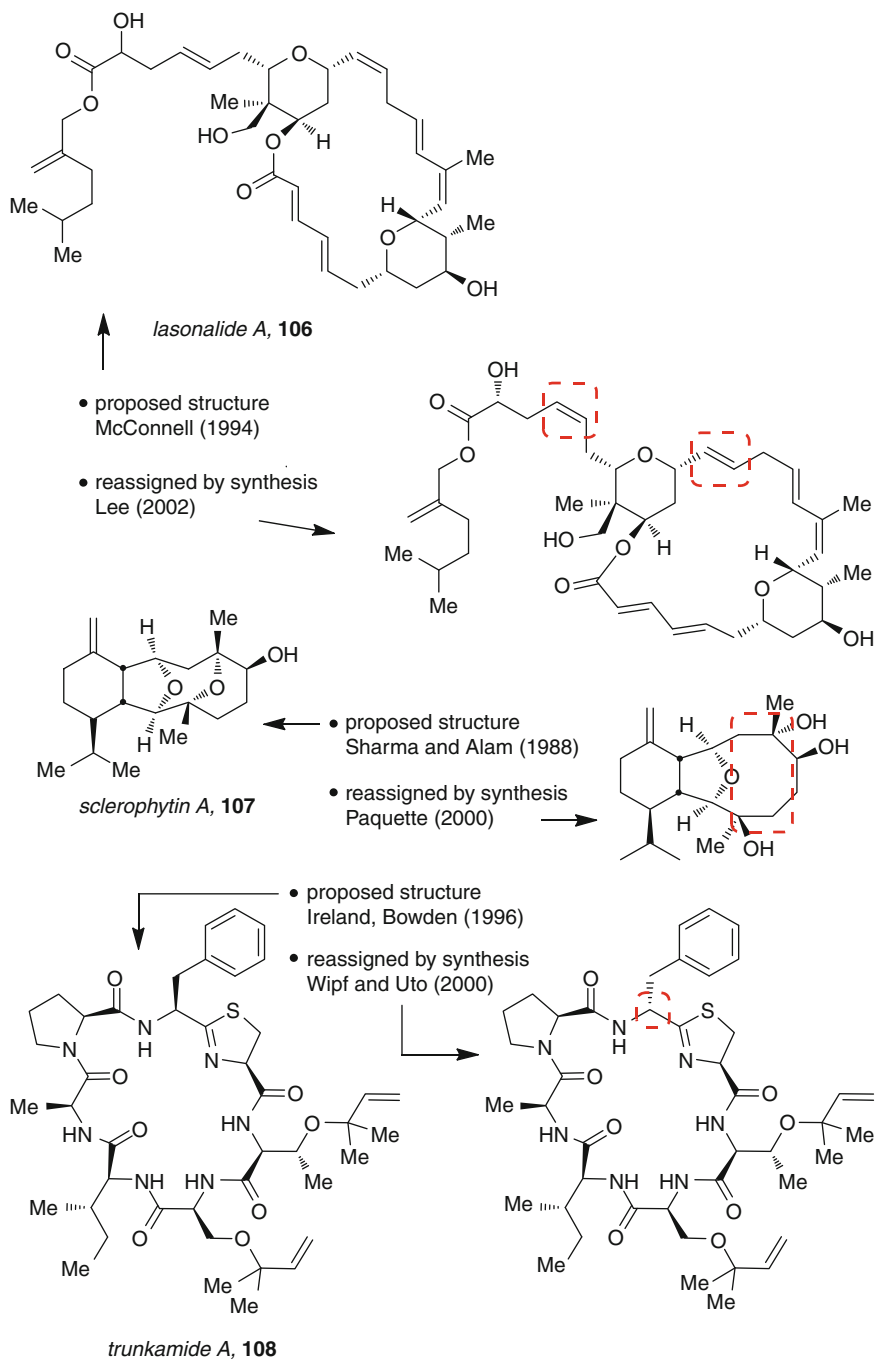


Fig. 11.4 (continued)

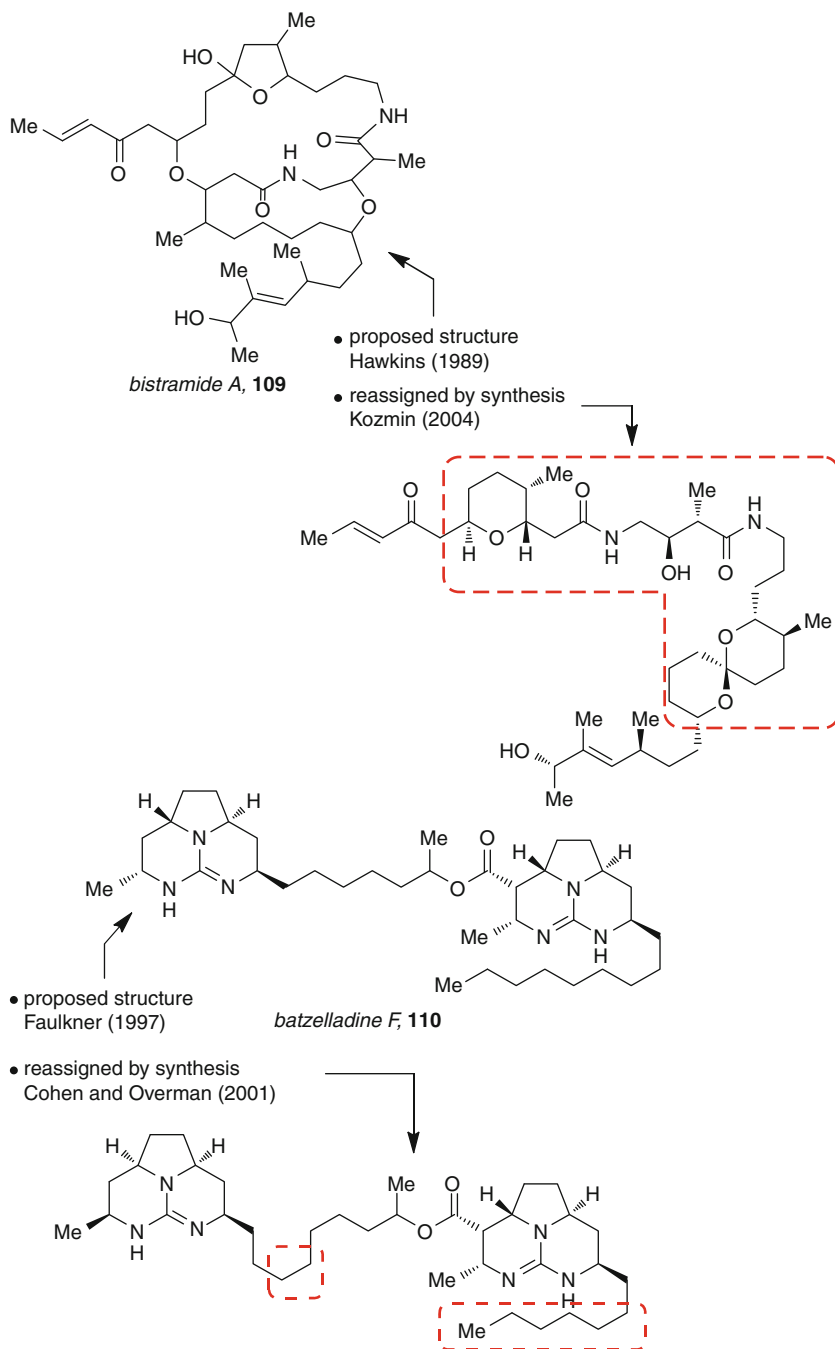


Fig. 11.4 (continued)

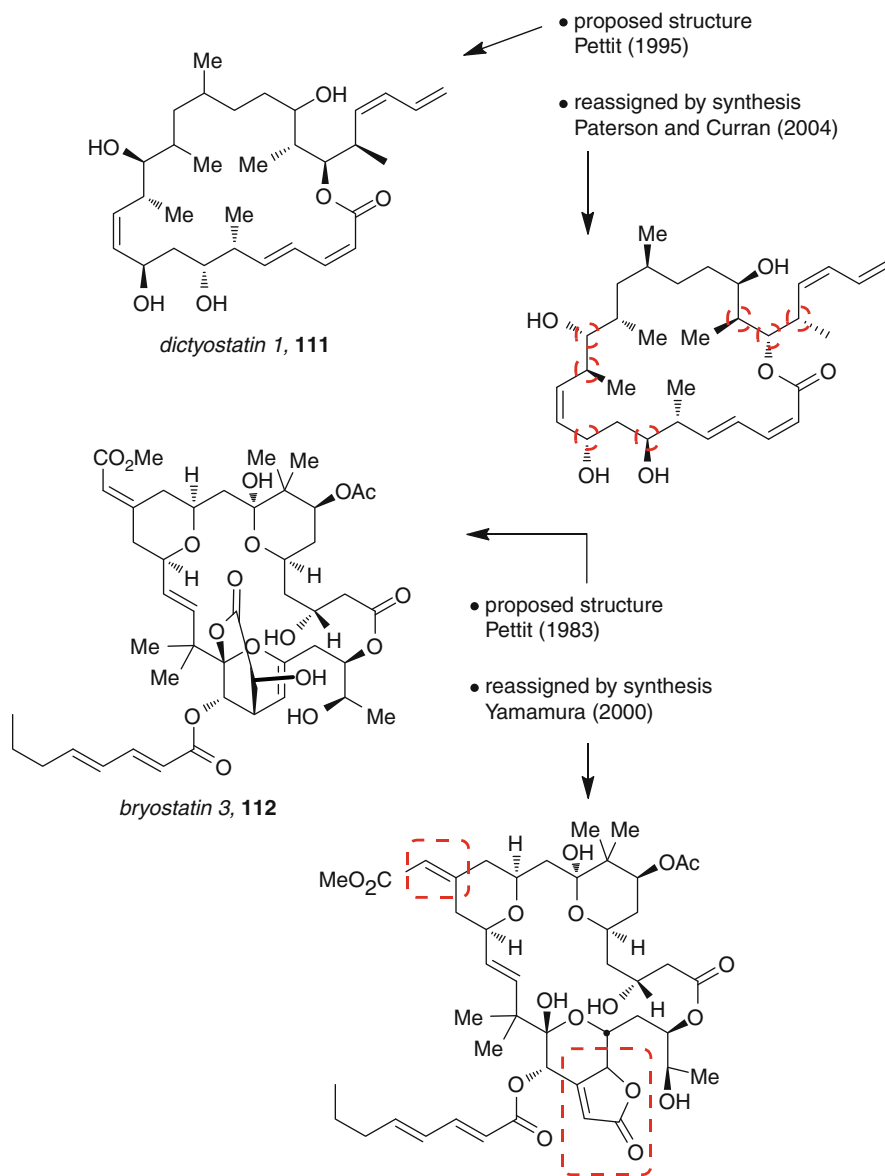
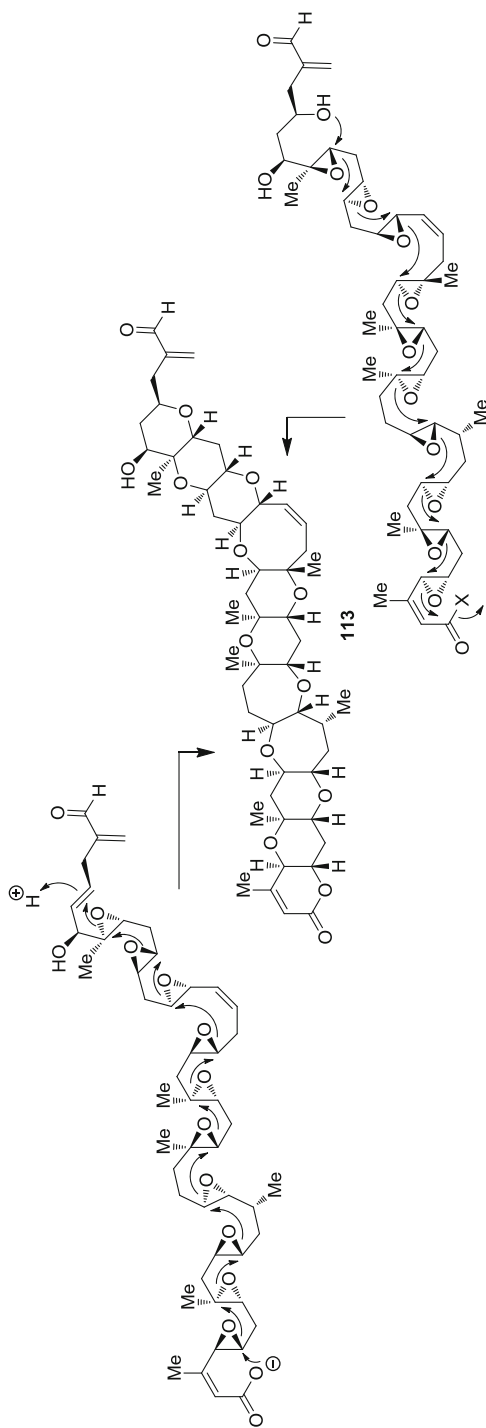
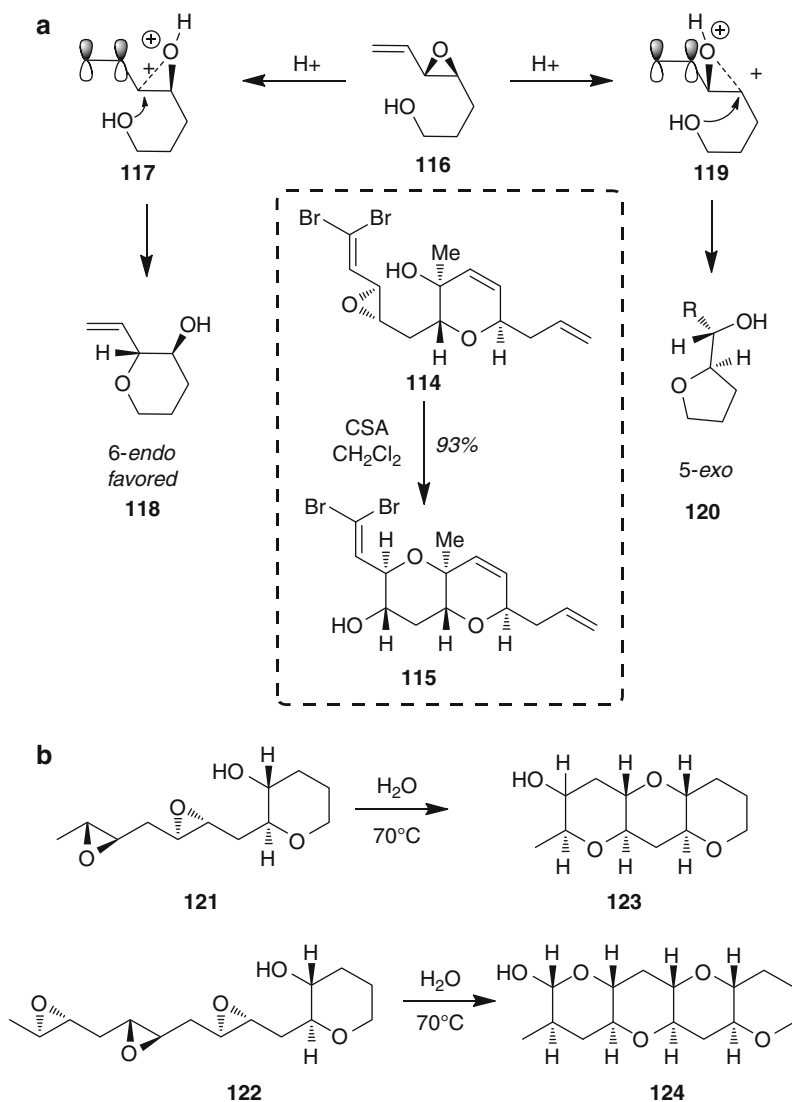


Fig. 11.4 Some initially misassigned structures where synthesis has played a key role in structure reassignment and confirmation: lasonolide (**106**) [111], sclerophytin A (**107**) [112], trunkamide (**108**) [113], bistramide (**109**) [114], batzelladine (**110**) [115], dictyostatin (**111**) [116], and bryostatin (**112**) [117]

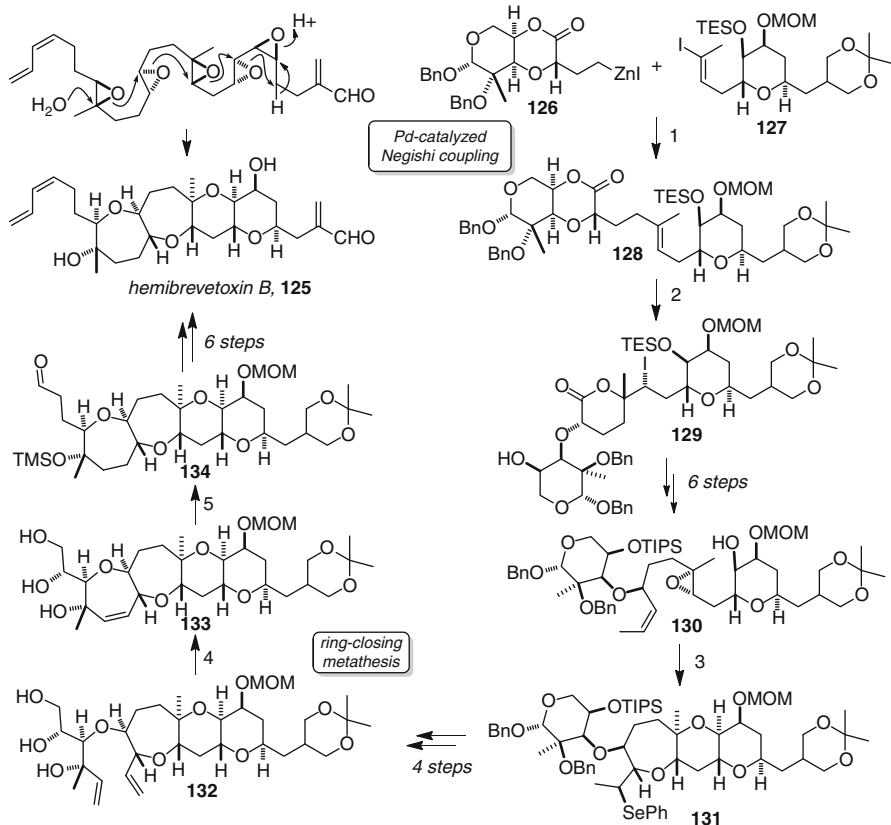


Scheme 11.15 Nakanishi-Nicolaou hypothesis [110]



Scheme 11.16 (a) Nicolaou's original approach to pyran formation from epoxy alcohols and (b) Jamison's discovery of the importance of H₂O as solvent

Holton's synthesis of hemibrevetoxin B125 [42] is based partly on these principles and is shown in Scheme 11.17 [43]. The first key union of subunits involved a Negishi coupling between organozinc **126** (Scheme 11.17, prepared from the corresponding iodide, which was in turn prepared from benzyl β -D-arabinopyranoside in 12 steps) and iodide **127** (prepared from tri-O-acetyl-D-glucal



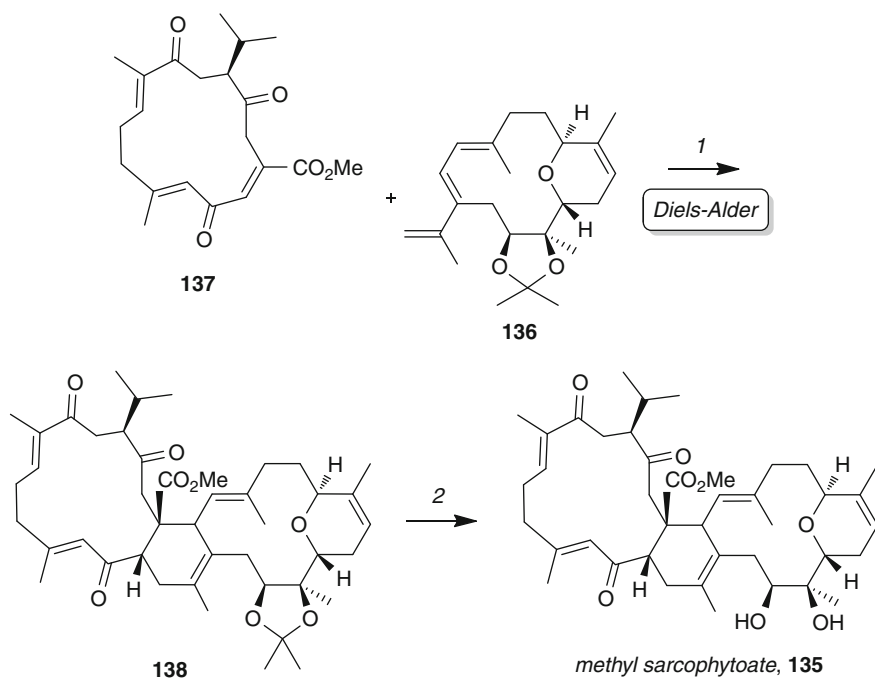
Scheme 11.17 Cascade epoxide cyclization-based biosynthesis of polyethers such as hemibrevetoxin B. Reagents and conditions: (1) 3 mol% PdCl₂(dppf), THF, rt, 76%; (2) (a) LiOH, THF–H₂O, 0°C; (b) NIS, 2,6-lutidine, –10°C, 75%; (3) *N*-(phenylseleno)phthalimide, (CF₃)₂CHOH, 0°C, 83%; (4) 10 mol% Grubbs II catalyst, PhH, 80°C, 85%; (5) (a) NaIO₄, Et₂O/*t*BuOH/H₂O; (b) (EtO)₂P(O)CH₂C(O)N(Me)OMe, NaH, THF; (c) H₂, 20% Pd(OH)₂/C, EtOAc; (d) TMSCl, Et₃N, CH₂Cl₂; (e) DIBAL-H, THF, –78°C, 79% (five steps)

via a 13-step sequence), which provided **128** in 75% yield. Lactone hydrolysis with lithium hydroxide, followed by iodolactonization with *N*-iodosuccinimide, produced iodolactone **130** (75%). A sequence of six steps converted **129** to epoxide **130**, which upon treatment with *N*-(phenylseleno)phthalimide underwent cyclization to give polycycle **131** as a single diastereoisomer in 83% yield. This sequence presumably is initiated by electrophilic selenation of the double bond, subsequent epoxonium ion formation, and termination by trapping by the free alcohol. Routine manipulations converted **131** to **132** via a sequence of four steps, and set the stage for formation of the oxepane ring by ring-closing metathesis (Scheme 11.17).

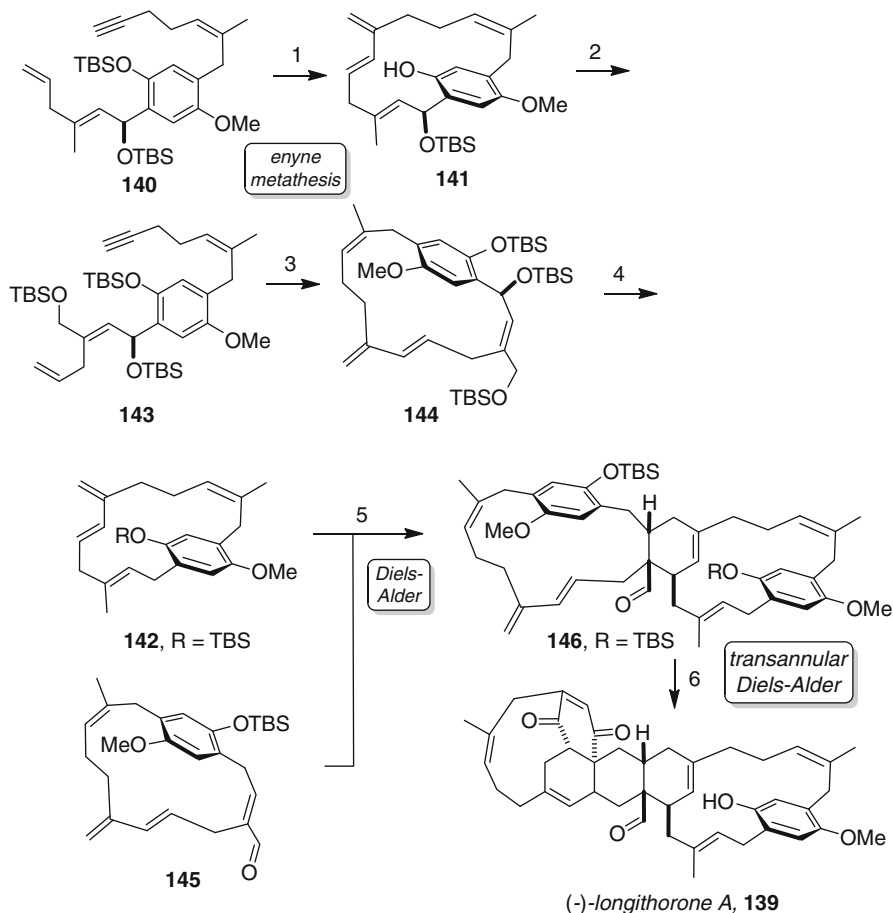
Upon exposure of **132** to Grubbs' second-generation catalyst, in benzene at reflux, ring-closure to yield **133** occurred in 85% yield. A sequence of 11 steps was used to convert **133** to hemibrevetoxin B, **125**.

11.3.2 Methyl Sarcophytoate and Longithorone A

Diels–Alder reactions have repeatedly proven their worth in the area of complex molecule synthesis, and in the cases of some natural products, the application of the Diels–Alder reaction after consideration of potential biosynthetic pathways can lead to the rapid assembly of molecules. Two recent examples are considered here. The synthesis of biscembranoid methyl sarcophytoate (**135**), which was developed by Nakata and coworkers [44], employs a Diels–Alder reaction between methyl sarcoate and another complex cembrane as the key step (Scheme 11.18). When **136** was heated with **137** in PhMe at 100°C for 1.5 days, the desired adduct **138** was obtained in 22% yield. Removal of the acetonide by treatment with aqueous AcOH completed the synthesis (50% for the final step). Notwithstanding the exact sequencing to reactions (and the use of protecting groups in the case of the laboratory synthesis), it seems likely that this process mimics the likely biogenesis.



Scheme 11.18 Synthesis of methyl sarcophytoate. Reagents and conditions: (1) PhMe, 100°C, 22%; (2) AcOH–H₂O, 50°C, 50%



Scheme 11.19 Shair's total synthesis of (-)-longithorone A. Reagents and conditions: (1) (a) 30–50 mol% Grubbs I, ethylene, 45°C, >20:1 atropisomer ratio; (b) TBAF, THF, 0°C, 31% (two steps); (2) (a) NaCNBH₃, TFA, CH₂Cl₂, 69% (b) TBSOTf, *i*Pr₂NEt, 0°C, 75%; (3) 0.5 eq Grubbs I, ethylene, 31%; (4) (a) TFA, Et₃SiH, CH₂Cl₂, (b) PPTS, EtOH 45°C, 46% (two steps), (c) Dess-Martin periodinane, CH₂Cl₂, 99%; (5) Me₂AlCl, CH₂Cl₂, -20°C, 70%; (6) (a) TBAF, THF, 0°C, (b) PhI(O), MeCN-H₂O, 0°C → 25°C, 90% (two steps)

The key elements of the Schmidt hypothesis for the biosynthesis of the longithorones were borne out in Shair's total synthesis of longithorone A (**139**) [45]. The synthesis highlights the strategic power of “biomimetic” Diels–Alder reactions and the utility of enyne metathesis reactions for the assembly of complex dienes. The key steps of the synthesis are shown in [Scheme 11.19](#).

Enyne **140** underwent enyne metathesis followed by TBS deprotection to give cyclophane **141** with excellent selectivity for the desired atropisomer. Deoxygenation and protection led to diene **142**. Alkyne **143** was treated with Grubbs' catalyst to give diene **144**. Ionic hydrogenation, followed by deprotection

and oxidation, afforded aldehyde **145**. An intermolecular Diels–Alder reaction between diene **142** and enal **145** gave cyclohexene **146**. Deprotection followed by transannular Diels–Alder cycloaddition completed Shair's total synthesis of (-)-longithorone A, **139**.

11.3.3 (+)-11,11'-Dideoxyverticillin A

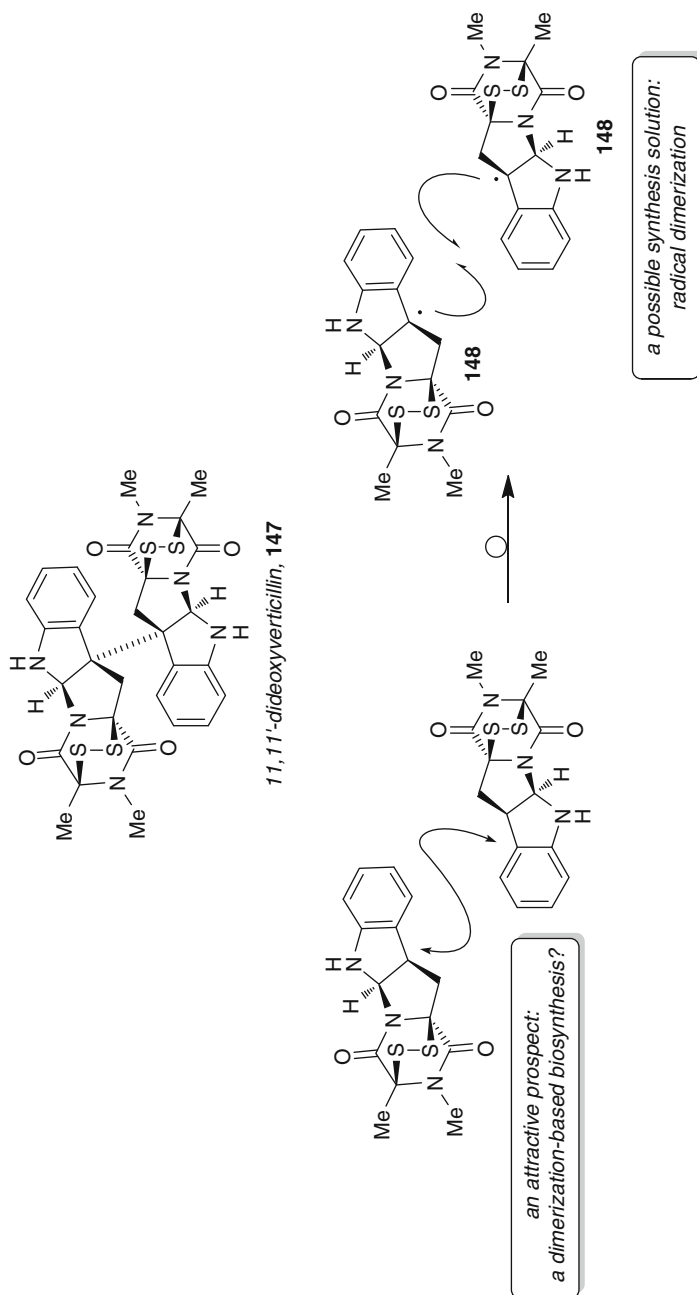
The dimeric epidthiodiketopiperazine alkaloids, as represented by (+)-11,11'-dideoxyverticillin A (**147**), are challenging synthetic targets that can be unraveled quickly by consideration of biosynthetic principles. Such an analysis led Movassaghi to a synthesis plan that was based on exploiting the dimerization of radicals **148** (Schemes 11.20) [46].

The dimerization precursor **149** was readily prepared in 58% yield by first reacting diketopiperazine **150** with bromine (MeCN, 0°C), then methylation with methyl iodide and potassium carbonate (Scheme 11.21). Reductive dimerization of **149** with tris(triphenylphosphine)cobalt (I) chloride in acetone gave the dimer **151** in 46% yield. After much experimentation, it was determined that the desired tetraol **152** could be prepared by oxidation with 4.8 equivalents of bis(pyridine) silver(I) permanganate in dichloromethane. This provided the tetraol **152** as a single diastereomer in an impressive 63% yield. However, it was found that **152** was highly acid and base sensitive, and while it could be transformed into the target molecule, it was a low-yielding process. It was discovered that these difficulties could be overcome by conversion to the diol **153**. This was prepared in 55% yield by selective protection using *t*-butyldimethylsilyl chloride and 5 mol% of Fu's PPY catalyst [47]. Reaction with potassium trithiocarbonate and trifluoroacetic acid, followed by addition of ethanolamine gave a tetrathiol **154**, which could be readily converted to the target molecule by reaction with potassium triiodide. This impressive sequence proceeded in 35% overall yield. Clearly, the success of this strategy suggests that the proposed biosynthetic sequence is plausible.

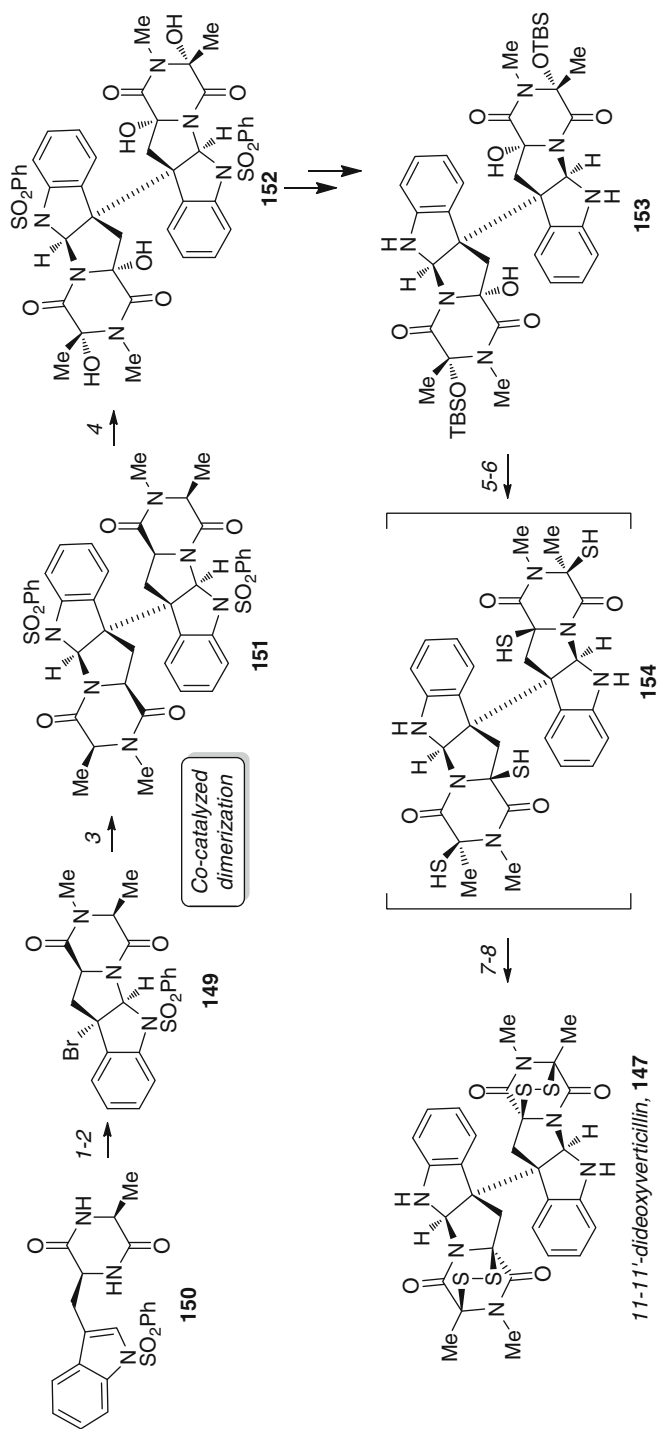
11.4 New Reactions and New Strategies: Azaspiracid-1, Amphidinolide A1, Bryostatin 16, Ningalin B, and Cyanthiwigins U and F

11.4.1 Azaspiracid-1

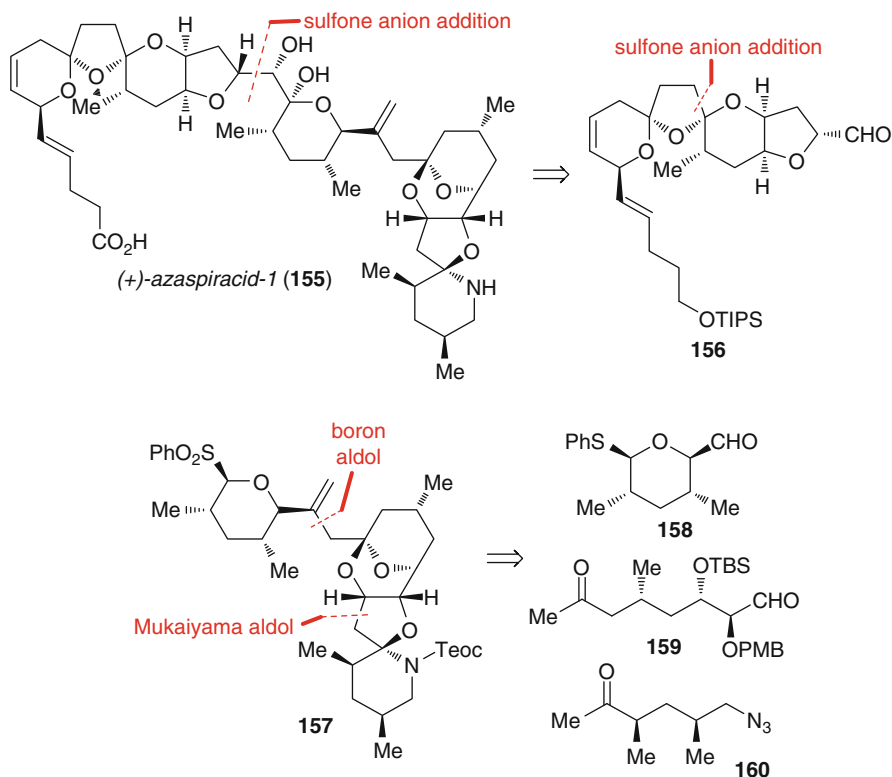
Complex natural products such as the azaspiracids have also served as excellent vehicles for the development and application of new synthetic methods. Subsequent to the Nicolaou synthesis, Evans reported a total synthesis of (+)-azaspiracid-1 (**155** the enantiomer of the natural product) [48]. An overview of the synthesis plan is shown in Scheme 11.22, and ultimately the key building blocks can be traced to compounds **158**, **159**, and **160**. This plan called for the preparation of these



Scheme 11.20 Strategic analysis of 11,11'-dideoxyverticillin through the eyes of biomimetic synthesis planning



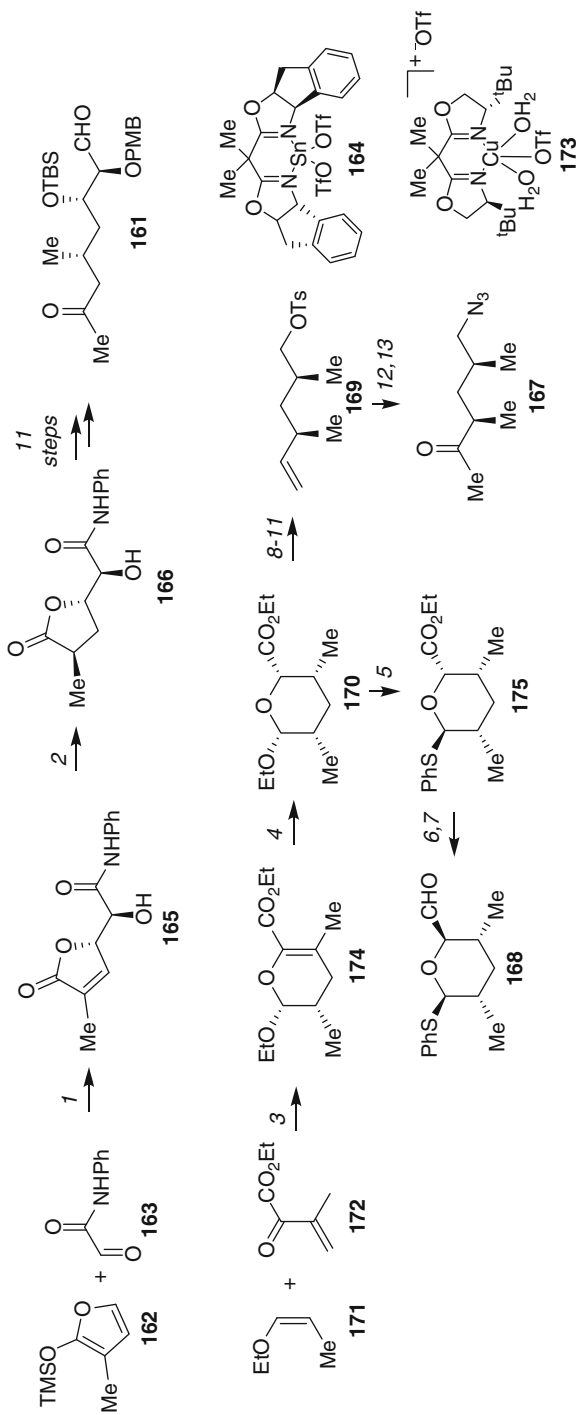
Scheme 11.21 Movassaghi's synthesis of (+)-11,11'-dideoxyverticillin. Reagents and conditions: (1) Br_2 , MeCN, 0°C , 76%; (2) MeI, K_2CO_3 , acetone, rt, 77%; (3) $\text{CoCl}(\text{PPh}_3)_3$, acetone, rt, 46%; (4) $\text{Py}_2\text{AgMnO}_4$, CH_2Cl_2 , rt, 63%; (5) TBSCl, 5 mol% PPY, NEt_3 , DMF, rt, 55%; (6) 5% $\text{Na}(\text{Hg})$, NaH_2PO_4 , MeOH, rt, 87%; (7) K_2CS_3 , TFA, CH_2Cl_2 , rt, 56%; (8) $\text{HOCH}_2\text{CH}_2\text{NH}_2$, acetone, rt, then KI_3 , pyridine, CH_2Cl_2 , rt, 62%



Scheme 11.22 An overview of Evans' analysis of (+)-azaspiracid-1 and the building blocks envisaged as being derived from asymmetric catalysis

compounds by Sn(II)- and Cu(II)-catalyzed asymmetric reactions that are part of a suite of powerful methods developed in the Evans group in the period 1990–2010, and azaspiracid-1 was expected to provide a worthy testing ground for the utility of these reactions in complex molecule synthesis.

Access to the ketone **161** was achieved in 13 linear steps, starting with an asymmetric Mukaiyama aldol reaction of (silyloxy)furan **162** with *N*-phenyl glyoxamide (**163**), in the presence of 10 mol% of chiral Sn²⁺ complex **164** (Scheme 11.23). This reaction afforded the lactone **165** in 67% yield and >99% *ee* after recrystallization, and was followed by reduction of the double bond using Crabtree's catalyst [49] to give **166**. Transformation of this material to the required aldehyde **161** was achieved in a further 12 steps. Ketone **167** and aldehyde **168** could be accessed from the same intermediate, chiral tetrahydropyran **165**. The initial step of the sequence used to prepare **170** was the hetero Diels–Alder cycloaddition between **171** and **172** in the presence of Cu²⁺ complex **173** to give **174** in 84% yield and with excellent control of enantio- and diastereoselectivity. Simple reduction over Pd/C with H₂ gave **170**, and access to the E-ring fragment



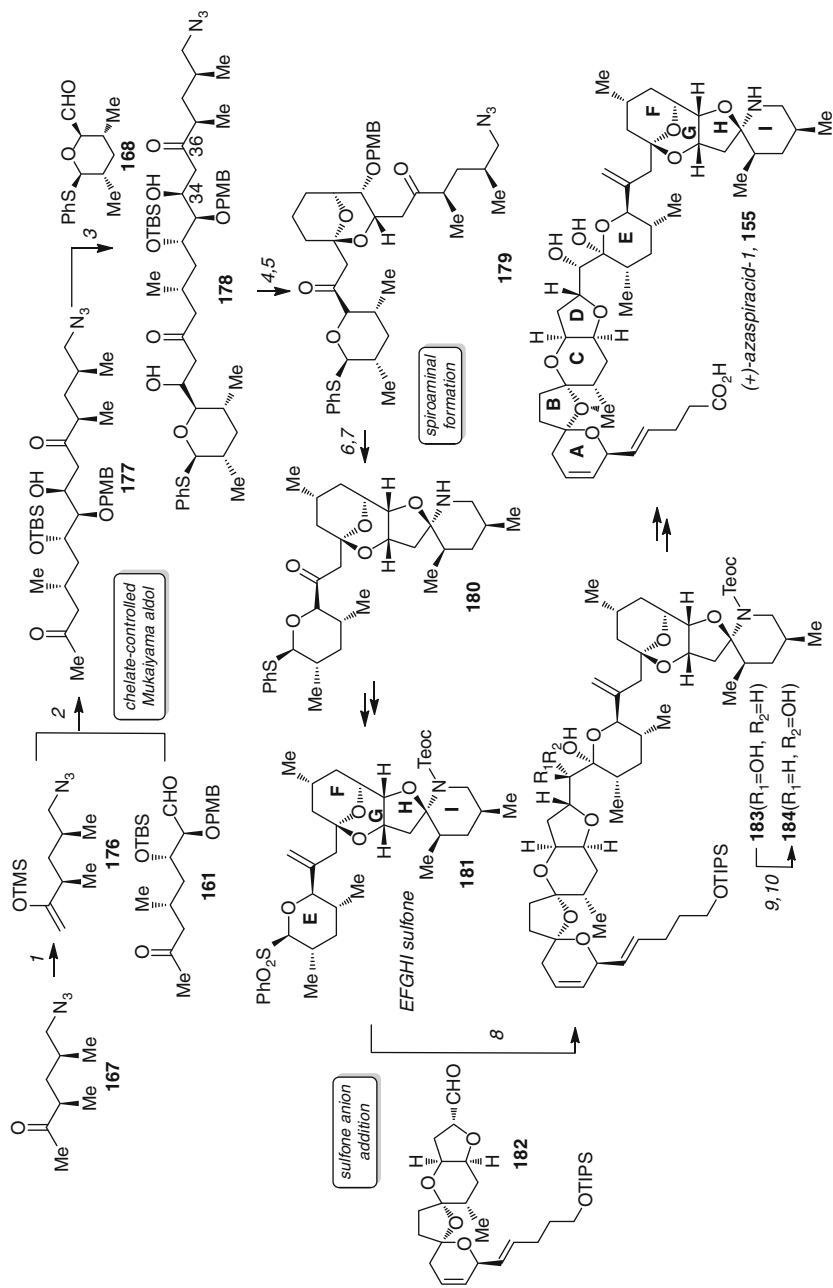
Scheme 11.23 Evans' synthesis of key building blocks for azaspiracid-1. Reagents and conditions: (1) 10 mol% **164**, CH_2Cl_2 , -78°C , 67% after recrystallization (>95% ee); (2) H_2 , 2 mol% $[(\text{cod})\text{Ir}(\text{PCy}_3)_3(\text{py})]\text{PF}_6$, CH_2Cl_2 , 98%; (3) 2 mol% **173**, 3 Å MS, Et_2O , -40°C , 84%; (4) H_2 , Pd/C, EtOAc, 95% of **170**; (5) PhSH, $\text{BF}_3 \cdot \text{OEt}_2$, CH_2Cl_2 , -20°C , 83%; (6) *t*-BuOK, THF, -50°C , 88% (d.r. 96:4); (7) DIBAL-H, toluene, -94°C \rightarrow -78°C , 93%; (8) Et_3SiH , $\text{BF}_3 \cdot \text{OEt}_2$, CH_2Cl_2 , 0°C , 91%; (9) LiAlH_4 , Et_2O , 0°C , 91%; (10) I_2 , PPh_3 , imid., $\text{CH}_3\text{CN}/\text{benzene}$, rt \rightarrow 60°C , 94%; (11) *t*-BuLi, THF, -78°C , then TsCl, -78°C \rightarrow 0°C , 95%; (12) O_2 , PdCl₂, CuCl, H₂O, DMF, 89%; (13) NaNa₃, DMSO, 50°C , 98%

167 from **170** was achieved by firstly forming the lactol thioether **175**, then epimerization of the ester substituent with potassium *t*-butoxide. This epimerization provides a tetrahydropyran with all four substituents equatorial. Reduction of the ester group with DIBAL-H afforded the aldehyde **168**. To access the third fragment required for the synthesis of EFGHI sulfone, the chiral tetrahydropyran **170** was transformed to the tosylate **169** via a four-step sequence as detailed in [Scheme 11.26](#). The tosylate was then converted to the desired HI-ring fragment **167** by Wacker oxidation and azide displacement.

With access to all the required fragments, attention was focused on fragment assembly by a series of aldol couplings ([Scheme 11.24](#)). First, ketone **167** and aldehyde **161** were coupled together using a chelate-controlled Mukaiyama aldol addition of enolsilane **176** with the aldehyde **161** in the presence of freshly prepared $\text{MgBr}_2 \cdot \text{OEt}_2$ to give the desired compound **177** as a single diastereomer in 93% yield. The second aldol coupling employed a boron-mediated aldol reaction between **172** and aldehyde **168** to give aldol adduct **178** as an inconsequential 60:40 mixture of diastereomers. Removal of the TBS ethers by aqueous HF in acetonitrile also resulted in cyclization to afford the FG bicyclic ketal as mixture of diastereomers. This mixture was oxidized with Dess–Martin periodinane to afford ketone **179**. At this juncture removal of the PMB ether with DDQ and reduction of the azide led to formation of the HI spiroaminal system **180** in 77% yield for the two steps. This ketone **180** was transformed to the desired EFGHI sulfone **181** and was methylenated using Tebbe's reagent in the presence of pyridine. Oxidation of the sulfide was carried out in the presence of pyridine to ensure that the sulfur group was not lost. With the assembly of the EFGHI sulfone **181**, the synthesis of azaspiracid-1 was almost complete. Coupling of the two major fragments was achieved by deprotonation of the sulfone **181** with *n*-BuLi, then addition of the aldehyde **182**. Quenching at -78°C with pH5 buffer afforded a near 1:1 mixture of lactol diastereomers, **183** and **184**, in 50% overall yield. Fortunately, the diastereomers are separable by chromatography and the undesired alcohol **183** could be transformed to the desired material **184** by oxidation under Swern conditions and diastereoselective reduction. Removal of the silyl protecting groups and a two-step oxidation of the C1 terminus provided (+)-azaspiracid-1 (**155**). The convergent approach allows the synthesis to proceed in just 26 linear steps, providing a nice example of complex molecule synthesis underpinned by powerful new asymmetric methods for the preparation of building blocks.

11.4.2 Amphidinolide A1

The amphidinolides have proven themselves a fertile environment for the development of new methods and strategies and, at the same time, have provided many instances of where synthesis has been able to assist in the structure assignment. This has always been a challenging task for this class in large part due to the minute amounts of material that are often initially isolated. The story of (+)-amphidinolide A1 [50] is noteworthy in this context as an example of the



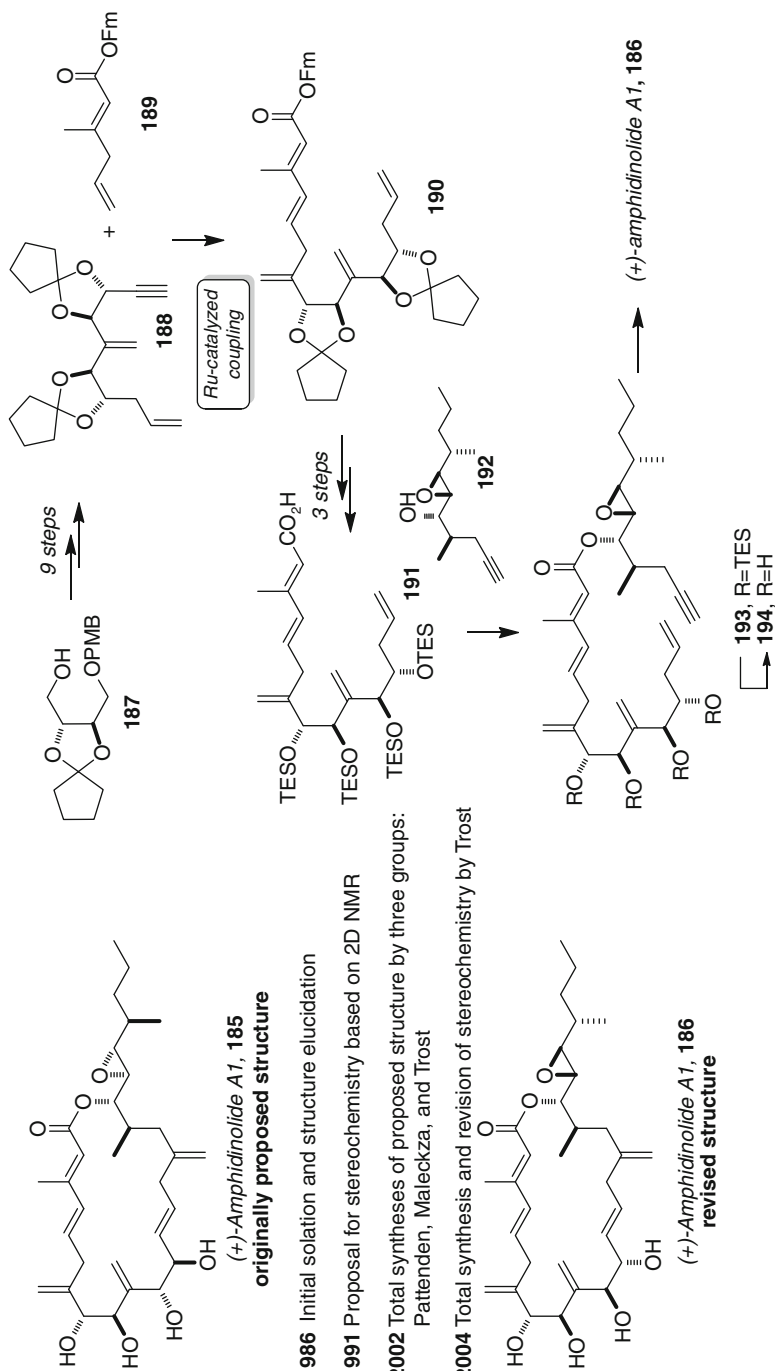
Scheme 11.24 (continued)

value of synthesis to the structure elucidation of complex marine natural products (Scheme 11.25). Kobayashi's initially proposed structure **185** was synthesized in 2002 in independent efforts by the groups of Trost [51], Pattenden [52], and Maleczka [53]. None of these efforts however produced material that matched the reported data which suggested that there were questions regarding the stereochemistry of the molecule remaining to be answered. This puzzle was solved in 2004 by Trost and Harrington when they described the structure elucidation of (+)-amphidinolide A1 (**186**) by a combination of total synthesis and NMR analysis [54] (Scheme 11.25).

The synthesis highlights Trost's new methodology for the construction of 1,4-dienes by the Ru-catalyzed coupling of alkenes and alkynes (Scheme 11.25) [55]. The first subunit coupling was achieved by reaction of **188** with **189** in the presence of Cp*Ru(MeCN)₃PF₆ as catalyst was employed. This catalyst provided the branched product **190** in 23% yield (39% yield based on recovered starting material). A straightforward sequence of three steps provided acid **191** which was coupled to the potentially sensitive epoxy alcohol **192** under Kita's conditions [56] to give ester **193** in 51% yield. After removal of the triethylsilyl ethers with TBAF–AcOH, [Cp*Ru(MeCN)₃]PF₆-catalyzed macrocyclization of **194** provided amphidinolide A1, **186**. Although the yield may seem modest (33% or 38% based on recovered starting material), this is an impressive example of the remarkable selectivity of the Ru-catalyzed alkene–alkyne addition. The spectral data for synthetic material matched very well to the natural product with only two protons deviating from that reported by greater than 0.01 ppm (the two deviations were by 0.03 ppm and by 0.02 ppm), the ¹³C NMR spectrum deviated by 0.1 ppm or less in CDCl₃, *J* values in three solvents were also in agreement, and the optical rotation was also consistent with reported data (synthetic [α]_D²⁴ +56° (*c* 0.05, CHCl₃) cf. reported [α]_D²⁴ +46° (*c* 1.0, CHCl₃)). Even with these excellent comparisons, in the absence of authentic material for comparison, Trost and Harrington conclude their paper with guarded comments:

In conclusion, we have employed a combination of synthesis and NMR spectroscopy as tools to determine the correct structure of amphidinolide A1. Although the lack of a sample of the natural product prevents a definitive comparison, the excellent correlation [of our synthetic compound] strongly suggests it is (+)-amphidinolide A1.

Scheme 11.24 Evans' synthesis of the EFGHI sulfone fragment of (+)-azaspiracid-1 and completion of the synthesis. Reagents and conditions: (1) LiHMDS, TMSCl, Et₃N, THF, –78°C, 89%; (2) MgBr₂·OEt₂, CH₂Cl₂, 0°C, 93%; (3) Cy₂BCl, *i*Pr₂NEt, CH₂Cl₂, –78°C, then **168**, –78°C → 0°C; (4) HF, H₂O, CH₃CN, 0°C, 92% (two steps); (5) Dess–Martin periodinane, pyr., CH₂Cl₂, 85%; (6) DDQ, pH 7 buffer, CH₂Cl₂, 0°C; (7) H₂, Pd/C, THF, 77% (two steps); (8) **181**, *n*-BuLi, –78°C, then **182**, NaOAc/AcOH buffer, –78°C → rt, 27% of **183** and 23% of **184**; (9) (COCl)₂, DMSO, Et₃N, CH₂Cl₂, –78°C → –20°C, 60%; (10) LiBH₄, CH₂Cl₂, –40°C, 56%

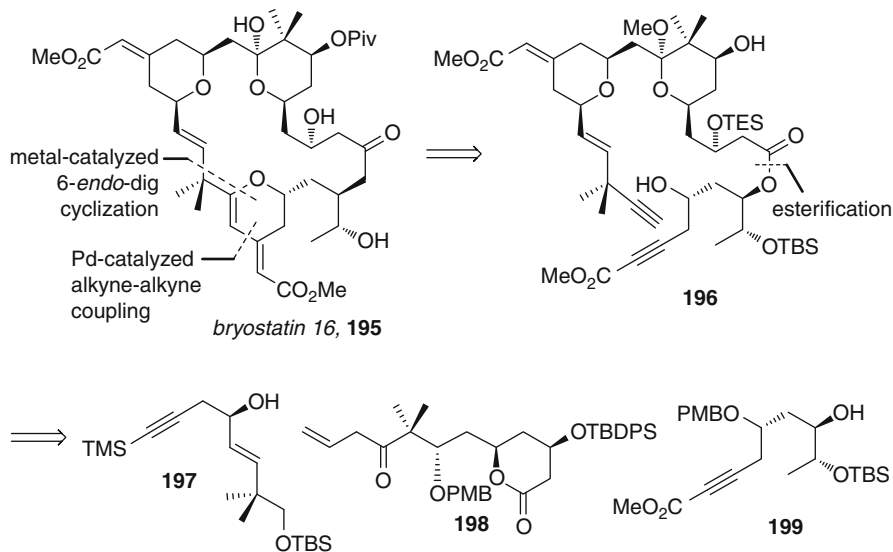


Scheme 11.25 Trost's synthesis of amphidinolide A1. Reagents and conditions: (1) **189**, [Cp**Ru*(MeCN)₃]PF₆, 23%; (2) piperidine, 88%; (3) AcOH/H₂O (3:1); (4) TESOTf, *i*-Pr₂NEt, 83% (two steps); (5) (1) [RuCl₂(*p*-cymene)]₂, ethoxyacetylene; (2) **192**, CSA, 51%; (6) TBAF, AcOH, 79%; (7) [Cp**Ru*(MeCN)₃]PF₆, 33%

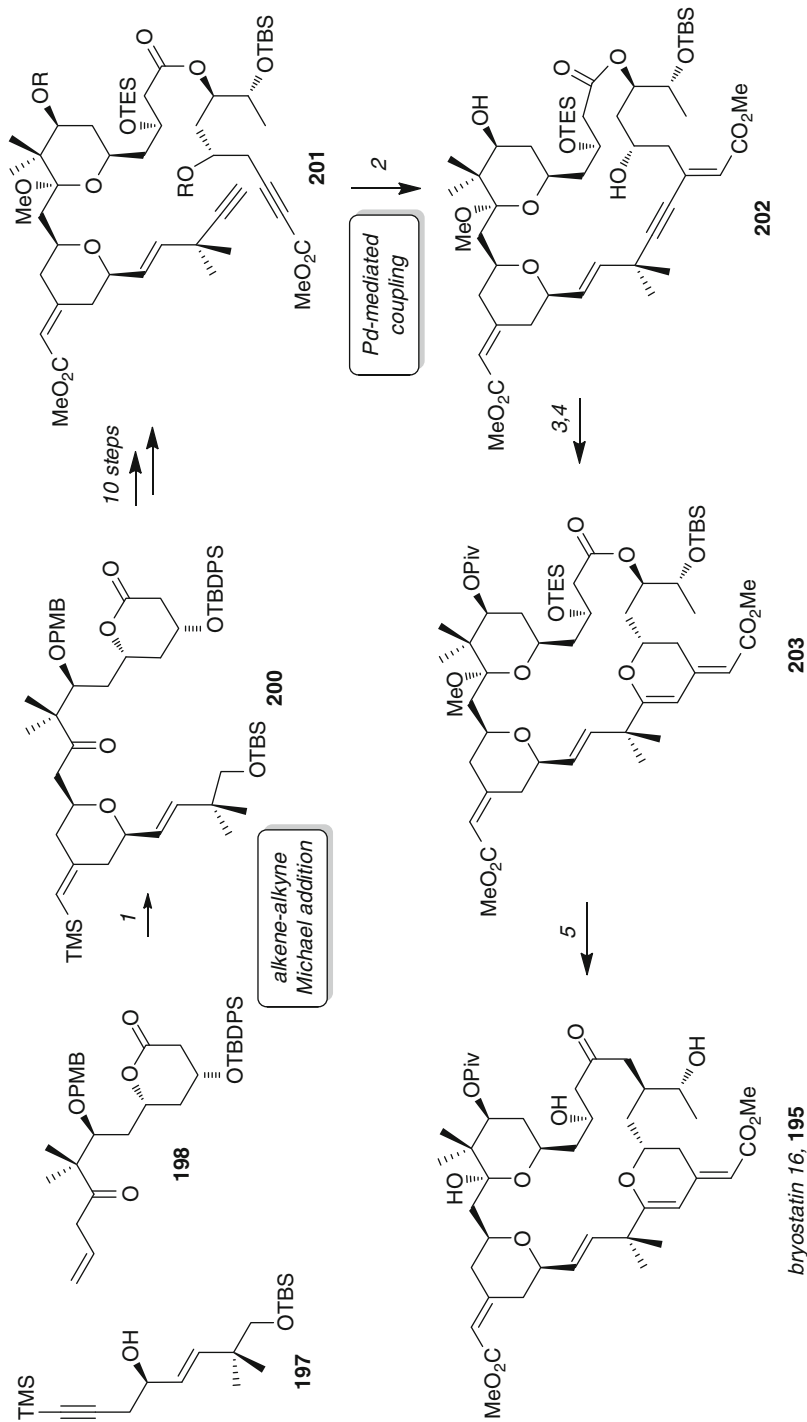
11.4.3 Bryostatin 16

The bryostatin family of macrolides have attracted significant attention over the years since the initial description of bryostatin 1 by Pettit and Clardy [57]. Synthetic highlights include five total syntheses [58], the development of a detailed pharmacophore model [59], and the preparation of much simplified functional analogs [60]. Here we highlight the total synthesis of bryostatin 16 (**195**) by Trost and Dong [39], which employs a number of new(er) transition metal-catalyzed reactions and underscores the value of new reactions in the arena of target synthesis: the longest linear sequence is only 26 steps. As detailed in Scheme 11.26, it was envisaged that the macrocycle could be formed from **196** using a palladium-catalyzed alkyne-alkyne coupling, followed by a metal-catalyzed 6-*endo-dig* cyclization. The key substrate **196** would be assembled from the fragments **197**, **198**, and **199**.

A chemoselective ruthenium-catalyzed tandem alkene-alkyne coupling/Michael addition (13 mol% CpRu(MeCN)₃PF₆, DCM) was used to form the *cis*-tetrahydropyran **200** in 34% yield (80% based on recovered starting material) (Scheme 11.27). Although modest in its conversion, the strategic power of this reaction for subunit assembly is impressive. The macrocycle **202** was generated in 56% yield by reaction of **201** with 12 mol% of palladium acetate and 15 mol% tris (2,6-dimethoxyphenyl)phosphine in PhMe at room temperature. It was found that the reaction had to be run at low concentration (0.002 M) and that the choice of solvent and the ligand/palladium ratio were critical to the success of the reaction. Treatment of the resulting alcohol **202** with a cationic gold catalyst (Au(PPh₃)SbF₆, NaHCO₃) initiated a 6-*endo-dig* cyclization and afforded the desired ring system in



Scheme 11.26 An overview of the Trost synthesis plan for bryostatin 16



Scheme 11.27 Trost and Dong's synthesis of bryostatins 16. Reagents and conditions: (1) CpRu(MeCN)₃PF₆, CH₂Cl₂, 34%; (2) Pd(OAc)₂ (12 mol%), TDMPP (15 mol%), PhMe, 56%; (3) AuCl(PPh₃), AgSbF₆, NaHCO₃, DCM/MeCN, 0 °C to rt, 73%; (4) Piv-O, DMAP, 73%; (5) TBAF, 52%

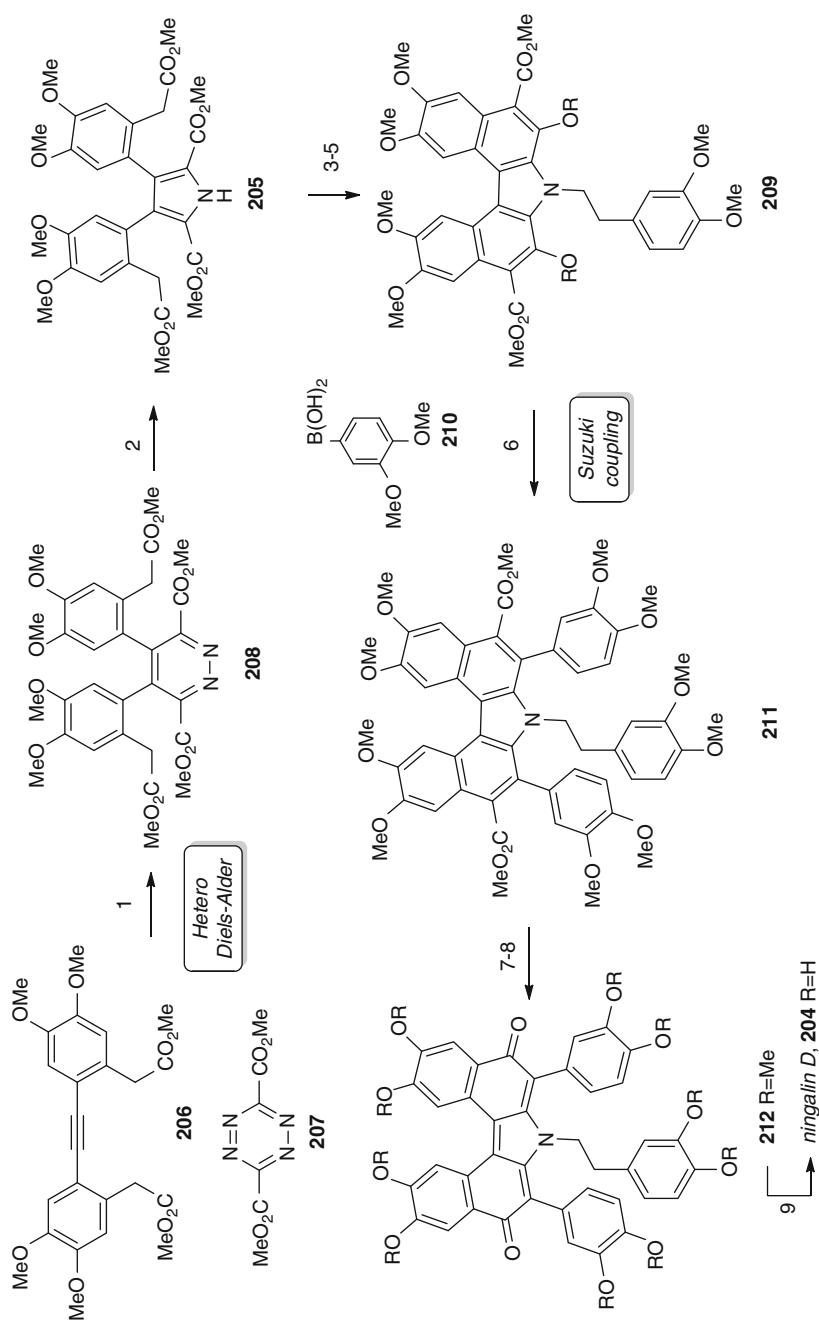
73% yield. After pivalation of the secondary alcohol to give macrocycle **203**, efforts focused on the global deprotection to afford bryostatin 16. After some experimentation, it was found that treatment of **203** with five equivalents of tetrabutylammonium fluoride gave bryostatin 16, **195**, in 52% yield.

11.4.4 Ningalin D

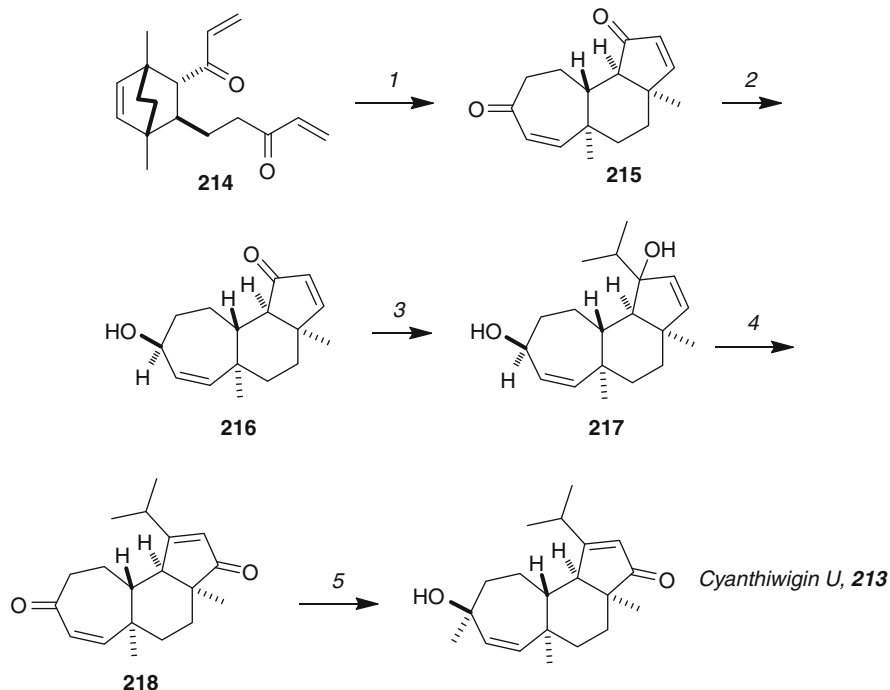
Complex alkaloids such as ningalin D (**204**) present substantial challenges for synthesis, and although cross-coupling chemistry is a dominant strategy for polyaromatic compounds, Boger has showcased the utility of alternative methods to produce an essentially ideal synthesis. In this case he completed a nine-step synthesis of ningalin D (**204**), which proceeds in 19% overall yield [61] (Scheme 11.28). The tetrasubstituted pyrrole **205** was rapidly assembled by firstly utilizing an inverse electron demand heterocyclic azadiene Diels–Alder reaction between symmetrical alkyne **206** and readily available tetrazine **207** to give symmetrical 1,2-diazine **208** in 87% yield. Reaction with 30 equivalents of zinc in trifluoroacetic acid at room temperature leads to cleavage of the diazine ring, followed by in situ cyclization to generate the pyrrole **205** in 64% yield. After alkylation of **205**, the aryl C and D rings were formed by double Dieckmann condensation by reaction with NaH in DMF at room temperature. The resulting diphenol **209** was triflated, and the F and G aryl rings were attached via a double Suzuki coupling with boronic acid **210**. Efforts to convert **211** into ningalin D were hampered by the steric congestion of the esters. However, hydrolysis of **211** with anhydrous hydroxide, followed by a modified Curtius rearrangement, afforded permethylated ningalin D **212** in a remarkable 70% yield. Clearly, the expected diamine was oxidized in situ and the resulting imines were hydrolyzed upon workup to generate the desired biphenylene quinone methide system. The ten methyl ethers were removed by reaction of **212** with 15 equivalents of BBr₃ to provide ningalin D, **204**, in 96% yield.

11.4.5 Cyanthiwigins U and F

The cyanthiwigin family of diterpenoids have stimulated the development of new methods and strategies (for a review see, [62]). For example, the Phillips–Pfeiffer synthesis of cyanthiwigin U (**213**) employed an efficient tandem metathesis reaction to convert bridged bicycle **214** into fused tricycle **215** in >43% yield (Scheme 11.29) [63]. Reduction of the more electrophilic carbonyl group with LAH gave **216**, and addition of isopropyllithium to the other carbonyl group gave bis-allylic alcohol **217**. Pyridinium chlorochromate oxidation resulted in formation of the cycloheptenone and, at the same time, gave Dauben oxidative transposition of the cyclopentenol to provide **218**. Simple addition of methyllithium completed the synthesis.



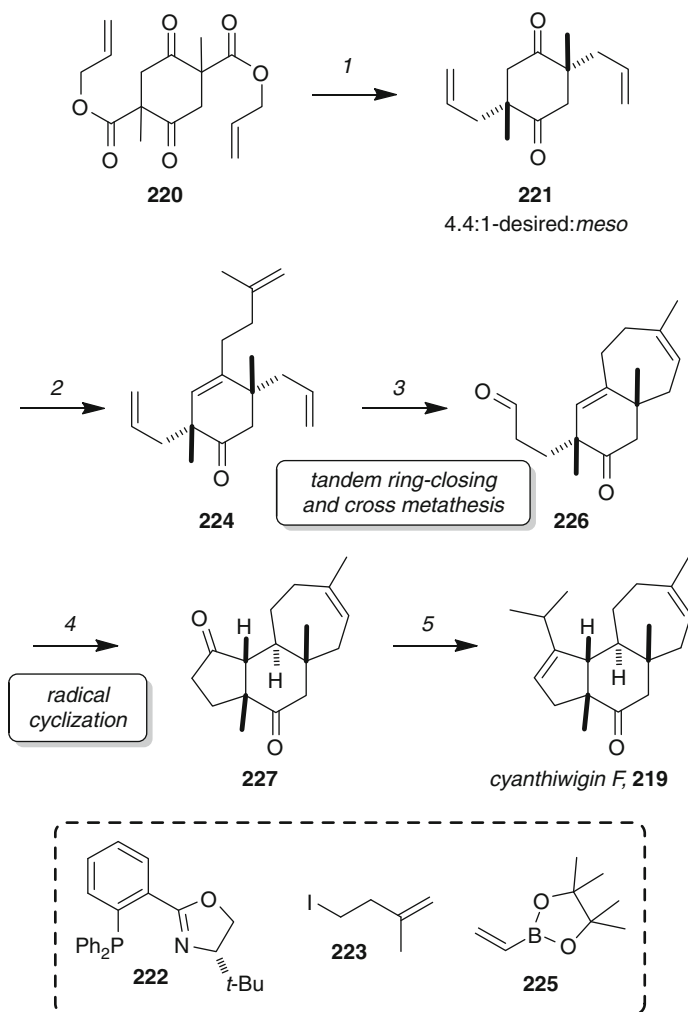
Scheme 11.28 (continued)



Scheme 11.29 Phillips and Pfeiffer's synthesis of cyanthiwigin U. Reagents and conditions: (1) 20 mol% Grubbs II, ethylene, PhMe, >43%; (2) LAH, THF, 92%; (3) *i*-PrLi, CeCl₃, THF; (4) PCC, CH₂Cl₂, 90% (two steps); (5) MeLi, THF, quantitative (*dr* = 9:1)

In a similar vein, Stoltz and Enquist completed a total synthesis of cyanthiwigin F (**219**) that was underpinned by reaction development (Scheme 11.30) [64]. Earlier studies into the asymmetric Tsuji decarboxylative allylation reaction [65] had provided a method for the conversion of **220** into **221** by treatment with catalytic Pd(0) in the presence of phosphino-oxazoline **222**. Subsequent enol-triflation and cross-coupling with the organozinc derived from iodide **223** gave **224** and set the stage for a ring-closing metathesis with Grubbs–Hoveyda catalyst (second generation) and simultaneous cross metathesis of the other olefin with vinylboronate **225**. An oxidative workup gave aldehyde **226** in 51% yield. Radical cyclization proceeded smoothly to produce tricyclic compound **227**, which could be advanced to cyanthiwigin F (**219**) by conversion of the cyclopentanone ring to the enol triflate and cross coupling with *t*-propylmagnesium chloride.

Scheme 11.28 The Boger synthesis of ningalin B, **204**. Reagents and conditions: (1) toluene, 110°C, 87%; (2) Zn, TFA, rt, 64%; (3) 3,4-dimethoxyphenyl ethyl iodide, CsCO₃, DMF, 60°C, 92%; (4) NaH, DMF, 25°C, 81%; (5) Tf₂O, pyridine-CH₂Cl₂, 0°C → 5°C, 92%; (6) (PPh₃)₄Pd, LiCl, 1 M aq. K₂CO₃-DME, 80°C, 88%; (7) *t*-BuOK, H₂O, DMSO, 80°C, 84%; (8) DPPA, *i*Pr₂NEt, CH₂Cl₂, 25°C; then H₂O, THF, air, reflux, 70%; (9) BBr₃, CH₂Cl₂, -78°C → rt, 96%



Scheme 11.30 Stoltz's total synthesis of cyanthiwigin F. Reagents and conditions: (1) **222**, Pd(dmdba)₂, Et₂O, 78%; (2) (a) KHMDS, PhN(Tf)₂, THF; (b) **223**, Zn, TMSCl, 1,2-dibromoethane, THF; Pd(PPh₃)₄, 57% (two steps); (3) Grubbs-Hoveyda II, **225**, PhH; NaBO₃, THF/H₂O 51%; (4) *t*-BuSH, AIBN, PhH, 57%; (5) (a) KHMDS, PhN(Tf)₂, THF; (b) *i*-PrMgCl, CuCN, THF, Pd(dppf)Cl₂, 38% (two steps)

11.5 At the Edges of the Known Universe of Molecular Complexity

The marine environment produces some remarkably complex structures, and these compounds have in turn stimulated tremendous efforts in total synthesis. In this section we briefly highlight the synthesis of ladder polyethers, but in

advance of doing so we present four molecules that represent substantial complexity in Fig. 11.5. All of these molecules are accessible by synthesis: ciguatoxin CTX3C (**227**) was made by Hirama and Inoue in 2001 [66]; palytoxin (**228**) by Kishi and Suh in 1994 [67]; norhalichondrin B (**229**) by Kishi (1992) [68] and Phillips (2009) [69]; and phorbaxazole A (**230**) by Forsyth (1999) [70], Smith (2001) [71], Williams (2003) [72], Pattenden (2003) [73], and White (2006) [74].

The Nicolaou group was one of the first to engage in synthetic studies directed toward the ladder polyethers, and among the many total syntheses from the group in this area there has been a significant amount of reaction discovery and development, which we briefly highlight here (Scheme 11.31). For example, the formation of cyclic ethers by thiohemiacetal formation (**231** → **233**) and reductive removal of the sulfur to give structures of type **234** has seen widespread use by many groups. An especially creative solution to the formation of bis-oxepane rings is the reductive cyclization of dithionolactones (**235** → **236**) and their subsequent conversion to **238** by desulfurization and hydrogenation [75].

Elements of the methods described above were employed in Nicolaou's first total synthesis of brevetoxin B (**113**), the closing steps of which are shown in Scheme 11.32 [76]. Subunit coupling by Wittig reaction between phosphonium salt **239** and aldehyde **240** gave **241** after removal of the TMS ether. Reductive etherification by the two-step approach outlined above gave **242** in an impressive 85% yield, and the synthesis was completed in five further steps.

More recently, Sasaki and coworkers have completed a synthesis [77] of gymnocin A (**243**), a polyether toxin from the red tide dinoflagellate *Karenia mikimotoi* [78]. The total synthesis employed some daring applications of their earlier-developed method for polyether synthesis based on a β -alkyl Suzuki–Miyaura coupling followed by hydroboration and reductive etherification as the key strategy for subunit couplings. The key steps involved in the assembly of the complete A → N ring system are summarized in Scheme 11.33. Hydroboration of complex enol ether **244** with 9-BBN to give borane **245** is followed by cross-coupling with nonacyclic enol triflate **246** in the presence of Pd(PPh₃)₄ to give **247**. Given the very high complexity of the substrates, the yield for this reaction is a remarkable 81%, and should serve to underscore the power of contemporary cross-coupling reactions in complex settings. Conversion of **247** to the precursor for acetal formation was achieved by a four-step sequence: (a) hydroboration-oxidation, (b) protection as the triethylsilyl ether, (c) removal of the *p*-methoxybenzyl ether, and (d) oxidation to produce ketone **248** (56% overall yield for four steps). Treatment of **249** with ethanethiol in the presence of Zn (OTf)₂ provided the desired thioacetal **250** in 40% yield along with 38% of thioacetal **251** in which one of the tert-butyl dimethylsilyl ethers had been removed. This compound was readily resilylated to produce **250**. Reductive desulfurization under radical conditions with AIBN and triphenylstannane converted the thioacetal into the desired ether **252** in an impressive 98% yield. Compound **252**, which contains the complete A → N ring system, was converted to gymnocin A, **243**, by an eight-step sequence.

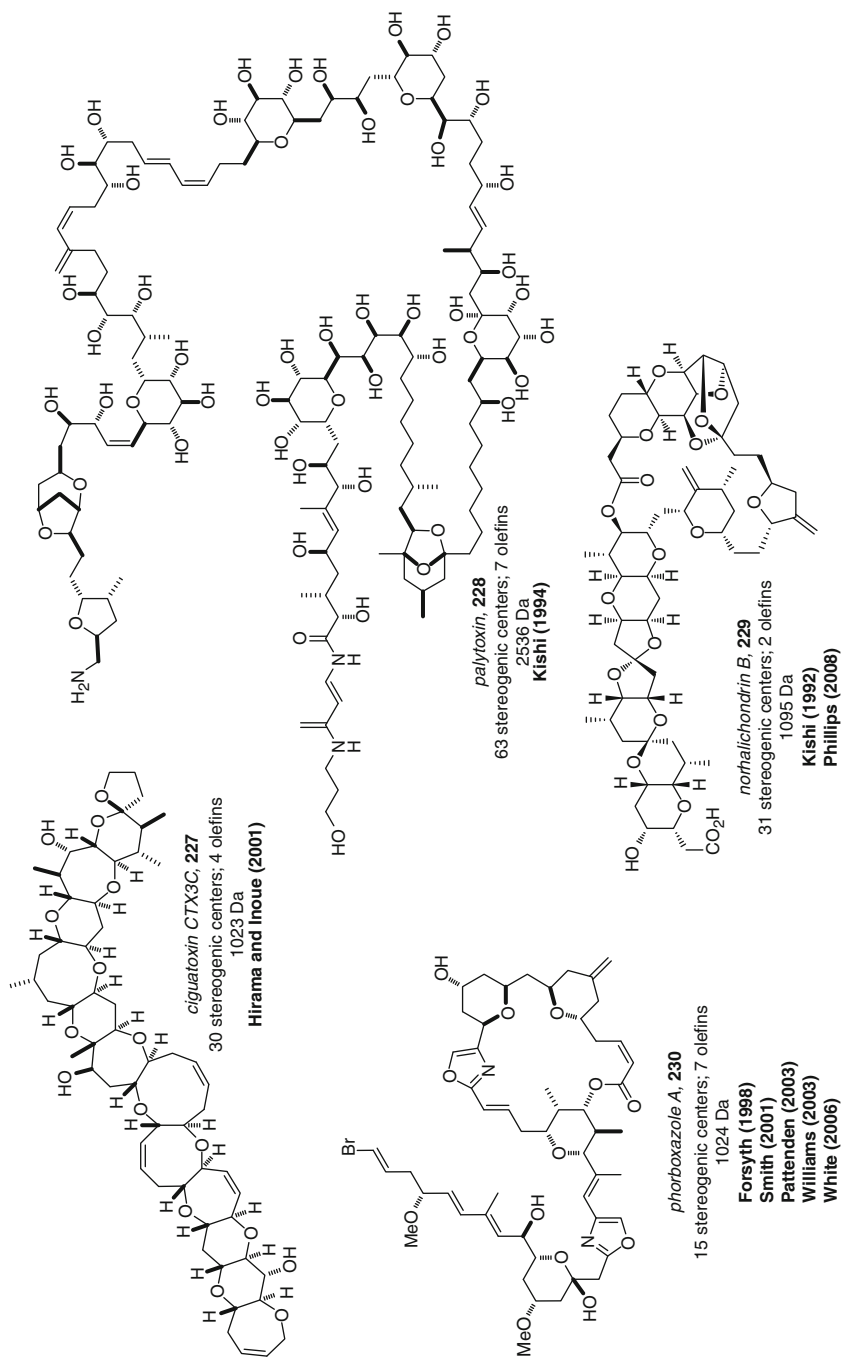
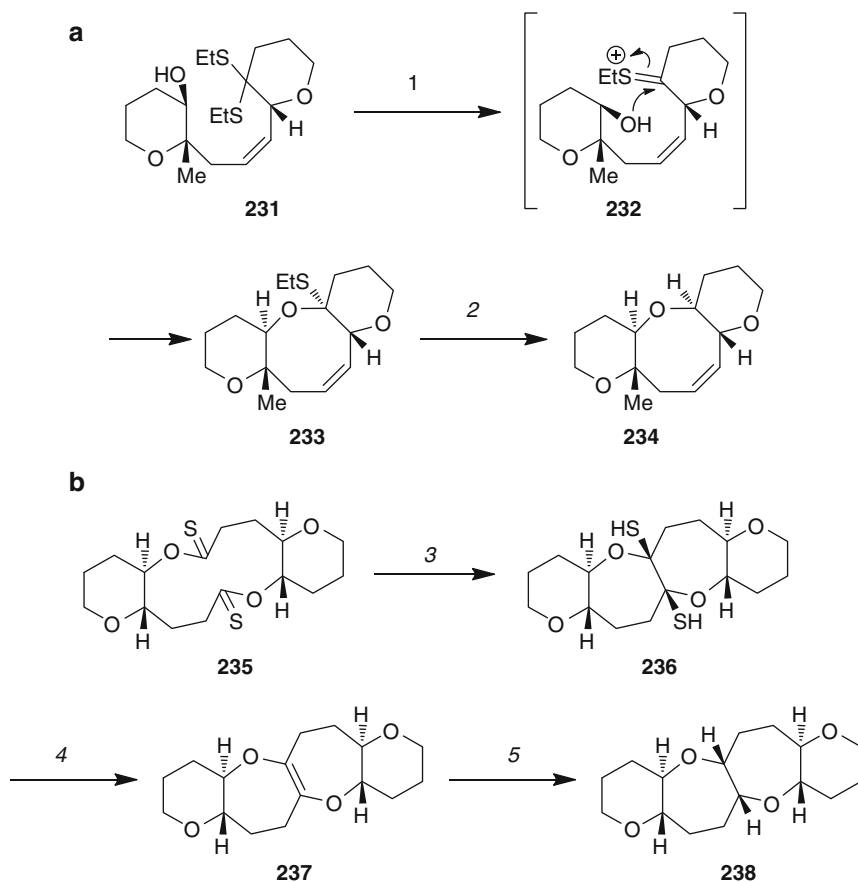


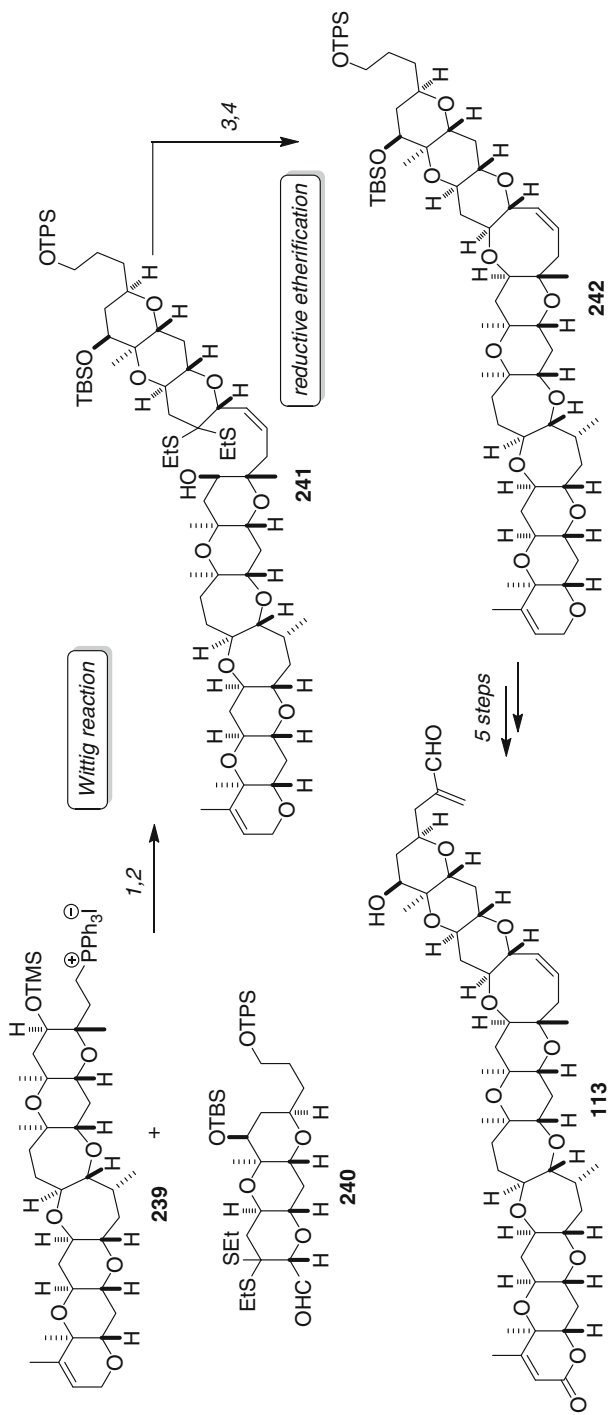
Fig. 11.5 Examples of the level of molecular complexity that can be attained by modern organic synthesis



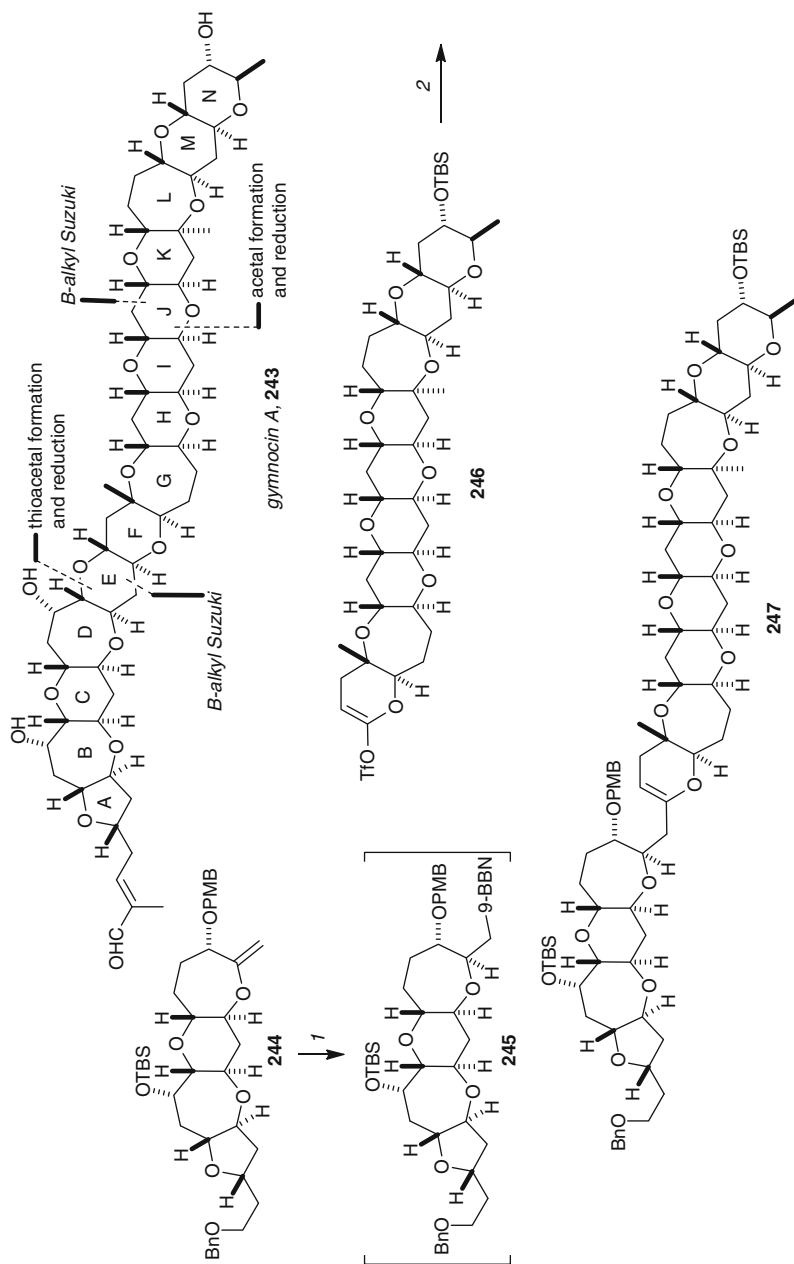
Scheme 11.31 Early technologies from Nicolaou for complex ladder polyether synthesis. (a) Reductive etherifications, and (b) formation of bis-oxepanes by reductive coupling of dithionolactones. Reagents and conditions: (1) AgNO_3 , NCS, SiO_2 , 2,6-lutidine, CH_3CN , 3 Å MS, 92%; (2) Ph_3SnH , AIBN, PhCH_3 , 110°C, 95%; (3) sodium naphthalenide, THF, -78°C; MeI, 80%; (4) $n\text{Bu}_3\text{SnH}$, AIBN, PhCH_3 , heat, 99%; (5) H_2 , $\text{Pd}(\text{OH})_2$, EtOAc, 70%

11.6 Gram-Scale Synthesis: Moving Toward Realistic Supply of Compounds for Preclinical Evaluation

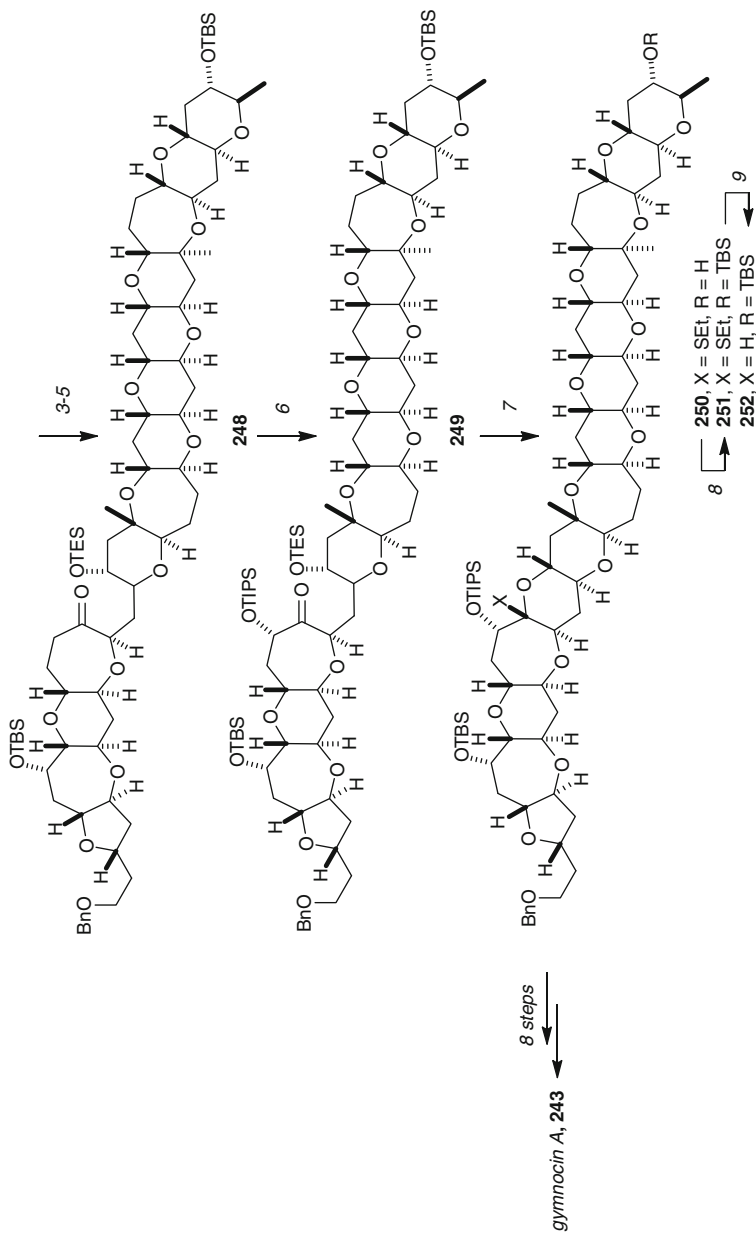
One of the major challenges of marine natural products is the limited supplies available from the natural source, which often stymies further investigation into the biological properties. Many marine natural products cannot be evaluated as clinical agents due to these limited supplies, and the development of a practical synthetic route is absolutely critical to the further development of such compounds.



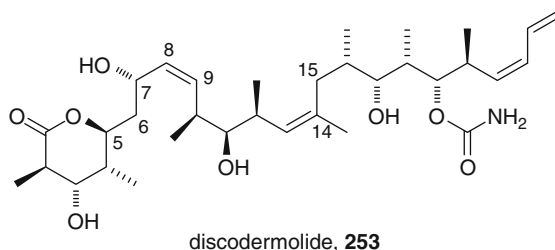
Scheme 11.32 Subunit couplings and completion of Nicolau's pioneering synthesis of brevetoxin B. Reagents and conditions: (1) *n*-BuLi, HMPA; (2) PPTS, MeOH, 25°C, 75% (two steps); (3) AgClO₄, NaHCO₃, SiO₂, 4 Å MS, MeNO₂, 25°C; (4) Ph₃SnH, AIBN, 110°C, 85% (two steps)



Scheme 11.33 (continued)



Scheme 11.33 Closing steps of Sasaki's total synthesis of gymnocin A. Reagents and conditions: (1) 9-BBN, THF, rt; (2) **245**+**246**, 3 M Cs₂CO₃, Pd(PPh₃)₄, DMF, rt, 81%; (3) BH₃·SMe₂, THF, 0°C → rt then NaOH, H₂O₂, 75%; (4) TESOTf, 2,6-lutidine, CH₂Cl₂, rt; (b) DDQ, CH₂Cl₂, pH 7 phosphate buffer, 0°C, 79% (two steps); (5) TPAP, NMO, 4 Å MS, CH₂Cl₂, rt, 95%; (6) (a) LiHMDS, TMSCl, Et₃N, THF, -78°C; (b) OsO₄, NMO, THF-H₂O, rt; (c) TIPSOTf, 2,6-lutidine, CH₂Cl₂, rt, 85% (three steps); (7) EtSH, Zn(OTf)₂, MeNO₂, 0°C → rt, 40% **252**, 38% **251**; (8) TBSOTf, 2,6-lutidine, CH₂Cl₂, rt, 71%; (9) Ph₃SnH, AIBN, PhMe, 110°C, 98%

**Schreiber (1993)**

4.3% overall yield, 24 steps LLS

Key fragments

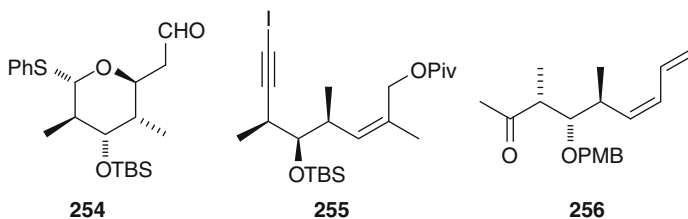
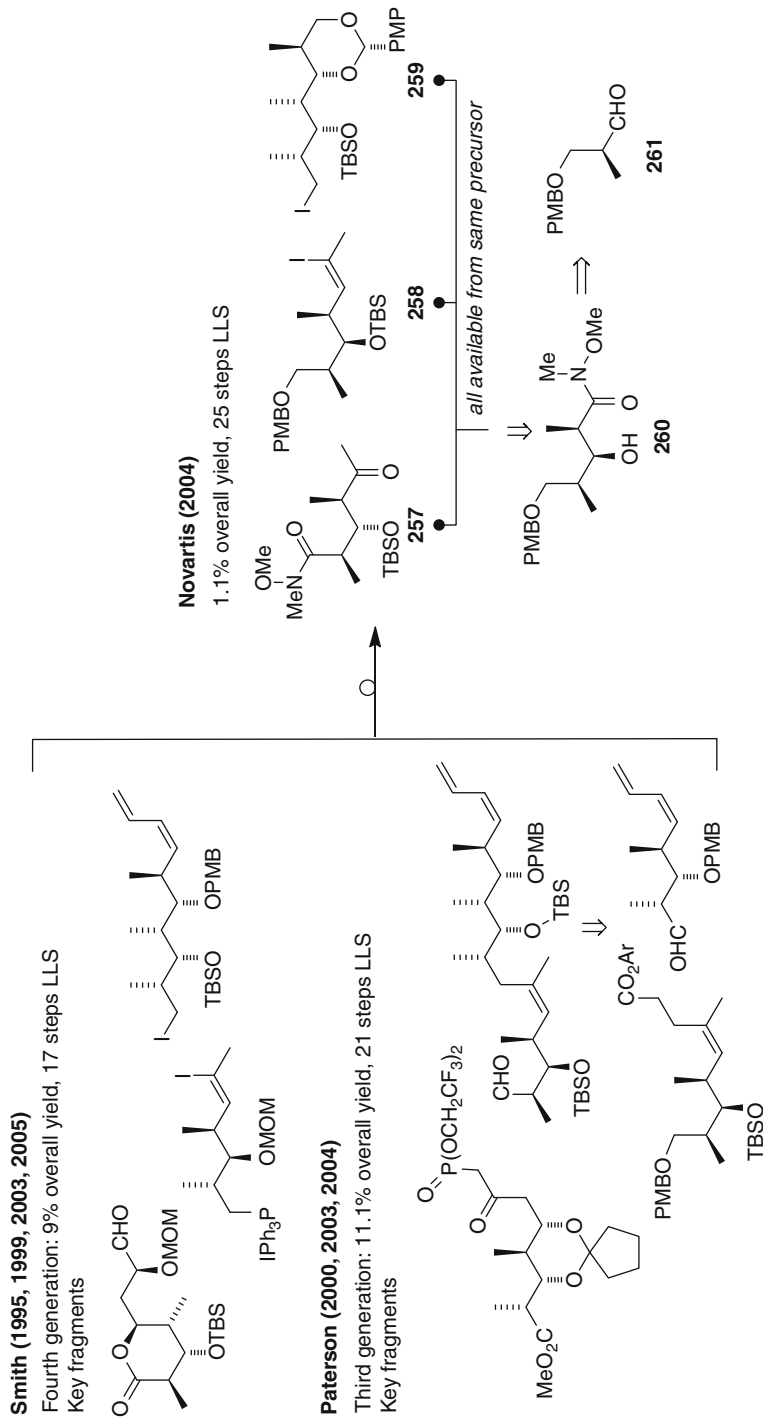


Fig. 11.6 The structure of discodermolide, and the main building blocks for Schreiber's initial total synthesis

One of the best examples of the value of total synthesis in providing realistic supplies of a natural product is discodermolide, **253**, which is a biologically active polyketide isolated in just 0.002 wt.% from the marine sponge *Discodermia dissoluta* [79]. The potent biological activity, coupled with the scarce supply from its natural source, has triggered intense activity in the total synthesis community [80]. Schreiber's group reported the first total synthesis, which confirmed the relative stereochemistry and established the absolute configuration [81]. As summarized in Fig. 11.6, his retrosynthetic analysis gave three key fragments, **254**, **255**, and **256**, with a Nozaki–Kishi coupling and an enolate alkylation being the critical bond-forming steps.

Since this work, a further 11 total syntheses have been reported from the academic groups of Smith [82], Paterson [83], Myles [84], Marshall [85], Panek [86], and Ardisson [87]. Of these syntheses, the groups of Smith and Paterson having refined their initial efforts and have reported fourth and third generation syntheses, respectively. As illustrated in Scheme 11.34, Smith's group utilized a Wittig reaction (C8–C9) and a Negishi cross-coupling (C14–C15) to assemble his key fragments, which allowed the generation of discodermolide in 9% overall yield and 17 steps for the longest linear sequence. While Paterson's initial syntheses had used boron aldol couplings, the difficulties of scale-up led his group to develop a third-generation synthesis where a Still–Gennari olefination was utilized. This resulted in an improved overall yield of 11.1%.



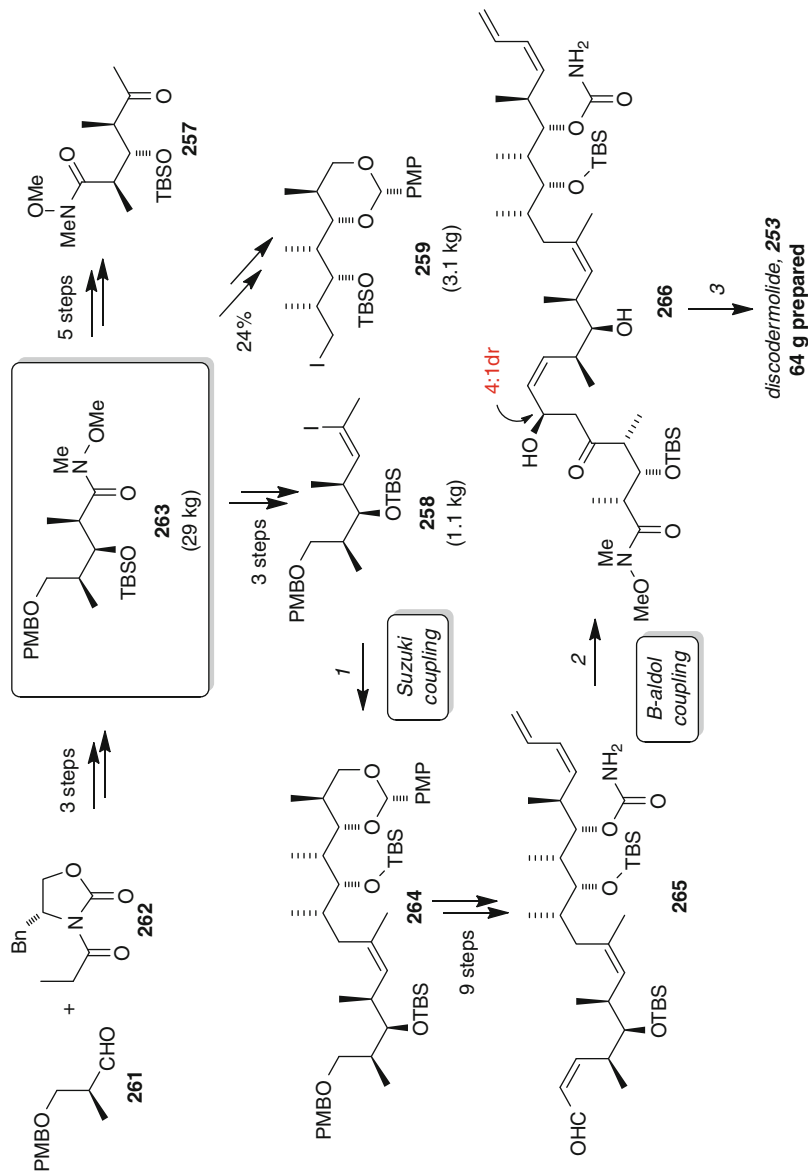
Scheme 11.34 Discodermolide synthesis: the foundational work for the Novartis synthesis

The advances made by these academic syntheses, in particular the efforts by the groups of Smith and Paterson, led Novartis to proceed with a total synthesis that could be carried out on an industrial scale so that over 60 g of discodermolide could be prepared [88]. This synthesis can be viewed as a hybrid of Smith and Paterson's routes, using the Paterson β -aldol disconnection at C6–C7 and the Smith–Marshall cross-coupling at C14–C15 as the key assembly steps. The three key fragments (**257**, **258**, **259**) are generated from the common precursor, **260**, originally reported by Smith. The synthesis proceeded in 25 steps (longest linear sequence) and 1.1% overall yield (Scheme 11.35). The common precursor **260** was prepared in three steps from the readily available aldehyde **261** and propionimide **262** and allowed the generation of 29 kg of material. As summarized in Scheme 11.35, **263** can be transformed into each of the key fragments (**257**, **258**, **259**), using routes related to Smith's syntheses. While Smith had used a Negishi cross-coupling to generate **264** from iodides **258** and **259**, the Novartis group chose to use a Suzuki cross-coupling, as originally reported by Marshall. Thus, iodide **259** was converted to the borane and coupled with iodide **258** using $\text{Pd}(\text{dppf})_2\text{Cl}_2$ as the catalyst. This key reaction proceeded in 73% yield on kilogram scale. To complete the synthesis, the Novartis group decided to utilize the endgame developed by Paterson. Accordingly, **264** was transformed into enal **265** in a nine-step sequence, with only two chromatographic separations required. After extensive experimentation, a reagent-controlled boron aldol coupling of aldehyde **265** and ketone **257**, using (+)- Ipc_2BCl , gave 67 g of the aldol product **266** (50–55% yield). An Evans-Saksena reduction ($\text{Me}_4\text{NBH}(\text{OAc})_3$, 73% yield) generated the C5-stereocenter stereoselectively and treatment with 3 N HCl was used to achieve global deprotection and lactonization and afforded discodermolide (**253**). This remarkable synthesis allowed the generation of 64 g of discodermolide, which allowed Novartis to initiate clinical trials. Unfortunately, toxicity issues have meant that these trials were discontinued [89].

Other complex marine natural products where “gram-scale” synthesis has provided materials for further evaluation include spongistatin (**267**) [90–96], kapakahines(**268**),(**269**)[97, 98],and iejimalide B (**270**) [99] (Fig. 11.7).

11.7 Supply by Synthesis: The Arrival of Halaven[®] and Yondelis[®] in the Clinic

In 2007, trabectedin (or ET-743, **271**), under the brand name Yondelis[®], was approved in the European Union for the treatment of soft tissue sarcoma, becoming the first marine natural product to be used in the treatment of cancer. It was originally isolated from the colonial ascidian *Ecteinascidia turbinata* and biological investigations revealed that it was a potent anti-cancer agent [100]. While aquaculture was initially used by PharmaMar to generate quantities of the compound for pre-clinical evaluation, the low yield, just 1 g being obtained from 1 t of ascidian,



Scheme 11.35 Synthetic strategy of the Novartis scale-up synthesis. Reagents and conditions: (1) 259, *t*-BuLi, 9-BBNOMe; 258, Pd(dppf)₂Cl₂, 73%; (2) 257, (+)-Ipc₂BCl, NEt₃, 63%; (3) (a) MeN₄BH(OAc)₃, 73% (b) 3 N HCl, 61%

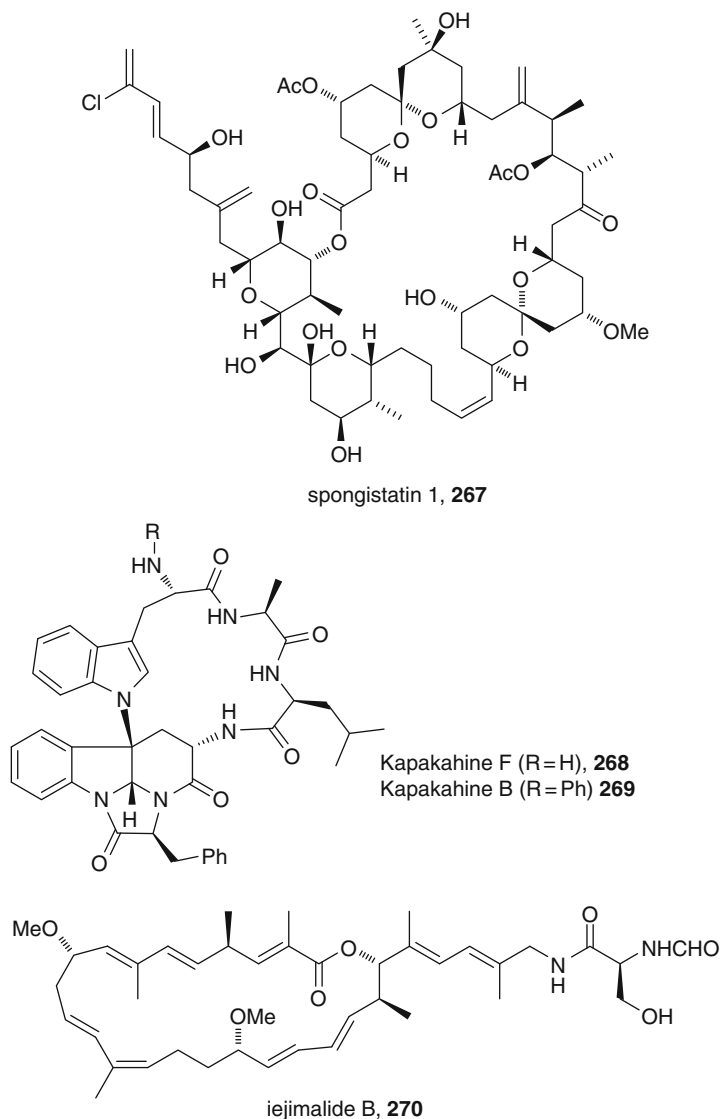


Fig. 11.7 Complex marine natural products available in appreciable amounts by synthesis

meant that this strategy would not be viable economically [101]. Thus, it was realized that an efficient, practical synthesis was the only realistic way that trabectedin could be supplied to the clinic.

The first total synthesis was developed by Corey and coworkers in 1996 and involved generation of the ten-membered lactone **272** via the trapping

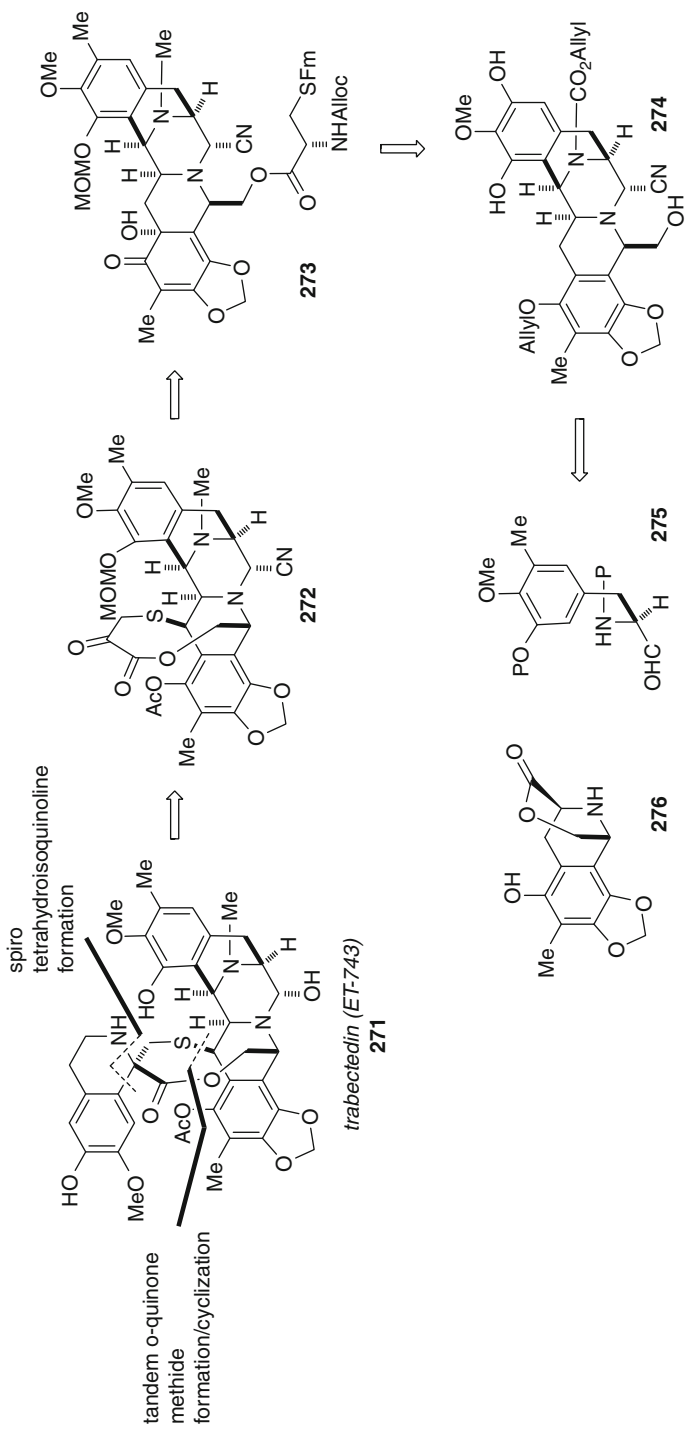
of a quinone methide intermediate as a key step (Scheme 11.36) [102]. Overall, the synthesis proceeded in 36 steps with a yield of 0.72%. Further work by Corey's group led to an enhancement in the overall yield (2.04%) but no reduction in the step count [103].

The synthesis provided an avenue for the generation of more material, but it was recognized by PharmaMar that the scale-up of this synthesis would be difficult. Using the key design principles of the Corey synthesis, they developed an efficient semi-synthesis from cyanosafracin B (**277**), which is readily available from fermentation from the bacteria *Pseudomonas fluorescens* [104]. As illustrated in Scheme 11.37, they were able to transform cyanosafracin B (**277**) into the alcohol **279** in 12 steps and 6% overall yield. Alcohol **279** can then be transformed into the quinone methide precursor **280** in three steps, using the protocols developed by Corey. The end game of the semi-synthesis was based on Corey's work, with some key changes in the protecting groups used and the ordering of the steps. Conversion to ten-membered lactone **282** was achieved in 58% yield, using the one-pot protocol developed by Corey. In contrast to Corey, the MOM and Troc protecting groups were removed first. The required α -keto lactone was generated in 57% yield using Corey's transamination protocol (4-methylpyridinium-4-carboxaldehyde iodide, DBU, $(\text{CO}_2\text{H})_2$). To complete the synthesis, the final tetrahydroisoquinoline system was introduced using a diastereoselective Pictet–Spengler condensation with 5-(2-aminoethyl)-2-methoxyphenol (**283**) in the presence of silica gel in 90% yield, and then, the nitrile group was substituted using silver nitrate in acetonitrile and water to afford trabectedin (**271**) in 90% yield. Overall, the semisynthesis requires 21 steps and proceeds in 0.96% overall yield. More importantly, it can be carried out on an industrial scale and is being used to provide the clinical supply of Yondelis[®].

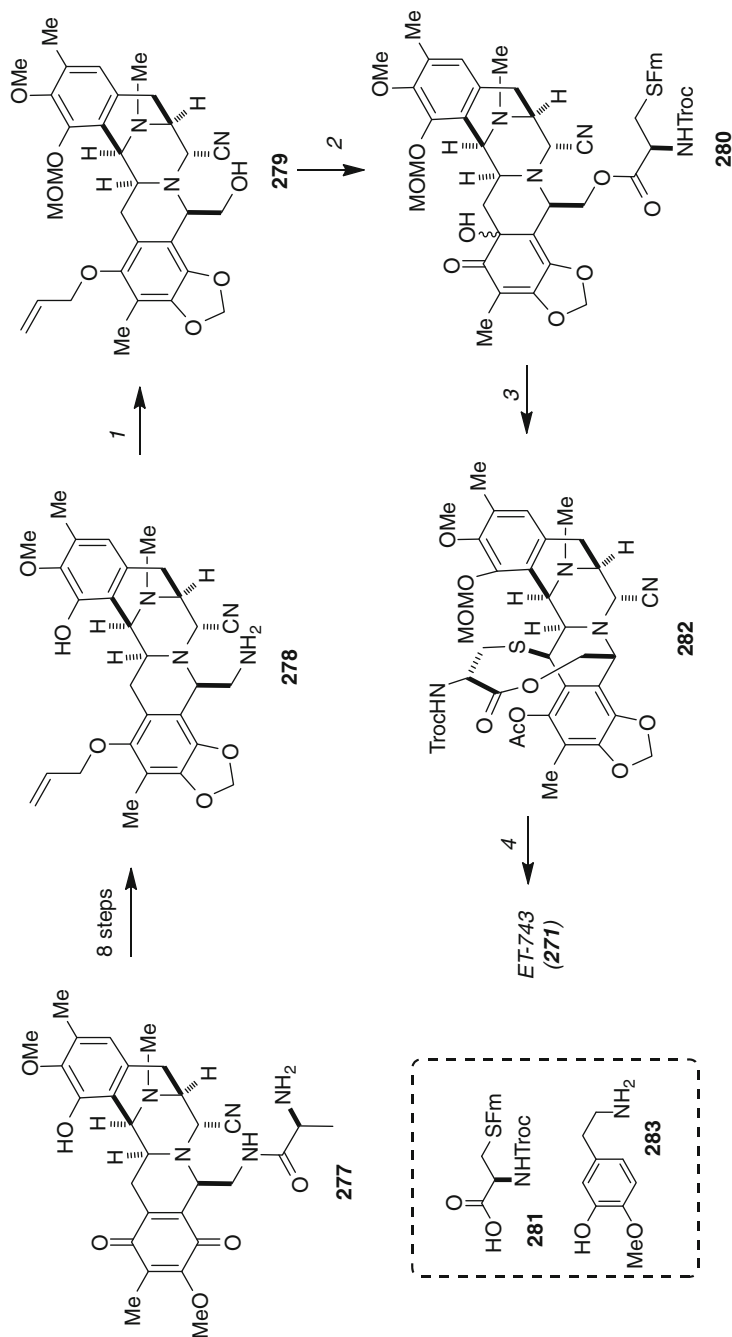
Other groups have been active in the area, with the groups of Fukuyama [105] and Zhu [106] each reporting total syntheses. Danishefsky [107] and Williams [108] have also reported formal syntheses, intersecting with key intermediates in the Fukuyama synthesis.

In 1992, samples of synthetic halichondrin B (**284**) and several intermediates were provided by the Kishi group to the Eisai Research Institute (Andover, MA) with a goal of evaluating *in vitro* and *in vivo* activity. In a significant discovery, the C1–C38 diol **285** was found to have a substantial fraction of the activity observed for the parent halichondrin B (Scheme 11.38) [109]. Evolution of this compounds ultimately produced E7389, eribulin mesylate (**286**), which was approved as a treatment for refractory breast cancer in November 2010 by the United States FDA.

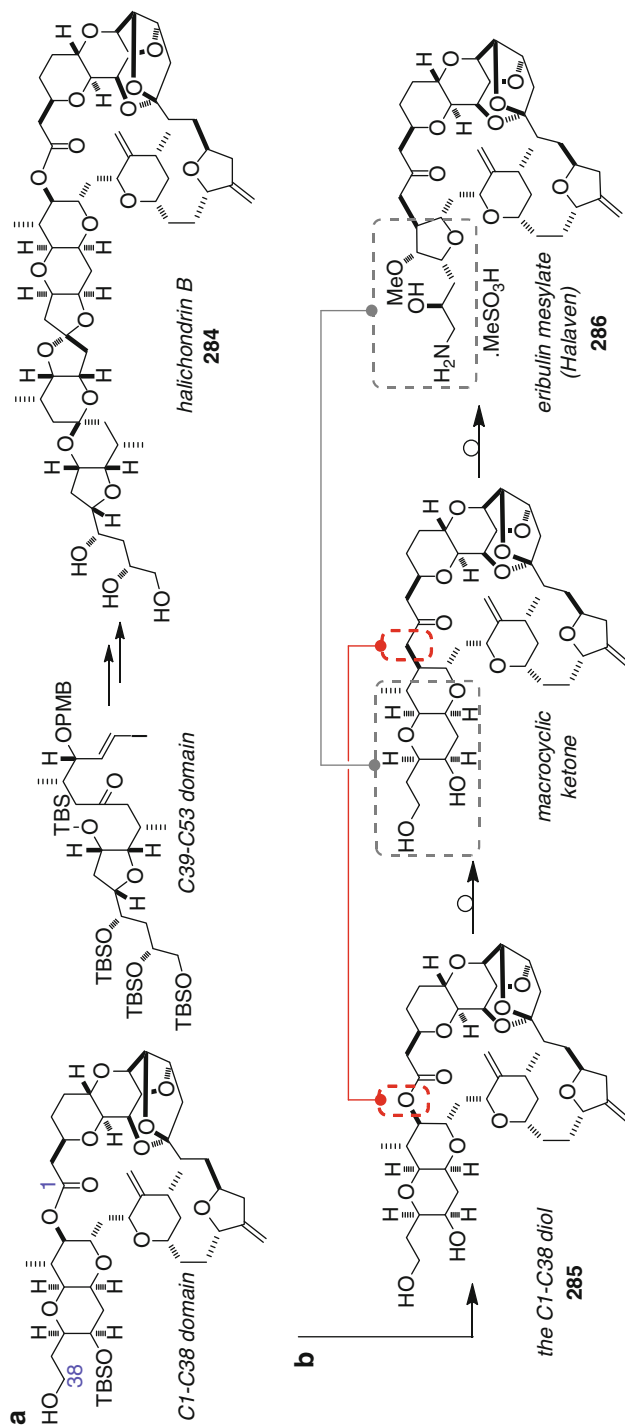
The Eisai synthesis of eribulin mesylate (**286**) employs much of the technology laid down in Kishi's studies on norhalichondrin B and halichondrin B (for a review see [110]). We pick up the synthesis here at the point of subunit couplings: Nozaki–Hiyama–Kishi coupling of aldehyde **287** with vinyl iodide **288** and subsequent base-induced cyclization provided a 3:1 mixture of C27 diastereomers favoring the desired product (Scheme 11.39). The PMB ether was then removed to yield **289**, at which point the diastereomers were separable. Alcohol **289** was converted to sulfone **290** in four steps. Deprotonation of **290** with *n*-BuLi, followed by addition to aldehyde **291** and oxidation gave **292**. Removal of the sulfone group with



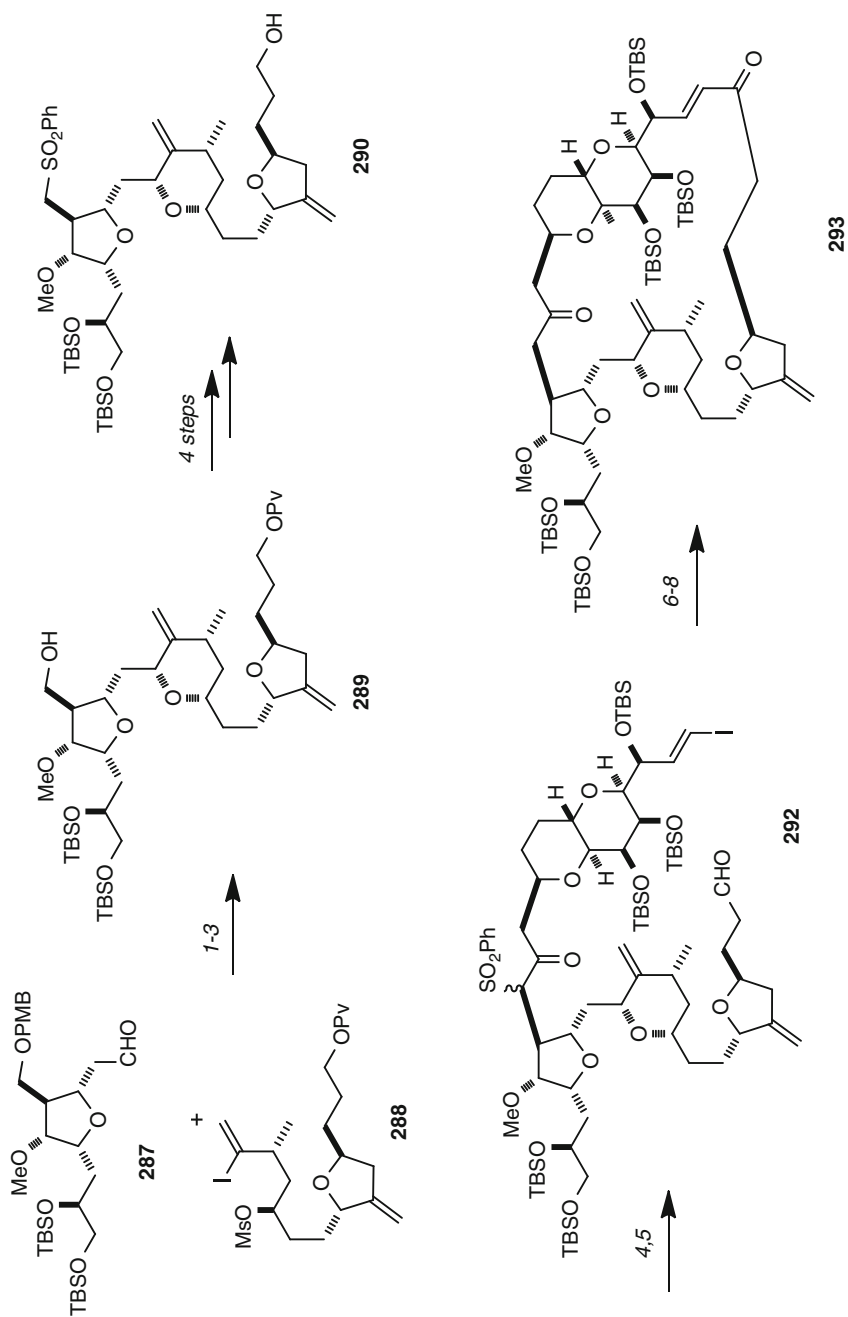
Scheme 11.36 The Corey retrosynthetic analysis for trabectedin



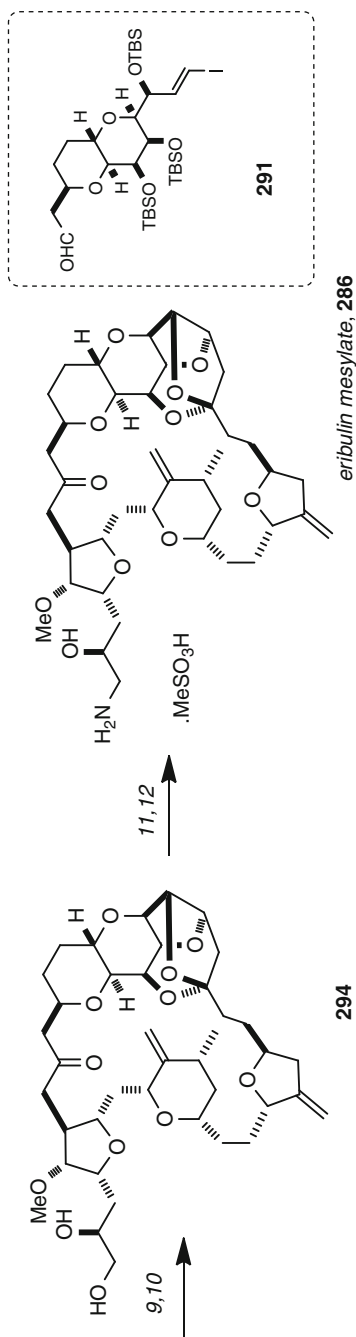
Scheme 11.37 The PharmaMar semi-synthesis of trabectedin (Yondelis[®]). Reagents and conditions: (1) (a) TrocCl, pyridine, CH₂Cl₂; (b) MOMBr, *i*-Pr₂NEt, DMAP, CH₃CN; (c) Zn, aq AcOH; (d) NaNO₂, AcOH, THF, H₂O, 36% (four steps); (2) (a) **281**, EDC·HCl, DMAP, CH₂Cl₂; (b) Bu₃SnH, (PPh₃)₂PdCl₂, AcOH, CH₂Cl₂; (c) (PhSeO)₂O, CH₂Cl₂; 78% (three steps); (3) DMSO, Tf₂O, CH₂Cl₂; *i*-Pr₂NEt; *t*-BuOH; (Me₂N)₂C = *N*-*t*-Bu; Ac₂O, 58%; (4) (a) TMSCl, NaI, CH₂Cl₂, CH₃CN; (b) Zn, aq AcOH; (c) [N-methylpyridinium-4-carboxaldehyde], DBU, (CO₂H)₂; (d) **283**, silica gel, EtOH; (e) AgNO₃, CH₃CN, H₂O, 36% (five steps)



Scheme 11.38 (a) The two key advanced building blocks of the Kishi total synthesis of halichondrin B, and (b) the evolution of the C1-C38 diol into a macrocyclic ketone and then into Halaven[®]



Scheme 11.39 (continued)



Scheme 11.39 The Eisai synthesis of eribulin mesylate (Halaven[®]). Reagents and conditions: (1) 0.5% NiCl₂/CrCl₂, 4:1 THF-DMF; (2) KHMDS, THF; (3) DDQ, CH₂Cl₂, aqueous buffer, 44% (three steps); (4) *n*-BuLi, then **291**; (5) Dess-Martin periodinane, 82% (two steps); (6) SmI₂, THF-MeOH; (7) 1% NiCl₂/CrCl₂, 4:1 THF-DMF; (8) Dess-Martin periodinane, 60% (three steps); (9) TBAF, imidazole.HCl; (10) PPTS, CH₂Cl₂, 90% (two steps); (11) MsCl, collidine, 90%; (12) EtOH saturated with NH₃, MsOH (five equiv), 93%

samarium (II) iodide, Nozaki–Hiyama–Kishi macrocyclization, and allylic alcohol oxidation gave enone **293**. Exposure of **293** to TBAF buffered with imidazole hydrochloride, followed by PPTS in CH_2Cl_2 , installed the polycyclic ketal domain, and the product **294** could be converted to eribulin mesylate by selective mesylation of the terminal alcohol and then aminolysis with NH_3 in EtOH. While current demand for clinical supply of Halaven is unknown, it is clear that Eisai's route has the capacity to provide multi-hundred-gram batches of API. Subsequent to regulatory approval by the FDA, Halaven has been approved for use in Singapore, Japan, and the European Union.

11.8 Conclusions and Future Perspectives

In this chapter, we have provided an overview of marine natural products synthesis that highlights some of the long-held rationales for the endeavor as well as the interplay between methods and strategy development in the context of challenging structures. These agendas will remain central to the science of synthesis, but the development of “gram-scale” syntheses and the arrival of Yondelis[®] and Halaven[®] in the clinic have ushered in an era in which synthesis may well be able to provide material that can address problems in human health.

11.9 Study Questions

1. In [Scheme 11.2](#), Kishi uses a series of stereoselective processes to prepare tetrodotoxin. Provide a stereochemical rationalization of the following reactions: (a) The conversion of **9** to **10** and (b) The conversion of **11** to **12**.
2. The Witkop reaction has been used by researchers to prepare the macrocycle of the diazonamide structure. Provide a mechanism for this reaction.
3. In Baran's synthesis of palau'amine, he generates the pyrrole **101** by reaction of bromide **104** and amino ester **105**. Provide a mechanism for this transformation.
4. Phillips' synthesis of cyanthiwigin U involves the conversion of bicyclic compound **214** to tricyclic compound **215**. Provide a mechanism.
5. Provide a mechanism for the intramolecular enyne metathesis that converts **140** to **141** in Shair's synthesis of longithorone A.
6. Evans uses a chelate-controlled Mukiyama aldol reaction to generate **177**. Provide a stereochemical rationale for the formation of **177** as a single diastereomer.
7. Boger's synthesis of ningalin D generates a tetra-substituted pyrrole **208** in two steps, from **206** to **207**. Provide a mechanistic rationale for each synthetic step.

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Part 3

**Marine Natural Products and
Chemical Ecology**

Antipredatory Defensive Roles of Natural Products from Marine Invertebrates

12

Joseph R. Pawlik

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Abstract

This chapter provides a broad and critical evaluation of investigations of the antipredatory defenses of marine invertebrates with a target audience of graduate students in ecology or natural products chemistry. After considering important concepts and theoretical issues associated with the research topic, techniques for assessing invertebrate chemical defenses against predators are detailed, with a focus on potential methodological problems. In particular, the importance of determining concentrations of metabolites in invertebrate tissues using a volumetric rather than gravimetric method is explained. Relevant concepts from the recent literature are reviewed and discussed, including the cost of

J.R. Pawlik

Department of Biology and Marine Biology, Center for Marine Science, University of North Carolina Wilmington, Wilmington, NC, USA

e-mail: pawlikj@uncw.edu

chemical defenses, synergistic effects of defenses, optimization of defenses, and structure-activity relationships of deterrent metabolites. Comparisons are made between the life histories and evolutionary environments of terrestrial and marine invertebrates to argue that the highly optimized chemical defense mechanisms and complex systems of color mimicry described for some terrestrial insects are unlikely to be equaled among marine invertebrates.

12.1 Introduction and Scope

Marine chemical ecology is a young discipline, having emerged from the collaboration of natural products chemists and ecologists in the 1980s with the goal of examining the ecological functions of the unusual secondary metabolites that were being isolated from the tissues of marine organisms. The result has been a progression of experimental protocols that have increasingly refined the ecological relevance of the research; some would argue, to a greater extent than the much older discipline of terrestrial chemical ecology.

The topic of this chapter is restricted to antipredatory chemical defenses of marine invertebrates, although much of what will be discussed is more broadly applicable to other defensive roles (allelopathic, antifouling, antimicrobial) and to other organisms, plants, and animals, both marine and terrestrial. In point of fact, it is not the author's intention to survey the primary literature for references pertaining to the topic, but only to cite examples that illustrate concepts as they are discussed. This contribution serves as an opportunity to address the subject in a broader, more analytical manner, with special attention to methodological problems, unanswered questions, and new research directions. Moreover, this chapter has been written for a target audience of *beginning graduate students* in ecology, or better, in chemistry, who might be considering marine chemical ecology as their field of study. For more thorough literature reviews, readers are directed to one excellent review of bioassay techniques [1], general reviews of marine chemical ecology [2], and the chemical defenses of marine organisms [3–5].

The author has contributed to the literature on this chapter's topic for over 25 years, and will unabashedly cite the work that he is most familiar with: his own. This might be interpreted as laziness or pretension, but more is now understood about the antipredatory defenses of a larger number of species of Caribbean marine invertebrates, specifically sponges, gorgonian corals, and ascidians, than for invertebrate taxa from any other marine biogeographic region. The Caribbean reef community is dominated by gorgonians and sponges, the species composition is remarkably similar across the entire region, and trophic relationships are well described. Within this framework, research has advanced from autecological characterizations of the defensive metabolites of individual species to community-level investigations that test higher-order ecological theory. As such, studies of Caribbean marine invertebrates provide the best body of work from which to draw examples that illustrate the concepts considered herein.

12.2 General and Theoretical Considerations

A series of interrelated research questions provide the framework for this chapter's topic: Do secondary metabolites produced by marine invertebrates defend them from predators? If they do, why? Are they toxic, or do they simply taste bad? Do metabolites require specific structural components to be active as defenses? How do they affect the behavior or physiology of the predator? Do the same metabolites affect all possible predators? Is predation a driving force in the evolution of defensive metabolites? Are defensive metabolites costly to the source invertebrate? If the defended invertebrate has endosymbionts, which of the two makes the metabolites, and how does that affect the cost to the invertebrate? Why don't predators surmount chemical defenses? If a secondary metabolite does not deter predation, does it have some other function? Does it only act in concert with other metabolites to deter predation? Might a secondary metabolite have no function at all?

12.2.1 Predator–Prey Interactions, Generalists and Specialists

It is well known that predation is an important force in controlling populations of marine invertebrates and in shaping their evolution. But it is not the only selective force; indeed, a host of abiotic and biotic factors interact to different degrees and at different times in structuring the ecology and evolution of any species (Fig. 12.1) [6, 7]. Because predation is often a dominant factor, organisms have evolved a number of defensive strategies to deter predators, ranging from behavioral mechanisms (nocturnal activity, rapid escape), to physical (spines, armor) and chemical defenses. Some predators have evolved counterstrategies to lesser or greater degrees, and in some cases, an evolutionary “arms race” has resulted in highly specialized predators that are adapted to eat highly defended prey [8]. At its most extreme, specialization can result in specific pairings of predator and prey, as for some nudibranch slugs that eat particular sponges, but more common are diffuse specializations that allow a predator to exploit a range of prey species that have developed a shared defensive trait, such as the jaws and pharyngeal mills of parrot fishes that allow them to eat many species of stony corals as well as calcified algae and sponges [9, 10]. The evolution of specialization has been the subject of considerable theoretical interest [11].

A high degree of prey specialization is comparatively rare, however, and most predators in marine environments are generalists, meaning that they consume many different prey species. So, to cite the example of sponges on Caribbean coral reefs, Randall and Hartman [12] examined the gut contents of the dominant predatory group, fishes, and they found the vast majority were generalist predators that did not eat sponges, a small minority were sponge predators that ate some sponges as part of their diet, and very few species ate sponges as most of their diet. One species appears to eat mostly one sponge species, making it more highly specialized than the rest. As we will see, knowledge of the generalist and specialist predators of

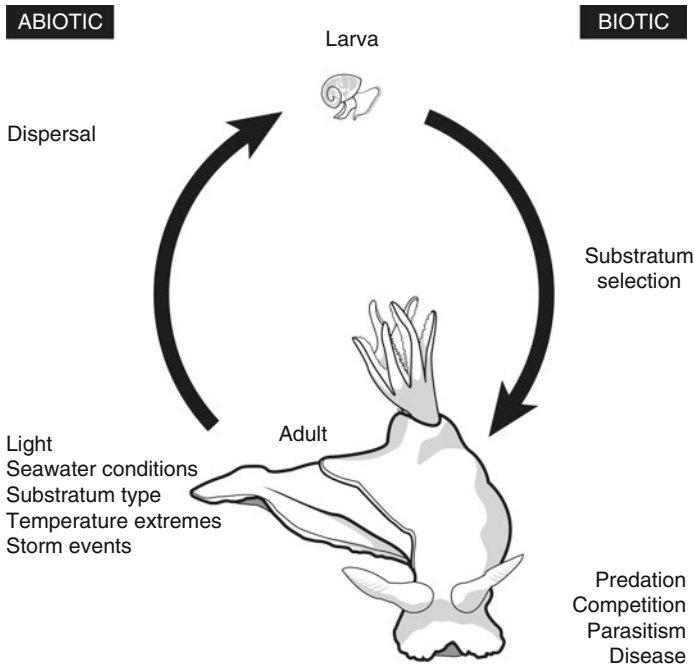


Fig. 12.1 Some of the abiotic and biotic factors that may affect the distribution and abundance of benthic marine invertebrates. For most species, the dispersive phase of the life cycle occurs during a planktonic (microscopic) larval stage, with the adult phase having limited mobility (the opposite situation is found for terrestrial insects). Note that predation is only one of the many factors that may impact the survival of a given species. Natural selection acts strongly on just a few characteristics of an organism at a time relative to the full range of factors that influence their survival; selective forces do not shape an “optimal” phenotype, nor does evolution permit only the best-adapted organisms to reproduce. Moreover, the focus of selection is likely to change over time as the relative influence of different abiotic and biotic factors change

a target invertebrate species within a community is a prerequisite for designing ecologically relevant experiments for assessing chemical defenses against potential predators. Few marine communities are characterized well enough that this level of understanding of trophic relationships exists [13, 14].

12.2.2 Palatability, Toxicity, Learning, and Aposematic Coloration

It is generally supposed that chemically defended prey produce metabolites that are unpalatable to predators (for the purpose of the discussion in this section, we will focus on fish predators, as they are the dominant predators in many marine ecosystems), and further, that this distastefulness is evidence of the toxicity of the metabolites. In the previous sentence, *toxicity* is understood to mean that a metabolite causes physiological damage to the predator that ingests it, while

unpalatability (distastefulness, detergency) means that food offerings containing the metabolite are rejected by potential predators without any necessary subsequent harm to the predator. However, any linkage between palatability and toxicity is far from clear. There are certainly examples of defensive metabolites that are known to be toxic in pharmacological assays [15], but little evidence that other unpalatable metabolites are toxic, and some strongly toxic metabolites may be quite palatable. Indeed, in the limited number of studies that have brought data to bear on the question, no relationship could be found between palatability and toxicity [16, 17].

There are good reasons to believe that palatability, and not toxicity, is the important driving force in the evolution of chemical defenses in marine invertebrates, although a defensive metabolite could have both properties. Distasteful secondary metabolites elicit an immediate response by a potential predator that permits the predator to learn to avoid chemically defended prey through the recognition of visual or chemical cues [18]. In aquatic systems, distastefulness is not perceived by predators at a distance, but only when prey mucus or tissue comes in contact with chemosensory structures in or around the mouth of the predator. Because an attack on distasteful prey is not usually fatal for the prey (particularly for clonal marine invertebrates), the prey and others like it will benefit from subsequent avoidance by the predator. If, however, the prey contained toxic metabolites that were not distasteful and had no physiological effect on the predator for many minutes or hours after ingestion, the predator could not learn to avoid the prey, as there would be no direct association between subsequent illness (or death) and the moment of attack on the prey. Moreover, the prey would likely be killed by the predator in the absence of the immediate deterrent effect of distastefulness. So, death of the predator, while seemingly a good strategy for the prey, is not so if it also means the death of the prey.

Why not produce chemical defenses that are both distasteful and highly toxic? The most likely reason is that highly toxic metabolites often have broad-spectrum, negative effects on living cells. Any prey producing a potent toxin would also have to contain it to prevent autotoxicity, and this could come at a high metabolic cost. In addition, if distastefulness alone prevents predatory attack, and confers a survival advantage to the prey, there is no need to bother with the cost of dealing with potent toxicity. But in the absence of toxicity, what would prevent a predator from circumventing distastefulness? Generalist predators (i.e., most predators) have other prey species available to eat, so there is no strong selective pressure to circumvent the distastefulness of one or a few species, as they can simply move on to other prey species. If, however, prey availability is limited to chemically defended species, predators may evolve behavioral and physiological mechanisms to circumvent defenses. Under enhanced predatory pressure, greater toxicity of the chemical defenses of prey may arise, leading to the “arms race” described frequently in the terrestrial chemical ecology literature [19].

So what is the evidence regarding distastefulness, toxicity, and learning among marine invertebrates and their predators? There is abundant confirmation that fish predators, like avian predators in terrestrial systems, use visual cues to discriminate among undefended and defended prey and learn to avoid the latter [18, 20].

Moreover, immediate regurgitation is the usual mode by which naïve predators reject defended prey, although in some cases learning occurs despite a lack of rejection, suggesting that toxic effects may be perceived quickly enough that some predators can learn to avoid prey despite being unable to reject novel defenses at the time of initial consumption [18]. It is conceivable that mildly toxic chemical defenses could have more insidious, long-term effects that alter growth rates, lifespan, or fecundity of predators [21], but the selective pressures that would favor a more complex mechanism over the straight-forward path of distastefulness are harder to imagine.

With visually acute predatory fish dominating many marine systems, and with good evidence of learned recognition of chemically defended prey by these predators, one might expect clear evidence of warning coloration (aposematism) and mimicry similar to that described for frogs and butterflies in terrestrial systems. Many sessile benthic invertebrates are brilliantly colored (e.g., sponges), and a clear candidate for mimicry are nudibranch mollusks, brilliantly colored shell-less slugs with potent chemical defenses that they derive from their diet or manufacture themselves, depending on the species [22]. Yet the evidence for these phenomena among marine invertebrates is not nearly as strong as for their terrestrial counterparts (butterflies, beetles, frogs, etc.).

No relationship has been found between bright colors and chemical defenses for Caribbean sponges [16]. Sponge-eating predators, including angelfishes, parrot fishes and hawksbill turtles appear to rely on visual cues that transcend color alone, quickly finding and eating preferred sponge species, whether brightly colored or drab, among similarly colored defended species in experimental arrays [23]. It had been proposed that spongivorous fishes used a “smorgasbord” strategy of alternating colors of sponges in their diets to avoid the accumulation of toxic compounds present in any one species [12, 24], but subsequent experimental work did not support this hypothesis [13, 23]. Indeed, the bright color of sponges may owe more to bacterial symbionts or dietary pigments than to the selective forces of predation [14, 16].

Among opisthobranch mollusks, herbivorous sea hares are mostly cryptically colored, and yet they often bear potent chemical defenses [25–27], although these may be targeted primarily at crustacean predators that rely less on visual cues. Blue and yellow stripes are a common color scheme for chemically defended Caribbean and Mediterranean nudibranchs [28], a pattern that blends to green at a distance, often rendering these slugs cryptically colored, although it has been proposed that the color pattern is indicative of a mimetic circle of species [29]. The large and brightly colored Spanish dancer nudibranch is primarily nocturnal and cryptically concealed during the day, but it reveals dramatically contrasting mantle markings when disturbed or swimming [30]. This species has a mantle that is bright crimson red in shallow water, but it would appear brown or black to potential predators at the range of depths it is most commonly found. Similarly, the alga-eating sacoglossan mollusk *Cyerce nigricans* also strongly chemically defended [31], appears mostly black in contrast to the bright green alga on which it feeds. Two congeneric gastropod slugs share the same chemically defended host sponge, and both are

similarly unpalatable, but while one has a strongly contrasting pattern on its body, the other is highly cryptic [32]. Even if it is arguable that visual cues help to protect some opisthobranch species, the general level of aposematism among marine slugs does not rise to that found in terrestrial insects, nor does it seem to provide a strong foundation for mimicry [33].

Stronger evidence for aposematism exists for Indo-Pacific nudibranchs of the family Phyllidiidae, but rather than settle the case, it only raises more questions. Natural assemblages of reef fishes consumed less of foods associated with the contrasting color patterns modeled after two of five species of these brightly colored, diurnal nudibranchs, providing evidence of aposematic coloration to the authors of the study [34]. However, the crude organic extract of one of the two nudibranch species having an avoided color pattern was not deterrent at the site in which feeding experiments were conducted, while at least one species with a color pattern that was not avoided by fish predators yielded a deterrent extract. The most strongly contrasting color pattern tested in the study and modeled after *Phyllidia polkadotsa* had no effect on predation.

In a thorough review of aposematic coloration in nudibranchs, Edmunds found the direct evidence inconclusive [33]. As part of his analysis, he noted the absence of extensive examples among nudibranchs of Batesian or Mullerian mimics, both of which are common among butterflies. A similar argument could be made against aposematism in marine flatworms [35] and for polychaetes with brightly colored feeding appendages [36, 37], although some claims have been made for mimicry among flatworms [35, 38]. Overall, the fact that the evidence for aposematism is nowhere near as pervasive for marine invertebrates as it is for their terrestrial counterparts further supports the contention that the relative selective pressures of predation on visual cues related to chemical defenses are not as intense in marine systems and do not result in the levels of optimized defenses, or complex chains of mimicry, that are seen in terrestrial insects.

Why should aposematism and associated mimicry be common among tropical terrestrial invertebrates (particularly butterflies) but rare among their marine counterparts? One possibility is that predation is a much more important selective force on insects than on marine invertebrates (Fig. 12.1) [7]. Butterflies are adults during the dispersive phase of their life history during which time they share the open air with their avian predators and cannot rely on crypsis, while adult benthic marine invertebrates crawl or are sessile. Female butterflies directly deposit their eggs on appropriate food plants for the nondispersive larval stage of their life history, while most marine invertebrates have a pelagic larval stage associated with considerable larval wastage and a very low probability of finding an appropriate settlement substratum [39]; in fact, the prevailing view of marine ecologists is that recruitment processes are a dominant, if not the most important, factor in determining distributions and abundances of marine invertebrates [40]. Many species of butterflies go through multiple generations in a season, greatly accelerating the evolutionary process compared to most marine invertebrates, which have generation times measured in years. Many of these life history differences may also explain why host specialization is often intense for insects, but not so for marine invertebrates.

An intriguing possibility for the limited existence of aposematism and mimicry among some opisthobranch mollusks is that it is evidence of past selection. Predation may have been a much more important factor guiding the evolution of opisthobranch species living in the warmer and more extensive shallow seas of the geological past than it is today.

12.2.3 Resource Limitation and Metabolite Function

All organisms have a finite amount of metabolic energy to allocate to the biological functions of maintenance, movement, growth, reproduction, and defense. Greater investment in one of these categories must come at the expense of the others. A marine invertebrate may defend itself in many ways, and it is conceivable that it may not defend itself at all. Mobile animals can hide or flee, while sessile species may exhibit armor, spines, or pincers. While the foregoing defense mechanisms have fairly obvious metabolic costs to the animals that use them, the situation is more ambiguous for chemical defenses. The cost of a chemical defense may be substantial if the invertebrate must synthesize a complex compound from primary metabolic building blocks, move the compound from the site of synthesis to a location where it will be most effective, and then either store the compound or release it. But what if the compound is an effective chemical defense in very small quantities, or it can be stored for long periods of time? What if it is derived directly from the diet of the animal, as for some nudibranch mollusks [30]? What if it is synthesized entirely by symbiotic algae or bacteria living within the tissues of the animal, as may be true for some sponges [41]? It is conceivable that a chemical defense could come at little or no cost to the invertebrate that uses it.

Just as it is likely that a chemical defense comes with a cost to the organism that exhibits it, it also seems reasonable to expect that any complex secondary metabolite found in the tissues of a marine invertebrate must have some sort of function, whether as a chemical defense or some other purpose. Again, this may not be the case. Secondary metabolites may be “biochemical baggage,” in that they are produced as by-products of the synthesis of other metabolites, whether primary or secondary, or that they are waste products that accumulate in the tissues of an organism [42]. If selective forces are neutral to the presence of these metabolites, or if they change over time from positive to neutral, they will continue to be produced in the population of organisms that exhibit them.

Marine natural products chemists are familiar with the broad diversity of unusual secondary metabolites present in the tissues of many benthic marine invertebrates, particularly sponges, ascidians, and gorgonian corals [43]. Often a single animal is the source of many compounds. Of this enormous chemical diversity, we can only ascribe ecological function, based on relevant experiments, to a tiny fraction. Bioassay-guided isolation techniques invariably exclude secondary metabolites that are not active in that assay system. It is entirely possible that these excluded metabolites have other important functions, but it is also possible that no particular function exists for these metabolites [42].

One interesting possible example of “biochemical baggage” is prostaglandins in the Caribbean gorgonian coral *Plexaura homomalla* [44]. This common sea whip grows among ten or more other species of gorgonians, including at least one congener, and yet only *P. homomalla* has very high concentrations of prostaglandins in its tissues (1–8% of tissue wet mass, mostly the acetoxymethyl ester of prostaglandin A₂(PGA₂)). Experiments conducted with the hydroxy acids of PGA₂ indicated that these compounds were potent antipredatory defenses against fishes [45], but when experiments were performed on the naturally occurring acetoxymethyl esters, they were not deterrent to potential predators [44], even though the crude organic extract of *P. homomalla* deterred predatory fishes, indicating the presence of other defensive metabolites [46]. Experiments also discounted antifouling and allelopathic roles for prostaglandins in *P. homomalla* [47]. Although specialist predatory snails of gorgonians, *Cyphoma* spp., exhibited higher levels of enzymes associated with detoxification when collected from *P. homomalla* [48], these snails are just as likely to graze on *P. homomalla* as any of the other gorgonian species that lack prostaglandins. Why should one common species of gorgonian contain such high concentrations of PGA₂ when all of the other species around it, many equally abundant, do not? It appears that the presence of PGA₂ in the tissues of *P. homomalla* makes very little difference to the survival of sea whips of this species.

12.3 Techniques for Assessing Invertebrate Chemical Defenses Against Predators

12.3.1 Historical Development

The field of marine natural products chemistry experienced a “gold rush” in the 1970s and 1980s when organic chemists took advantage of two emerging technologies: SCUBA diving and rapidly advancing spectroscopic methods (mostly NMR). The result was a rapid increase in the number of publications describing novel metabolites from benthic marine invertebrates and algae. Relying upon the assumption that secondary metabolites must serve some purpose (see previous section), many of these publications ascribed ecologically important properties to new compounds without empirical evidence; in point of fact, whole reviews of “chemical ecology” from this period were compiled of references with little or no assay data to support an ecological function for secondary metabolites [49].

At about the same time, ecologists were also taking advantage of the advent of SCUBA diving and describing the distributions and abundances of benthic animals and plants previously known only from much less effective sampling methods, such as dredging. The assumption of these researchers was that anything sessile and soft-bodied must be chemically defended to avoid consumption by abundant and ever-present predators [12]. In an effort to introduce empiricism to what was otherwise descriptive work on species abundances, some ecologists began extrapolating chemical defenses from toxicity assays in which fish (usually goldfish or guppies)

were exposed to aqueous suspensions of crude organic extracts of invertebrate tissues [50]. Looking back, it is surprising that publications in prestigious journals used similar techniques having little or no ecological relevance [51, 52] and that these studies are still widely cited today!

Indeed, not only are past studies that purport to investigate marine invertebrate chemical defenses on the basis of toxicity data cited in the current literature, studies based on toxicity data continue to be published [53–55]. In fact, one of the most up-to-date citations in this chapter is a study that attempts to link greater conspicuousness of nudibranch coloration with chemical defense by drawing entirely on brine shrimp toxicity data [56]! This is not entirely surprising because data from toxicity assays, particularly brine shrimp, Microtox, and fish toxicity experiments, are very easy to generate relative to time-intensive feeding experiments conducted with ecologically relevant predators. But beyond possible (and rather limited) pharmacological significance, toxicity data have no ecological value because these assays have no bearing on the manner in which potential predators perceive prey under natural conditions. In point of fact, studies that have compared data from toxicity and feeding assay experiments have found no relationship between them [16, 17]. Simply put, marine chemical ecologists should dispense with toxicity assays, editors and reviewers should not allow toxicity data to be published in the ecological literature, and past studies consisting of toxicity assays should not be cited as evidence of ecologically meaningful information.

12.3.2 Current Approach

In brief, the approach for assessing the antipredatory activity of the tissues of a marine invertebrate can be summarized as follows, and is further detailed in the paragraphs below: (1) determine the appropriate generalist predators for feeding experiments, (2) collect target invertebrates and properly extract secondary metabolites, (3) use an appropriate assay, and (4) employ suitable experimental and statistical methods.

1. *Determine the appropriate generalist predators for experiments.* It seems obvious that an appropriate, co-occurring generalist predator should be chosen for feeding experiments, but many past studies have instead opted for a more convenient “model” predator, which, while certainly better than using toxicity assays (above), nevertheless reduces the ecological relevance of the study. Clearly, a generalist coral reef fish should not be used to investigate defenses of a target invertebrate from a Norwegian fjord; instead, the local population of potential predators, whether vertebrate or invertebrate, should be determined, either from past studies or as part of a survey of the habitat of the target invertebrate. Some examples: fishes are the primary predators of invertebrates on Caribbean coral reefs [12, 23], while sea stars are the primary predators of the Antarctic benthos in McMurdo Sound [14], and crabs and lobsters are the dominant predators on some temperate reefs [57]. Generalist predators, and not specialists, are chosen for feeding experiments because specialists may

have surmounted prey defenses, and the research question addresses defenses against the most common classes of predators for the habitat of the target invertebrate.

2. *Collect organisms and extract secondary metabolites properly.* Under the best of circumstances when collecting target invertebrates, several geographically distant collections of individual specimens are obtained so that independent feeding experiments can be performed on each, thereby revealing potential variability in chemical defenses at the species or population level [58]. However, this is not always practical because multiple collections are not possible, the organism is rare, or the organism is small, and insufficient organic extract is available from individual organisms for assays. Under any of these circumstances, it is better to extract a mass collection of the target invertebrate and assume that the extract reflects a composite mean level of defense for the population of organisms from that collection site [59].

In preparing crude organic extracts of a target invertebrate, it is best to extract freshly collected tissue to avoid any possibility of sample degradation. As an alternative, fresh collections are quickly frozen and maintained solidly frozen until processed. Some older studies were performed on air-dried invertebrate tissues [60], which necessitated re-evaluation of the experiments performed on extracts from these species with better techniques that resulted in some very different findings [46].

Prior to extraction, the total volume of the tissue must be determined. This is usually done by adding the tissue samples to a graduated cylinder partially filled with either water or the extraction solvent and recording the displaced volume. After tissue volume has been determined, the tissue may be further chopped or shredded to expedite the extraction process. Each step in the extraction process should use a volume of solvent about twice that of the tissue sample. The solvent mixture of choice for extracting wet tissue is a mixture of equal parts dichloromethane and methanol, which rapidly permeates tissue, solubilizing membranes and dehydrating cellular material. Separation of the dichloromethane phase from the resulting miscible mixture of methanol and water from the tissue occurs very quickly, so it is best to agitate the extraction containers to keep the semi-emulsified extraction liquid in contact with the whole tissue sample. After a minimum of 6 h, preferably under cold and dark conditions, the first extraction solvent mixture is poured off and the tissue squeezed before the same volume of methanol alone is used for the second extraction, which again is best done with agitation for a minimum of 6 h. A third extraction round, also with methanol, is necessary only when the tissue is particularly dense. Evaporation of the solvents should be done to minimize exposure of the extracts to heat and light; for example, the dichloromethane partition of the extract can easily be separated from the aqueous methanol partition in a separatory funnel and evaporated nearly to dryness on low heat by rotary evaporation. Rotary evaporation will also quickly remove solvent from the last methanol extract. The aqueous methanol partition is best evaporated using a vacuum evaporator system. When most of the solvent has been removed

from each, the partitions of the extract are combined into a single vial, completely dried by vacuum evaporation, and stored frozen under nitrogen, if not used immediately for feeding experiments.

3. *Use an appropriate assay.* Feeding experiments can be performed in the laboratory or in the field, with the advantage of the former in simplicity and speed, and of the latter in enhanced ecological relevance. Optimally, feeding experiments will begin in the laboratory and then be duplicated at some level in the field [61]. Feeding experiments are most often behavioral assays in which consumption or rejection of an artificial food that predators do not otherwise recognize is scored. Artificial foods are used because they allow precise control of the nutritional quality of the food as well as the concentration of crude organic extract or metabolites from the invertebrate under investigation. Additionally, the predatory subjects are unfamiliar with artificial foods, have neither learned to avoid nor prefer them, and tend to sample them carefully, resulting in a behavioral assay that is easier for the investigator to observe. For assays in which fish are the predatory subject, artificial foods made from a polysaccharide gelling agent such as agar, carrageen, or Phytigel are commonly employed. These gelling agents add little nutritional value to the artificial food and have the distinct advantage of solubilizing many lipid-soluble metabolites in suspension in the gel matrix, allowing a homogeneous presentation of secondary metabolites in the food. One minor disadvantage of these gelling agents is that they must be heated to boiling after being mixed in water in order for solidification to subsequently occur, and there is always some concern that heat-labile secondary metabolites may be degraded as they are mixed in the molten gel. However, it seems unlikely that wholesale degradation of otherwise stable natural metabolites would occur from such a brief exposure to heat, and the author knows of no example to support this concern. Nevertheless, as an alternative, the sodium salt of alginic acid can be mixed in much the same way as the previously cited gelling agents, but rather than requiring heat, alginic acid forms a solid gel when exposed to a solution of calcium chloride. Proper solidification requires a high surface-to-volume ratio, however, so use of this gelling agent is largely restricted to small volumes of artificial food that are extruded through a syringe housing and into the calcium chloride solution to form long noodles that are then cut to form food pellets [16]. When food pellets are prepared, the feeding assay scores consumption or rejection of individual pellets [16], but when larger food samples are prepared, changes in the mass of treated and control food samples are scored after exposure to predatory fishes [62].

Whatever the artificial food matrix used to volumetrically reconstitute the secondary metabolites from the tissues of the target invertebrate, the food should match the nutritional quality of the same tissues by addition of a nutritional substitute, such as fish meal, or squid mantle. This is important because it is likely that the same sensory processes that predators use to reject feeding deterrent metabolites also perceive the nutritional quality of foods. Foods with very low nutritional quality may be rejected by potential predators at much lower levels of chemical defense [63], and conversely, secondary metabolites may

only be deterrent at higher-than-natural concentrations if those metabolites are presented in an artificial food that is more nutritious than the tissue from which it was derived. Nutritional quality of tissues is determined using calorimetry (to assess total energy content) as well as specific assays for protein, lipid, and carbohydrate [46, 64]. Of these, it is generally agreed that matching the protein content of the invertebrate tissue in the artificial food is the most important. Powdered, freeze-dried squid mantle is a particularly useful nutritional substitute because it is readily available, easy to measure, and its nutritional characteristics have already been determined [64]. Avoid nutritional substitutes that are excessively oily (e.g., tuna packed in oil) or those that may have high levels of free amino acids (e.g., some commercial fish foods) as the stimulatory effects of these substances may act against potential feeding deterrent metabolites present in the tissues of the target invertebrate.

Feeding experiments involve potential predators making choices between foods treated with secondary metabolites from the target invertebrate and control foods, which lack the secondary metabolites, but may contain the solvents (often methanol) used to dissolve the metabolites for homogeneous addition to the food matrix. Because crude organic extracts of invertebrate tissues are often strongly pigmented while most control food mixtures are not, it may be necessary to color-match the treated and control food samples. This is done to prevent assay fish from learning to reject pigmented food samples when multiple assays of different target invertebrate species are being performed in succession with the same group of assay fish, as when doing a survey for chemical defenses [16]. Color-matching can be done by adding drops of food dye while preparing artificial foods, and it is easier to add dye to both treatment and control mixtures to give the same color (masking the natural pigment of the extract in the treatment mixture) rather than trying to match the color of the treatment mixture by adding dye solely to the control mixture.

Once artificial food has been prepared containing a natural volumetric concentration of secondary metabolites from the target invertebrate and having a nutritional quality that approximates the tissues of the target invertebrate, food samples can be presented to assay predators in laboratory or field assays. A single feeding experiment is made up of multiple replicate assays, each of which must be independently performed. For laboratory feeding experiments with fish, independent replication is achieved by splitting up the population of assay fish into separate cells so that no group of fish is assayed more than once with the same treatment. Independent replication can be more difficult for field assays because one or a few hungry fish may monopolize a SCUBA diver who exposes food samples to fishes in the field, and multiple samples eaten by the same predator would not constitute independent replicates. One way around this problem is to place paired treatment and control food strips at replicate feeding stations that are a sufficient distance apart so that the same fishes are not feeding from more than one station [44, 65]. Paired samples are then removed after predators have had a chance to consume some of the food, with feeding deterrence evident when more of the control has been eaten relative to the

treatment food, as determined by measuring the remaining food strips. The difficulty with this type of field assay is that it works well only with “nibbling” fish predators – those that grab the whole food sample and swim off, only to reject the sample after moving away from the feeding station, will render this field assay method useless.

This review has largely focused on fish feeding assays because fishes are often the dominant predators in marine habitats, but there are many examples of feeding assays that have been designed around invertebrate predators. Invertebrate feeding assays are of two types: those that measure consumed assay foods directly and those that score behavioral differences in response to assay foods. The latter category is often necessary because many invertebrate predators feed slowly, consume little, or feed in such a way that it is difficult to score loss of food material. There are examples of invertebrate assays performed in the laboratory with pelleted assay foods that parallel those described previously for fishes [66, 67]. But the most common method for direct measurement of assay food consumption by invertebrates is the “screen gel assay” adapted from sea urchin assays of algal metabolites [68] and adapted for use with crabs [69], sea stars [70], and other invertebrate predators [71]. For these assays, paired treatment and control gel-based foods (as previously described) are solidified onto fiberglass window screen as a thin coating, and the relative number of squares in the screen within the gel area that are consumed over a certain period of time are recorded. For invertebrates that consume larger amounts of material, cubes or strips of gel-based foods can be incorporated onto the screen and weighed before and after the feeding experiment [72]. An assay designed for the opposite situation, to test whether shrimp feed on small amounts of brightly colored control or treatment foods, scores the color change of the shrimp gut by observing it through its clear carapace [55].

Perhaps the best example of a behavioral assay performed with an invertebrate predator for the purpose of testing for chemical defense is the “tube-foot retraction” assay used to test the responses of sea stars, the dominant benthic predators of McMurdo Sound, Antarctica, to potential prey sponges and mollusks and to the organic extracts from these target invertebrates [73–75]. The assay consists of touching the tube feet along one arm of a replicate sea star with the experimental treatment and then measuring the time it takes for the retracted tube feet to extend again from the ambulacral groove. For assays of extracts or pure compounds, the control used is a glass rod coated with silicone grease, and this elicits a retraction time of about 25 s for tube feet of the sea star *Perknaster fuscus*; the response to grease with fish tissue extract is about 28 s, while the response to grease treated with metabolites from the chemically defended sponge *Latrunculia apicalis* is about twice that amount of time [76].

4. *Employ suitable experimental and statistical methods.* The importance of appropriate experimental methods has already been discussed to some extent in describing collection and assay techniques, particularly regarding replication of sampling and when performing feeding experiments. Additionally, if an

investigator wishes to compare the chemical defenses of one or a group of invertebrates relative to a previous study, it is imperative that the same methodology be used, or any comparative conclusions will be compromised by technical differences between the two studies.

One important concern when isolating the chemical defense of a target invertebrate is in the use of bioassay-guided fractionation. Once the presence of a chemical defense has been ascertained by assaying the crude organic extract of the tissues of the target invertebrate, the same assay is employed as the crude extract is chromatographically fractionated into smaller subsets of compounds that make up the mixture. Again, this should be done on a volumetric basis, using “mL equivalents” of tissue extract rather than mass equivalents. As the separation proceeds, fractions are best assayed as a serial dilution relative to the natural volumetric concentration: 4×, 2×, and 1×. This span of concentrations takes into account the likely reduction in deterrent activity that comes from splitting the active metabolites over two or more chromatographic fractions or from loss of active metabolites through decomposition, reaction, or attachment to chromatographic media. Once the active metabolites have been isolated by bioassay-guided fractionation, the investigator should endeavor to identify them using standard spectroscopic techniques and should also do the same for inactive fractions that may have secondary metabolites. For the reasons explained earlier in this chapter regarding their functional significance, it is equally important to know which secondary metabolites are active in ecologically relevant experiments as to know which metabolites are not.

Appropriate statistical analyses of data are as important for behavioral assays as for any other scientific research that involves determining the significance of differences in experimental outcomes. Fortunately, these analyses are usually simple and routine. The significance of most laboratory feeding experiments, in which consumption of control and treated foods is compared, is usually determined with some form of contingency table analysis of which Fisher’s exact test is commonly employed [16]. The assumption for these experiments is that all of the control food offerings will be consumed because the investigator would not be using experimental predators that were not feeding on control foods. In one example, a useful boundary in food pellet consumption was designated that separates palatable from defended treatment foods, based on Fisher’s exact test, in which a treatment is considered deterrent if six or less of ten food pellets are eaten [16].

To analyze data from field experiments, paired, nonparametric statistical tests are usually employed, such as the Wilcoxon paired-sample test [63]. Nonparametric, paired tests are necessary because the variance in the amount of food consumed between replicate pairs of samples positioned in different places in the field is often greater than the difference in consumption between the control and treatment food sample within a pair, a reflection of the “patchiness” of predators in field situations. These nonparametric tests analyze the directionality of the results rather than comparing the mean consumption of control and treated foods.

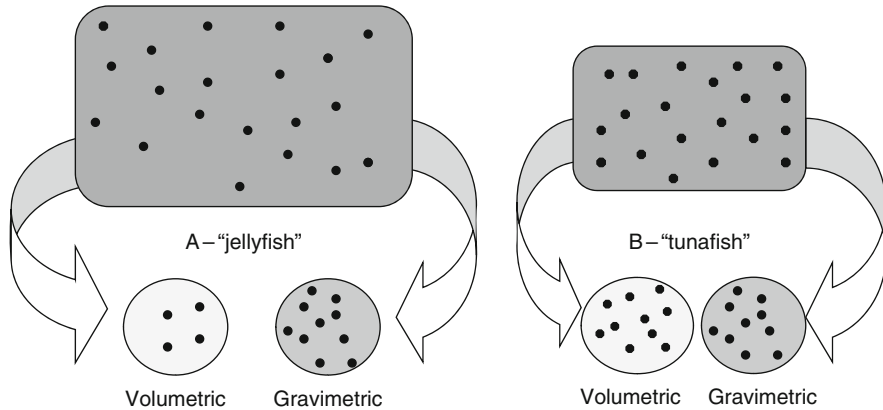


Fig. 12.2 Comparison of volumetric and gravimetric methods for reproducing the concentration of a defensive component in invertebrate tissues. In these diagrams, the *black dots* represent the components of interest (secondary metabolites, spicules, sclerites, etc.) that are assumed to be homogeneously dispersed in the freshly collected (wet) tissue. In example A, the components are sparsely distributed in highly hydrated tissue (jellyfish), while in B, the same amount of components are distributed in about half the volume (tuna fish). Any predator taking an equal volume bite out of A would experience the defensive components at half the concentration of the same bite of B. If the components are reconstituted in an artificial food matrix as a function of wet tissue volume (volumetric), the concentration of the components are identical to the original tissue concentration for both A and B, but if the components are reconstituted as a function of dry mass (gravimetric), they are likely to be more highly concentrated than the original tissue for A (depending on the dry mass of the artificial food used)

12.3.3 Technical Problems

Gravimetric vs. volumetric concentration determination. One long-standing technical problem plaguing the marine chemical ecology literature is with the determination of extract or metabolite concentration in an organism and duplication of the natural metabolite concentration in artificial assay foods. Natural products chemists are accustomed to reporting metabolite concentrations as a function of dry tissue mass, but predators eat wet tissue, and marine invertebrate tissues vary widely in the amount of water contained in their tissues. From the perspective of a predator, a bite of a jellyfish or sea anemone would contain substantially more water per unit dry mass than the same sized bite of a squid or sea slug. For highly hydrated tissues, the concentration of metabolite per unit dry mass would be much higher than per unit volume, but volume (bites) is the measure that is ecologically relevant (Fig. 12.2).

In addition to differences in water content, tissues of marine invertebrates may have very different densities because of skeletal inclusions. For example, some sponges have tissues that are perfused with glass spicules, which have a very high density, but are not part of the living organism (similarly dense limestone inclusions are found in soft corals and tunicates). Dry mass calculations of metabolite concentration would include the heavy mass of these spicules, which are not part of the

living tissue of the sponge, driving down the relative mass of any metabolite found in the tissue. Because the concentration of skeletal inclusions can vary greatly between organisms of the same species, and sometimes between parts of the same organism, perceived differences in metabolite concentration based on dry mass could be accountable entirely to differences in skeletal element concentrations.

The problem of gravimetric concentration determination particularly affects any study aimed at testing for differences in levels of defense between parts of the same organism or between individuals in a population. For example, investigators wishing to test for differential allocation of chemical defenses in one part of the body of a study organism are faced with potential differences in hydration or skeletal inclusions that could confound any differences in metabolite concentration on a dry mass basis. Similarly, investigations of seasonal cycles in metabolite concentration may be confounded by changes in hydration, tissue quality associated with changes in diet (e.g., presence of more lipids in well fed organisms), changes in skeletal inclusions due the changes in flow or wounding, or changes in the abundance or development of gametes.

Determination of metabolite concentration by volume solves both the problems of differences in tissue hydration and density variation from skeletal and tissue inclusions, and it is the most relevant measure from the standpoint of consumption of tissue by a potential predator. It requires that tissue volume be measured at the onset of an extraction protocol, by displacement of water or solvent in a graduated cylinder, and that the resulting extract be treated as a *volume-equivalent* (e.g., “mL equivalents”) throughout the bioassay-guided metabolite isolation process. Dry mass determinations should also be performed during the isolation process because these comparative data are necessary for the marine natural products literature should a novel metabolite be isolated and reported.

The importance of using volumetric methods for determination of metabolite concentration is illustrated in surveys of the chemical defenses of Caribbean gorgonian corals against the generalist predatory bluehead wrasse, *Thalassoma bifasciatum*. The initial survey of 1987, one of the earliest to systematically examine chemical defenses of a broad range of species from a biogeographic community, used a gravimetric approach to estimate natural concentrations of metabolites in experimental foods and documented considerable variability in chemical defenses among common Caribbean gorgonian corals [60]. Subsequent studies introduced the technical superiority of volumetric concentration determination [77]. The gorgonian survey was repeated 15 years later, using volumetric concentration determination and improved techniques for sample processing, and this time, all 32 gorgonian species yielded deterrent crude organic extracts [46]. As an example from the technically improved study, the dry masses and volumes of two tissue samples from the common Caribbean sea fan, *Gorgonia ventalina* were 19.72 g and 27 mL and 22.86 g and 57 mL, respectively (i.e., the mass of the second was 16% greater than that of the first but occupied 111% more volume). In a gravimetric assay, the extracts of these two samples would be applied to similar masses of food of unknown volume because the assay food is also measured and prepared on the basis of mass, not volume. In a volumetric assay, however,

the extract of the second sample would be applied to more than twice the volume of food as the first. The relative concentrations of each extract would be very different in the gravimetric and volumetric assays, as likely would be the feeding responses by the assay organisms.

As was also pointed out in the foregoing technically improved survey of Caribbean gorgonian chemical defenses [46], gravimetric feeding assays fail to control for the nutritional quality of the target organisms. Invertebrate tissues contain nutritionally valuable (e.g., protein) and inert components (e.g., mineralized skeletal elements). When assay foods are prepared gravimetrically, the mass of the nutritionally poor portion is replaced almost entirely by an equivalent mass of nutritionally valuable matrix. As a result, a gravimetrically prepared assay food cannot replicate the nutritional quality of tissue. When assay foods are prepared volumetrically, however, organic extract from a volume of tissue is added to a volume of assay food that can be modified to have a similar nutritional quality (more or less powdered freeze-dried squid mantle). The proportion of the nutritional components is controlled for in a volumetric assay. Thus, volumetric assays are more ecologically relevant than their gravimetric counterparts because the assay food more closely models hydrated tissue in both nutritional quality and extract concentration. A note of caution, however: the foregoing assumes that tissue constituents (secondary metabolites, skeletal elements, etc.) are homogeneously distributed in the tissue under investigation. If it is suspected that the tissue constituent of interest is, for example, concentrated in the surface of the target organism, then a more careful, separate extraction of inner and outer layers of tissue will be required.

Extraction protocol. Experiments designed to assess chemical defenses of marine invertebrates require that secondary metabolites be extracted and assayed separately from any structural defenses that may be present in their tissues. To this end, the full range of potential defensive metabolites, from nonpolar (e.g., terpenes) to polar (e.g., glycosides), must be extracted from tissues and recovered in nearly 100% yield with minimal degradation prior to reconstituting the metabolites in assay foods and performing feeding experiments with potential predators.

Very little comparative work has been published on extraction protocols, but the choice of wet or freeze-dried tissue and extraction solvent can substantially alter extraction efficiency [78]. Minor variations on the aforementioned extraction scheme are the norm for most studies of marine invertebrate chemical defenses [16, 46], particularly when natural products chemists are involved as collaborators. Substitution of one extraction solvent for another of the same polarity is unlikely to have much effect on the extraction outcome, particularly if the extract is prepared from freshly distilled solvents and processed quickly. Tissue extraction may be incomplete, however, if an inappropriate solvent is used. Extraction with methanol alone, for example, may not liberate all the nonpolar metabolites from the tissue. Freeze-drying tissue before extraction, which is often done to speed and simplify the process by removing water, may also be problematic because very polar metabolites may not be extracted from freeze-dried tissue with methanol unless the tissue is first rehydrated. Experience in the author's laboratory has

shown that yields of some metabolites from sponges are higher when using wet tissue than freeze-dried tissue, as has been determined for similar extractions of macroalgae [78].

A combination of the aforementioned technical pitfalls is illustrated in a recent set of studies that claims to demonstrate latitudinal variation in sponge chemical defenses as a function of relative predation pressure, comparing species that are found off the coast of the southeastern United States, where fish predators are scarce, and in the Caribbean, where predators are common [79, 80]. Sponge tissue samples were freeze-dried and then extracted only in a mixture of equal parts dichloromethane and methanol, a protocol that would likely not liberate the most polar secondary metabolites from the tissues of some sponge species. Data from feeding assays performed using sponge extracts prepared in this manner were compared to those done on wet-extracted tissue using the protocol described previously [16], and the authors found lower levels of chemical defense in the sponges from the coast of the southeastern US than had previously been documented from the Caribbean [79]. Unfortunately, incomplete extraction of sponge tissue is an alternative and more parsimonious explanation for the difference in feeding assay outcomes for the more recent study, and a less equivocal test of the latitudinal variation hypothesis will require complete and identical extraction protocols. Moreover, the preceding example provides a cautionary tale in support of using identical methodologies when seeking to compare data from two studies.

Nutritional quality of assay foods and the feeding state of assay predators. When conducting feeding experiments to determine whether organic extracts of marine invertebrates contain chemical defenses, it is important that other variables that affect assay food quality not confound or interact with the effects of the metabolites being tested. In particular, the nutritional quality of assay foods is important [63, 81]. Metabolites that are mildly deterrent are more likely to induce predators to reject them when they are incorporated into foods with little or no nutritional quality than when they are incorporated into high-quality foods. High food quality is usually linked with protein content, and many associated amino acids and peptides are strong feeding stimulants [82], which may interact with feeding deterrents. Indeed, the converse may also be true – assay foods with very high nutritional quality may mask the deterrent effects of minimally effective defensive metabolites.

It is incumbent on the investigator to match the nutritional quality of the artificial assay food with that of the marine invertebrate from which the crude organic extract or metabolites have been derived. Sometimes this is relatively simple; for example, the mantle tissue of a nudibranch and a squid are likely to be fairly similar in food value, so an artificial food prepared from the latter should be a good stand-in for the tissue of the former. But the tissues of sponges, ascidians, and soft corals may contain high concentrations of both water and skeletal elements that make their interspecific nutritional quality highly variable, particularly on a volumetric basis (see above, Fig. 12.2) [46, 64, 83]. Therefore, replicate tissue samples should minimally be subjected to a combination of bomb calorimetry for total caloric content and a suitable assay of soluble protein to determine reasonable nutritional

parameters for artificial assay foods [46]. Because the gelling agent used in most assay foods (agar, carrageenan, alginic acid, or similar) has little nutritional value, a nutritional component can be added to the gelling agent to approximate the food value of the invertebrate tissue. Performing the same analyses on the selected nutritional component, such as powdered, freeze-dried squid mantle or a commercial flake food for aquarium fish, will provide the comparative basis for determining the recipe to match the invertebrate tissue, which, again, should be calculated on a volumetric basis.

Along the same lines, the feeding state of the assay predator can have an important effect on the outcome of feeding experiments. Predators that have been starved are likely to consume artificial food offerings despite the presence of a chemical defense that would otherwise deter them. This problem is well known to experimentalists who regularly run feeding experiments, but few studies have quantified the importance of the feeding state of consumers [84]. It is likely that predators of marine invertebrates are well fed; observations of fishes on coral reefs certainly support this contention [10, 23]. Therefore, if experiments are to be performed in the laboratory, assay predators should be maintained on a healthy diet to observe normal feeding behavior. However, it is not uncommon to deny assay predators food for a short period of time prior to a feeding experiment in order to boost the speed at which a feeding choice is made.

12.4 Additivity and Synergism

Complicating any exploration of chemical defenses of marine invertebrates is the possibility that a single metabolite does not act in isolation but in association with other metabolites or in association with physical defenses. The interaction of the individual component defenses may be *additive*, that is, their combined deterrent effect is equal to the sum of their individual effects, or it may be *synergistic*, wherein their combined deterrent effect is greater than the sum of their individual effects. A third case, in which the interactive effect of components leads to a loss of activity, is termed *antagonistic* and is exemplified in the previously cited interaction between compounds that enhance feeding (e.g., amino acids) and chemical defenses.

Marine invertebrates are likely candidates for interactive effects of potential defenses. Many species of sponges, soft corals, and ascidians are known to contain in their tissues: (1) mixtures of secondary metabolites of the same structural class, (2) multiple secondary metabolites of different structural classes, and (3) skeletal elements, such as glass spicules (sponges) or calcitic inclusions (soft corals, ascidians). The possibilities for exploring the interactions among these components quickly become numerically astronomical, but what remains ecologically relevant is whether their sum is deterrent to potential predators, and this is an experimentally approachable question using the techniques already described. However, when components are separated and are no longer deterrent at natural concentrations, two questions arise: (1) Did degradation or loss of metabolites during isolation or

purification result in activity falling below some threshold level? (2) Did separation of multiple active components from each other result in activity falling below threshold? Additionally, the effectiveness of any combination of chemical or physical defenses may depend on the nutritional quality of the prey [85].

Experimental examinations of additivity or synergism are rare in chemical ecology [86], and the terms may be used improperly. The complexity of evaluating additive vs. synergistic effects is illustrated in an exchange of publications on the chemical and physical defenses of calcified marine algae against herbivorous fishes [68, 87, 88].

In only one case has a systematic statistical approach for identifying additivity or synergism been undertaken: Jones et al. [89] used an isobolographic analysis and logit model to examine the interaction between chemical defenses and spicules in the tissues of Caribbean sponges. For each sponge species examined, multiple assays of each defensive component (crude organic extract or isolated siliceous spicules) in artificial foods were performed using the bluehead wrasse fish as the experimental predator. Assays of serial dilutions of each defensive component were performed to determine the 50% effective dose (ED_{50}) of each, and then a series of combination assays were carried out at concentrations equal to or less than the ED_{50} of each component in isolation. Synergism between chemical and physical defenses at natural component concentrations was observed for three of seven sponge species that exhibited intermediate levels of chemical defenses, suggesting that spicules may synergistically enhance chemical defenses for some sponge species, but the authors suggested that this effect was more likely to be an exaptation of the primary function of spicules in sponges, which is to provide structural support to the organism. While Jones et al. [89] provided a novel analytical technique and an important proof of concept, their procedure has yet to be applied to defensive variability within a single species.

12.5 Optimization, Differential Allocation, Induction, and Activation

It is generally supposed that organisms are “optimized” in all respects for their environment by natural selection, but as discussed previously, this is certainly not true: The physical and biological environment changes through time, and evolution acts on the sum of the phenotypic characteristics that make up an individual organism – some will be more important at any one time, some less, some perhaps not at all. If defense is particularly important to the survival of an organism because predation is intense, and a coevolutionary “arms race” develops in which the prey must develop ever more sophisticated methods of combating predatory attack while somehow keeping the cost of those methods to a minimum, we might expect optimization of chemical defenses. In fact, optimization strategies have been described in the terrestrial chemical ecology literature, particularly for insects, and include mechanisms like differential allocation or induction of chemical defenses, as well as other protective measures, such as mimicry.

Chemical defenses that are *differentially allocated* are found at higher concentrations in the parts of an organism that are more susceptible to attack, thereby saving the organism the cost required to make and store defensive metabolites throughout its body. *Induction* describes the initiation of metabolite synthesis in response to tissue damage caused by predatory attack. An *induced chemical defense* is very economical because metabolites are produced only when needed, but the process would not provide immediate protection because metabolite synthesis would require some time. Another strategy often confused with induction is termed activation. An *activated chemical defense* is stored by the organism in a less bioactive form but is converted to a more potent form either when tissue is damaged or the defense is released in response to attack. The advantage of an activated defense to the prey is one of storage, in that it is potentially less costly to maintain relatively nontoxic precursor metabolites than to deal with autotoxicity from storing the product metabolite.

Evidence for optimized chemical defenses of marine invertebrates has been relatively scarce. This is interesting, because marine chemical ecologists often look for examples of optimized defenses in the system they are studying that parallel those described in terrestrial systems, not only to provide additional examples of the phenomena but also because they are intrinsically interesting, “just so” evolutionary narratives. When optimized defenses are found in a system, it is often interpreted that they can be generalized to other organisms, but when optimized defenses are not found, the research results are generally not published. Therefore, the paucity of reports of optimized chemical defenses among marine invertebrates more likely reflects scarceness rather than insufficient effort in uncovering the phenomena.

Differential allocation is certainly present in nudibranch mollusks, which have higher concentrations of deterrent metabolites in their dorsal surface and eggs [30], or associated with specialized glands on the dorsum and sides of the slugs [90]. For sessile benthic marine invertebrates, it has been claimed that some gorgonian corals invest higher levels of chemical defenses in their polyps than in the coenenchyme tissue that surrounds the axial skeleton of the coral [91], but the comparative data used to support this conclusion were based on gravimetric determinations of metabolite concentration (dry mass basis) rather than on a volumetric determination. Because the polyps of most gorgonians are free of calcitic sclerites, while the coenenchyme is infused with them to varying degrees, the high density of sclerites would result in much lower concentrations of metabolites on a dry mass basis in coenenchyme than on a volumetric basis, as explained previously [46]. Therefore, claims of differential allocation of chemical defenses in gorgonian corals await confirmation using a volumetric approach.

For sponges, differential allocation of defenses has been investigated for several species, with no evidence of the phenomenon in some [92] and some evidence in others [76, 93–95]. Here, the issue may be complicated by the method by which a predator feeds or whether the metabolite plays multiple roles. Fish predators of sponges take large bites of sponge tissue [23], which would make differential allocation ineffective [92]. But sea stars, the dominant invertebrate predators in

Antarctic benthic communities, feed by everting their guts on the surface of prey and appear to have driven the evolution of differential allocation of defenses to the surface tissues in some co-occurring sponge species [76]. The same may be true for sponges that are grazed by nudibranch mollusks [94] or have chemical defenses against fish predators that also serve as antifouling agents [93].

Differential allocation has been invoked for one species of morphologically distinct sponge from the Indo-Pacific, *Oceanapia* sp., which grows buried in the substratum but produces a stalk and cap structure that sticks up into the water column, where it is ostensibly subject to greater predatory attack [95]. As with the previous gorgonian example, the claim that the protruding structures contain higher concentrations of deterrent metabolites is confounded by the gravimetric (dry mass) method of determining metabolite concentration [95] because the concentration of glass spicules in the sponge tissue is highly variable, much greater in the sponge base and decreasing to the tip of the protruding structure. While the growth form of *Oceanapia* sp. certainly makes it a likely candidate for differential allocation of chemical defenses, volumetric measurements of metabolite concentrations will be needed to confirm this.

Induced defenses of marine invertebrates have been the subject of far fewer published studies than differential allocation of defenses, and in no case is there unequivocal evidence of the phenomenon. The chicken liver sponge *Chondrilla nucula* presents an excellent candidate for induced defenses: it has a high degree of intraspecific variability in chemical defense [16] and is abundant in a variety of habitats in the Caribbean, from reefs where fish predators are common to mangrove and grass bed habitats where they are rare. A more in-depth study of variation in chemical defenses of this species failed to resolve site-specific patterns in chemical defenses or induced increases in defense as a function of simulated predation [92].

Following up on preliminary data that suggested an induced defense [96], a transcriptome profiling approach was taken in a study of an Indo-Pacific soft coral *Sinularia polydactyla* that tracked changes in mRNA pool complexity as well as metabolite concentration for corals reciprocally transplanted to areas of high and low predation [97]. While there were clear differences in transcriptome complexity between transplanted corals, perhaps representing induced changes in metabolite production, the metabolite profiles in transplanted corals did not necessarily support induced defenses [97].

One of the more interesting and controversial areas of research into marine invertebrate antipredatory defenses has been that of activated defenses. It is important to remember that activated defenses are not optimized in the same way that differentially allocated or induced defenses are because these last two mechanisms reduce the overall expenditure of the organism on defensive metabolite production: They are cost-saving measures that optimize the use of defenses. An activated defense requires the synthesis of a full complement of precursor molecules, in addition to whatever enzyme or catalyst is required for conversion of the precursors into the defensive metabolite after the organism is attacked. As such, an activated defense could conceivably be *more expensive* to maintain than a constitutive defense. The potential advantage of an activated defense is one of

potency: A nonreactive precursor can be stored easily until attack, at which time tissue disruption and interaction of precursor and catalyst results in the nearly instantaneous formation of a highly deterrent (and possibly autotoxic) product metabolite. The foregoing is important because although it is easy to understand the evolution of resource-saving optimization schemes like differentially allocated or induced defenses (despite the paucity of evidence for their general existence among marine invertebrates), the evolution of activated defenses is more difficult to envision. After all, if the organism has to go to all the trouble of making the full complement of a chemical defense, why not make it constitutive?

An activated antipredatory defense was originally proposed for the Mediterranean sponge *Aplysina aerophoba* on the basis of laboratory experiments with freeze-dried sponge tissue [98]. Mechanistically, high molecular weight brominated tyrosine derivatives were thought to be rapidly converted by a putative enzyme to form smaller, more active chemical defenses after predatory damage to the sponge tissue. Because *Aplysina* spp. are found worldwide and all contain very similar secondary metabolites, it was proposed that this “biotransformation” was a common feature of the chemical defense of the genus. However, no evidence of activation was found in a combination of rigorous laboratory and field experiments with living specimens of two species of *Aplysina* in the Caribbean [99]. Without going into excessive detail, well over a decade after the initial report [98] and despite the rigorous field experiments performed in the Caribbean [99], there are now more than ten publications that directly relate to the putative activated defenses of *Aplysina* spp. [100]. The putative enzyme responsible for this activation defies isolation and characterization, and it is now suggested that the smaller brominated metabolites are important as antimicrobial agents that defend the wounded sponge tissue but not as antipredatory defenses [100, 101].

Another curious example of an activated defense has been described for the hydroid *Tridentata marginata*. Like most hydroids, *T. marginata* has stinging cells (cnides), but in addition it has a chemical defense against generalist fish predators that is effective even after the cnides have been discharged [102]. Further research suggested that the metabolites responsible for the chemical defense were stored in a nondeterrent form in the cnides, and that the crushing action associated with predation resulted in release and conversion to the deterrent metabolites, tridentatols A-C [103]. At one level, it is unclear why one species of hydroid should develop chemical defenses along with cnides while other co-occurring species have cnides alone, although the authors suggest that cnides offer a relatively ineffective physical defense in this species [102]. But in this example, the justification for activated defenses based on autotoxicity seems to be obviated by the isolation of the defensive precursors in cnide capsules.

The most recent example of an activation scheme has been proposed for the Indo-Pacific reef sponge *Aplysinella rhax*, a close relative of sponges of the genus *Aplysina* [104]. Maceration or wounding of the sponge tissue caused the rapid formation of psammaphin A from its sulfate salt, a reaction that was suggested to be enzyme catalyzed. The activated metabolite was claimed to be a more deterrent defense on the basis of feeding assays using fractions of extracts of the sponge, but

when the purified metabolite and the sulfate salt were assayed in the field, there was no difference in consumption of the two, casting doubt on the importance of the conversion as a requirement for an enhanced chemical defense. The authors of this study [104] suggest that evidence of activated chemical defenses have been underreported in the literature on marine chemical ecology, but an alternative explanation is that activated defenses are very rare (if they exist at all) for the simple reason that they do not provide an evolutionary advantage over constitutive defenses. Past observations of activated defenses in sponges may be attributable to differential tissue extraction efficiency, hydrolysis from less soluble precursors, or the heterogeneous distribution of metabolites in sponge tissue [99].

In summary, research to date warrants that claims of optimized or activated defenses among marine invertebrates be assessed with skepticism and with a higher standard of evidence. While the evolutionary narrative inspired by studies of terrestrial plants and insects is highly appealing, marine invertebrates in general have not been under the same selective predatory pressures that result in more complicated optimized defense strategies (Fig. 12.1). Comparing the basic aspects of the biology and ecology of marine invertebrates to terrestrial invertebrates (insects) may give us clues that explain why induction, differential allocation, and activation, as well as complex levels of aposematism and mimicry are common to the latter but not to the former: Marine invertebrates are fairly long-lived and exhibit indeterminate growth (some sponges may live thousands of years [105]), and while predation is an important part of their ecology, so too are other aspects, particularly recruitment. Terrestrial insects, on the other hand, may complete multiple generations in a single summer and exhibit determinate growth, and their populations are under intense and directed predatory pressure. Therefore, it is not surprising that many of the interesting phenomena found among butterflies and beetles are not evident among sponges, corals, and nudibranchs.

12.6 Resource Trade-Offs and the Cost of Chemical Defense

While terrestrial chemical ecologists have addressed costs in some systems [106–108], few studies in marine ecology have attempted to demonstrate that chemical defenses have a cost to the marine invertebrates that produce them. Perhaps the easiest way to address the cost of defense is to compare resource parameters within a species that has defended and undefended individuals, whether by constitutive (genotypic) or facultative (induced) means. As we have seen above, there are few examples of intraspecific variability in defenses among marine invertebrates, and none in which costs have been examined.

An alternative method for investigating the cost of chemical defenses is to quantify relative rates of growth or reproduction among co-occurring species that exhibit different levels of defense. Assuming that all life functions (respiration, growth, reproduction) have a cost, the production of chemical defenses should result in a trade-off, such that defended species exhibit lower rates of growth or reproduction than undefended species. Making this comparison can be difficult,

either because relative levels of defense among species in the community are unknown or because all the species in the community are similarly well defended, as in Caribbean gorgonian corals [46]. Moreover, different species may invest in mechanisms other than chemical defenses, which are also likely to have costs. Also, if endosymbionts of a chemically defended invertebrate (e.g., zooxanthellae in hard and soft corals) are responsible for the production of the chemical defense, it may come at little or no cost to the host invertebrate.

The Caribbean coral reef sponge community has provided an interesting system in which trade-offs between chemical defense and life functions have been evident. The most common sponges on Caribbean reefs are either chemically defended or undefended [16], and the latter group is consumed by a suite of sponge-eating fishes [10, 23]. When the rate of wound healing was compared between the two groups, undefended species were found to heal much faster than defended species [109]. More indicative of resource trade-offs between the two groups, however, were the results of surveys of an artificial reef shipwreck that provided new substratum for sponge recruitment and growth [110]. If undefended sponge species are able to divert metabolic resources to growth and reproduction, they would be expected to colonize new substrata faster than defended species that use their resources to synthesize and store chemical defenses. And in fact, undefended sponge species dominated an artificial reef shipwreck off the Florida Keys 4 years after it was sunk (96.0% of sponge cover was made up of undefended species vs. 15.2% on adjacent reefs), with initial recruits of defended species observed 18 months later [110], corroborating a resource trade-off between chemical defense and reproduction or growth.

12.7 Structure-Activity Relationships and the Commonality of Chemical Defenses

In pursuit of developing more effective insecticides, plant–insect chemical ecologists have systematically investigated the relationships between metabolite structure and feeding deterrent activity for many insect species [111]. Similar efforts have been rare in marine chemical ecology. When multiple pure compounds have been assayed together for feeding deterrent activity, it is not uncommon for comparisons to be made and preliminary conclusions drawn about relationships between structure and activity [59, 112], but these have not addressed the issue in a systematic way.

One study has examined the relationship between metabolite structure and feeding-deterrent activity for a series of analogs having minor modifications to determine the importance of metabolite size, shape, and functionality [113]. Using a fish feeding assay, 21 compounds, including pyrrole-imidazole alkaloids isolated from sponges of the genus *Agelas* and synthetic analogs, were tested at a range of concentrations. Additional observations of structure-activity relationships for metabolites from *Agelas* sp. were reported in a companion publication [114]. The pyrrole moiety was required for feeding deterrent activity, while the imidazole

group enhanced activity. Imidazole metabolites lacking the pyrrole were not active, while feeding-deterrent activity was enhanced by dimerization, increased polarity, or the addition of bromine.

Interestingly, there do not yet appear to be any common structural themes among secondary metabolites that have been isolated and identified as chemical defenses of marine invertebrates. Compounds of several classes and of very different polarities are represented among feeding deterrents, from nonpolar terpenoids [115] to polar glycosides [116]. This variability suggests that compound polarity, and therefore solubility in water, is not a critical factor in the evolution of marine invertebrate chemical defenses. Bad-smelling volatile compounds present in some sponges do not appear to act as chemical defenses [61]. While acidity is known to deter feeding, and is used by some ascidians as a chemical defense [83], this mechanism of defense is surprisingly uncommon, and many ascidians also have secondary metabolites as chemical defenses [59], perhaps suggesting that the metabolic demands of containing inorganic acids within invertebrate tissues are greater than their advantages relative to organic compounds as chemical defenses.

Recent technical developments in molecular genetics may permit structure-activity relationships to be addressed at the cellular level. Metabolites from the sponges *Ectyoplasia ferox* and *Erylus formosus* that had previously been identified as feeding deterrents using co-occurring fish predators [116, 117] also deterred feeding of the freshwater zebra fish [118]. Transcripts made from a zebra fish cDNA library were expressed in the oocytes of the frog *Xenopus laevis* and tested for chemoreceptor activation using electrophysiological techniques. Oocytes expressed gene sequences from the library and exhibited electrophysiological responses when exposed to the deterrent metabolites formoside and ectyoplasides A and B, indicating that the chemical defense-activated signaling pathway was reconstituted in *Xenopus* oocytes [118].

There is some evidence that chemical defenses may be broadly effective against predators, not only against different species (such as fishes) [79, 119], but also against different predatory taxa (crabs, seastars) [69, 70]. This commonality in response suggests that chemoreceptive responses of diverse taxa of predators are similar at the molecular level. In at least one case, for triterpenoid glycosides from two Caribbean sponges, multiple defensive roles have been proposed that extend beyond antipredatory effects to allelopathic and antifouling functions [93]. In terms of resource allocation, the advantages of multifunctional defenses are clear, and this is an area that is ripe for further investigation.

12.8 Study Questions

1. An eminent Ivy League bryozoan taxonomist finishes her survey of Indonesian coastal waters and sends 410 dried bryozoan samples representing 53 species ($N > 2$ for each) to her first-year graduate student, with instructions to investigate their chemical defenses. Following the advice of the elderly entomologist in the lab next-door, the graduate student decides to use diethyl ether as the sole

extraction solvent and to run Microtox toxicity assays on serial dilutions of each extract as a function of extract dry mass. He is delighted to discover very clear differences in toxicity between mangrove and coral reef species and runs a complex statistical analysis to support his conclusions. He submits their work on “The chemical defenses of Indonesian bryozoans” to a top-rated ecology journal.

Q1: What problems are reviewers of this manuscript likely to cite in recommending that it not be published?

Q2: What should the graduate student do after receiving the negative decision?

2. A graduate student in a natural products laboratory is studying the variability of secondary metabolites in a species of soft coral that produces a potential anti-cancer drug, xenopterolide. She determines that there is a significant difference in the mean concentration of xenopterolide, which is also a well-known fish feeding deterrent, in replicate samples ($N = 20$) from high-flow reef crest environments ($30 \mu\text{g}$ xenopterolide/mg dry tissue mass) vs. low-flow patch reef environments ($100 \mu\text{g}/\text{mg}$). She concludes that fish predation on this soft coral is more intense in patch reef environments.

Q3: What is an alternative explanation? Hint: Soft corals increase the density of their skeletal elements (limestone sclerites) as a function of increasing flow regime.

Q4: How would you re-design the methodology for this project?

3. A postdoctoral researcher is studying seasonal variation in secondary metabolite concentration in a species of sponge by removing a tissue sample from each of 20 sponges every month for a year (no sponge is sampled more than once). The sponge is hermaphroditic, producing sperm and eggs in the spring, brooding large numbers of large embryos throughout its tissue for several months, and then releasing them in late summer. The researcher determines metabolite concentrations as a function of both volume and mass.

Q5: What pattern of metabolite concentration might the researcher expect to see, on a gravimetric vs. volumetric basis, if the sponge tissue is full of glass spicules, but the embryos are free of spicules?

Q6: What if neither sponge nor embryos have spicules?

Q7: What if the sponge differentially provisions embryos with high levels of chemical defenses?

Q8: For a seasonal study like this, why might the investigator also want to measure the mass of the crude organic extract for each tissue sample?

4. An MS graduate student completes his 2-year dissertation research on the ecological functions of a suite of previously characterized secondary metabolites in a temperate colonial ascidian. He uses all the proper extraction and assay techniques to explore possible defenses against several co-occurring predators, as well as meticulously investigating antifouling, allelopathic, and antimicrobial functions. His data show no defensive effect of the metabolites in any of his assays. His advisor is sympathetic but tells him that his work is not publishable because “nobody should publish negative results” and that “all secondary

metabolites must have ecological functions, otherwise the organism wouldn't make or store them."

Q9: Why is the advisor wrong about each of the statements in quotes?

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Antipredatory Defensive Role of Planktonic Marine Natural Products

13

Adrianna Ianora, Antonio Miralto, and Giovanna Romano

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Abstract

This chapter deals with chemical ecology and the role of antipredatory metabolites in the plankton and how such plant–herbivore interactions structure communities in the pelagic zone of the oceans. The first section deals with antiproliferative compounds produced by unicellular diatoms that induce abortions or congenital defects in the offspring of zooplankton crustaceans such as copepods exposed to them during gestation. Such teratogenic compounds include numerous oxylipins, and polyunsaturated aldehydes (PUAs) in particular, that are very similar to those produced in higher terrestrial plants. Oxylipins are believed to play a pivotal role in plant defense because they act as chemical attractors (e.g., pheromones, pollinator attraction) or alarm signals against

A. Ianora (✉) • A. Miralto • G. Romano
Functional and Evolutionary Ecology, Laboratory Stazione Zoologica Anton Dohrn,
Villa Comunale, Naples, Italy
e-mail: adrianna.ianora@szn.it, antonio.miralto@szn.it, romano@szn.it

herbivore attack (e.g., in tritrophic interactions) and as protective compounds (antibacterial, wound healing). The second section in this chapter deals with neurotoxic compounds (e.g., saxitoxins, brevetoxins, and others) produced mainly by dinoflagellates which induce severe pathologies (i.e., paralytic, neurotoxic, diarrhetic, and amnesic shellfish poisoning) in humans that consume shellfish containing high levels of these toxins and which are generally considered as feeding deterrents in the plankton. Strong physiological responses have also been reported in several copepod species after <24 h of feeding on these cells, such as elevated heart rates, regurgitation, loss of motor control, and twitching of the mouthparts, decreased feeding, decreased fecundity, delayed development, and direct mortality. Another important feeding deterrent in the plankton includes dimethylsulfoniopropionate (DMSP) found in numerous species of phytoplankton, but most prominently in the prymnesiophytes and dinoflagellates, which appears to act as a signal molecule or indicator of inferior prey rather than as a toxin. We discuss the environmental conditions which promote increased production of these metabolites and some of the classic bioassays to test their biological activity. We also discuss the multiple functions of antipredatory metabolites and the importance of chemical interactions in the plankton for shaping biodiversity and ecological functioning both at the community and cellular level.

13.1 Introduction

Plankton is the collective name for small or microscopic organisms that float or drift in large numbers, especially in the photic zone of the oceans. Plankton is of great importance because it serves as food for fish and larger organisms, and indirectly for humans whose fisheries depend on plankton. The plant-like component of the plankton is called phytoplankton and includes single-celled algal groups such as diatoms, dinoflagellates, coccolithophores, and other protists. The animal component is called zooplankton and is dominated mainly by crustaceans that subsist on phytoplankton and other small zooplankton. Copepods and other zooplankton crustaceans graze on large quantities of phytoplankton cells that must escape, deter, or tolerate herbivores in order to persist. Herbivory is therefore an important pressure for the evolution of defensive compounds in marine phytoplankton, as for terrestrial higher plants, and for shaping prey–predator relationships in the pelagic environment. These chemicals are secondary metabolites or natural products that are not directly involved in primary metabolism. They differ from the more prevalent macromolecules, such as proteins and nucleic acids that make up the basic machinery of life. Often, secondary metabolites constitute a very small fraction of the total biomass of an organism, and it is not always clear what the biological function of these compounds actually is. In recent years, it has become increasingly apparent that these metabolites have important ecological functions and may at times contribute as much as primary metabolites to the survival of the producing organism. The science that considers chemical interactions between

organisms and their environment is termed chemical ecology, considered one of the fastest growing and rapidly evolving environmental subdisciplines.

Research on chemically mediated interactions in the marine environment has historically focused on predator–prey interactions in the benthos, and there is now a considerable amount known about feeding preferences and deterrent molecules in macroalgae, sponges, mollusks, and corals (see ► [Chapter 12](#)). Much less is known on the chemical ecology of planktonic marine organisms. We also know very little as to why zooplankton avoid certain compounds, and few studies have assessed what happens when secondary metabolites are consumed. Studies on chemical interactions in the plankton are still in their infancy, but there is an increased awareness that natural products play fundamental roles as defenses against predators, competitors, and pathogens, and therefore drive ecosystem functionality in the plankton. In this chapter, we focus on some of the better studied antipredatory defenses in the plankton, and more specifically on where the specific compounds have been identified and tested in pure or semipurified form in manipulative experiments. The chapter does not attempt to provide a comprehensive overview on this subject, but rather to illustrate some examples of the diversity and importance of chemically mediated interactions involving planktonic organisms ([Fig. 13.1](#)), and some of the methodologies that have developed in this field in recent years. In the following sections, we focus on compounds that induce reproductive failure in grazers and those that induce feeding deterrence and mortality (summarized in [Table 13.1](#)). We then discuss the environmental conditions which promote increased production of these metabolites and some of the classic bioassays to test the biological activity of phytoplankton natural products on predatory copepods.

13.2 Antiproliferative Compounds

13.2.1 Diatom Oxylipins

The strongest evidence that phytoplankton use chemical defense to deter planktonic grazers comes from the work initiated over a decade ago on diatom oxylipins. Diatoms have traditionally been viewed as beneficial to the growth and survival of marine organisms and to the transfer of organic material through the food chain to top consumers and important fisheries. However, while diatoms may provide a source of energy for copepod larval growth, they often reduce fecundity and/or hatching success. These results constitute the paradox of diatom–copepod interactions in the pelagic food web [[12](#)]. This biological model is new and has no other equivalent in marine plant–herbivore systems, since most of the known negative plant–animal interactions are generally related to repellent or poisoning processes, but never to reproductive failure.

In terrestrial environments, there are many reports of compounds produced by plants that interfere with the reproductive capacity of grazing animals, and which act as a form of population control. These compounds are referred to as teratogens or substances that induce abortions or congenital malformations in the offspring of

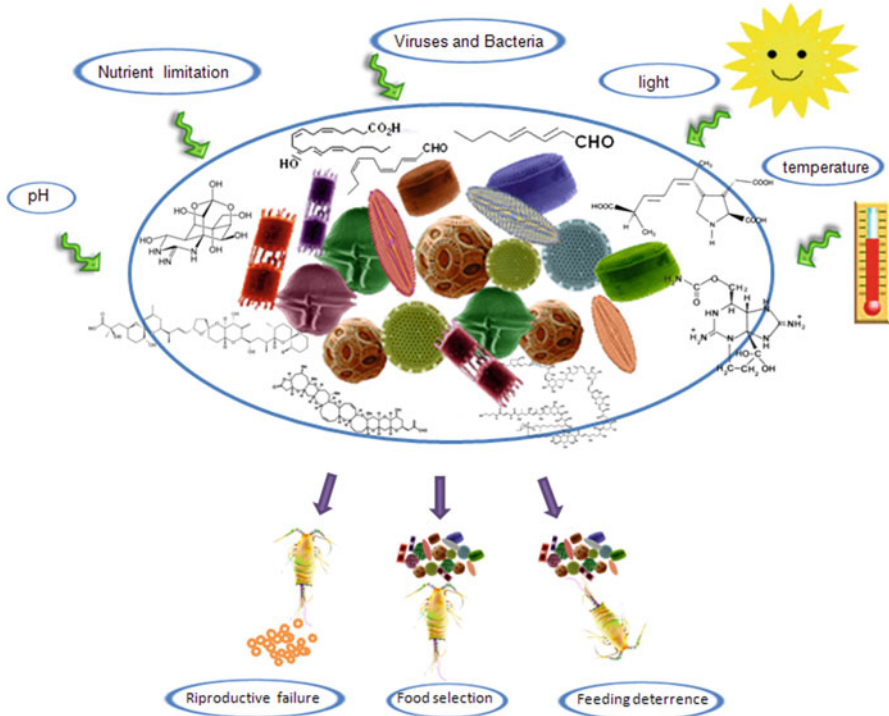


Fig. 13.1 Schematic representation of the environmental factors affecting the production of phytoplankton secondary metabolites (*green arrows*) and the effects of these metabolites on planktonic predatory copepods (*blue arrows*)

mothers exposed to them during gestation. Some classic examples of teratogens include caffeine, present in many plants processed for use as beverages and foods, and nicotine, the principal chemical present in tobacco. Nicotine has been shown to have possible teratogenic effects on fetal development in humans, and it is now widely accepted that pregnant woman should avoid smoking during their pregnancy. The same compound has been shown to have strong effects also in range animals that ingest tobacco plants, with newborns showing limb deformities and palate closure defects associated with the high content of nicotine in their tissues [13].

Nothing was known on the presence and effects of such compounds in the marine environment until the discovery of diatom oxylipins, including polyunsaturated aldehydes (PUAs), produced by diatom cells from precursor membrane-bound lipids [5, 14–16]. Diatom PUAs were first isolated by Miralto et al. [1] who showed, *in vitro*, that they reduced copepod hatching success, cleavage of sea urchin embryos, and proliferation of human adenocarcinoma cells. The same authors showed that diatoms also modified copepod hatching success in the field in February 1997 and 1998 during two major diatom blooms in the North Adriatic

Table 13.1 Effects of secondary metabolites produced by phytoplankton on predatory copepods. Only characterized compounds known to be produced by microalgae and for which the specific toxicity has been determined are reported (modified from Ianora et al. [152])

Compounds	Producer	Target organism	Effect	Mode of action	References
Decatrienal PUAs	<i>Thalassiosira rotula</i> and other <i>Thalassiosira</i> species	Copepods	Reduced hatching success, abnormal nauplii, growth inhibition	Antimitotic, apoptosis	[1, 2]
Octatrienal, octadienal, heptadienal	<i>Thalassiosira rotula</i> , <i>Skeletonema marinoi</i>	Copepods	Reduced hatching success, abnormal nauplii, growth inhibition	Antimitotic, apoptosis	[3, 4]
Hydroxy- and epoxy-fatty acid pool	<i>Thalassiosira rotula</i> , <i>Skeletonema marinoi</i> , <i>Pseudo-nitzschia delicatissima</i> , <i>Chaetoceros affinis</i> , <i>Chaetoceros socialis</i>	Copepods	Reduced hatching success, abnormal nauplii, growth inhibition	Antimitotic, apoptosis	[5, 6]
Fatty acid hydroperoxides	<i>Thalassiosira rotula</i> , <i>Skeletonema marinoi</i> , <i>Pseudo-nitzschia delicatissima</i> , <i>Chaetoceros affinis</i> , <i>Chaetoceros socialis</i>	Copepods	Reduced hatching success, abnormal nauplii, growth inhibition	Antimitotic, apoptosis	[5, 6]
Oxoacids	<i>Pseudo-nitzschia delicatissima</i>	Copepods	Reduced hatching success, abnormal nauplii, growth inhibition	Antimitotic, apoptosis	[7]
DMSP: acrylate, DMS	<i>Emiliana huxleyi</i>	Protistan, crustacean	Feeding deterrence, search behavior	Unknown	[8]
Apo-fucoanthin	<i>Thalassiosira weissflogii</i> , <i>Phaeodactylum tricorutum</i>	Copepods	Feeding deterrence	Unknown	[9, 10]
PSP ^a	<i>Alexandrium</i> sp.	Copepods	Feeding deterrence	Unknown	[11]

^aPSP saxitoxin (STX), neo-STX, gonyautoxin (GTX), C-toxins

Sea. Egg viability in these periods was only 12% and 24%, respectively, of the total number of eggs produced compared to 90% after the bloom in June indicating that copepod recruitment was higher during postbloom conditions and not during the bloom as previously assumed.

Oxyplins, and PUAs in particular, have important biological and biochemical properties including the disruption of gametogenesis, gamete functionality,

fertilization, embryonic mitosis, and larval fitness and competence [17]. PUAs are also apoptogenic inducers through the activation of specific caspases that lead to the enzymatic breakdown of DNA [18, 19]. PUAs may be sequestered during oocyte development and be passed maternally to the embryo, or may act directly on embryos. By whichever route, the timing of reproduction in relation to toxic diatom abundance will have important consequences for invertebrate recruitment [20–22].

The PUA decadienal is the best-studied metabolite of this group and thus has become a model aldehyde for experimental studies on the effects of oxylipins on marine organisms. Numerous functions have been proposed for this highly reactive molecule, such as grazer defense [1, 23], allelopathy [24, 25], cell to cell signaling [26, 27], antibacterial activity [28], and bloom termination initiator [7, 29]. In terms of grazer defense, decadienal has been shown to negatively affect reproductive processes in planktonic copepods (reviewed by Ianora and Miralto [30]) and cladocerans [31], and benthic echinoderms [17, 18, 22], polychaetes [32], ascidians [33], mollusks [34], and benthic copepods [35] with widespread consequences on ecosystem functionality (Table 13.1).

The discovery of an enzyme cascade leading to the production of volatile biologically active oxylipins in marine phytoplankton is rather new [30] even though the oxidative cleavage of fatty acids to form similar defensive compounds is well known in higher terrestrial plants [36, 37] and freshwater microalgae [38]. Several papers have described the biochemical pathways leading to PUA production [6, 39]. Pohnert [40] described that the transformation of polyunsaturated fatty acids (PUFAs) such as C20 in the diatom *Thalassiosira rotula* was initiated by phospholipases, in particular phospholipase A2, that act immediately after cell damage. Liberated C20 PUFAs such as eicosapentaenoic (EPA) and arachidonic acids are then further converted by lipoxygenases and lyases to PUAs. Pohnert [40] suggested that in contrast to higher terrestrial plants that use lipases acting on galactolipids to release C18 linoleic fatty acids for the production of aldehydes, diatoms rely on phospholipids and the liberation of C20 EPA fatty acids by phospholipases to produce decadienal and decatrienal.

However, d'Ippolito et al. [15] described an alternative biochemical pathway from other complex lipids in the diatom *Skeletonema marinoi* which involves the hydrolysis of chloroplastic glycolipids and release of C20 EPA and C16 PUFAs such as hexadecatrienoic and hexadecadienoic acids. They showed that chloroplasts have a direct role in the production of PUAs in diatoms, similar to what occurs in higher terrestrial plants [36]. They proposed a biochemical pathway leading to the production of PUAs in diatoms whereby C20 and C16 PUFAs are liberated from chloroplast glycolipids and phospholipids by lipolytic acyl hydrolases. These PUFAs are then rapidly transformed into unstable hydroperoxides by either 9-lipoxygenase (LOX), 11-LOX, or 14-LOX enzymes. Hydroperoxides are, in turn, rapidly transformed to PUAs such as 2,4-heptadienal, 2,4-octadienal, and 2,4,7-decatrienal depending on the LOXs and other downstream enzymes present in the diatom cells.

The synthesis of PUAs begins immediately after cell wounding, thus implying that the proteins responsible for the oxidative metabolism of C16 and C20 fatty

acids are expressed constitutively in diatom cells. By studying the downstream enzymatic activity responsible for PUA synthesis, d'Ippolito et al. [41] demonstrated that the diatom *T. rotula* possesses an enzymatic arsenal capable of transforming C16 and C20 PUFAs to 2,4-octadienal or 2,4,7-decatrienal, whereas in the diatom *S. marinoi*, C16 and C20 PUFAs serve as specific substrates for the production of 2,4-heptadienal and 2,4-octadienal.

A mechanism for the production of PUAs only after cell lysis has been proposed so that toxins are released directly into the body of grazers [42], thereby avoiding intoxication to the diatom cells [24]. Fontana et al. [6] measured PUA production with time and showed that formation of PUAs begins soon after sonication of cells and increases steadily for several minutes thereafter, reaching concentrations of up to 50 fg cell⁻¹ in the diatom *T. rotula*. When PUAs are removed by keeping the cells under vacuum for 15 min, production is reinitiated immediately, giving rise to even higher levels (up to 100 fg cell⁻¹) 40 min later. More recently, Romano et al. [22] have shown that decadienal can be detected spectrophotometrically for up to 14 days in closed culture containers.

A major advancement in the study of the chemistry of diatoms was the discovery that they produce cytotoxic compounds other than PUAs (Fig. 13.2). Wichard et al. [2] had shown that only 36% of the investigated 51 species released PUAs upon cell damage, with PUA concentrations ranging from 0.01 to 9.8 fmol cell⁻¹ depending on the species or strain, thereby suggesting that many diatoms do not produce these compounds. But, at about the same time, d'Ippolito et al. [43] showed that the diatom *T. rotula* had an oxidizing potential capable of converting PUFAs to a variety of other unprecedented oxylipins, as later confirmed by Fontana et al. [5]. Fontana and coworkers compared the effects of the well-known PUA-producing diatom *S. marinoi* [1, 23] with two *Chaetoceros* (*C. similis* and *C. affinis*) species which did not produce PUAs, but which nonetheless impaired hatching success. They showed that when the *Chaetoceros* species were damaged, they produced fatty acid hydroperoxides and oxylipins such as hydroxyacids (HEPEs) and epoxyalcohols (HepETEs), as well as highly reactive oxygen species (ROS) of low acute toxicity to adult copepods but which depressed the viability of copepod gametes and offspring. Two of these compounds, 15S-HEPE and threo-13,14-HepETE, have now also been reported by d'Ippolito et al. [7] in the non-PUA-producing pennate diatom *Pseudo-nitzschia delicatissima* which produces large amounts of these metabolites in the late exponential and stationary phase of growth. d'Ippolito et al. also reported the presence of another metabolite, 15-oxo-5Z,9E,11E,13E-pentadecatetraenoic acid, which was only present in small amounts in the late stationary phase of the culture, demonstrating a precise timing in the production of these compounds during various stages of the cell cycle. Pohnert et al. [44] had already suggested the presence of aldehydic 9-oxo-nonadienoic and 12-oxo-dodecatienoic acids (12-ODTE) in the non-PUA-producing diatom *Phaeodactylum tricorutum* on the basis of the detection of high amounts of the C11-hydrocarbon hormosirene and the C8-hydrocarbon fucoserratene after wounding. Indeed, as reported by Pohnert and Boland [45], these hydrocarbons are released together with the aldehydic acids 9-ONDE and 12-ODTE by

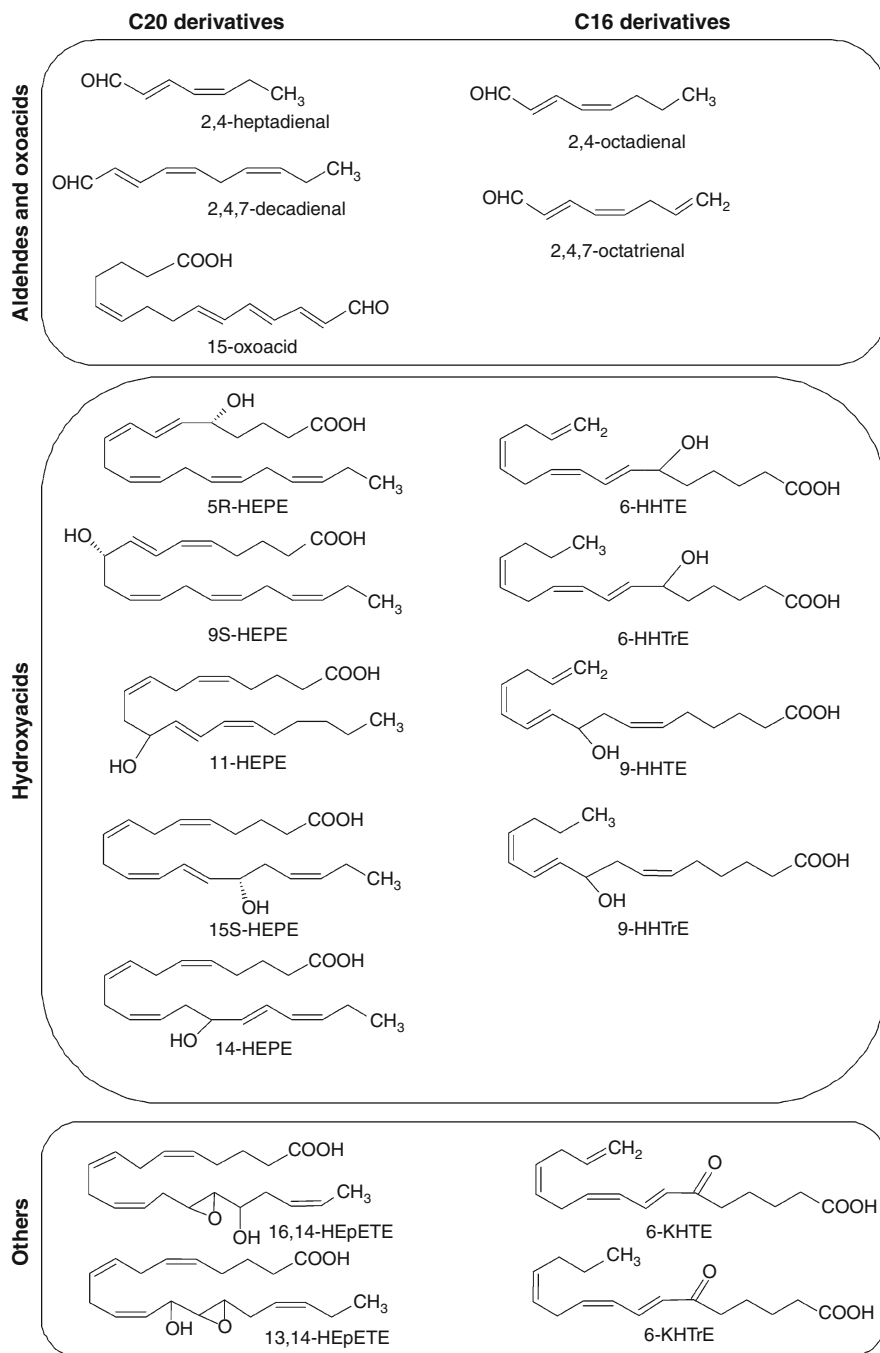


Fig. 13.2 (continued)

freshwater diatoms. These products are very similar to those produced by terrestrial plants [37], as shown in Fig. 13.3. A major difference, as in the case of PUAs, is in the precursor PUFAs, C16 and C20 fatty acids, used to synthesize these compounds in diatoms [39, 43] compared to the C18 fatty acids in terrestrial plants [36, 37]. Oxylipins formed in flowering plants include fatty acid hydroperoxides, hydroxyl- and keto-fatty acids, oxoacids, epoxyalcohols, divinyl ethers, PUAs, and the plant hormones 12-oxo-phytodienoic acid and jasmonic acid [46], several of which have not yet been found in diatoms (e.g., jasmonic acid). Oxylipins are believed to play a pivotal role in plant defense because they act as chemical attractors (e.g., pheromones, pollinator attraction), alarm signals against herbivore attack, and protective compounds (antibacterial, wound healing). Diatom oxylipins also show a high similarity to volatile organic carbons released from brown algae which are suggested to be involved in chemical signaling and pheromone attraction between gametes of different sex [46].

Testing the biological activity of oxylipins other than PUAs is quite recent. Pohnert et al. [44] reported that the lethal dose to induce 50% mortality (DL-50) in sea urchins with 12-ODTE was reached at concentrations around 9–10 μM which was in the range observed for decadienal (7.3 μM). Fontana et al. [5] found that a pool of oxylipins, other than PUAs from the diatom *S. marinoi*, blocked hatching success of the copepod *Calanus helgolandicus* at about 70 μM compared to a pool of aldehydes from the same diatom (32 μM) with induction of apoptosis and malformations in hatched nauplii for both pools of compounds. More recently, Ianora et al. [47] tested the hydroxyacid 15S-HEPE on newly spawned eggs of the copepod *Temora stylifera*, showing that this metabolite blocked hatching success at about 94 μM compared to heptadienal and decadienal (45 and 32 μM , respectively). All three compounds induced apoptosis and malformations in hatched nauplii. Taken together, these results indicate that PUAs are not the only class of molecules inducing reproductive failure in copepods. The “diatom effect” is therefore not due to a single class of compounds (i.e., PUAs), as previously believed, but rather to a blended mixture or bouquet of toxins which grazers are exposed to during feeding. Oxylipins such as 9S-hydroxyhexadecatrienoic (9S-HHTrE) and 9S-hydroxyhexadecatetraenoic (9S-HHTe) have also been found at sea, during a late spring bloom in the North Adriatic Sea of the non-PUA-producing diatom



Fig. 13.2 Diatom oxylipins characterized to date deriving from the oxidation of C16 and C20 fatty acids. Information on diatom species producing these compounds is given in Ianora and Miralto [30]. 5R-HEPE = 5R-hydroxy-(6,8,11,14,17)-eicosapentaenoic acid; 9 S-HEPE = 9 S-hydroxy-(5,7,11,14,17)-eicosapentaenoic acid; 11-HEPE = 11-hydroxy-(5,8,11,15,17)-eicosapentaenoic acid; 15 S-HEPE = 15 S-hydroxy-(5,8,11,13,17)-eicosapentaenoic acid; 14-HEPE = 14-hydroxy-(5,8,11,15,17)-eicosapentaenoic acid; 6-HHTe = 6-hydroxyhexadeca-(7,9,12,15)-tetraenoic acid; 6-HHTrE = 6-hydroxyhexadeca-(7,9,12)-trienoic acid; 9-HHTe = 9-hydroxyhexadeca-(6,10,12,15)-tetraenoic acid; 9-HHTrE = 9-hydroxyhexadeca-(6,10,12)-trienoic acid; 13,14-HEpETE = 13-hydroxy-(14,15)-epoxy-5,8,11,17-eicosatetraenoic acid; 16,14-HEpETE = 16-hydroxy-(14,15)-epoxy-5,8,11,17-eicosatetraenoic acid; 6-KHTe = 6-ketohexadeca-(7,9,12,15)-tetraenoic acid; 6-KHTrE = 6-ketohexadeca-(7,9,12)-trienoic acid

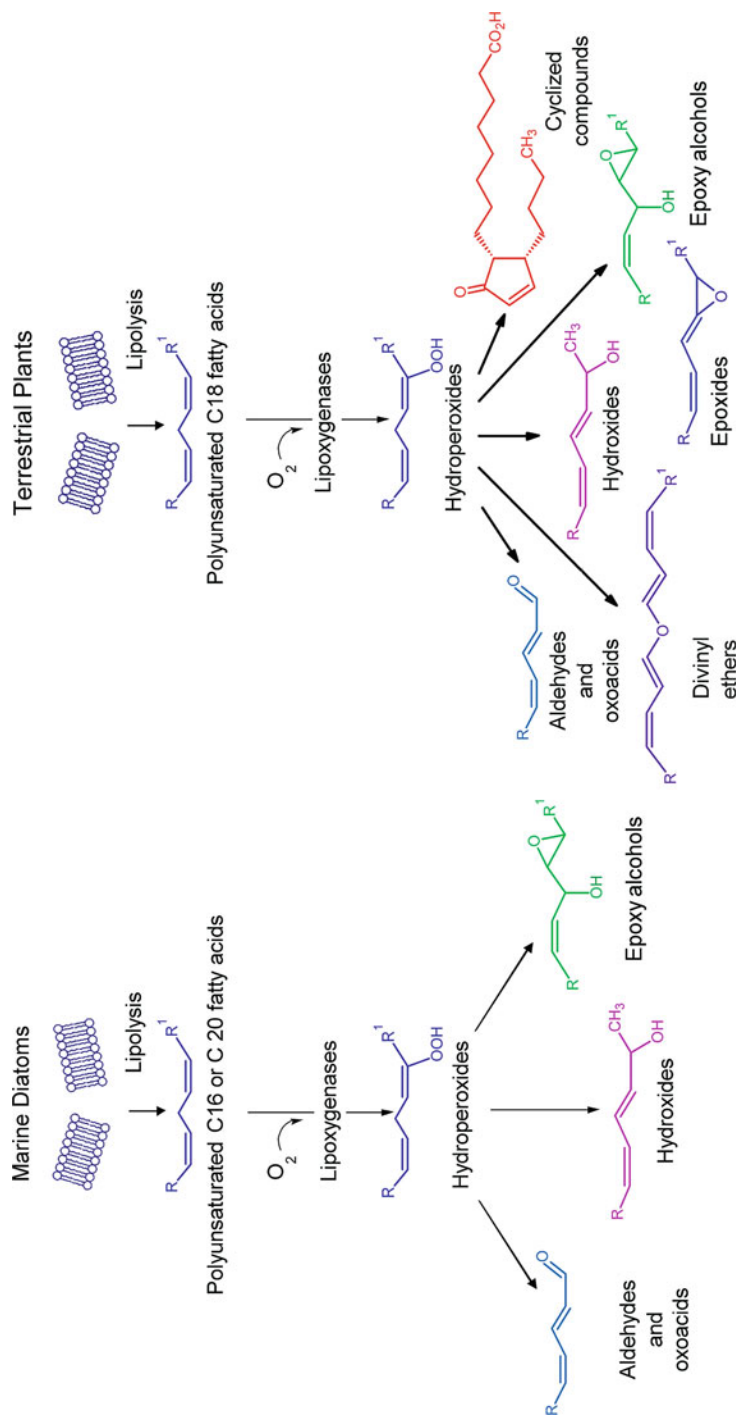


Fig. 13.3 Oxidative metabolism of fatty acids in (a) marine diatoms and (b) terrestrial plants. Starting mainly from eicosapentaenoic (C20) and exadecatetraenoic (C16) fatty acids in diatoms or from octadeca(e)noic (C18) fatty acids in plants, both oxidative pathways involve oxygenation of these fatty acids by oxygen addition through lipoxygenase activity to a *cis,cis*-1,4-pentadiene moiety

Cerataulina pelagica, the likely cause for reduced egg production and hatching success in *Acartia clausi*, *Calanus helgolandicus*, and *Temora longicornis* [48].

Diatoms are not the only class of marine phytoplankton to produce oxylipins. The bloom-forming phytoplankter *Phaeocystis pouchetii* (Prymnesiophyceae) has been shown to produce and release decadienal [19] even though it remains unclear as to what amounts are produced. In freshwater environments, PUAs are commonly released by diatoms and chrysophytes (see [49] and references therein) through cell lysis, independently from grazing, conferring rancid smells to source drinking water [50]. In this case, PUAs may not only serve to deter grazers [51] but may also function as intra- or interspecific signals, for example, to modulate population density or to signal the presence of pathogens or predators [52]. Their widespread occurrence in marine and freshwater photoautotrophs may be an indication of the great ecological importance of these compounds.

An alternative hypothesis for the ecological function of PUAs by diatoms was recently developed by Jüttner ([49] and references therein). Upon cell damage, diatom-dominated biofilms release small quantities of PUAs that are efficient repellents for herbivorous zooplankton. These substances probably function as “warning cues,” since upon cell damage, diatoms release high amounts of the polyunsaturated eicosapentaenoic acid (EPA) which is highly toxic for crustacean herbivores. Following cell wounding, a small fraction of the released EPA is further converted into PUAs which, in turn, can be detected by the grazers. Thus, grazers that initiate feeding on these diatoms cause the liberation of an activated warning cue that repels them, thereby protecting them from the toxic EPA and protecting the diatom from herbivores. A major challenge for the future will be to understand the ecological function of these metabolites and the physiological factors that lead to their production. We have just begun to understand the role of diatom oxylipins in the plankton, and there remains great scope for research into the effects of these toxins on gamete, embryonic, and larval development of herbivorous grazers.

13.2.2 Dinoflagellate Antiproliferative Compounds

Hatching failure in copepods can also depend on poor sperm quality. Interestingly, such effects have mainly been reported in copepods fed with dinoflagellate diets. For example, *Prorocentrum micans*, *Gymnodinium sanguineum* and *Gonyaulax polyedra* significantly modified spermatophore production and reduced the fertilization capacity of male sperm after 6–12 days of continuous feeding in the copepod *T. stylifera* [53]. A reduction in fertilization capacity was neither due to maternal effects nor to male age since hatching success returned to normal when males were substituted with freshly caught wild males or males conditioned with a good diet such as the dinoflagellate *Prorocentrum minimum* for the same length of time as couples fed with the poor diets. Microscope images of unhatched eggs colored with a nucleus-specific fluorescent dye showed that these eggs had not been fertilized.

Ianora et al. [54] later showed that extracts of a nontoxic strain of the dinoflagellate *Alexandrium tamarense* blocked fertilization but not cell divisions in sea

urchin embryos. Of the two organic extracts of *A. tamarensis*, the one obtained in MeOH was the more active, and one of the fractions obtained by its separation on Sephadex LH-20 resin blocked fertilization of sea urchin oocytes at concentrations of $1 \mu\text{g mL}^{-1}$. The PUA decadienal, used as a control, had little or no effect on fertilization success at any of the concentrations tested. By contrast, the *A. tamarensis* active fraction had little or no effect on sea urchin first cell cleavage as opposed to decadienal, which blocked cell cleavage at concentrations of $1 \mu\text{g mL}^{-1}$.

There are several examples of compounds isolated from marine dinoflagellates that block cell divisions in the classic sea urchin bioassay. These include goniodomin-A from *Goniodoma pseudogoniaulax* [55], amphidinolide-A from *Amphidinium* sp. [56], and okadaic acid and its derivative dinophysistoxin-1, which are common in some species of the genera *Prorocentrum* and *Dinophysis*, respectively [57]. Extracts of *A. tamarensis* may also inhibit egg hatching and larval survival in the scallop *Chlamys farreri* [58]. In all of these studies, the molecules or extracts tested showed antimitotic activity with blockage of cell divisions in developing sea urchin embryos. In Ianora et al. [54], however, there was little or no adverse effect on cell cleavage, but very strong effects on fertilization success when oocytes were incubated for 30 min in *A. tamarensis* extracts.

Clearly, these compounds were not feeding deterrents since both male and female *T. stylifera* copepods fed well on this *A. tamarensis* strain, with fecal pellet production rates comparable to other dinoflagellate (*P. minimum*) diets [53]. Nonetheless, there were adverse effects on other life-history parameters such as fecundity, egg viability, and adult female survivorship.

Why do microalgae produce such compounds if they do not serve to deter feeding in their predators? According to chemical defense theory, there should be a selective survival advantage for species that can “protect” themselves from grazers, allowing such species to grow explosively, because the growth of the populations of their predators has been suppressed. This could occur through the production of chemicals that not only deter feeding activity but also reduce population growth. For example, diatom oxylipins reduce egg production and/or hatching success, thereby sabotaging copepod population growth and, consequently, predator grazing impact. In the case of *A. tamarensis*, the defense machinery is potentially even more effective, because female longevity is reduced as well. The chemical structures of these compounds remain unknown.

13.3 Feeding Deterrents

13.3.1 HAB Toxins

Phytoplankton are among the most diverse organisms in the oceans, and due to the complexity of the habitat in which they live, these unicellular eukaryotes have evolved some of the most unique metabolites ever isolated in nature. Some of these are potent neurotoxins that can make their way up the marine food chain and are responsible for massive fish kills, both wild and farmed, as well as the deaths of

many aquatic birds and mammals, including whales and sea lions [59, 60]. There are a wide range of organisms that produce toxic compounds that are often referred to as harmful algal bloom (HAB) toxins. These include flagellates especially dinoflagellates, cyanobacteria, and some species of diatoms, silicoflagellates, prymnesiophytes, raphidophytes, and other phytoplankton. It is estimated that of the 300 species reported to be HABs, only 2% (60–80 species) actually produce toxins. The other HABs cause mortality of marine organisms after reaching high concentrations that may cause damage due to clogging or oxygen depletion. A detailed description of the different types of HAB toxins is beyond the scope of this chapter. Here, we consider only some examples of toxins which potentially serve as antipredatory defense compounds in the plankton (Table 13.1, Fig. 13.4).

Interestingly, the neurotoxic compounds produced by dinoflagellates which induce severe pathologies (i.e., paralytic, neurotoxic, diarrhetic, and amnesic shellfish poisoning) in humans that consume shellfish containing high levels of these toxins may have little or no effect on their direct zooplankton grazers. Several studies have demonstrated that some copepods show little or no behavioral effects of consuming toxic dinoflagellates (e.g., [61, 62]). On the other hand, there are other studies showing that certain dinoflagellates induce strong physiological responses in copepods after <24 h of feeding on these cells, such as elevated heart rates, regurgitation, loss of motor control, and twitching of the mouthparts [63], decreased feeding [64], decreased fecundity [65], delayed development [66], and direct mortality [61]. Furthermore, the copepods *Calanus finmarchicus* [67], *Eurytemora herdmani*, and *Acartia tonsa* [68] have been shown to avoid feeding on paralytic shellfish toxin (PST)-containing prey when offered together with a nontoxic food option. Based on these findings and the negative effects that PST-containing phytoplankton have on some grazers, PSTs have been suggested to act as a protection against grazers [69], but direct demonstrations of paralytic shellfish toxins functioning as antigrazer defenses have not been demonstrated to date.

Most of these toxins are always present in the cells and are referred to as constitutive as compared to induced defenses that are produced only upon damage of the cells by predators (e.g., diatom oxylipins). If the primary function of these compounds is to protect the producers against grazers, the optimal defense theory predicts that cell-specific toxin content should correlate to the probability of attack [68]. Hence, their concentration in the cell should increase following contact with herbivore-specific chemicals [70]. This has, in fact, been shown for the marine copepod *A. tonsa* whereby waterborne chemicals produced by this copepod caused an increase in PST production in the harmful algal bloom-forming dinoflagellate *Alexandrium minutum* [11]. *A. minutum* contained up to 2.5 times more toxins than controls and was more resistant to further copepod grazing. Further investigations [71] showed that when *A. minutum* was grown under nitrate-rich conditions, but not in low-nitrate treatments, the presence of waterborne cues from grazers resulted in significantly increased cell-specific toxin content, implying that the magnitude of grazer-induced PST production is directly proportional to the degree of nitrogen availability. This response was also grazer-specific, with some species of copepods inducing a higher production of toxins (up to 20-fold increase in the presence of the

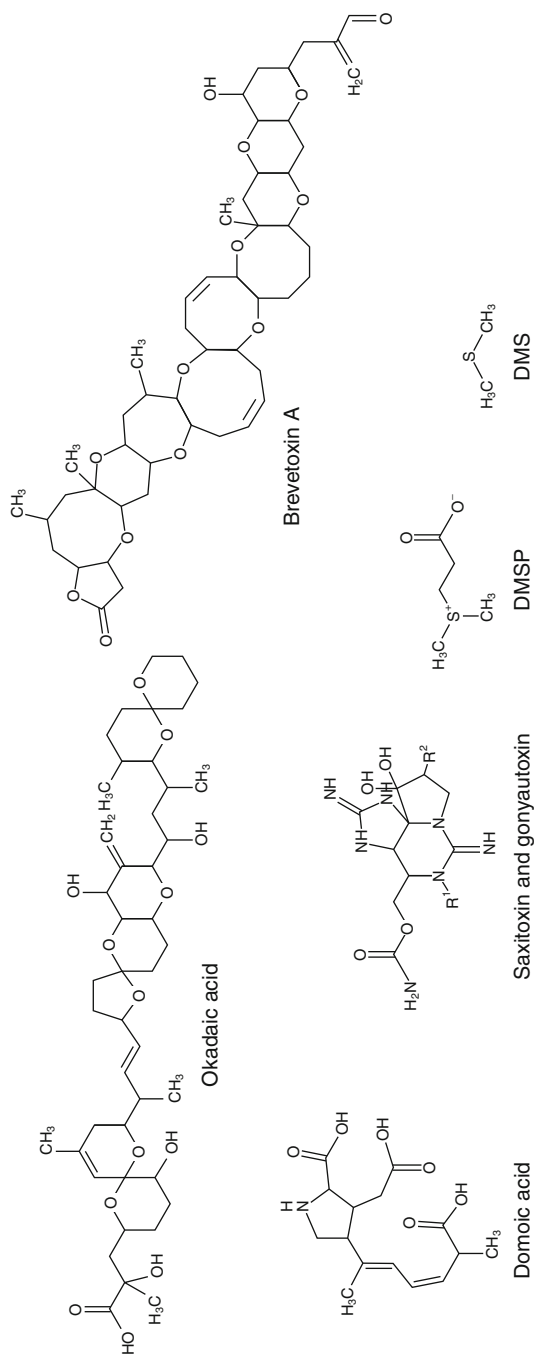


Fig. 13.4 (continued)

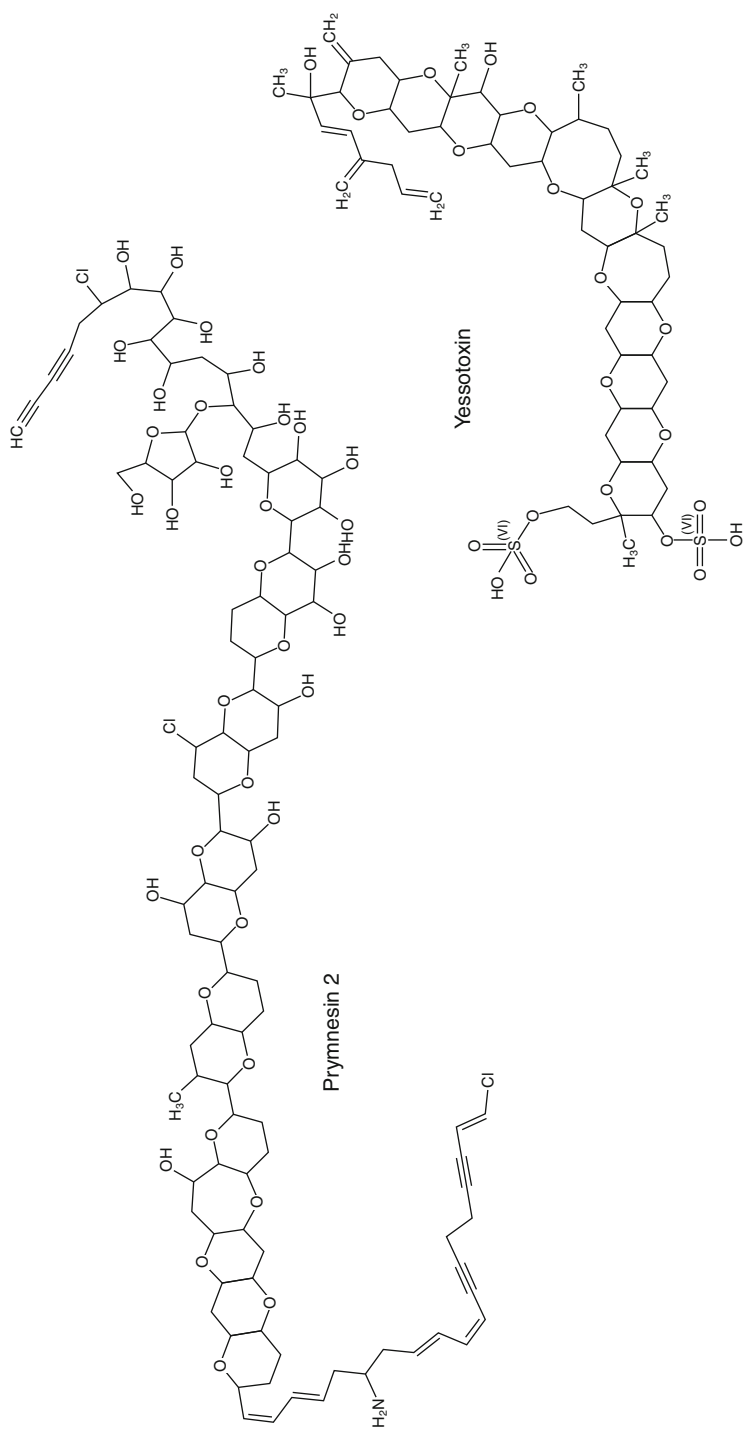


Fig. 13.4 Dinoflagellate and diatom neurotoxins suspected to have antifeeding and antireproductive activity on planktonic predatory copepods. Saxitoxin: $\text{R}^1 = \text{H}$, $\text{R}^2 = \text{H}$; Neosaxitoxin: $\text{R}^1 = \text{OH}$, $\text{R}^2 = \text{H}$; Gonyautoxin1: $\text{R}^1 = \text{OH}$, $\text{R}^2 = \text{H}$; Gonyautoxin2: $\text{R}^1 = \text{H}$, $\text{R}^2 = \text{OSO}_3^-$

copepod *Centropages typicus*) than others, which may induce no change at all (*Pseudocalanus* sp.). The ability of *A. minutum* to sense and respond to the presence of grazers by increased PST production, and the associated negative effect on grazers, is a strong evidence that these compounds are defensive metabolites, the purpose of which is not necessarily to intoxicate and kill the predator but to discourage further consumption.

The discovery and characterization of the molecules responsible for this biological activity are relatively recent (mainly 1980s). Okadaic acid was the first toxin isolated from a marine dinoflagellate even though it had previously been found in the sponge *Halichondria okadae*. The toxin was identified from a Tahitian strain of the dinoflagellate *Prorocentrum lima* and a derivative of this toxin, dinophysistoxin, was later isolated from temperate species of the dinoflagellate genus *Dinophysis*. Both okadaic acid and dinophysistoxin are associated with episodes of diarrhetic shellfish poisoning in humans (see [68, 72] for reviews on dinoflagellate toxins). Okadaic acid is a potent inhibitor of protein phosphorylase phosphatase 1 and 2A in the cytosol of mammalian cells that dephosphorylate serine and threonine. It is not only a potent tumor promoter but is also capable of reversing cell transformation in some oncogenes.

Other neurotoxins such as the brevetoxins are sodium channel activators causing repetitive depolarization of nerve membranes with an increase in the influx of sodium ions that ultimately deplete cellular reserves of acetylcholine at the synapses. The saxitoxins cause the opposite effect to the brevetoxins. They bind to the sodium channels and specifically block sodium permeability of the nerve membrane, ultimately causing paralysis and respiratory failure in humans. The differences in structure of the various saxitoxins alter the rates at which they bind to and depart from the binding site on the sodium channel. Yessotoxin, isolated from the dinoflagellate *Ptychodiscus brevis* (previously *Gymnodinium breve*), partially resembles the brevetoxins in structure and toxicity. Ciguatera poisoning produces various symptoms such as cardiovascular, gastrointestinal, sensory, and motor disturbances. No effective drug is currently known for therapy. The toxin is produced by a benthic dinoflagellate, *Gambierdiscus toxicus*, and is transmitted to fish along the marine food chain. *G. toxicus* also produces a more polar toxin, maitotoxin, which, together with ciguatoxin, is probably the most potent neurotoxin ever isolated from marine organisms.

There is high species-specific variability in the effects of these toxins on grazers, with effects ranging from severe physical incapacitation and death in some species [61] to no apparent physiological effects in others [73]. This variability may depend on the capability of some predators to detoxify or activate defense systems against these compounds. Recent studies [74] have shown that two days of feeding on a strong oxylipin-producing diatom (*Skeletonema marinoi*) is sufficient to inhibit a series of genes involved in aldehyde detoxification, apoptosis, cytoskeleton structure and stress response in the copepod *Calanus helgolandicus*. Of the 18 transcripts analyzed by RT-qPCR at least 50% were strongly downregulated (aldehyde dehydrogenase 9, 8 and 6, cellular apoptosis susceptibility and inhibitor of apoptosis IAP proteins, heat shock protein 40, alpha- and beta-tubulins) compared to animals fed

on a weak oxylipin-producing diet (*Chaetoceros socialis*) which showed no changes in gene expression profiles. These results provide molecular evidence of the toxic effects of strong oxylipin-producing diatoms on grazers showing that primary defense systems that should be activated to protect copepods against toxic algae can be inhibited. On the other hand other classical detoxification genes (glutathione S-transferase, superoxide dismutase, catalase, cytochrome P450) were not affected possibly due to short exposure times. At the same time, each herbivore species is likely to show unique features in detoxification/transport mechanisms as is the case for insect detoxification. Colin and Dam [62, 75] have shown that when two geographically distant populations of the copepod *Acartia hudsonica* were reared on the toxic dinoflagellate *Alexandrium fundyense*, the one that had not experienced recurrent blooms of the toxic algae had lower somatic growth, size at maturity, egg production, and survival, compared to the other population that showed no effects on these life-history parameters. Some copepod species also seem capable of concentrating toxins in their body tissues [76, 77], and such biotransformations typically yield the formation of more potent analogs of these toxins, as occurs in mollusks. Although there is no evidence that copepods are capable of long-term sequestration of such toxins, these predators provide not only a link for toxin flux in pelagic food webs but they may also act as a sink for toxins by metabolizing and removing them from the environment. Provided that they are not incapacitated by the toxin, in some cases, the accumulated toxin may even serve as a transient defense against more sensitive predators. Many benthic invertebrates are capable of sequestering compounds from the food they consume and using them as defensive molecules against predators [78]. There is no reason why this should not also occur in the plankton.

Some diatom species of the genus *Pseudo-nitzschia* produce the potent neurotoxin domoic acid which mimics the excitatory activity of the neurotransmitter L-glutamic acid, inducing destructive neuronal depolarization and successive degeneration of the hippocampus of the brain. In severe cases of this pathology, known as amnesic shellfish poisoning, victims show permanent loss of recent memory. Bioassays with pure compounds (<20 μM domoic acid) induced 100% mortality after 24 h in the copepod *Tigriopus californicus* [79]. However, domoic acid has not been shown to induce negative effects on planktonic organisms that consume *Pseudo-nitzschia* species [80]. Olson et al. [81] found that copepod grazing impacts on field populations of *Pseudo-nitzschia* sp. were negligible, but this lack of grazing was not attributed to domoic acid. In a similar field-based study, Olson et al. [82] found no correlation between low grazing rates and particulate or dissolved domoic acid concentrations in field samples. On the other hand, Bargu et al. [83] found that krill exposed to abnormally high concentrations of dissolved domoic acid fed significantly less on a nontoxic food source than krill unexposed to domoic acid. However, due to the high concentrations and exposure methods used by these authors, little can be concluded about the putative antipredatory role of this toxin. If domoic acid is not a feeding deterrent to zooplankton grazing, zooplankton may facilitate vectorial transmission of the toxin which could have serious impacts on the marine ecosystem as well as on

the marine economy and human health. The genome sequence for *Pseudo-nitzschia multiseriis* which will soon be available, should provide more insights into domoic acid biosynthesis, allowing researchers to profile production capabilities across different species, to better characterize their responses to environmental triggers, and to examine the molecular interactions between toxin-producing cells and their predators.

Blooms of the haptophyte *Prymnesium parvum* are well-known nuisances in brackish waters around the world that are usually accompanied by massive fish kills due to the production of prymnesins which exhibit potent cytotoxic, hemolytic, neurotoxic, and ichthyotoxic effects. These secondary metabolites are especially damaging to gill-breathing organisms, and they are believed to interact directly with plasma membranes, compromising integrity by permitting ion leakage. Several factors appear to function in the activation and potency of prymnesins including salinity, pH, ion availability, and growth phase [84]. Prymnesins may function as defense compounds to prevent herbivory, and some investigations suggest that they have allelopathic roles. Exposure to *P. parvum* can cause inactivity in the copepods *Eurytemora affinis* and *Acartia bifflora*, without the copepods actually consuming the toxic alga, resulting in reduced copepod reproductive success [85]. Sopanen et al. [86] found that cell-free filtrates of *P. parvum* also negatively impacted copepod survivorship. No studies are available testing the effects of pure compounds on grazers.

Karlodinium veneficum is a small athecate dinoflagellate commonly present in low levels in temperate, coastal waters. Occasionally, *K. veneficum* forms ichthyotoxic blooms due to the presence of cytotoxic, hemolytic compounds named karlotoxins. Exposure to a toxic strain of *K. veneficum* significantly lowered clearance and ingestion rates compared to a nontoxic strain and mixed diets dominated by the toxic strain, but did not induce mortality in the copepod *A. tonsa* [87]. These results support the hypothesis that karlotoxins in certain strains of *K. veneficum* deter grazing by potential predators and contribute to the formation and continuation of blooms. Another HAB dinoflagellate *Karenia brevis* produces brevetoxins, polyketide neurotoxins with acute toxic activity in waterborne or aerosol form against vertebrates [88]. However, according to Poulson et al. [89], negative effects of *K. brevis* on copepod egg production and survivability are not due to a chemical deterrent, but likely caused by the nutritional inadequacy of *K. brevis* as a food source. Again, there are no studies testing the effects of pure molecules on grazers.

There is also the possibility that compounds inducing negative effects on grazers are not only the PSP toxins produced by HABs but also other unknown allelopathic compounds that inhibit the growth, survival, and reproduction of competing algae [90, 91]. In *A. tamarensis*, these compounds are presumably large molecules (>5 kDa), stable over broad temperature and pH ranges, and refractory to bacterial degradation [92]. *Alexandrium* allelochemicals have lytic activity targeting both competitors and grazers underlying the success of this species during blooms [93], suggesting that they are very important for structuring plankton communities.

13.3.2 DMSP and DMS

Dimethylsulfoniopropionate (DMSP) is found in numerous species of phytoplankton, but most prominently in the Prymnesiophyceae and Dinophyceae [94]. DMSP is cleaved during feeding by predators into the gas dimethyl sulfide (DMS) and acrylate which was originally hypothesized to act as a grazing deterrent (Table 13.1) via the accumulation of acrylate in grazer food vacuoles [95]. However, Strom et al. [96] showed that DMSP, not DMS or acrylate, acted as a chemical defense against protist grazers, causing a notable feeding rate reduction in several species.

DMSP released by phytoplankton into ambient seawater appears to act as a signal molecule or indicator of inferior prey rather than as a toxin. Fredrickson and Strom [97] have shown that adding DMSP (20 mM) to laboratory cultures of two ciliates (*Strombidinopsis acuminatum* and *Favella* sp.) and one dinoflagellate (*Noctiluca scintillans*) causes a 28–75% decrease in feeding rates and that these decreases were concentration-dependent with 20 nM as the lower threshold for an effect. Partial but not complete recovery of grazing rates occurred during long-term (24 h) exposure to dissolved DMSP, as long as concentrations remained above 12 mM.

There are other studies showing that DMSP-producing species of phytoplankton do not deter grazers, suggesting that some predators are less sensitive to or more capable of detoxifying this metabolite. The bloom-forming coccolithophore *Emiliania huxleyi* contains high intracellular levels of DMSP, yet some strains of *E. huxleyi* are a suitable food source for protist grazers [98–100]. Copepods also consume *E. huxleyi*, though not as a preferred food source [99]. Like *E. huxleyi*, the prymnesiophyte *Phaeocystis* is a suitable food source for some protist grazers even if it is a strong DMSP producer [101]. However, studies of copepod feeding upon *Phaeocystis* generally give varied results, many of which related to sizes of colonies, differences between copepod species and experimental techniques. Turner et al. [102] concluded that even though copepods may feed well upon *Phaeocystis*, resulting poor fecundity on this diet may inhibit copepod population increases during blooms, thereby contributing to the perpetuation of blooms. The high egg-hatching success on this diet argues against *Phaeocystis* containing chemical compounds that act as mitotic inhibitors reducing copepod egg viability, such as those found in diatoms and dinoflagellates.

Phaeocystis may also use morphological defenses to deter grazers. The life cycle of *Phaeocystis* includes solitary flagellated cells 3–8 μm in diameter, which are usually succeeded by blooms of colonial aggregations with hundreds of nonflagellated cells embedded in gelatinous colonies of up to 2 mm diameter ([102] and references therein). Gelatinous *Phaeocystis* colonies can form enormous nuisance blooms contributing to anoxia, beach fouling, and clogging of bivalve gills and fishing nets. Colony formation in *Phaeocystis* has been interpreted as a defense strategy against small grazers, because large colonies create a size-mismatch problem for small zooplankton ([70] references therein). *Phaeocystis* cells may therefore face a dilemma in a more complex food web context since colony formation will make the cells more vulnerable to larger grazers in the system

such as copepods. Long et al. [103] have shown that *Phaeocystis* colony formation was suppressed in the presence of a larger grazer (the copepod *A. tonsa*), but when small ciliate (*Euplotes* sp.) grazers attacked this alga, it shifted to the colonial form which was too large to be grazed by these ciliates. These results provide strong evidence that *Phaeocystis* cells not only sense that neighbors were being attacked but also that they “identified” the attacker and responded with opposing phenotypic shifts depending on the identity of the attacker [104]. The chemicals responsible for colony formation in this species have not yet been identified.

Not all induced morphological changes involve colony formation. For example, Pondaven et al. [105] reported grazing-induced changes in cell wall silicification in a marine diatom. Grazing-induced silicification may increase the mechanical resistance of the diatom’s frustule to copepod mandibles [106]. Pondaven et al. [105] compared changes in cell wall silicification of the marine diatom *Thalassiosira weissflogii* grown on three different preconditioned media which only differed by the fact that they had contained, either diatoms alone (control medium), nonfed copepods of the species *Calanus helgolandicus* (starved-copepods medium), or both diatoms and copepods (“diatoms and copepods” medium) before being used for culture experiments. Cells grown in preconditioned media that had contained both diatoms and herbivores were significantly more silicified than diatoms grown in media that contained diatoms alone or starved herbivores. These observations indicate that diatom cell wall silicification is not only a constitutive mechanical protection for the cell but also a phenotypically plastic trait modulated by grazing-related cues [70]. At present, it is still unknown which chemical compound(s) induces this defense.

DMS derived from the breakdown of DMSP also shows biological activity. A wide range of organisms seem to use DMS as a cue for food finding [107, 108]. It is possible that DMS odor plumes produced during zooplankton grazing are used by predators to detect, locate, and capture their prey. Plumes of DMS trigger a tail-flapping response in the copepod *Temora longicornis* which results in altered flow patterns and probably assists copepods in locating food [8]. The identification of the involved signal is important for general considerations about food finding by copepods. Since grazers are involved in the cell disintegration that triggers DMS production, this process could attract herbivores to patches with high food concentrations or assist predation on actively feeding herbivores. Carnivores can also benefit from the production of these infochemicals (information-conveying chemicals) which they sense and use to detect herbivores, thereby reducing the grazing pressure exerted by the herbivores on the plants [107]. Very little is known on such tritrophic (involving three trophic [feeding] levels) interactions in the plankton. A classic example of such complex feeding interactions in terrestrial ecosystems involves flies that sip nectar from flowers and are, in turn, eaten by spiders.

Despite the abundance and obvious presence in the plankton of these compounds, we still know little about the regulation of their production and their direct delivery to the interacting organisms. In phytoplankton cells, DMSP functions as a compatible solute, a cryoprotectant and, perhaps, an antioxidant [109–111]. Variation in phytoplankton intracellular DMSP concentration appears to facilitate

phytoplankton survival in a fluctuating environment. For example, increased DMSP production may occur under nutrient limitation [112] and when there is a decrease in temperature [113].

13.3.3 Apo-fucoanthinoids

Another class of feeding deterrents in the plankton is the apo-fucoanthinoids produced by the diatoms *Phaeodactylum tricorutum* and *Thalassiosira pseudonana* [9]. The compounds were identified as apo-10'-fucoxanthinal, apo-12'-fucoxanthinal, apo-12-fucoxanthinal, and apo-13'-fucoxanthinone. Feeding deterrent responses in the copepod *Tigriopus californicus* were observed at concentrations of 2–20 ppm which is about 1,000 times lower than the total apo-fucoanthinoid concentration in *P. tricorutum* [10]. Mortality occurred at concentrations ranging from 36.8 to 76.7 ppm. Thus, these compounds are present in concentrations which may have ecological significance in the control of bloom formation and grazing, even if *P. tricorutum* and *T. pseudonana* are not major blooming species.

The activity of these molecules was tested by dissolving them into the water in which copepods had been incubated, and fecal pellet production was used as an indication of feeding activity. A decrease in fecal pellet production after 24 h was interpreted as a result of feeding deterrence compared to control containers that had not been inoculated with these compounds. A reduction in fecal pellet production as an indication of feeding deterrence has also been inferred in other studies on copepod feeding behavior, although it remains unclear if negative effects on copepod fitness are due to reduced ingestion of cells, toxins interfering with digestive processes, or enhanced energy expenditure due to detoxification.

13.4 Environmental Factors Affecting Toxin Production

In general, changes in toxin content are associated with disturbed (unbalanced) physiology with the up-shock or down-shock of cells exiting or entering stationary phases (see [114] and references therein). Table 13.2 illustrates the importance of up/down-shock events in affecting toxicity for some of the toxin-producing species discussed until now. Phosphorus limitation often seems to enhance cellular toxin content. N limitation does so to a lesser extent, or may in the cases of domoic acid and PSPs do the opposite and lead to a fall in toxin content. Si-limited growth of *Pseudo-nitzschia* promotes synthesis of domoic acid [115]. The same occurs for PUA production in the diatom *S. marinoi* with a 7.5-fold increase ($27.5 \text{ fmol cell}^{-1}$) in Si-limited cells with respect to controls [116]. In most instances, toxin content is relatively low under nutrient-balanced conditions (N:P = 16:1). Physical factors can also affect toxin production. For example, low temperature decreased the growth rate of the PSP-producing dinoflagellates *Alexandrium catenella*,

Table 13.2 Toxic species and factors affecting toxin production

Toxic species	Factors increasing cell toxin	Toxin ^a	References
Toxins containing nitrogen			
<i>Alexandrium catenella</i> , <i>A. cohorticula</i>	Low temperature, low growth rate	PSP	[117]
<i>A. fundyense</i>	N- and P- limitation, temperature	PSP	[118–120]
<i>A. minutum</i>	P-limitation	PSP	[64]
<i>A. tamarense</i>	P-limitation, N-excess, organic matter	PSP	[117, 121–123]
<i>Pseudo-nitzschia australi</i> , <i>P. delicatissima</i> , <i>P. multiseriata</i> , <i>P. pungens</i> , <i>P. seriata</i>	P-/Si-limitation, N excess, growth phase, high light, high pH, high or low temperature, organic matter, Fe-limitation or Cu-stress	DA	[114, 124, 125]
Toxins with little or no nitrogen			
<i>Chrysochromulina leadbeateri</i> , <i>C. polylepis</i>	P-limitation, salinity, high pH, N or P-limitation	ICHT	[117, 126, 127]
<i>Dinophysis sp.</i> , <i>D. acuminata</i> , <i>D. acuta</i>	N-/or P-limitation, N-limitation; N-/P-sufficiency	OA, DTX, PTX	[117, 128]
<i>Fibrocapsa japonica</i>	Low salinity	PUFA	[129]
<i>Gymnodinium catenatum</i>	Low temperature, P-limitation	GYM	[117, 121, 130]
<i>Heterosigma akashiwo</i>	High temperature, Fe-limitation	ROS	[131]
<i>Karenia brevis</i>	Urea	Brevetoxin	[132]
<i>Ostreopsis ovata</i>	High temperature	Ostreocin	[133]
<i>Prymnesium parvum</i> , <i>P. patelliferum</i>	N-/or P-limitation	Prymnesin	[134, 135]
<i>Prorocentrum lima</i>	N-/or P-limitation, organic matter	OA, DTX	[117]
<i>Pseudo-nitzschia delicatissima</i>	Growth phase	15-HEPE, 15-oxoacid, 13,14- HepTE	[7]
<i>Skeletonema marinoi</i>	Growth phase, N- and P- limitation; Si- limitation	PUAs	[29, 115, 136]

Adapted from Graneli and Flynn [114]

GYM gymnodimine, ICHT ichthyotoxins, DA domoic acid, OA okadaic acid, DTX dinophysistoxin, PTX pectenotoxin, 15-HEPE 15-hydroxyeicosapentaenoic acid, 13,14- HepTE 13,14-hydroxy, epoxyeicosatetraenoic acid, PUAs polyunsaturated fatty aldehydes, ROS reactive oxygen species

^aPSP saxitoxin (STX), neo-STX, gonyautoxin (GTX), C-toxins

A. cohorticula, and *Gymnodinium catenatum*, whereas it increased toxin content per cell. In contrast, a low growth rate due to light inhibition did not cause an increase in toxin content, compared to cells growing at optimum illumination. In other studies, light seems to be essential for toxin production (e.g., *Prymnesium parvum*) with higher irradiance augmenting toxin production, but once the toxins were extracellular, they were rapidly inactivated by exposure to both visible light and UV radiation [117]. Briefly, there is wide variation in toxin production not only

between algal groups but also species and strains in response to different environmental conditions, and this will affect toxin production levels at sea in different years with cascading effects on predators.

13.5 Laboratory Protocols to Assess the Effects of Phytoplankton Metabolites

Marine chemical ecology is a young science, and the methodologies to study the effects of natural products on marine organisms are subject to rapid change. During the last two decades, bioassays have progressed from those that detected bioactivity without much concern for ecological relevance, to ecologically relevant tests to investigate possible functions of secondary metabolites in the phytoplankton. The problem is that often the natural concentrations of a compound, and therefore the concentrations that should be tested, are not known. Most feeding deterrents have been isolated and identified by natural products chemists looking for unusual secondary metabolites. Rarely have chemical studies provided information on the yield of these compounds after extraction. Hence, it is difficult for ecologists conducting bioassay experiments to know the natural concentrations of these metabolites to be tested. To further complicate matters, there are geographical variations in the concentration of secondary metabolites and within-region variation in some cases. Notwithstanding, much progress has been made in recent years in designing ecologically relevant bioassays with natural concentrations of a compound in many feeding trials. Here, we give a few examples of bioassay methods currently used to study chemical interactions in the plankton especially those involving antipredation and antigrowth activities.

The antiproliferative activity of phytoplankton metabolites on plankton predators has been tested mainly on zooplankton copepods ([30] and references therein) and cladocerans [31]. The majority of these studies have tested the effects of aqueous solutions containing toxic compounds by incubating embryos, larvae, or adults and studying the effects on fertilization, embryogenesis, and postembryonic development. Although the ecological relevance of these assays is questionable, because animals usually come into contact with these metabolites only through direct grazing and possibly during lysis of cells during the decay of a bloom, these assays are very useful for a preliminary screening of bioactive compounds in phytoplankton. They are also very useful for bioassay-guided separation of bioactive compounds or for testing the effects of pure compounds.

For example, Miralto et al. [1] tested the effects of PUAs which they had isolated for the first time from marine diatoms by incubating *T. stylifera* copepods in 5-mL tissue culture wells containing PUAs (2-*trans*-4-*cis*-7-*cis*-decatrienal, 2-*trans*-4-*trans*-7-*cis*-decatrienal, and 2-*trans*-4-*trans*-decadienal) at concentrations ranging from 0.5 to 5 $\mu\text{g mL}^{-1}$ (Fig. 13.5d). Fertilized eggs were freely spawned by females into containers, and the percentage of hatched eggs was determined 48 h later when

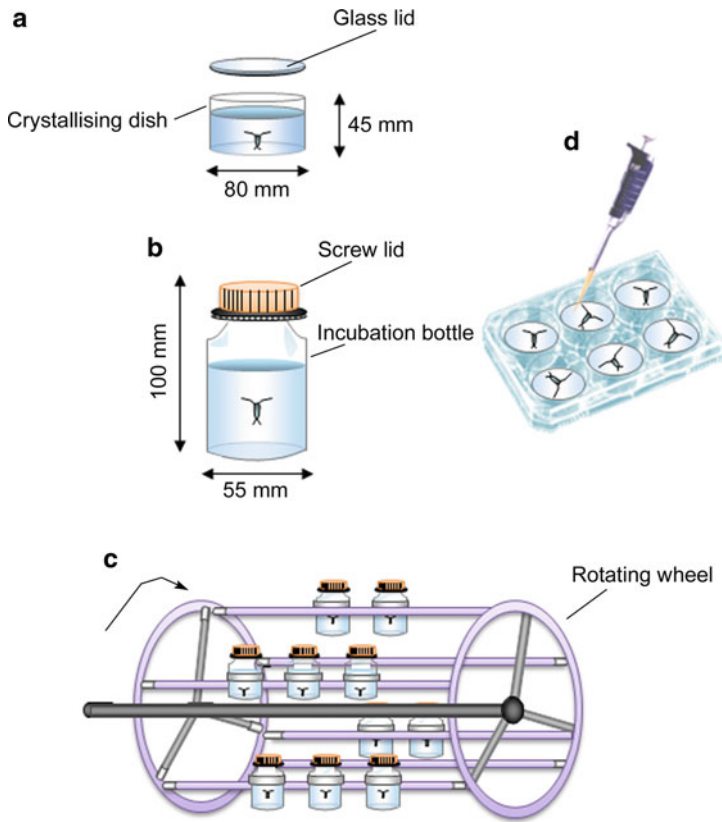


Fig. 13.5 Classic bioassays to test the biological activity of phytoplankton secondary metabolites on planktonic copepods. (a) 100-mL crystallizing dishes containing single females or male and female couples and natural food suspensions. (b): 1-L jars containing up to 20 copepods and food suspensions are placed on rotating wheel, as shown in (c). (d) 5-mL multitissue culture wells containing single copepods exposed to phytoplankton extracts or pure molecules. For explanation see text

control untreated eggs had hatched. Ianora et al. later used the same protocol to compare the effects of PUAs and 15S-HEPE on egg-hatching success of *T. stylifera*. Females were incubated individually in 5-mL tissue culture with known solutions of compounds and were removed when they had spawned to avoid cannibalization of eggs (Fig. 13.5d). Hatching was observed 48 h later.

More ecologically relevant studies on the antigrrowth activity of phytoplankton metabolites have been conducted using grazing experiments whereby copepods are fed microalgae that are known to produce toxic metabolites (e.g., diatom oxylipins) for several days (usually 15 days). Using these long-term feeding assays, Ceballos and Ianora [138] followed the effects of diatoms that produced toxic metabolites on reproductive success of adult copepod females (egg production and hatching viability of eggs), demonstrating that the microalgae tested arrested cell divisions

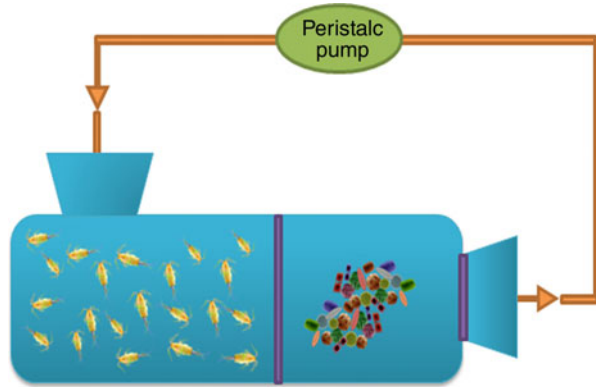
and embryonic development compared to control microalgae that did not produce these compounds. Feeding assays consisted in incubating females individually in 100-mL crystallizing dishes filled with 0.45- μm filtered seawater and a known quantity of toxic-producing and nontoxic-producing microalgae, at saturating food concentrations equivalent to about $1 \mu\text{g C mL}^{-1}$ (Fig. 13.5a). Females were transferred to new containers with fresh algal suspensions daily for 15 days. A daily tally was kept of egg production and hatching success.

Feeding assays testing the effects of different algal diets have traditionally used larger experimental jars that are filled with food suspensions and then mounted on a rotating wheel (0.5 rpm), to keep the food suspended, in a controlled temperature room and on a fixed day–night light cycle (Fig. 13.5b). In this case, several copepods (5–10 in the case of 500 mL jars) are added to each of triplicate 500-mL experimental jars containing food suspension. A control jar with no copepods is treated in the same manner as the experimental jars, and an initial sample of food suspension is preserved at the beginning of each experiment. Experimental jars are filled and sealed, without air bubbles inside, and mounted on a rotating wheel (0.5 rpm), in a controlled temperature room at 20.5°C , on a 12:12 h L:D cycle for 24 h (Fig. 13.5c). After 24 h, copepods are removed from the experimental jars by pouring them into bowls to check for dead copepods. Food suspensions are then preserved with Lugol's solution, and phytoplankton cell numbers counted in Sedgwick-Rafter cells. At least 400 cells are counted in all cases to ensure $\pm 10\%$ precision. Ingestion rates are determined from differences in phytoplankton cell concentrations in initial, control, and triplicate experimental suspensions using the formulae of Frost [139]. Grazing rates for dead copepods are calculated assuming that they had fed for half of the experiment. Using these assays, Turner et al. [140] demonstrated that copepod egg-hatching success was strongly modified by some diatom diets, with hatching diminishing to 0% after 10 days of feeding on a diatom diet, and that this effect was diluted but not removed when the diatom was mixed with a dinoflagellate diet.

Bioassays have also been designed to test the antigrowth activity of metabolites on larval development to adulthood. Development assays consisted in incubating hatched copepod nauplii in experimental jars mounted on a rotating wheel with known quantities of algal food and following the development of nauplii to adulthood (Fig. 13.5b, c). Ianora et al. [23] sampled juveniles daily, counted and checked them under the microscope to determine the stage of development, and transferred them to new jars with fresh algal medium. A tally was kept of the most abundant larval stage and percentage of surviving individuals to calculate development and survival curves. Using this assay, Ianora et al. [23] showed that maternal diets affected offspring fitness. When mothers and their offspring were fed a diatom that produced unsaturated aldehydes, none of the larvae reached adulthood compared to control mothers and offspring that were fed a nondiatom diet. The effects on development were less severe when mothers received the control food and the offspring the treatment food.

A recent study has explored the possibility of using liposomes as a delivery system for copepods [141]. Giant liposomes were prepared and characterized in the

Fig. 13.6 Device to assess the effect of phytoplankton exudates on copepod activity. Phytoplankton and copepods are separated by a glass filter (see also Miralto et al. [143])



same size range of food ingested by copepods (mean diameter = 7 μm) and then encapsulated with the fluorescent dye fluorescein isothiocyanate (FITC) to verify copepod ingestion with fluorescence microscopy. Females of the calanoid copepod *T. stylifera* were fed with FITC-encapsulated liposomes alone or mixed with the dinoflagellate alga *P. minimum*. Control copepods were incubated with the *P. minimum* diet alone. When liposomes were supplied together with the algal diet, egg production rate, egg-hatching success, and fecal pellet production were as high as those observed for the control diet. On the contrary, egg production and hatching success was very low with a diet of liposomes alone, and fecal pellet production was similar to that recorded in starved females. This suggests that liposomes alone did not add any nutritive value to the diet, making them a good candidate as inert carriers to study the nutrient requirements or biological activity of different compounds.

In another study, Buttino et al. [142] used these giant liposomes to encapsulate decadienal in order to investigate the effect of PUAs on the reproductive biology of the copepods *T.* and *C. helgolandicus*. After 10 days of feeding, liposomes reduced egg-hatching success and female survival with a concomitant appearance of apoptosis in both copepod embryos and female tissues. Concentrations of decadienal-inducing blockage were one order of magnitude lower than those used in classical feeding experiments (e.g., Ianora et al. [23]), demonstrating that liposomes were a useful tool to quantitatively analyze the impact of toxins on copepods. This type of technology for the delivery of toxins and drugs in feeding trials has considerable potential as a means of delivering a known quantity of toxin under seminatural conditions, allowing the toxins ingested to be determined.

An experimental flow-through chamber was designed by Miralto et al. [143] to verify if copepod fertility was modified due to the release of chemical cues by other conspecifics. The apparatus (Fig. 13.6) was divided into two chambers, each of which had a 50-mL volume capacity. The chambers were separated by a glass fiber filter (20 μm pore size), and a peristaltic pump ensured diffusion of 0.45- μm filtered SW water at a flow rate of 8 mL min^{-1} . A similar chamber could be used to test if copepod exudates induce an increased production of defensive metabolites in

phytoplankton, as described by Selander et al. [72] who observed a 2.5-fold increase in PST production in the dinoflagellate *A. minutum* when exposed to waterborne cues from copepods.

The application of “omics” technologies (genomics, transcriptomics, proteomics, metabolomics, etc.) to studies of biosynthesis and regulation of bioactive secondary metabolites, and the concomitant effects on plankton population dynamics is an emerging but rapidly advancing field. Complete genome sequences have been reported for two diatoms, *Thalassiosira pseudonana* [144] and *Phaeodactylum tricorutum* [145], but others will soon be available for representative species of major groups (e.g., heterotrophic and photosynthetic bacteria, prasinophytes, diatoms, *Emiliana huxleyi*, *Phaeocystis*, and copepods). With access to these tools, chemical ecologists have an unprecedented opportunity to learn more about the biochemistry and ecological functioning of pelagic systems more quickly and comprehensively than ever. This is manifested by altered expression of superoxide dismutase and metacaspases, key components of stress and death pathways. Transgenic approaches for manipulating genes in key signaling and stress-related pathways in phytoplankton may provide the opportunity to gain further insights into trophic-level interactions.

Given the massive genome size and complexity characteristic of marine dinoflagellates, whole genome sequencing remains impractical. A functional genomics approach, involving generation of a cDNA library and sequencing of expressed sequence tags (ESTs), has proven useful in the search for putative biosynthetic genes for secondary metabolites, stress response genes, and those involved in growth regulation leading to bloom formation [146]. Particularly, when coupled with DNA microarrays, molecular approaches have the potential to reveal novel pathways that are up- or downregulated during certain stress situations and might reveal the biochemical and chemical basis for some observed species interactions that cannot be explained to date. One detailed study of intrapopulation diversity within the toxic dinoflagellate *A. tamarensis* [147] revealed that the abundant genetic diversity, determined by two independent molecular markers, was not directly correlated with the phenotypic variation in toxin spectrum and intracellular concentration.

Another powerful postgenomics tool, advanced metabolite profiling, also termed “metabolomics,” allows mapping of the chemical diversity and dynamic range of bioactive secondary metabolites of potential importance in ecological interactions. Thus, the response of phytoplankton cultures or communities to competing organisms, predators, and viruses can be monitored with limited bias toward a certain compound class. Statistical evaluation of the data provides insight into the metabolic changes within the cells as well as into the released metabolites that might represent the chemical language of the cells [148]. It is likely that knowledge of the complex patterns of chemicals released by microalgae and other plankton species will result in a paradigm shift revealing new mechanisms for processes such as community function, food location, or complex defensive and allelopathic interactions. The marriage of metabolomics and metagenomics has the potential to be a particularly powerful

combination in shedding light on planktonic and microbial interactions in marine ecosystems [149].

Another important tool in plankton chemical ecology studies will be the adoption of model organisms that will provide insight into the functioning of other organisms. This approach is widely used in the biomedical field to explore potential causes and treatments for human disease and is based on the concept of conservation of biochemical pathways and genetic material over the course of evolution. Models are chosen on the basis that they are suitable for experimental manipulation, have characteristics such as a short life cycle, are amenable for maintenance and breeding in the laboratory, and have nonspecialist living requirements. In terrestrial chemical ecology, the introduction of *Arabidopsis thaliana* as the first fully sequenced plant proved to be highly successful for the elucidation of rather general plant defensive pathways. Such an approach could also be useful in the plankton and would allow for the elucidation of fundamental biochemical mechanisms such as regulatory and metabolic pathways in producer organisms as well as the identification of the mechanisms of action in target organisms. Ideally, the models selected in plankton ecological studies would also be supported by genomic and postgenomic resources, databases, and infrastructure.

13.6 Concluding Remarks

In comparison to the large number of studies on the antipredatory compounds produced by terrestrial plants, those regarding marine phytoplankton are underrepresented. Most studies on the secondary metabolites of these microalgae have focused on bioactivity and structural elucidation, with a view toward potential pharmaceuticals or other commercial purposes. Nevertheless, the environmental and human health consequences of HABs have provided great impetus to conduct ecologically relevant studies on microalgae in the last decade (reviewed by Poulson et al. [89] and Sieg et al. [150]).

Marine chemical ecology is a young science that requires the collaborative effort of biologists, ecologists, and chemists. Identifying the compounds responsible for mediating feeding, reproduction, and behavioral interactions is only the first step in understanding the ecological relevance of a compound. These effects then need to be translated from laboratory assays to their natural context in order to provide the ultimate test and major challenge for field ecologists. An increased understanding of chemical defenses will be achieved when we know how ecologically realistic doses of these metabolites affect growth, reproduction, and survivorship of consumers. In the long run, such studies will lead to a better understanding of how these compounds can help regulate ecosystem functionality by underpinning the chemical and molecular processes that are crucial for the fitness and survival of the producing organisms.

A major challenge for the future will be to understand the multiple simultaneous functions of many of these secondary metabolites. For example, diatom PUAs may have an antipredatory function [14] and also act as allelopathic agents [135]. Furthermore, PUAs can affect growth of some bacterial strains [28] and possibly also

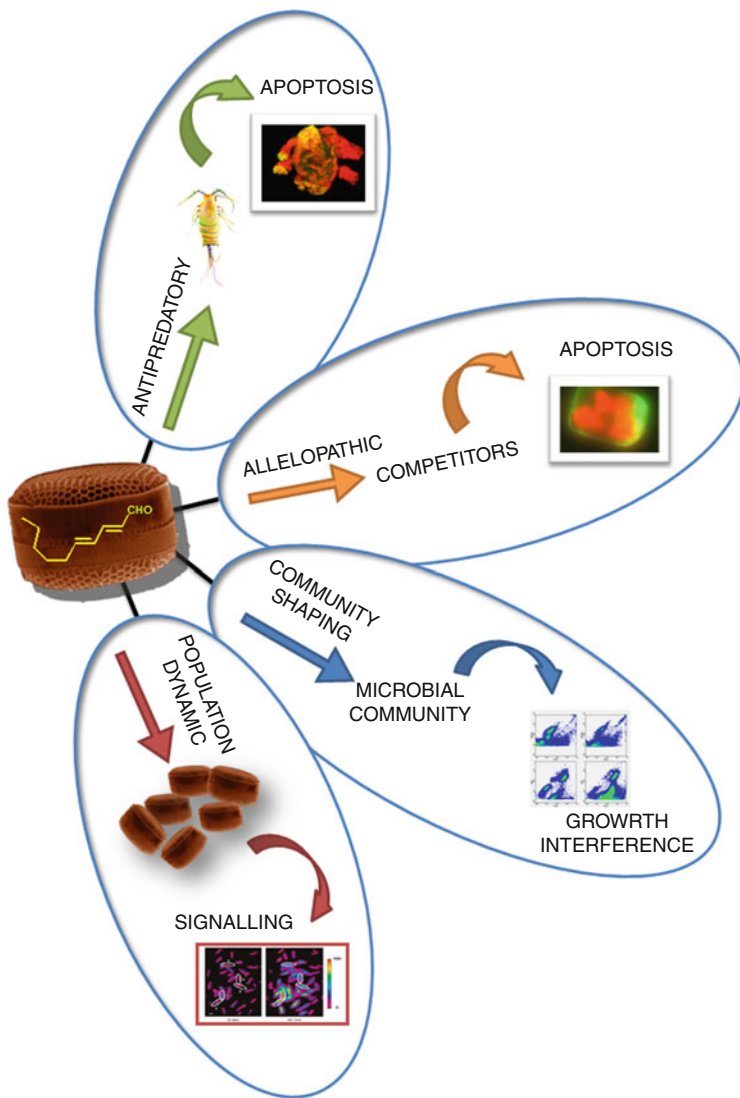


Fig. 13.7 Multiple effects of diatom polyunsaturated aldehydes (PUAs): From the top, Antiproliferative (teratogenic) effect on copepods. Abnormal *Calanus helgolandicus* copepod nauplius hatched from a mother fed with the PUA-producing diatom *Skeletonema marinoi*. Yellow parts indicate TUNEL-positive apoptotic tissues (from Ianora et al. [23]). Allelopathic effect on phytoplankton species in culture, *Skeletonema marinoi*, cell after incubation with decadienal. Red fluorescence indicates annexin positivity (apoptosis) (from Casotti et al. [24]). Growth interference of picoplankton. Flow cytograms represent a natural seawater sample from the Adriatic Sea; left panels are controls, right panels are picophytoplankton (top) and heterotrophic bacteria (bottom), after 24 h inoculation with a mixture of octadienal and heptadienal [28]). Signaling effect. Intracellular transmission of decadienal-derived signal induces NO in neighboring (from Vardi et al. [26]) influencing population dynamic

have a stress-signaling function [17], with potential consequences for food web structure and community composition (Fig. 13.7). Thus, the same secondary metabolites may act to deter different groups of organisms by different modes of action.

The chemical multifunctionality of secondary metabolites is well documented in higher terrestrial plants. For example, the anthraquinone emodin, identified in 17 plant families distributed worldwide, has numerous biological activities, some of which exhibit a wide spectrum of ecological impacts by mediating biotic or abiotic interactions of plants with their environment. In vegetative organs emodin may help protect plants against herbivores, pathogens, competitors and extrinsic abiotic factors (e.g., high light intensities). In unripe fruit pulp, emodin may facilitate seed dispersal by protecting the immature fruit against predispersal seed predation whereas in ripe pulp it may deter frugivores and thus reduce the chances that seeds will be defecated beneath the parent plant [151]. Natural selection should favor secondary metabolites with multiple functions because they protect the plants against a variety of unpredictable biotic and abiotic environments. Such metabolites also enhance plant defenses by using different molecular targets of specific enemies through a variety of mechanisms of action. As discussed in a recent paper [152] herbivores also vary profoundly in their tolerance to secondary metabolites, and future research should be directed to better understanding detoxification processes, or lack of such processes, in the plankton. The complexity of planktonic food webs allows a multitude of pathways for infochemicals that need to be better understood. The role of parasites and viruses, both in introducing toxins into the plankton, as well as removing them through detoxification or species-specific host-pathogen interactions is poorly known. Resulting trophic cascades may have important repercussions in plankton community structure with implications for higher trophic levels including important fisheries.

We have only barely begun to understand the importance of chemical interactions in the plankton and their role in shaping biodiversity and ecological functioning both at a community and cellular level. An increased understanding of the natural function of these compounds may lead to new strategies for the correct management and protection of these potentially important natural resources for the future and help find new biotechnological applications for these products in our day-to-day lives. Antifeedants have already been used to derive anticancer, antiviral, and antiaging products; toxins have been used to develop pain killers; and functional products have been obtained from the materials used by sessile organisms to colonize free surfaces. Knowledge of ecophysiological interactions may serve as a platform to facilitate the search for new biotechnological candidates, as well as to optimize culture conditions and achieve production of biomass for industrial applications.

13.7 Study Questions

1. What types of antipredator defensive strategies occur in the plankton and do these differ from those in benthic habitats?

2. How do antipredator defensive strategies in marine organisms compare to those in terrestrial habitats?
3. What is the function of oxylipins in diatoms?
4. Are dinoflagellate neurotoxins defensive metabolites against predators?
5. Are some classes of molecules more common as defensive metabolites than others?
6. How do toxin production levels vary in relation to environmental changes?

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P.-Y. Qian (✉) • S.Y. Xu

KAUST Global Collaborative Program, Division of Life Science, Hong Kong University of Science and Technology, Clear Water Bay, Hong Kong, China

e-mail: boqianpy@ust.hk

Abstract

With the global ban of application of organotin-based marine coatings by International Maritime Organization in 2008, there is a practical and urgent need of identifying environmentally friendly low-toxic and nontoxic antifouling compounds for marine industries. Marine natural products have been considered as one of the most promising sources of antifouling compounds in recent years. In antifouling compound screening processes, bioassay systems often play most critical/vital roles in screening efforts. To meet various needs, a variety of bioassay systems have been developed and/or adopted in both research and commercial laboratories. In this chapter, we provide a brief outline of common bioassay procedures for both antimicrofouling and antimacrofouling assays, which can serve as a general guideline for setting up bioassay systems in laboratories engaged in antifouling compound screening. Some bioassay procedures currently practiced in various laboratories are not included in this book chapter for various reasons. Individual laboratories should modify bioassay protocols based on their research interests or needs. Nevertheless, we highly recommend the research laboratories to adapt high-throughput assays as much as possible for preliminary screening assays, followed by more complex bioassay processes using multiple target species. We argue strongly for studies in mode-of-action of antifouling compounds against settling propagules, which shall lead to discovery of molecular biomarkers (genes, proteins, receptors, or receptor system) and will allow us to design more targeted bioassay systems.

14.1 Introduction of Biofouling: Microfouling and Macrofouling

Biofouling commonly refers to the undesirable accumulation of microorganisms, plants, algae, and animals on surfaces submerged in marine environments, particularly on the surface of ship hulls, fish cages and nets, and seawater intake systems. Although in natural environments, the biofouling process can also take place on innate surfaces, such as the surface of large marine organisms including sponges, corals, crabs, whales, and marine mammals, it is often termed as epibiosis. In fact, biofouling occurs on almost every exposed surface in natural environments other than marine, such as development of molds on walls, bacterial film on human teeth, microbial growth on membrane systems of bioreactors and desalination systems. In general, we often classify the biofouling phenomena in aquatic systems into two types: microfouling and macrofouling.

Microfouling (Fig. 14.1) refers to the formation and development of biofilm on the surface. Biofilms are a conglomerate of organic molecules, bacteria, diatoms, fungi, and other microorganisms such as protozoans. Microfouling often begins with adsorption of dissolved organic matter to the surface within seconds of the initial exposure of a new surface to an aquatic system, which leads to formation of a very thin (about 100 nm) conditioning film – called molecular fouling [1].

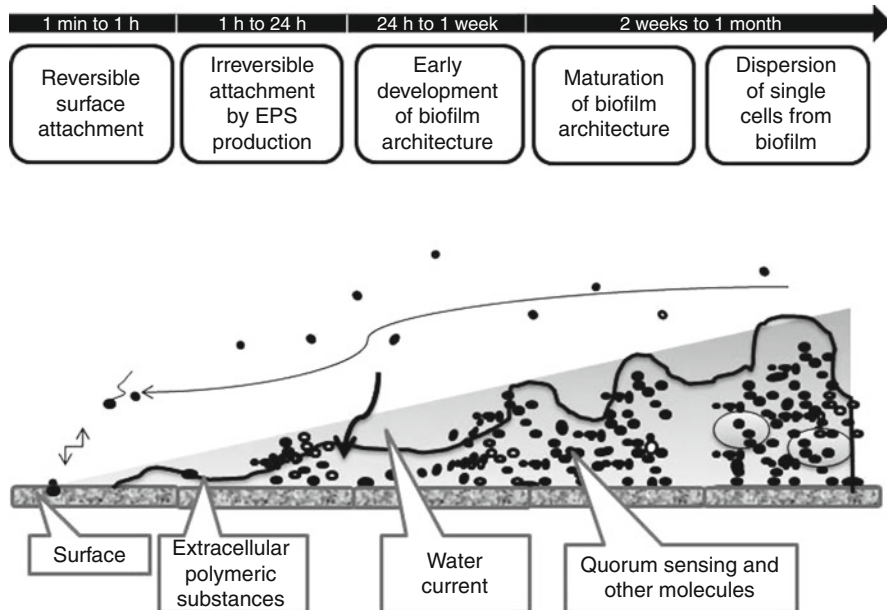


Fig. 14.1 The process of bacterial biofilm formation, showing attachment of bacteria, and extracellular polymeric substance (EPS) production. Quorum sensing and other molecules are involved in the process. This figure is adapted from Fig. 3 on page 2 from Todar's Online Textbook of Bacteriology (Todar 2008), <http://textbookofbacteriology.net/normalflora2.html>

This thin film changes physical and chemical characteristics of the original surface [2], which, in turn, affects subsequent primary colonizers. Since bacteria often dominate the aquatic environment by number (besides viruses and macromolecules), they often attach to and interact with the conditioning film first. An early sequential model of biofilm development is thus primarily based on the relative abundance of each type of microfouling organisms in aquatic environment which follows the sequence of dissolved molecules > bacteria > fungi > diatom, protozoans, and algal spores. However, it is also apparent that physical and chemical characteristics of a new surface as well as behavior of settling microfoulers will also affect the early colonizers of the surface, which determines the development of a new biofilm [3].

Of course, the development of a biofilm is a continual process on any surface since microbial communities will go through continuous succession/evolution. Synergistic and/or competitive interactions among colonizers, together with the arrival of new recruits and/or loss of previous colonists, continuously shape the biofilm community [4]. Biofilm succession (development of microfouling) is influenced by physical and chemical conditions of the external environment as well as colonizers' physical and chemical conditions and behavior. The highly dynamic development and succession/changes of microbial communities in biofilms make it difficult for controlling microfouling processes in nature.

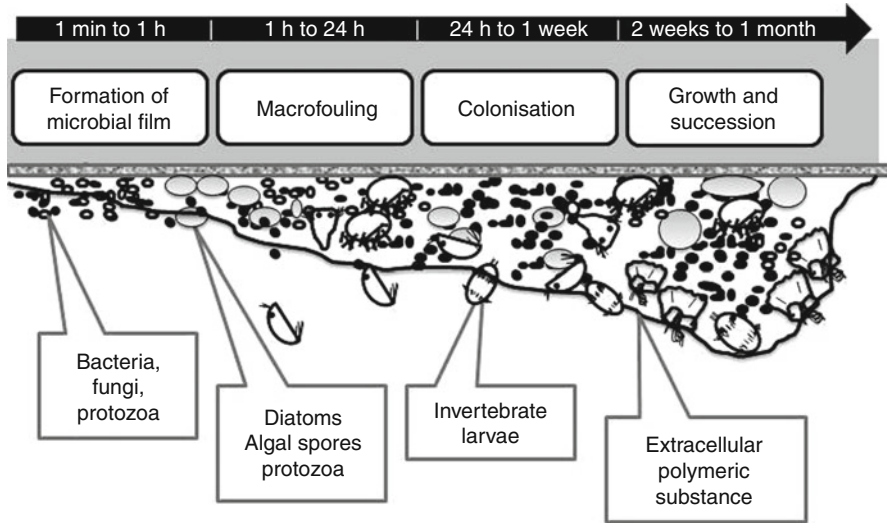


Fig. 14.2 The process of macrofouling, showing settlement and accumulation of primary settlers – bacteria, fungi, and protozoa followed by diatoms, spores of macroalgae, and larvae of marine sessile invertebrates. As with biofilm formation, EPS production is involved

Development of microfouling is also closely linked with marine corrosion since microbial metabolites released from the biofilm can corrode marine structures, which will not be discussed here as it is not the focus of this chapter.

Macrofouling refers to settlement of spores of macroalgae and larvae of marine sessile invertebrates and subsequent growth of these macroorganisms on marine surfaces. Accumulation of biomass of macroorganisms, such as seaweeds, mussels, oysters, calcareous tube-building polychaetes, clams, and barnacles that are often called as macrofoulers, is the real concerns of maritime industry and operation. In fact, some macrofouling species are small in size, but they can form enormous biomasses on ship hulls or in seawater intake systems that severely affect the performance of marine structure and system. Macrofouling often leads to substantial economic costs and operational challenges/difficulties in maritime industry, such as mariculture, shipping industry, naval vessels, power plants, and desalinization facilities. Therefore, how to control macrofouling has always been the top priority of the antifouling industry.

In summary, the development of biofouling community can be described as follows (Fig. 14.2).

Antifouling refers to the processes and means of controlling and/or preventing biofouling to take place or to clean up the biomass accumulation of fouling organisms, such as the control of biofilm development or preventing larvae or spores of macrofoulers from settlement on a new surface, and/or removal of biofilm and accumulated biomass of macrofoulers. For detailed information on pros and cons of different antifouling coatings, please see a nice review by Yebra et al. [5].

It is well known that larval or spore settlement of macrofoulers and their subsequent growth and development are affected by many factors, such as chemical and physical characteristics of marine surfaces, biophysical condition and behavior of settlers, hydrodynamics near the surface, physical, chemical, and biological environmental conditions. Due to complexity of interaction between macrofoulers and external environmental conditions, it is very difficult to stop the settlement process of settlers without using very destructive means (such as toxic antifouling compounds) in nature.

As biofouling has been a real challenge for as long as the history of human navigation at sea and in the rivers, antifouling technology was developed almost in parallel, which can be traced back to thousands of years. The ultimate goal of antifouling control is to stop the attachment of marine macrofoulers before they are allowed to grow on the ship hull surface. Before rapid industrialization era, raw materials, such as plant oil, tars, and brimstone, were commonly used as primary antifouling coating of ships and boats. In general, there were three major types: white antifouling coatings consisting of train oil, brimstone, and rosin; brown coatings consisting of tar, brimstone, and pitch; and black coatings consisting primarily of tar (giving the black color) and pitch. These coatings were proven to be very effective in protecting wooden structure from biofouling for a relatively long time. Of course, toxicity of these coatings was not the concern of navigation industry at that time (see Chapter 1 in [6]).

Metal-based antifouling coatings were proposed in the early seventeenth century when copper sheathing was suggested and finally applied to ship keels in the mid-seventeenth century. It was then discovered that copper-based antifouling coatings can effectively prevent the underwater structure from biofouling by seaweeds, worms, and mussels since copper can be oxidized and interact with chlorine in seawater to form toxic films that either deterred larval or spore settlement of macrofoulers or even killed the foulers coming close to ship hulls. Quickly, the British navy adopted copper-based coatings to their fleet, and the same or similar technology that was based on copper coatings was rapidly adopted by other industries. Since then, various types of metal-based coatings were developed and used until the discovery of tributyltin (TBT)-based coatings about half a century ago. TBT-based coatings were considered as the most cost-effective and non- or low-toxic antifouling coatings in the market for almost 40 years as it can effectively prevent attachment of macrofoulers at extremely low concentrations (at ng/L concentrations). Unfortunately, it was found in the 1980s that TBT can cause deformation of oyster shells at a concentration of 20 ng/L and imposex – development of male organs in female genitalia- in marine snails at 1 ng/L. TBT was also found to be accumulated through food chains and at high concentrations in marine mammals. These new discoveries led to the complete ban of organotin-based coatings by International Maritime Organization in September 2008 (although some countries still produce and apply them to marine structures at this point). Together with the ban of a number of toxic biocides, the marine coating industries are facing serious problems on what kind of coatings can be developed and marketed. At this point, many coating industries are forced to return to metal-based coating technology (with reduced metal concentrations) in combination with so-called booster biocides since

copper fails for some macroalgae. However, the environmental safety of most of those “booster biocides” has not been rigorously evaluated in the marine environment. These facts combine to demand for the discovery of nontoxic or low-toxic antifouling compounds. Developing alternative antifouling coating technology becomes an urgent but challenging issue, which calls for the rapid screening and discovery of marine natural products as non- or low-toxic antifouling compounds.

Besides chemical means of antifouling control, surface–polymer chemistry has recently been a major area of antifouling technology development, with the ultimate goal to create physical/chemical surfaces which weakens the strength of the attachment of settling spores, microbes, and larvae, so that these foulers will be washed away by the water flow (see reviews [5, 7]). The details will not be discussed here as it is not so relevant to the scope of this chapter.

As long as biofouling continues to develop on underwater structures, foulers need to be removed physically and the surfaces need to be repolished and repainted, which will not be discussed here either.

14.2 Methods of Assessment of Biofouling

Assessment of the biofouling condition of ship hulls, membrane filter systems (desalination facilities), inside pipelines, and other underwater services is a very important step for developing antifouling control and maintenance strategies in maritime operations. Highly diverse methods and technologies have been developed to carry out biofouling monitoring, which vary based on practical needs. However, in general, the methods can be divided into two types based on the purpose of the assessment.

Methods of assessing microfouling which are commonly used to qualify and quantify biofilm development, particularly for bioreactor systems, membrane filter systems, and newly submerged surfaces [8] include (but do not exclude others that are not listed here):

- (a) Direct cell counting of bacteria, diatoms, algal spores, and other microscopic organisms under the microscope with or without staining methods
- (b) Counting the number of microbes (bacterial colonies) formed on agar plates with various culture media, and/or type of colonies and species
- (c) Determination of biomass, thickness, microbial density, and matrix of the biofilm under a confocal laser microscope
- (d) Determination of polymer matrix under atomic force microscope and 3-D structures of biofilms under scanning electronic microscope
- (e) Determination of biomass (wet weight, dry weight) or percentage of coverage of biofouling organisms within a given area
- (f) Determination of organic matter contents, proteins, lipids, hydrocarbons, ATP, or humic substances extracted from a harvested biofilm

As some of these methods are commonly used in antifouling bioassay systems, no details will be provided in this section, while others can be easily found in the literature.

Assessment of macrofouling involves routine monitoring of underwater marine installations, and most of these methods are relatively simple and easy to follow. They include:

- (a) Visual inspection of the seriousness of the fouling condition (either by naked eye, or video camera or camera imaging (which is particularly useful for pipeline inspection))
- (b) Determination of the percentage of coverage of surfaces
- (c) Determination of biomass and/or species composition (in terms of wet weight, dry weight, or numbers)
- (d) Determination of the thickness of fouling coverage
- (e) Determination of the attachment/adhesion strength of macrofouling organisms
- (f) Determination of the fouling rate, and so on

Again, these methods are not the real focus of this chapter and will not be reviewed extensively.

14.3 Screening of Marine Natural Product as Antifoulants

14.3.1 General Strategies

To screen marine natural products for effective antifouling compounds, the following general procedure is commonly practiced by different research groups, which can be divided into the following steps (Fig. 14.3):

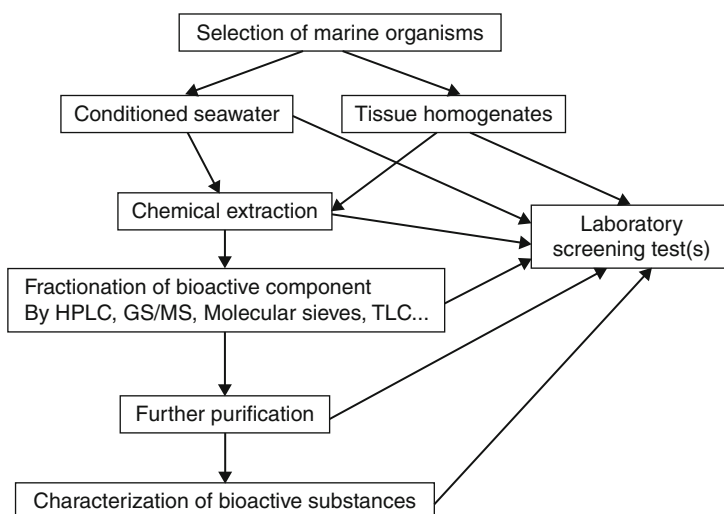


Fig. 14.3 General process for identification of natural antifouling compounds in marine natural products. Fractionation of bioactive components can be done through high-pressure liquid chromatography (HPLC), gas chromatography/mass spectrometry (GC/MS), molecular sieves, and thin layer chromatography (TLC)

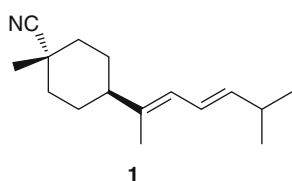
1. Selecting marine organisms as a source of natural products
2. Obtaining sufficient raw biological materials through either fermentation (of microbes) or harvesting (of macroorganisms from either natural populations or marine farms)
3. Testing the antifouling potency of either conditioned seawater or homogenized tissues with screening bioassays
4. Extracting biomass with various solvents if the preliminary bioassay result is promising
5. Testing antifouling potency of various extracts with bioassay systems
6. Fractioning and partitioning extracts and identification of active fraction(s) based on bioassay results
7. Purifying bioactive compounds and testing their activities with bioassay systems
8. Characterizing chemical compounds using various instrumentation such as MS, NMR, X-ray, and so on
9. Confirming the bioactivity of the pure compound with further bioassays

14.3.2 Current Status

Screening of marine natural products for antifouling compounds has been a hot topic over the last few decades; many compounds isolated from marine invertebrates, seaweeds, and microbes showed promising activities, but so far, hardly any of those compounds have been commercialized as antifouling products due to various challenges (see reviews [9–11]). In total, about 200 compounds isolated from marine organisms have shown good antifouling activities against some major fouling organisms. These compounds are highly diverse in terms of molecular size, structure group, and solubility in seawater [9–11]. It is anticipated that more and more marine natural products will be patented as potential antifouling compounds each year as this area of research has been intensively carried out in recent years.

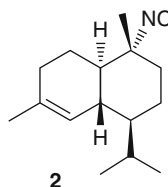
14.3.2.1 Natural Antifouling Compounds and their Synthetic Analogues

Over the last two decades, a considerable number of natural compounds have been reported to have antifouling activities from many marine organisms including sponges, algae, corals, as well as microorganisms. For some of these compounds, their structure–activity relationships have been extensively studied, and analogues with improved activity and reduced complexity of structure have been synthesized, which paves the way for future industrial application. Fusetani published a very nice book “*Antifouling Compounds*” in which many antifouling compounds isolated from marine sources were included. Herein, we will extract a few examples from that book about marine natural compounds and their synthetic analogues with pronounced antifouling activities. Please refer to the book for more in-depth reading as well as for the related references (Fig. 14.4).



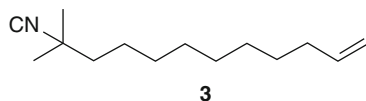
$EC_{50} = 0.13 \mu\text{g mL}^{-1}$

$LC_{50} > 100 \mu\text{g mL}^{-1}$



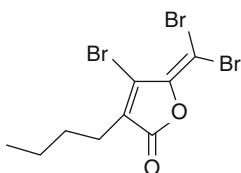
$EC_{50} = 0.14 \mu\text{g mL}^{-1}$

$LC_{50} > 100 \mu\text{g mL}^{-1}$

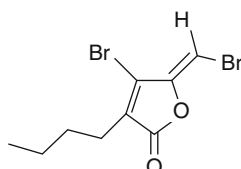


$EC_{50} = 0.046 \mu\text{g mL}^{-1}$

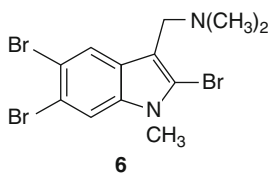
$LC_{50} > 30 \mu\text{g mL}^{-1}$



$EC_{50} = 20 \text{ ng mL}^{-1}$

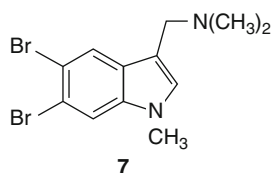


$EC_{50} = 20 \text{ ng mL}^{-1}$



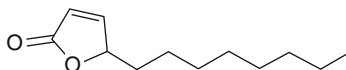
$EC_{50} < 0.01 \mu\text{g mL}^{-1}$

$LC_{50} > 1 \mu\text{g mL}^{-1}$



$EC_{50} < 0.06 \mu\text{g mL}^{-1}$

$LC_{50} > 0.6 \mu\text{g mL}^{-1}$



$EC_{50} = 0.5 \mu\text{g mL}^{-1}$

$LC_{50} > 50 \mu\text{g mL}^{-1}$

Fig. 14.4 Natural antifouling compounds and their synthetic analogues. EC_{50} values refer to their activity against barnacle cypris settlement. LC_{50} values refer to the half lethal concentration

A number of isocyanate compounds (Fig. 14.4: 1–3) were isolated from the marine sponge *Acanthella cavernosa* and nudibranchs of the family Phyllidiidae. These compounds show potent inhibitory activity against settlement of cypris of *Balanus amphitrite* without significant toxicity. Two compounds, 3-isocyanatotheonellin and 10-isocyanato-4-cadinene, have notable antifouling activity with EC_{50} values of 0.13 and 0.14 $\mu\text{g mL}^{-1}$, respectively, while their LC_{50} values are more than 100 $\mu\text{g mL}^{-1}$. Further structure–activity relationship studies and structural optimization led to the synthesis of a simple linear alkyl isocyanate whose EC_{50} was even lower than the original natural products. Field testing with this simple compound further proved its efficiency in controlling settlement of barnacles, ascidians, and bryozoans.

Halogenated furanones were isolated from red alga *Delisea pulchra*, and their ecological role and bioactivities were extensively investigated. These 2(5 *H*)-furanones showed excellent activities in preventing fouling of both macroorganisms and bacteria. In particular, they control bacterial fouling by interfering with the quorum sensing system in bacteria. Among these furanones, two compounds (Fig. 14.4: 4–5) can inhibit settlement of cypris of *Balanus amphitrite* with EC_{50} values around 20 ng mL^{-1} , which is 20 times more active than CuSO_4 . A large number of synthetic analogues of these furanones were screened for their bioactivity, and several of them are now in industrial uses for antimicrofouling and antimacrofouling purposes.

A heterocyclic compound, 2,5,6-tribromo-1-methylgramine (TBG) (Fig. 14.4: 6), was isolated from several marine bryozoans species. It showed remarkably strong antifouling activity with an EC_{99} of 0.03 $\mu\text{g mL}^{-1}$ against *B. amphitrite* cyprids. In subsequent studies, more than 150 gramines and related compounds were tested and compared for their antifouling compound, and 5,6-dichloro-1-methylgramine (DCMG) (Fig. 14.4: 7) was selected for further investigation because of its outstanding performance in antifouling assays. Field test and various toxicity tests were carried out for DCMG, and the results were quite satisfactory.

Other than marine macroorganisms, marine microorganisms are becoming a more important source for bioactive natural compounds. A group of simple butenolides were isolated from marine *Streptomyces*, and they showed moderate antifouling activity with EC_{50} values around 20 $\mu\text{g mL}^{-1}$. After localizing the functional group, Xu et al. had a simple alkyl butenolide (Fig. 14.4: 8) synthesized whose antifouling activity was greatly improved. In laboratory antisettlement assays, it could inhibit three major fouling organisms with EC_{50} values all less than 1 $\mu\text{g mL}^{-1}$, while its toxicity was quite low. In a field test carried out on a highly fouled fish farm, less than 5% of the compound (w/w) mixed with the basal paint could protect the surface from fouling for 3 months when compared to control surfaces which only had basal paint [99].

These examples give us confidence that it is promising to develop nontoxic antifouling compounds from marine-derived natural compounds. The marine environment, especially the microbes living in it, is an enormous untapped resource for us to find such treasures, and we shall be optimistic.

14.3.3 Selection of Marine Organisms for Chemical Extraction

The most important first step in antifouling studies is to select the right organisms as raw materials. Although there has not been a well-defined guideline for selecting marine organisms, for macroorganisms, we tend to select species that are:

1. Free of biofouling on their surfaces while their neighboring species are heavily fouled
2. Easy to be harvested in large biomass
3. Able to produce various chemical compounds as documented in the literature
4. Easy to be extracted with various chemical solvents (as some marine organisms that produce a large amount of mucous are very difficult to be extracted)
5. Not on the species list to be protected, and so on

For microorganisms, the species are often selected for further study after a preliminary screening bioassay. However, certain bacterial groups such as *Actinomyces* and microbes associated with sponges and corals are favorable targets.

14.3.4 General Extraction Procedures and Partition Methods

14.3.4.1 Extraction of Macroorganisms

Fresh marine macroorganisms are collected from the field (Figs. 14.5–14.7). The specimen is first washed with filtered seawater and then freeze-dried (alternatively, it can be dried in a fume hood). The dried specimen is homogenized and extracted by pure methanol for 24 h for three successive times. In addition, sonication can be included to assist the extraction of metabolites, but the temperature of the water bath must be controlled to avoid overheating the solvent. The combined methanol extract is evaporated under vacuum to generate the total organic extract (TOE). The TOE is subsequently extracted using distilled water (sample code W) and dichloromethane (sample code O as for organic). The W fraction is then partitioned using *n*-butanol (sample code WB). As butanol has a relatively high solubility in water, water-saturated butanol is preferred if a quantified extraction needs to be carried out. Inorganic salts are mostly present in the remaining water fraction (sample code WW), which is usually discarded. The dichloromethane, F fraction, is dissolved or sometimes suspended in 90% aqueous methanol and then partitioned using hexanes (sample code OH) to remove very lipophilic substances, such as lipids. The 90% aqueous methanol layer is then diluted to 50% aqueous methanol and partitioned using dichloromethane (sample code OD), and the remaining aqueous methanol is dried (sample code OM). This conventional lipid–lipid extraction and solvent partitioning is outlined in Fig. 14.5. Alternatively, some other routinely used partitioning schemes can be adopted, and a good example is the one described in [12].

In recent years, accelerated solvent extraction (ASE) has been occasionally adopted in extraction of marine macroorganisms and has proven to be an efficient

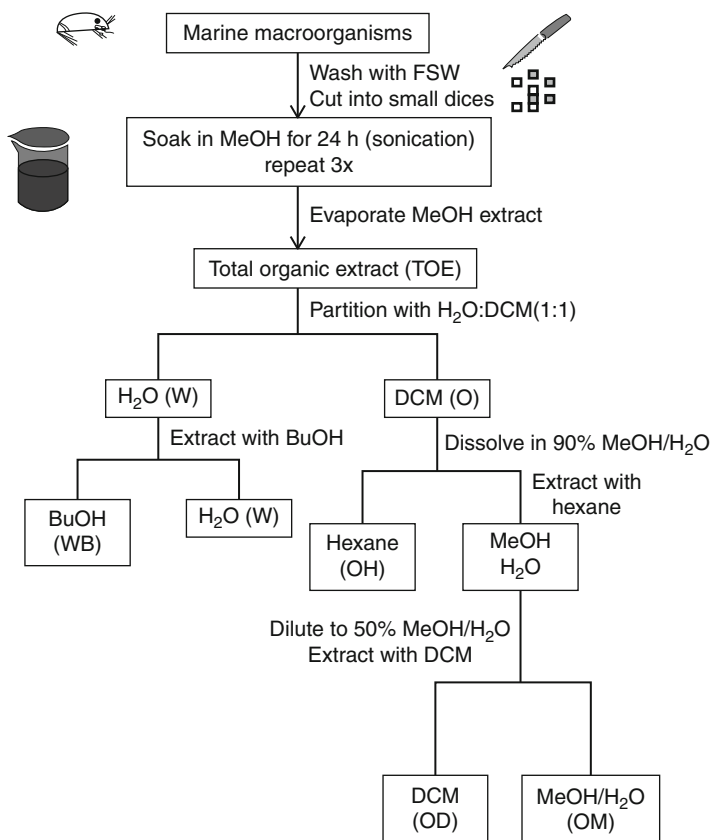


Fig. 14.5 Standard solvent partitioning of extracts of marine organisms, which is a conventional lipid–lipid extraction methodology. Abbreviations: *FSW* filtered seawater, *3x* three times, *MeOH* methanol, *DCM* dichloromethane, *BuOH* butanol

and environmentally friendly extraction method [13]. ASE employs higher pressure to keep the solvent at a temperature higher than its normal boiling point at atmospheric pressure. With higher temperature and reduced viscosity, the solvent is able to extract the specimen thoroughly in a very short period of time. Briefly, the specimen is loaded to an extraction cell in the ASE system and exposed to solvents at high temperature for a short period of time. Johnson et al. [13] first extracted 50 g of sponge sample using distilled H₂O to remove most of the inorganic salts. They then successively extracted the sponge sample with solvents that are routinely used in extraction, such as hexanes, dichloromethane, and methanol, which cover different levels of polarity. Moreover, at the end of each extraction, a purge with nitrogen dries the specimen so that less overlapping takes place between successive extractions. By using the ASE, Johnson et al. [13] demonstrated that the extraction efficiency of ASE is higher than conventional solvent extraction and partition.

Meanwhile, ASE requires much less time and labor. For example, grounding of the sample is unnecessary. However, researchers need to determine variables such as extraction temperature and time in order to optimize the extraction program and fulfill extra safety requirements. Nevertheless, ASE offers a new, efficient, and economically and environmentally friendly method.

14.3.4.2 Extraction of Microbial Cultures

Marine microorganisms – mainly bacteria and fungi – can be isolated from different marine habitats, such as seawater, sediments, surface and internal tissues of macroorganisms. Usually, a small-scale fermentation of isolated microorganisms is carried out and screened in specific antifouling bioassays. After the active strain is selected, a large-scale fermentation will be performed in order to isolate and characterize the pure compounds that exhibit the desirable antifouling activity. Most of the fermentation is carried out in liquid culture for a certain period of time, which is very critical for the production of the bioactive compounds. At the end of the fermentation, the first step is the separation of the microbial cells from culture medium, which is very important if one wants to know whether the bioactive compound is an extracellular or intracellular metabolite. This step usually can be done by either filtration or centrifugation depending on the nature of the microbial cells. For fungi, the easiest way is just to filter the whole liquid culture by several layers of cheesecloth. The filtrate is then extracted by liquid–liquid extraction using ethyl acetate or solid extraction using adsorbent resins such as Amberlite XAD-7 and Diaion HP20. The solid extraction method is preferred when dealing with a large-scale culture. The ethyl acetate extract or the eluent washed from the resin is then evaporated, and the obtained crude extract can then be processed using the standard solvent partition scheme described above. Metabolites associated with or inside the microbial cells are usually obtained by using methanol to extract the lyophilized mycelia or bacterial cells.

Sometimes, solid fermentation for microbes, especially for fungi, can be carried out. If the material is agar, then the agar plate/disk is usually cut into small pieces and extracted by 100% ethyl acetate or 80% ethyl acetate, 15% methanol, and 5% acetic acid. To achieve optimum extraction, the sliced agar and extraction solvent should be kept on a shaker for 24 h to increase extraction efficiency. The contents are then filtered and the filtrate is dried under vacuum on a rotary evaporator to obtain the crude extract for further separation and analysis. The work flow is described in [Fig. 14.6](#).

14.3.4.3 Extraction of Volatile Metabolites

Volatile compounds are sometimes responsible for the chemical defense mechanisms of marine macroorganisms, such as sponges and algae. Volatile chemicals from bacteria or biofilms are involved in inducing or inhibiting larval settlement. To collect volatile chemicals, a simple closed-loop stripping apparatus (CLS) can be used according to Grob and Zürcher [14] and later modified by Harder et al. [15]. For macroorganisms, such as sponges, the sample will be first washed with filtered seawater and then submerged in filtered seawater in a clean

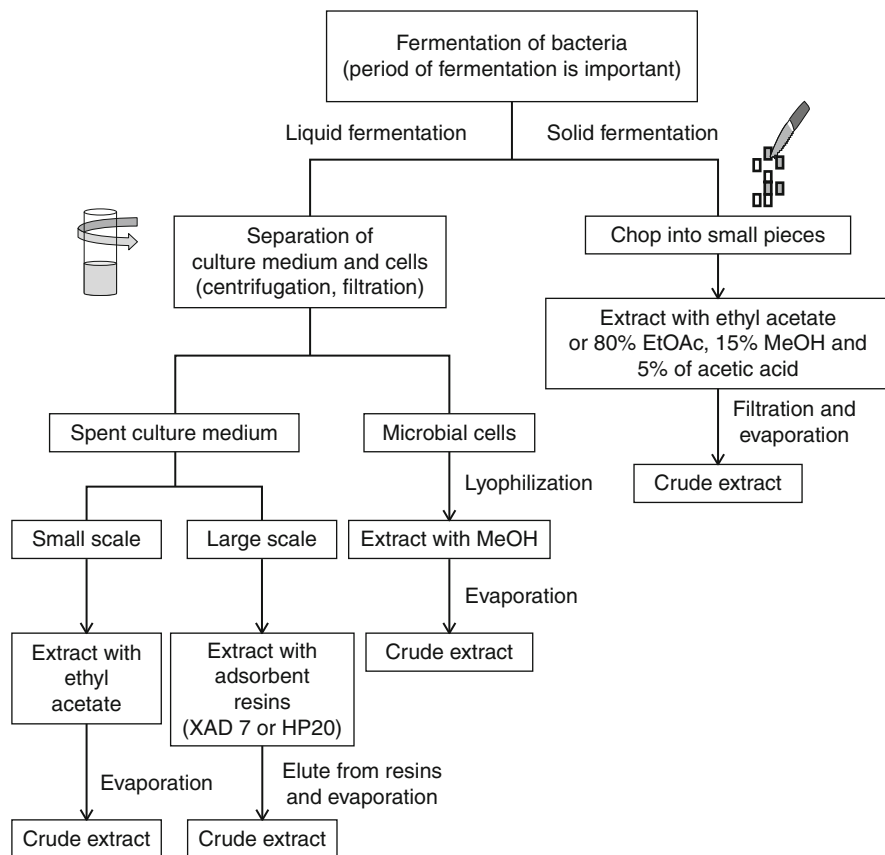
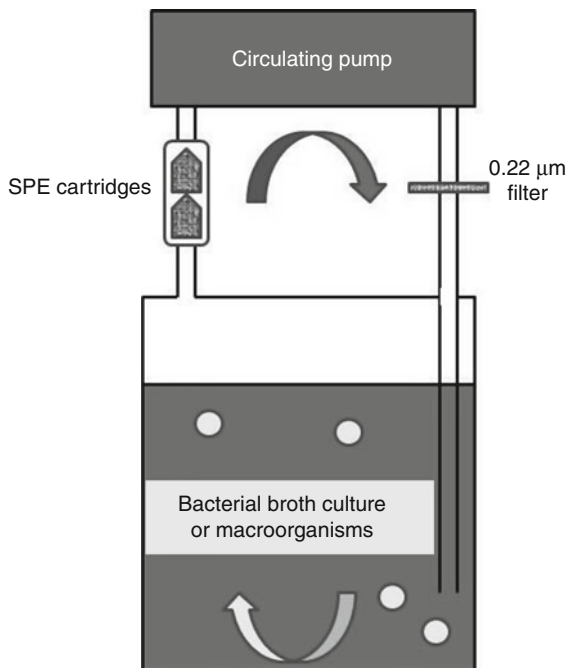


Fig. 14.6 Extraction workflow of marine microorganisms using fermentation to isolate and characterize pure compounds with antifouling activity

vessel. The closed loop will be formed by connecting the vessel to a pump generating air, a 0.22- μm membrane filter, and a solid extraction cartridge. A sketch of the apparatus is provided in Fig. 14.7. The air generated by the pump will pass through the membrane filter, enter the seawater which contains the macroorganism sample, and sweep volatile compounds out of the aqueous phase. The solid-phase extraction cartridge, which is commercially available in many forms, will absorb the volatile compounds. In addition, this system is also applicable for the extraction of volatile compounds from microorganisms. To do that, the seawater is replaced by sterile medium which is subsequently inoculated with microorganisms. In fact, the whole system becomes a mini-bioreactor with adequate aeration. After being absorbed, volatile compounds can be eluted from the cartridge using acetone, and then the constituents of the volatile compounds can be analyzed by GC-MS.

In recent years, a more advanced solid-phase extraction technique called Stir Bar Solid Extraction (SBSE) was developed by Baltussen et al. [16].

Fig. 14.7 Apparatus for extraction of volatile compounds. A closed loop is formed by connecting the vessel to a pump, a 0.22- μm membrane filter, and a solid-phase extraction (SPE) cartridge. This figure adapted from Harder et al. [15]



The main advantage of this technique is its high sensitivity, enabling identification of trace amounts of volatile compounds. Moreover, SBSE is a solvent-less, simple method which allows extraction and concentration in a single step. The principle of this method is to use a magnetic stir bar coated with a polydimethylsiloxane (PDMS) film. The PDMS-coated stir bar is firstly introduced into the sample (either gaseous or aqueous matrices), and a predetermined extraction method (extraction temperature, time and speed of stirring) is used to extract the compounds from the sample. Compounds are desorbed from the stir bar by thermal desorption using a commercial TDU (thermal desorption unit, Gerstel) with a programmed-temperature vaporization injector (Gerstel) and analyzed by GC-MS. The whole process can be done automatically, and high-throughput screening is therefore made possible. Many volatile compounds have been analyzed using this technique. Demyttenaere et al. [17] used SBSE coupled to GC-MS to analyze the organic volatile compounds produced by fungi and found that this technique is able to enrich compounds normally present in trace amounts. Therefore, this new technique could provide an alternative to traditional methods.

14.3.4.4 Extraction of Metabolites from Parts of Marine Macroorganisms (Also Applicable to Localization of Metabolites)

To isolate a natural antifouling compound, which really plays the same ecological role in protecting its host from biofouling (epibiosis), it is important to know where the metabolite is localized in the macroorganism. Many compounds with

antifouling activity have been isolated from sponges. However, to know if these compounds play a real antifouling role in nature will require more evidence, such as the localization of the compounds. Furthermore, as many marine invertebrates contain microbial symbionts, determining the origin of a secondary metabolite (from the host or the microbial symbionts) is also important in understanding its possible antifouling function in nature. Here we describe a method for extraction of a metabolite from different types of cells that is applicable to sponges, algae, and tunicates. The macroorganism sample is collected from the field and cleaned of debris, rinsed with calcium- and magnesium-free artificial seawater (CMF-ASW), pH 7.4 to replace the natural seawater. The tissue is then cut into small pieces using a razor blade and completely immersed in aerated CMF-ASW. After 2 h, the cloudy water which contains dissociated cells is filtered through a 100- μm nylon mesh using vacuum filtration to remove large spicules and cell aggregates. This step is repeated using a 50- μm mesh. The cells are then fixed in 3% glutaraldehyde in artificial seawater, pH 7.4, and left overnight at 4°C in the dark. The purpose of fixation is to protect dissociated cells from rupturing and to prevent aggregation of cells. Just prior to fractionation, the fixed cells are diluted with CMF-ASW, spun down at 600 g and 4°C for 5 min and then washed twice with fresh CMF-ASW to completely wash away the fixative. The fixed cell suspension is then fractionated according to density via centrifugation (600 g at ambient temperature) across discontinuous Percoll gradients, such as 20%, 40%, 60%, and 80% in CMF-ASW, or other gradients that have been predetermined. The bands of cells that accumulate at the density interfaces are then carefully collected by pipette and washed twice with CMF-ASW and centrifugation. The fractions can then be extracted by organic solvents such as dichloromethane and methanol and further separation and analysis of the extract can be done in the same way as described in previous sections. A flow chart is provided for reference in Fig. 14.8.

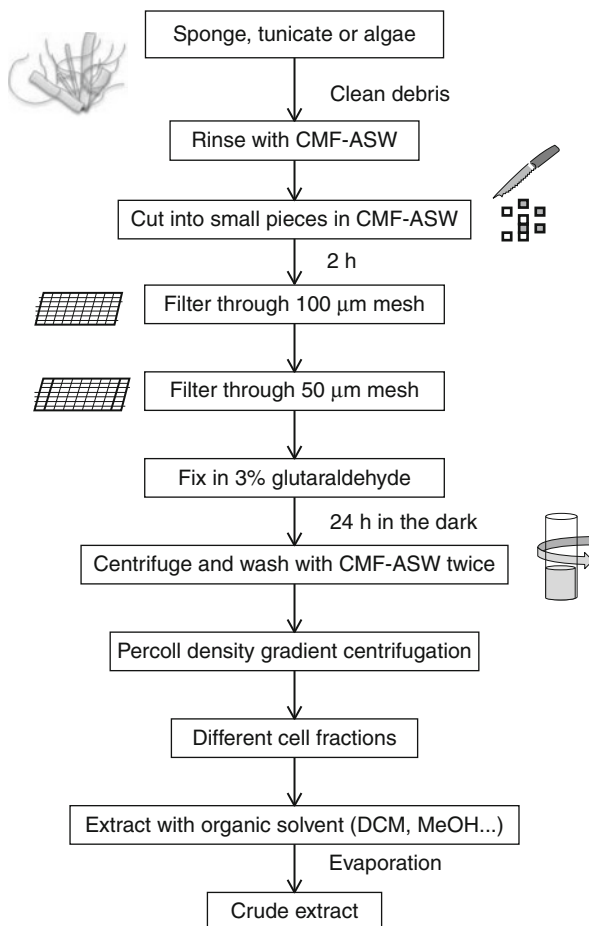
14.4 Methods for Screening Antimicrofouling Compounds

For microbial fouling on submerged surface, we need to control the attachment and growth of microbes, particularly bacteria (which are dominant components of biofilms), and biofilm formation and development. Therefore, antibacterial attachment and growth, antibiofilm formation, and quorum sensing bioassays are the most commonly used antimicrobial assays, while antifungal and antidiatom attachment and growth assays are often the secondary assays.

14.4.1 Antibacterial Assay

Antibacterial growth and attachment assays are the laboratory bioassays most commonly used for many decades and are primarily based on the performance of individual bacterial species/strains. Selection of bacterial species and strains is target-driven. For instance, pathogenic bacterial strains and species are commonly

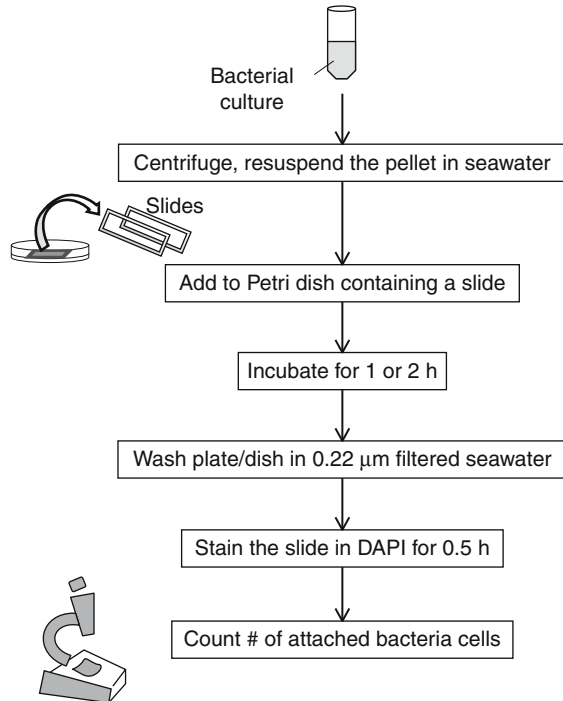
Fig. 14.8 Extraction of metabolites from different types of cells in marine macroorganisms such as sponges, algae, and tunicates (also applicable to localization of metabolites). Abbreviations: *CMF-ASW* calcium- and magnesium-free artificial seawater



used in antibiotic screening (to be covered in other chapters). In general, for antimicrobial assay screening, the following characteristics can make bacterial species and strains ideal target organisms:

- Being the common and dominant ones in natural biofilms
- Having good motility
- Attaching quickly on an agar or exposed surface (such as glass or Petri dishes)
- Being stable under laboratory conditions (they do not mutate frequently)
- Being easy to grow and maintain in laboratory conditions
- Growing well on common bacterial culture media
- Forming a good biofilm
- Having the property either inducing algal spore attachment or larval settlement of marine invertebrates

Fig. 14.9 General antibacterial attachment assay. The treatment solution should contain the test solution of extract or compound, the negative controls should use a small amount of solvent used to dissolve the extract in the treatment, and the positive controls should use an antibiotic solution. Abbreviations: *DAPI* 4',6-diamidino-2-phenylindole, a fluorescent stain that binds strongly to DNA



We have used the following species in our laboratory bioassays: *Loktanello hongkongensis*, *Micrococcus luteus*, *Pseudoalteromonas* sp., *Rhodovulum* sp. (MB253), *Ruegeria* sp., *Staphylococcus haemolyticus*, *Vibrio fluvialis*, *Vibrio halioticoli*, *Vibrio* sp. (NAP-4), and 7 strains of common marine pathogens: *Moraxella phenylpyruvica*, *Pseudoalteromonas piscida*, *Shewanella algae*, *Vibrio alginolyticus*, *Vibrio furnissii*, *Vibrio harveyi*, and *Vibrio vulnificus*.

Stock culture of selected bacterial strains to be used for bioassays is obtained from either bacterial culture collections or from a research laboratory deposit and inoculated into sterile culture broth (with a suitable culture medium, which can be species specific in order to provide optimal growth, attachment, and performance of the test species) and grown at a defined temperature until the culture reaches its stationary phase. Suspended bacteria are harvested by centrifugation and diluted in autoclaved FSW to an optical density of 0.1 at a wavelength of around 600 nm or optimal density for the bioassays described in following sections.

14.4.1.1 Antibacterial Attachment

Various antibacterial attachment assays have been developed and applied. Here, we only introduce one protocol. Other methods such as bacterial attachment onto agar surfaces and Petri dish surfaces more or less follow the following steps (Fig. 14.9):

- Adding bacterial suspension into a Petri dish containing an acid-washed slide
- Incubating for a desired period of time

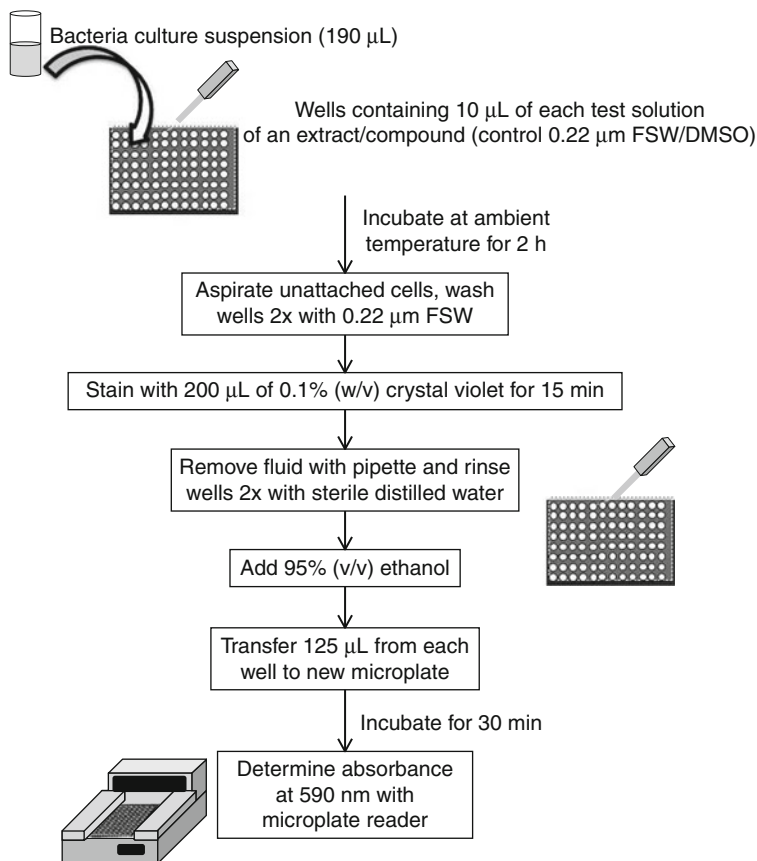


Fig. 14.10 Anti-adhesion/attachment assay in microplates for bacteria

- Washing the plate or dish in 0.22- μm filtered seawater
- Staining the slide in DAPI for 0.5 h
- Counting the number of attached bacterial cells in at least 10 fields of view under an epifluorescence microscope

In these assays, for treatment, the test solution of extract or compound is either incorporated into the agar plate or added directly into Petri dishes; for the negative controls, the small amount of solvent that is used to dissolve the extract is added instead; for the positive controls, antibiotic solution will be used.

Anti-adhesion/attachment assay in microplates (Fig. 14.10): Ten μL of DMSO or solution of dissolved extracts/compounds in seawater is placed into each well of a 96-well microplate containing 190 μL of diluted bacterial culture suspension and incubated at ambient temperature for 2 h. Unattached cells are then aspirated off, and wells are washed twice with sterile 0.22- μm filtered seawater. Attached bacterial cells are stained with 200 μL of 0.1% (w/v) crystal violet for 15 min at room temperature. The fluid in each well is removed with pipette, and the wells

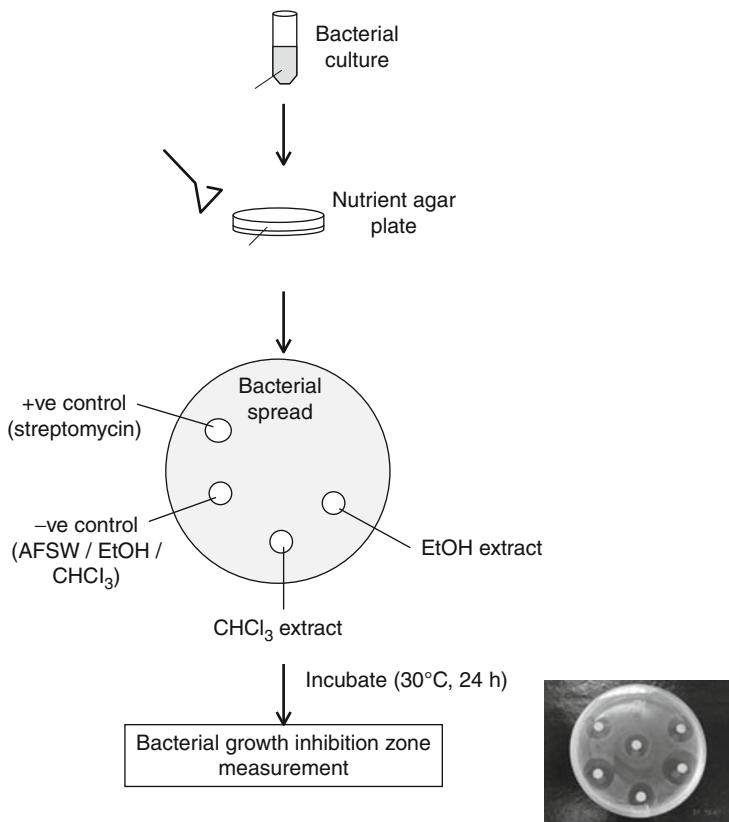


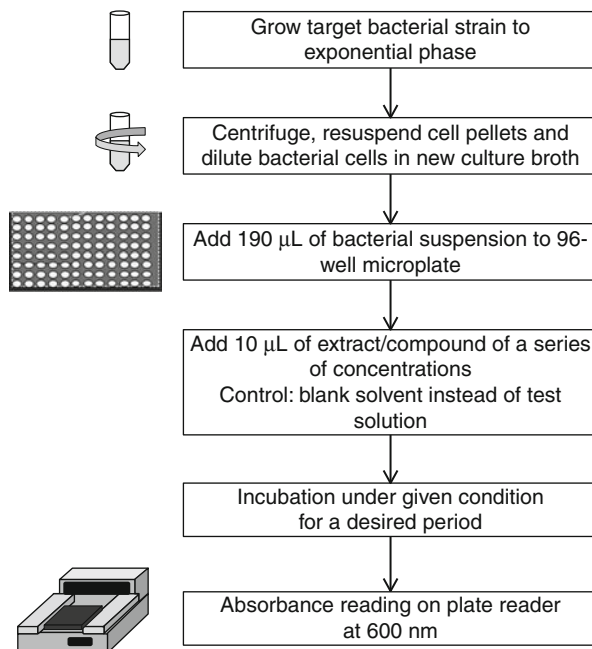
Fig. 14.11 Disk diffusion assay to test antibacterial property of chemical extract or compound against target bacterial strains. Abbreviations: +ve positive, -ve negative, *EtOH* ethanol, *CHCl₃* chloroform

are rinsed twice with sterile distilled water. A solution of 95% (v/v) ethanol is added to the wells and incubated for 30 min. The contents are briefly mixed, and 125 μL of the ethanol containing solubilized crystal violet is transferred to the wells of a new microplate. Afterward, the absorbances of the wells are read at 590 nm in a microplate reader. As a control for treatment, 10 μL of DMSO or sterile 0.22- μm filtered seawater can replace the test solution in the wells and incubated for 2 h. Wells are washed, stained, and read as above.

14.4.1.2 Antibacterial Growth

Disk Diffusion Assay (Fig. 14.11): A standard disk diffusion assay can be used to test the antibacterial property of a chemical extract or pure compound [18–20] using target bacterial strains. For antimicrofouling testing, we recommend using bacterial strains that can induce attachment of dispersing propagules of marine seaweeds or invertebrates or a dominant species in natural biofilms [3]. Each sterile

Fig. 14.12 Microtiter bioassay using bacteria, using a 96-well polystyrene cell culture plate with flat bottom, for screening for drugs and antibiotics



filter paper disk (Whatman No. 1; 6 mm in diameter with disk volume = 20 mm³) is prepared and loaded with a given volume (usually less than 20 µL for a disk with a diameter about 6 mm) of the test extract or compound dissolved in a solvent (such as acetone which can easily be evaporated and be able to dissolve the extract or compound); the amount loaded onto each disk is dependent on potency of the extract and compound. After evaporation of the solvent, the paper disk is placed onto agar plates (plastic Petri dishes) that have already been spread with a culture suspension of a test bacterium prepared, as described above. Again, agar medium is suitable for bacterial growth. Two disks, one containing streptomycin at a concentration of 10 µg disk⁻¹ and one pretreated with the same solvent, may serve as the positive and negative controls, respectively. There should be at least three replicates for each test concentration of the chemical extract or compound. The plates are incubated at a temperature suitable for the test bacterium to grow as a confluent film on the agar. The diameter of bacterial growth inhibition zones or halos (growth inhibition zones between the disk and the unaffected bacterial lawn) is recorded to the nearest 0.5 mm and compared.

Microplate reader assay [21] (Fig. 14.12): Microtiter plate bioassay (96-well polystyrene cell culture plate with flat bottom) for antibacterial growth is the common method for screening for drugs and antibiotics and has been covered in other chapters of this book; therefore, we will not give a very elaborate account on this method. Briefly, a bacterial culture suspension prepared above is further diluted in the broth medium to a concentration ranging from 0.5×10^3 to 2.5×10^3 CFU mL⁻¹.

Each well of the plate is filled with 175 μL of bacterial culture. To each well, 20 μL solution of the test extract or compound, or the appropriate solvent or antibiotic solution is added as the treatment or negative or positive controls, respectively. The plates are incubated for a desired period of time. The turbidity of each well is determined by running the entire plate through an automatic multiple plate reader. The relationship between turbidity and cell density of bacteria can be determined easily as the number of bacterial cells in a well can be counted with a Flow Cell Cytometer.

In fact, there are numerous types of antibacterial growth assays developed by various groups for various purposes, which can be modified for antimicrofouling compound screening. We have no intention to provide an exhaustive list of such assay protocols here.

14.4.1.3 Antibiofilm Formation

Biofilm development assessed by Laser Confocal Microscopy (Fig. 14.13): A pure bacterial culture at stationary phase of the test species or strain is centrifuged ($3,000\times g$, 10 min) first, and bacterial cell pellets are resuspended in autoclaved 0.22-mm filtered seawater (FSW) to achieve an optical density of 0.15 at 600 nm. Four mL of the suspension is then added to a polystyrene Petri dish (diameter, 50 mm; Falcon no. 1006) [22]. Each Petri dish contains an acid-washed glass slide. A small volume ($<40 \mu\text{L}$) of a test solution (usually DMSO) of the extracts or compounds is then added to the Petri dish. After incubation at a suitable temperature for a desired period of time (bacterial species-dependent), biofilm biomasses are determined indirectly by quantification of acridine orange (Sigma, USA) which is used to stain the biofilm according to the method described by Genevaux et al. [23] with slight modifications. Briefly, the glass slides covered by biofilms are rinsed three times with AFSW, incubated in $50 \mu\text{g mL}^{-1}$ acridine orange in the dark for 10 min, and then rinsed again by AFSW. Acridine orange from stained biofilms is then redissolved with 3-mL ethanol, and its fluorescence is measured spectrophotometrically at 430 nm.

Biofilms on the glass slides are stained with fluorescein isothiocyanate-conjugated (FITC) concanavalin A (Sigma, USA; concentration = 1 mg mL^{-1}) for 30 min in the dark. Then the biofilms are rinsed in AFSW before being viewed under a Nikon C1 Confocal Microscope (Japan). The argon laser line at 488 nm for scanning excitation and a 515–565 nm band-pass filter is used to detect green-fluorescence emission signals. The alignments of the laser and monitor setup are checked according to the manufacturer's instructions. Samples are observed under $40\times$ (dry: NA 0.75) and $100\times$ (oil immersion: NA 1.4) lens, with the latter used for image acquisition. EZ-C1 software is used to generate pictures and data through the biofilms. The threshold value is set manually and retained for all sections in the same plane. Biofilm biomass, cell density, and thickness are compared among treatments and the control.

Gel-based assay [24] (Figs. 14.14, 14.15): The immobilization of chemical extracts or compound under test in agar gel or phytogel was originally developed for both laboratory and field assays for chemical defenses against

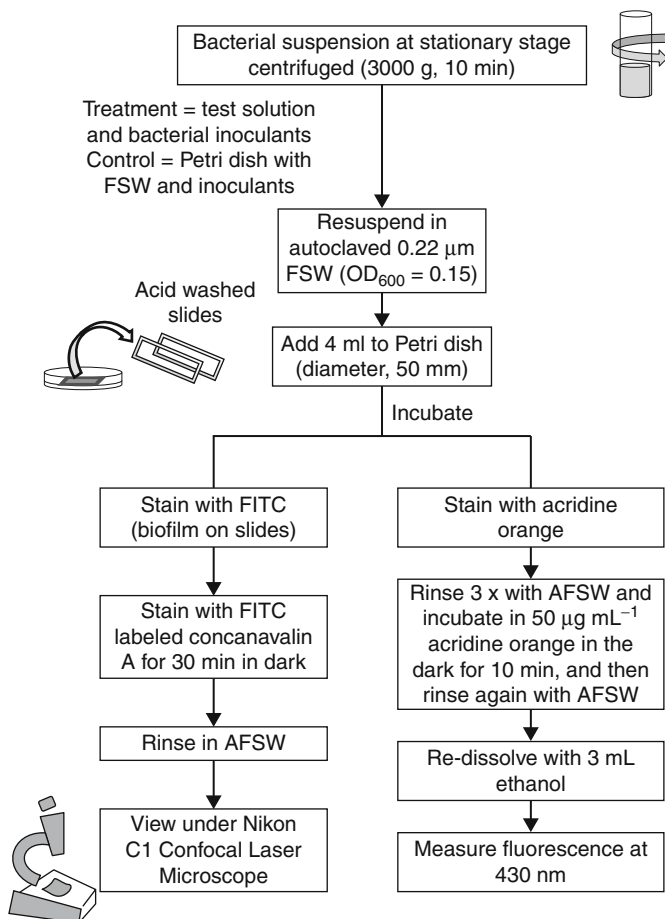
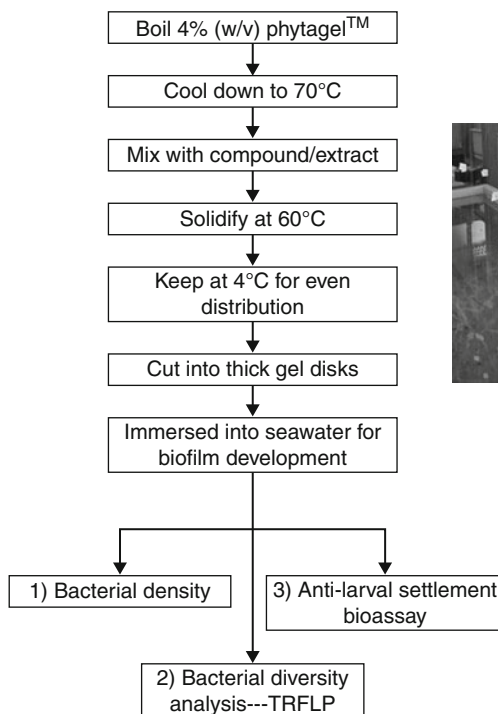


Fig. 14.13 Antibiofilm development assay, which can be assessed by Laser Confocal Microscopy. Abbreviations: *FITC* fluorescein isothiocyanate-conjugated concanavalin A

fish predation [25]. This method has at least the following advantages over the conventional antibacterial assays: (1) a culture-independent approach, i.e., there is no bias with respect to the choice of ecologically relevant test bacteria because the gels are exposed to a natural assemblage of microbial colonizers, (2) no restriction to particular modes of inhibitory microbial colonization, i.e., antibiotic and/or repellent, (3) extracts are incorporated into gels at presumably natural volumetric concentrations, (4) extracts within the gel matrix do not alter the physical characteristics of the settlement surface, (5) the ability to perform this assay under flow conditions, and (6) avoiding problems associated with laboratory assays such as unrealistic water flow and exposure to only one or a few species of test organisms. In addition, as assay gels contain a concentration of chemical extract or pure compound that decreases with time, this technique should provide conservative

Fig. 14.14 General procedure of assay using Phytigel to screen for antifouling activity, with microbial community structure and biomass of biofilm as end points. Abbreviations: *TRFLP* terminal restriction fragment length polymorphism



evidence of antifouling activity. As such, our research team developed a phytigel assay that can be used to screen for antifouling activity, using microbial community structure and the biomass of biofilm as end points.

The chemical extract/compound is dissolved in DMSO to test concentrations and transferred into sterile 50 mL Corning tubes. Gels are prepared by adding Phytigel™ (Sigma Chemical) into a stirred beaker of boiling distilled water to yield a 4% (w/v) gel concentration. After the gel solution is cooled to 70°C, the test solution in DMSO is vigorously mixed with the liquid gel solution in corning tubes to evenly distribute the extract/compound in the viscous hydrogel. Due to the high boiling point of DMSO (189°C), the extract volume will remain constant during this procedure. A control can be prepared accordingly with pure DMSO instead of test solution. The closed tubes are turned upside down and allowed to slowly solidify in a water bath at 60°C. After 5 min, the trapped air bubbles will migrate out of the solution yielding a transparent gel cylinder. The cylinders should be kept at 4°C overnight to allow for a homogenous diffusion of test solution through the gel. Subsequently, cylinders are removed and sliced into 5-mm-thick gel disks with a sterile razor blade. The gel disks are pierced with fishing line and anchored 10 cm below the water surface in individual 10 L aquaria that are continuously supplied with natural seawater from the same source at a flow rate of 60 Lh⁻¹. To avoid potential cross contamination of experiments by leached test solution, only the experimental gels of the same group are kept in the same

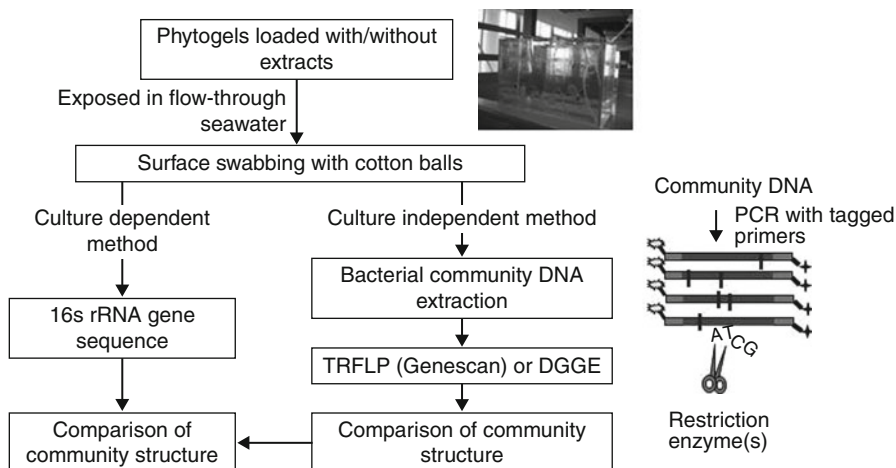


Fig. 14.15 Procedure to analyze community structure using PhytoGel assay. Abbreviations: *PCR* polymerase chain reaction, *DGGE* denaturing gradient gel electrophoresis

aquarium. After a 48-h exposure to natural seawater, the phytogel disks are retrieved to determine bacterial and diatom density, and for microbial community structure analysis. For bacterial counts, phytogels (3 replicates per treatment or control) are fixed in 4% formaldehyde in seawater, and the bacterial density is determined under a microscope after DAPI staining. The surfaces (6 cm²) of each of the other three disks are swabbed with sterile cotton buds for the collection of epibiotic microbes. Swabs from each gel will be individually suspended in 0.8-mL extraction buffer (100 mM Tris-HCl, 100 mM EDTA, 100 mM sodium phosphate, 1.5 M sodium chloride, 1% CTAB; at pH 8) in 2-mL microcentrifuge tubes [26]. To lyse the cells, the samples are subjected to three cycles of freezing and thawing followed by 2 h incubation in 20% SDS at 65°C. Cotton buds are removed, and the total DNA is extracted with an equal volume of 24:1 chloroform:isoamylalcohol followed by precipitation in isopropanol at room temperature for 15 min. The precipitated DNA is washed with cold ethanol and resuspended in 50 µL of autoclaved double-distilled water and frozen until use.

PCR of 16 S rRNA genes (rDNA) in bacterial community DNA is performed according to method described in [26]. Fluorescently labeled PCR products are purified and analyzed using TRFLP or DGGE methods [26, 27]. Microbial community structures among the treatments and controls are compared accordingly [26, 27], for which the protocols and procedure are not discussed in details.

14.4.1.4 Antiquorum Sensing Bioassay

Quorum sensing (QS) molecules produced by marine bacteria are very important for development of bacterial films, and blocking production of QS molecules can lead to prevention of biofilm formation. Therefore, screening for quorum sensing blockers is a valuable way for controlling biofilm development. Over the last

30 years, several strategies with various QS blocker screening assays have been developed, and there is a very good review on this topic [28]. A general strategy is to expose a biosensor strain to test solution that may or may not cause a loss of signal response. Alternatively, a wild-type strain containing a QS-regulated phenotype can be used as a biosensor and grown in liquid media before being added into microtiter plate wells containing test solution of an extract or compounds. Changes in pigmentation of bacteria can be probed at a given time during or after incubation.

In a QS blocker screening assay, the most important first step is to select appropriate reporter strains. Although many species have been used for such a purpose [28], two bacterial species are commonly used: *Chromobacterium violaceum* [29] that produces purple violacein and pigmented *Pseudomonas aureofaciens* strain 30–84 that produces orange phenazine [29]. The QS blocking activity can be observed via a loss of their colorful pigmentation, which can be detected by eye and quantified by spectrophotometers.

Here, we will only introduce two basic methods.

Microplate assay (modified from [30–32]) (Fig. 14.16): *Chromobacterium violaceum* CV026, which is a mini-Tn5 mutant of the wild-type strain, is not able to produce the purple pigment violacein. Its violacein production is dependent on external addition of *N*-hexanoylhomoserine lactone (HHL). To screen for quorum sensing blockers, strain CV026 is grown to the stationary phase in culture medium containing 0.5% yeast extract and 1% tryptone. One hundred μL of bacterial culture is added into each well of 96-well microplates (with flat bottom). Then *N*-hexanoylhomoserine lactone (optimal concentration: 3.7×10^{-8} M for violacein induction) and 5 μL of DMSO containing an extract/compound is added into the well, respectively. The wells without test solution but with HHL and without HHL serve as the positive and negative controls. After exposure for 16 h at 27°C, the microplate is centrifuged at 13,000 *g* for 10 min to precipitate the insoluble violacein. The culture supernatant is then discarded, and 200 μL of DMSO is added to the pellet. The solution is then vortexed vigorously for 30 s to completely solubilize violacein and centrifuged at 13,000 *g* for 10 min to remove the cells. One hundred μL of the violacein-containing supernatants is then transferred to the wells of a new 96-well flat-bottomed microplate where the absorbance can be recorded with a microplate reader at a wavelength of 585 nm.

Agar overlay technique (Fig. 14.17): QSI indicator bacterial strains such as *Chromobacterium violaceum* 12472 and *Pseudoalteromonas aureofaciens* 30–84 are grown overnight in LB broth [29]. Following overnight growth, the test solution is placed onto an LB agar plate and then overlaid with LB soft agar containing the indicator organism. After incubation, the production of color around the bacterial colonies is observed.

In the case of screening for QS blocker producing bacteria, the test bacterial strains are streaked to the central part of LB agar plates and allowed to grow overnight. Alternatively, several test strains can be streaked onto one agar plate for high-throughput screening. After overnight growth, 5 μL of the organisms is vigorously mixed with 5 mL of molten LB soft agar of the indicator organisms

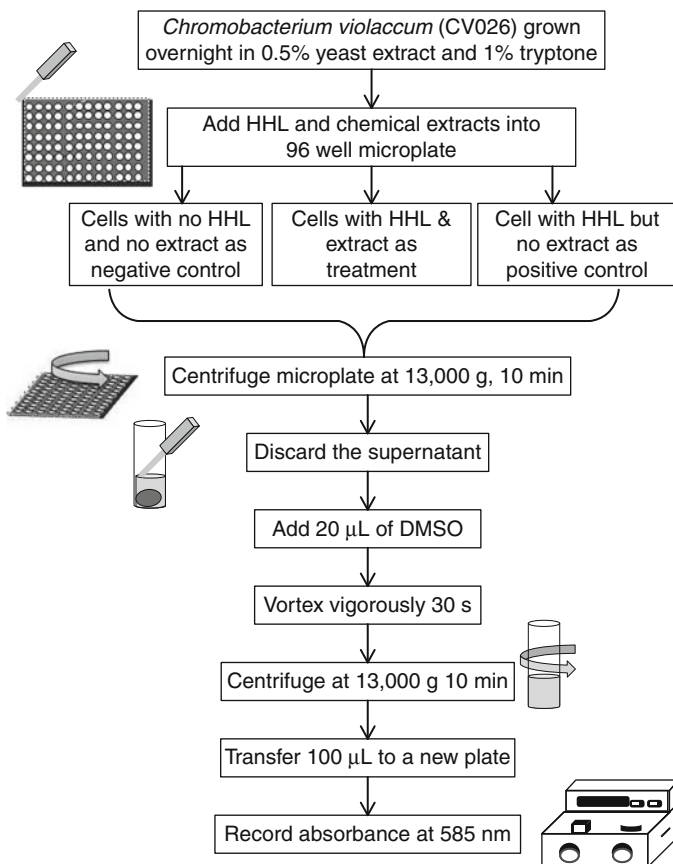


Fig. 14.16 Microplate assay for quorum sensing blockers using reporter bacterial strain *Chromobacterium violaceum* CV026. This strain is unable to produce the purple pigment violacein, so violacein production is dependent on an external addition of *N*-hexanoylhomoserine lactone (HHL). This figure is adapted from McLean et al. [28]

C. violaceum ATCC 12472 [29] or *P. aureofaciens* 30–84 and quickly overlaid onto the agar containing the testing bacterial strain. After incubation, a positive QSI result can be detected by the growth of living, but nonpigmented indicator organisms in the vicinity of the test organism.

14.4.2 Antidiatom Assay

Diatoms are common microfouling organisms and one of major component of marine biofilm [33]. The diatoms in biofilm can release inductive and/or inhibitive materials for spore and/or larval settlement of macrofouling organisms, in addition to causing microfouling problems. Therefore, controlling diatom

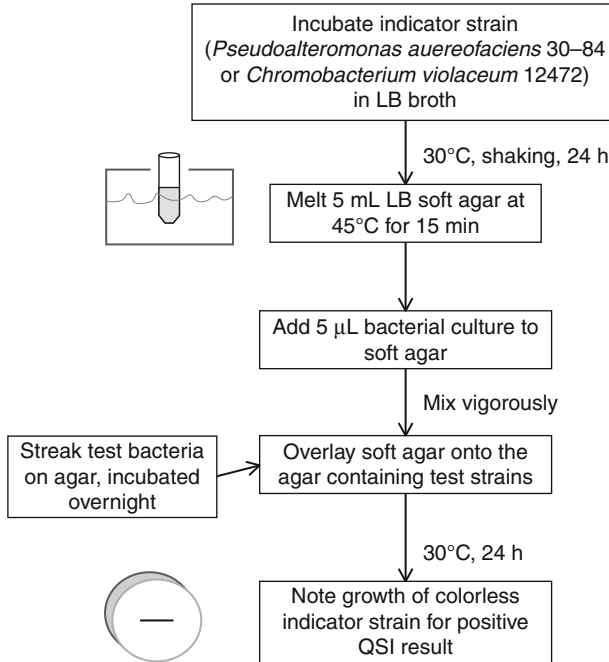
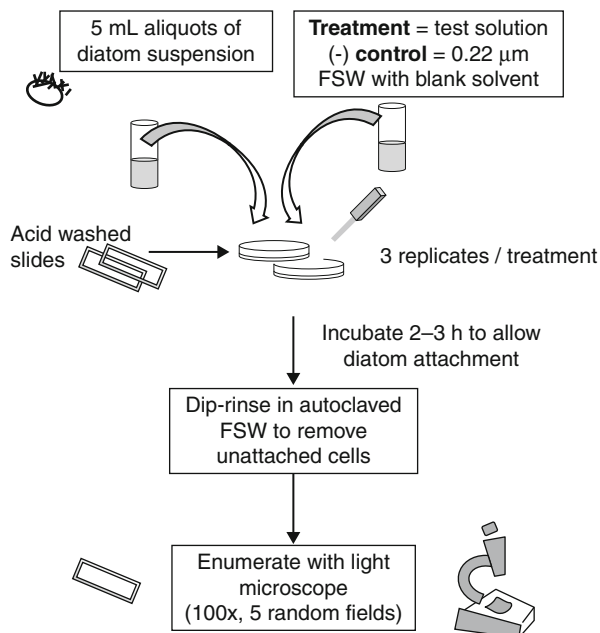


Fig. 14.17 Assay for quorum sensing blockers using the overlay method. Lysogeny broth (LB) agar plate with test solution is overlaid with LB soft agar containing the indicator organism. This figure is adapted from McLean et al. [28]. Abbreviations: *QSI* quorum signal inhibition

attachment and growth is also a target of antifouling efforts. Antidiatom attachment and growth assays have been developed and adopted; however, many antifouling compounds failed in microfouling control, simply due to failure in preventing diatom attachment and growth in biofilms.

Selection of diatom species and strains for antidiatom assays may follow guidelines similar to selection of bacterial species. Basically, test strains/species should be able to grow fast, to attach to surfaces quickly and firmly, and to form good biofilms that can induce attachment of other microfoulers and macrofoulers [15]. Prior to each bioassay, pure diatom stock cultures are inoculated into 400-mL Erlenmeyer flasks containing autoclaved *F/2* nutrient medium in 0.22- μm filtered seawater (FSW) [34] and incubated at 24°C with overhead fluorescent illumination (0.3×10^{16} quanta $\text{s}^{-1} \text{cm}^{-1}$) under a 15:9 h L:D photo cycle until the formation of a visible diatom film on the culture flask walls. Diatom cells are brushed off the flask interior wall with a sterile paintbrush and suspended in a fresh culture medium. Known volumes of cell suspensions of diatoms are filtered through 0.45- or 1.0- μm filter membranes (Osmonics) and resuspended in 50-mL FSW, which will be ready for use in subsequent antidiatom attachment and growth assays.

Fig. 14.18 Antidiatom attachment assay, with three replicates per treatment and 0.22- μm filtered seawater used in place of testing solution for negative control



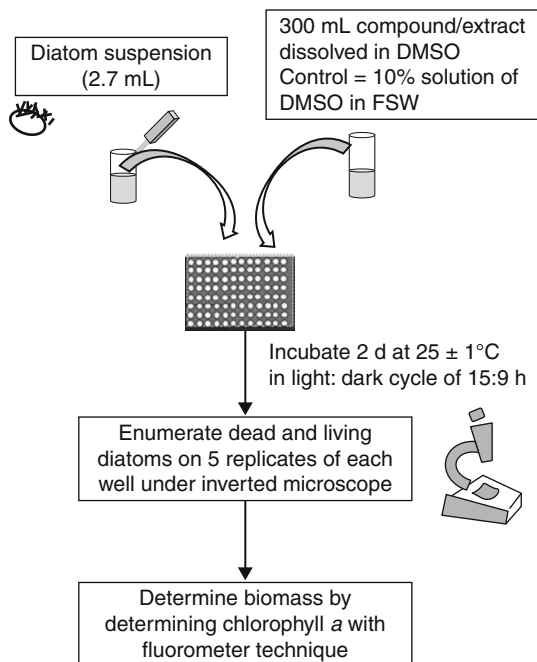
14.4.2.1 Antidiatom Attachment

Briefly, 5-mL aliquots of the suspensions are added into sterile Petri dishes each containing an acid-washed glass slide. In the negative control, only 0.22- μm filtered seawater is added while in the treatment, test solutions are added (Fig. 14.18). There should be at least three replicates per treatment. After incubation for 2–3 h (depending on species) to allow diatom cells to attach, filmed glass slides are dip-rinsed in autoclaved FSW to remove unattached cells. Diatom cells on glass slides are enumerated by light microscopy at a magnification of 100X in 5 randomly chosen fields of view (Zeiss Axiophot; $\lambda_{\text{Ex}} = 359 \text{ nm}$, $\lambda_{\text{Em}} = 441 \text{ nm}$) [35] or are counted using image analysis similar to that described for algal spore attachment in Sect. 5. The effect of the extract/compound on attachment of diatoms is determined by comparing the result of each treatment with that in the control. For cell detachment assays, slides are exposed to shear stress also according to the methods described for testing algal spore adhesion strength in Sect. 5. Percentage removal of diatom cells will be calculated accordingly [36].

14.4.2.2 Antidiatom Growth

Prior to the experiment, an extract or compound is dissolved in DMSO to a given concentration (Modified from [33]; Fig. 14.19). Three hundred μL of the test solution is added to each Petri dish or each well of a multiwell plate that contains 2.7 mL of diatom suspension (about $2 \times 10^5 \text{ cells mL}^{-1}$). A 10% (v/v) solution of

Fig. 14.19 Antidiatom growth assay. This figure is adapted from Dobretsov et al. [33]. Abbreviations: *DMSO* dimethylsulfoxide



DMSO in filtered (pore size $0.22 \mu\text{m}$) seawater (FSW) is used as a control. The dishes or plates are incubated for 2 days at $25 \pm 1^\circ\text{C}$ at a light:dark cycle of 15:9 h. Then, the numbers of dead and living diatoms are counted on 5 replicates of each well or dish under an inverted microscope. Empty diatom shells are treated as dead diatoms and those with distinct chloroplasts are considered as live ones. In addition, the amount of *chl a* of each Petri dish or well can be determined by a fluorometer technique [37] as an indication of the diatom biomass.

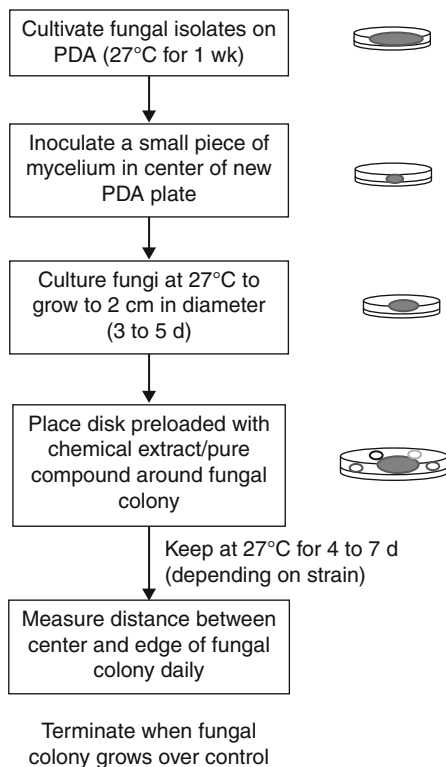
14.4.3 Antifungal Assays

Fungal strains/species isolated from marine biofilms are used as test organisms, and selection criteria are similar to those outlined for selection of bacteria species/strains in Sect. 4.1.

14.4.3.1 PDA Plating Assay

Prior to each assay, selected fungal isolates are cultivated on a PDA (potato dextrose agar, Sigma) plate at 27°C for 1 week or other culture media under a given culture condition, depending on species to be tested (Fig. 14.20). A small piece of mycelium is then inoculated in the center of a new PDA plate. The fungi is cultured at 27°C and allowed to grow to 2 cm in diameter (3 to 5 days). An autoclaved paper disk loaded with the test solution of a chemical extract or pure compound is then placed around the fungal colony (1 cm to the edge of the

Fig. 14.20 Antifungal assay using potato dextrose agar (PDA). This figure is adapted from Miao and Qian [20]



fungal colony) and kept at 27°C for 4 to 7 days, depending on the growth rate of the fungal strain. For the control, 5 μL of the blank solvent without extract/compound is used. For screening for bacteria with antifungal activity, bacteria strains can be directly inoculated near the fungal colony. The assay is terminated when the fungal colony grows over the control. The distance between the center and the edge of the fungal colony is measured daily. The inhibition of fungal growth is determined by comparing the radii of the fungal colony under the treatment and control conditions [20].

14.4.3.2 Microtiter Plate Assay

Prior to assay, fungal strains are cultured with a suitable culture medium under a given culture condition, and the commonly used culture medium often consists of yeast extract, soluble starch, and agar. After inoculation for several days, the conidia are collected by a sterile swab, suspended in filtered seawater, filtered to get rid of the mycelia, and adjusted to 1×10^4 to 5×10^4 CFU mL^{-1} of conidia by adding sterilized 0.22- μm filtered seawater. Two hundred μL of the conidia suspension is allocated to each well of a microplate. Ten μL of the extract/compound dissolved in DMSO is added to each well. A selected antibiotic chemical is used as positive control. The assay plates are incubated at 27°C until the shape of fungal growth can be observed and compared with the controls under an inverted microscope [38] (Fig. 14.21).

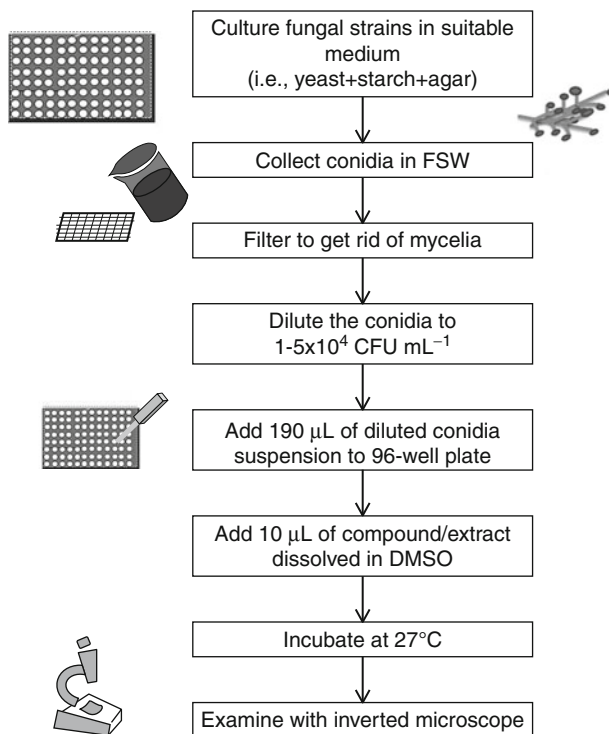


Fig. 14.21 Antifungal assay using a microtiter plate. This figure is adapted from Byun et al. [38]. Abbreviations: *CFU/mL* colony forming unit per milliliter

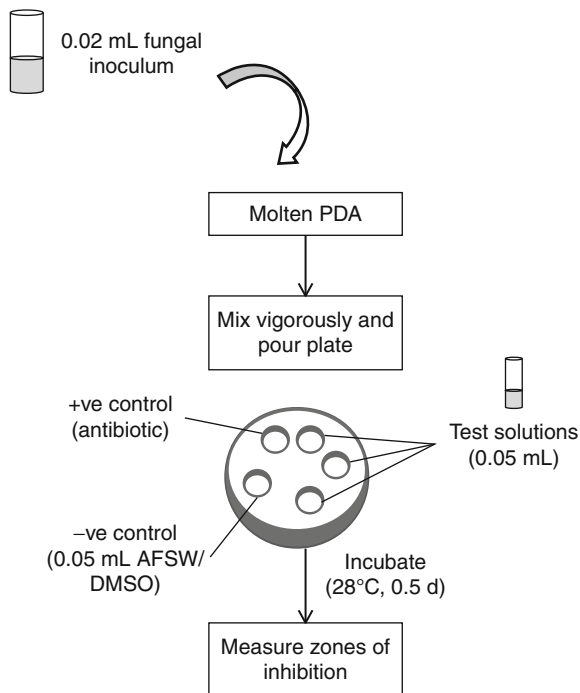
14.4.3.3 Agar Well Diffusion Assay

The agar well diffusion assay is also used for measuring antifungal activity. An aliquot (0.02 mL) of fungal inoculum is added to molten potato dextrose agar (PDA) and then poured into a Petri dish using sterile technique. After solidification, wells of 6.0 mm in diameter are drilled with a sterile cork borer on the agar plate. Then, 0.05 mL of test solution of a chemical extract or pure compound is added into each well. Similarly, 0.05 mL of either sterile filtered seawater or solvent is added into the wells that serve as the negative control, while antibiotic solution is added into the wells that serve as the positive control. The plates are incubated for 1 to 2 days at 28°C or until fungal growth can be observed in the negative control. The antifungal activity is evaluated by measuring zones of inhibition of fungal growth surrounding the wells in mm. There should be at least three replicates per treatment [39] (Fig. 14.22).

14.4.4 Bacterial Challenge Culture

Selected fungal strains are inoculated into appropriate culture medium and inoculated at 25°C for 5 days, while target bacterial strains are cultured in suitable

Fig. 14.22 Antifungal assay using agar well diffusion assay. In this assay, wells are created by drilling with a sterile cork borer after solidification of molten potato dextrose agar. Test or control solutions are poured into the wells. There should be at least three replicates per treatment. This figure is adapted from Matti et al. [39]



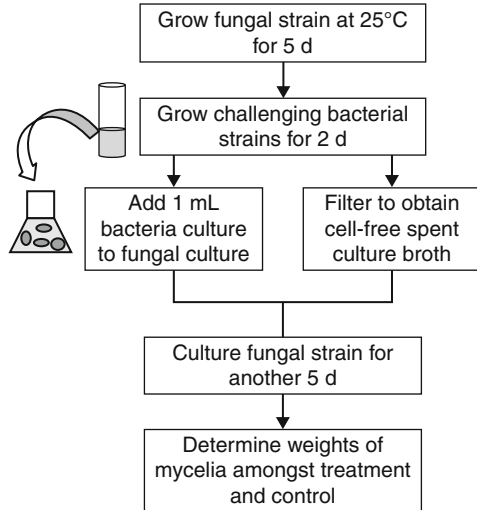
culture medium for 2 days. The bacterial cultures are then centrifuged at 5000 rpm for 15 min, and the cell pellets are resuspended in 5-mL fresh autoclaved culture medium. The resuspended bacterial cells are added into 5-day fungal cultures (3 replicates per sample). In case that bacterial extract or bacterial metabolites are tested, a given amount of the test solution is added into each fungal culture container. The treatments are cultured for another 5 days. The control set is added with 5-mL fresh autoclaved medium only. The fungal growth is determined according to the dry weights of mycelia and compared among the treatments and the controls [40] (Fig. 14.23).

14.5 Antilarval Settlement and Antialgal Bioassay

14.5.1 Antialgal Assays

Marine macroalgae (seaweeds) are common foulers on marine surfaces and often form dense mats that can clog seawater intakes, increase drag coefficients, or increase the weight of buoys. Therefore, controlling attachment and growth of macroalgae has been as challenging as controlling hard foulers such as barnacles and calcareous tubeworms. Here, we introduce antialgal bioassays that are commonly used in research laboratories.

Fig. 14.23 Competition assay, in which bacterial challenge strains are cultured against fungi. This figure is adapted from Miao et al. [40]

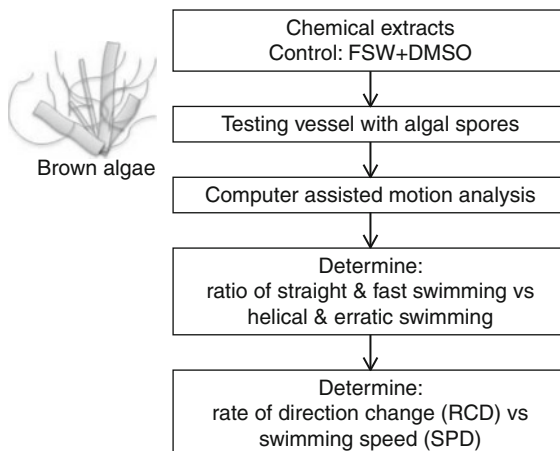


14.5.1.1 Preparation of Algal Spores

The most commonly used macroalgae are various green algal species of the genus *Ulva* since this group of seaweeds is not only common foulers on marine underwater surfaces but also on a wide distribution of organisms. The procedure to induce release of algal zoospores from *Ulva* spp. has been well developed [41–43] and is easy to follow. As described by Joint et al. [44], prior to permanent attachment onto a surface, free-swimming spores often undergo a behavior change from random swimming to a “searching” pattern of exploration close to the substratum [41]. Like some marine invertebrate larvae, during the searching process, the spores often spin downward using their flagella as propellers, and thus, their apical domes may come in close contact with the substratum. They may temporarily attach to the substratum and thus extrude a pad of elastic material that is left behind on the surface if they reject the surface and continue their search for a suitable place for permanent attachment. During the attachment process, the spores secrete an N-linked, polydisperse, self-aggregating glycoprotein that anchors them to the substratum and also makes the attachment irreversible. Therefore, surface texture, chemical characteristics, and microbial films all play important roles in spore attachment [41].

Briefly, fertile individuals of *Ulva* spp. are collected from the field and used immediately or kept in seawater tables with a flow-through seawater supply and illuminated with full spectrum light for as short a period of time as possible. To induce sporulation, each algal blade is rinsed with fresh seawater to remove loosely attached epibionts and mucous on the blade surface, and then placed in separate glass beakers containing sterile 0.22- μm filtered fresh seawater. The beakers are placed directly near a pointed light source (but avoid overheating due to light energy). Newly released zoospores swim toward the light and thus can be easily collected with a pipette. Newly released spores are then transferred to a small beaker containing sterile 0.22- μm filtered fresh seawater and are used immediately

Fig. 14.24 Antialgal spore swimming behavior assay, using computer-assisted motion analysis to determine swimming properties



for antismimming behavior, antisetlement, and adhesion strength experiments, as described below. Sometimes, in order to collect enough spores, the collected spores can be placed in a beaker on ice to prevent their settlement, and this procedure does not change the settling rate of the spores compared to freshly used spores in later experiments [41]. Similar procedures can be used to induce spore release in brown algae and red algae, however, with some minor modifications such as drying the algal blades in cold and dark conditions and then applying thermal shocks.

14.5.1.2 Zoospore Swimming Behavior Assay

This bioassay was developed by Callow et al. [42] and has been used in many of their studies. For a preliminary screening bioassay, this may be considered to be more challenging and may not be suitable for high-throughput purposes. However, it may be very useful for in-depth study of individual compounds (Fig. 14.24).

A slide is placed in each Petri dish (9 cm in diameter). Twenty-five mL of a spore suspension (2×10^6 spores mL⁻¹) together with the test extract/compound is added into the Petri dish that is placed on the stage of a Zeiss Universal microscope in a darkroom to prevent phototactic spore movements. Spore movement is filmed using a video camera. After 10 min, the microscope is focused on a plane just above the slide surface so that both swimming and settled spores can be observed. Time-lapse images are collected every 3 min for 60 min by using a timer controller. Single images are captured on the video camera. At the end of the filming, unsettled spores are washed off by rinsing slides gently with filtered seawater. The number of firmly attached spores to each sector is assessed by recording images of the slide. Finally, the slide is fixed and processed by using the standard cell counting procedure. Spores are counted using three consecutive video images representing each time point. The mean number of attached spores per square millimeter is calculated for each group of three images. Attached spores are counted by using the single video image after the slide is washed. Settled spores on the fixed slide are counted in 20 fields of view located at 100- μ m intervals along the diagonal of each square, starting at the central corner. The mean number of attached spores mm⁻² is calculated.

14.5.1.3 Algal Spore Settlement Assays

Different types of antialgal spore attachment assays have been used in previous studies [41, 42, 45], with some being more complicated than others. Here we introduce one of the simplest assays developed by an Australian research group [43]. One hundred μL (about 50 spores) of the algal spore suspension is added into each well of a 24-well culture plates containing 1 mL of 0.22- μm filtered seawater within which a testing extract/compound (treatment) or DMSO (the control) is preincluded. The plates are incubated in the dark for 2 h to allow for an even settlement of spores and then incubated at room temperature under natural light. After 24 h, the solution in each well is removed by pipette and 1 mL of 0.22- μm filtered seawater is added to each well. Algal spore settlement is assessed after 3 days using an inverted light microscope (Zeiss). Counts of germinated spores are conducted for ten fields of view under the microscope. All of the samples are tested in at least two to three replicate wells with spores pooled from at least three separate algal thalli. The results are compared to the controls (Fig. 14.25).

One may use 5-mL Petri dishes instead of 24-well culture plates in assays and also change incubation times for algal spore germination, depending on the germination speed of the individual species. In addition, the number of settled (attached and germinated) and unsettled (not in contact with the surface) spores can be determined under a microscope after 1 to 2 days (before unattached spores are washed out of the test vessel). In this situation, the percentage of settlement rather than the actual number of settled spores among treatments is determined and compared [43].

14.5.1.4 Settlement and Adhesion Assays

Prior to conducting a settlement and adhesion strength assay, glass microscope slides should be washed in a mixture of 50% methanol/50% concentrated HCl and then placed in 100% concentrated HCl for at least 2 h ([41, 42, 46], Fig. 14.26). Then, the slides are rinsed in double-distilled water to remove acid. One glass slide is placed in individual glass dishes. Ten mL of the zoospore suspension ($1\text{--}5 \times 10^6$ spores mL^{-1} in seawater (control) or in test solution (treatment)) is added into each dish. The dishes are placed in the dark at room temperature for at least 1 h to allow zoospores to settle evenly onto the glass slide (they will also settle on the dish, which is not used for assessment). The slides are then gently rinsed in sterilized 0.22- μm filtered natural seawater (or artificial seawater made of Instant Ocean in case natural seawater is unavailable); this removes unattached zoospores from the slides. At least three replicate slides are immediately fixed in 2% (v/v) glutaraldehyde in seawater for 10 min, washed carefully according to the method described in Callow et al. [41], and used as the “control” group, i.e., not exposed to the water jet. The remaining slides are incubated for various periods of time before exposing them to calibrated surface pressures in the water jet, followed by fixation. To ensure reproducible evaluation of short-term attachment strength on microscope slides, glass slides are mounted on a motorized holder with computer-controlled stepper motors that allow the bank of slides to be moved horizontally and vertically in a raster pattern across the path of the water jet, at speeds between

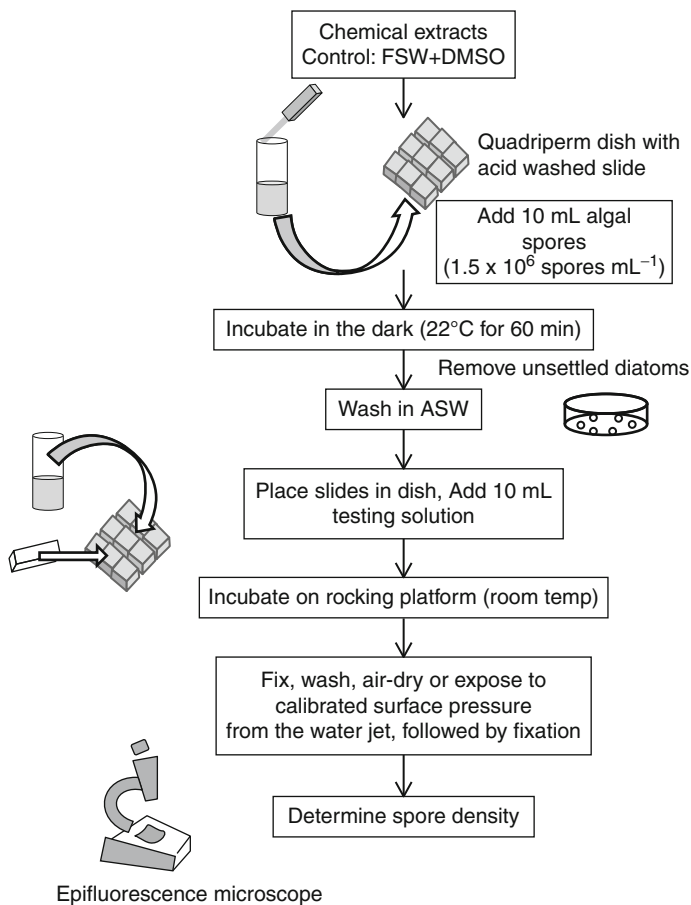


Fig. 14.25 Antialgal zoospore settlement assay. This figure is adapted from assay developed by Holmström et al. [43]

2.5 and 12.5 mm s^{-1} . The pitch of movement in the vertical direction at the end of each horizontal traverse is set at 2 mm . The water jet nozzle with an internal exit diameter of 1.6 mm is mounted 25 mm from the bank of slides. The instrument is typically operated at a speed of 10 mm s^{-1} for ten swathes to allow an area of 500 mm^2 in the mid-region of each slide to be exposed to water jet. The water supply is housed in a pressure resistant tank and pressurized using a compressed air supply from a conventional SCUBA tank as described by Swain and Schultz [47] who designed the original water jet apparatus for assessment of fouled panels in the field. The pressure of the water jet is increased until all attached spores are removed or until the maximum pressure of the apparatus is achieved.

Adhered zoospores are counted under epifluorescence microscope equipped with an image capture analysis system [42]. Counts are taken for 30 fields of view on each of 3 replicate slides. The number of spores that remain attached to

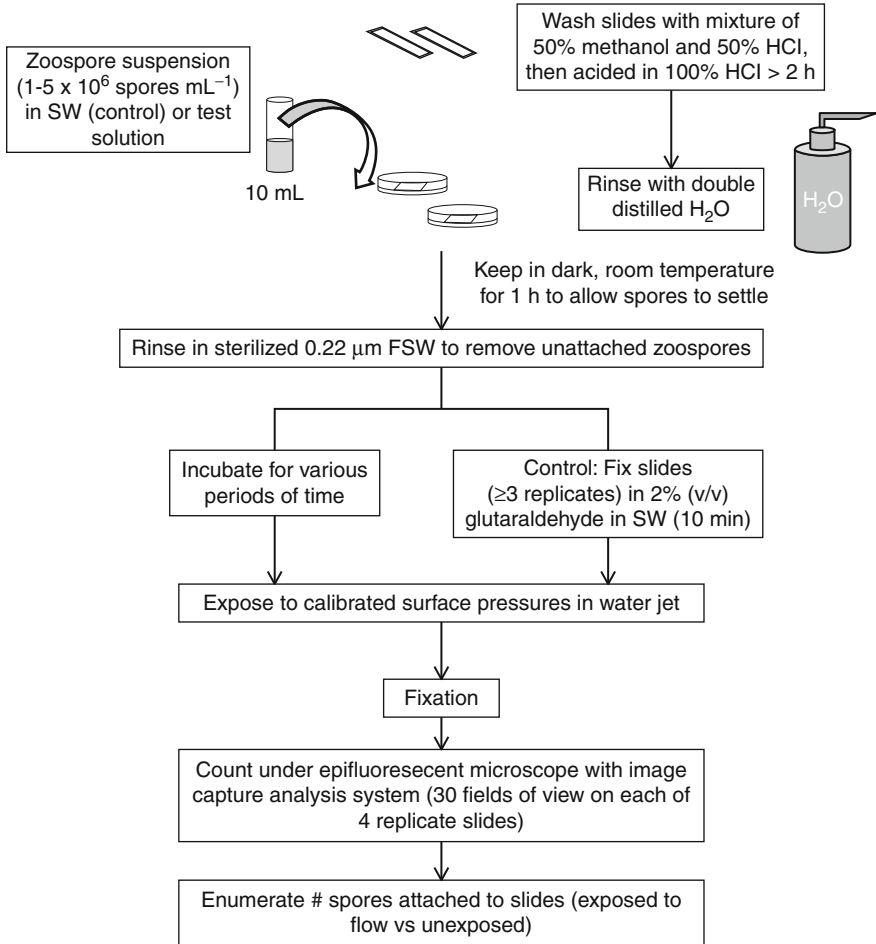


Fig. 14.26 Zoospore settlement and adhesion assay. This figure is adapted from method described by Callow et al. [41]

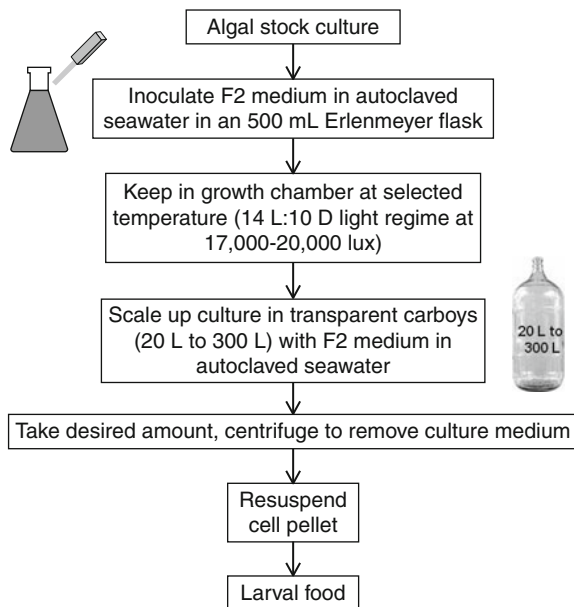
slides exposed to flow is determined and compared with unexposed controls. Since the level of settlement in each experiment may be different (because different spore batches may be used), data is presented in terms of percentage of spore removal in comparison with the controls.

14.5.2 Antilarval Settlement Assays (Various Systems)

14.5.2.1 Microalgal Culture as Feed of Invertebrate Larvae

Different invertebrate larvae prefer different algal foods, and different algal species also have different nutrient values that are also affected by culture condition of the algal species. Furthermore, it has also been proven that a mixture of algal species is

Fig. 14.27 Microalgal culture, to be used as feed for invertebrate larvae



often better than single algal species food. Therefore, it is very important to select the right algal species for individual larval species and also work out the optimal culture condition of individual algal species before developing large and routine larval culture for antifouling bioassays. Numerous studies have demonstrated that larval physiological conditions affect attachment and metamorphosis [48, 49], and these have a drastic impact on bioassay results and interpretation. Nevertheless, one can still follow the general protocol illustrated in Fig. 14.27 to get started with algal culture.

A review of literature on larval cultures of major fouling organisms that are routinely used in laboratory antifouling bioassay reveals the following tips as a general guideline:

1. *Isochrysis galbana*, *Chaetoceros gracilis*, *Thalassiosira pseudonana*, and *Skeletonema costatum* are common larvae food for barnacle larval culture. Energy reserves of larvae fed on different diatoms at a concentration of 1×10^6 cells mL^{-1} are ranked in the order: silicate-limited *C. gracilis* > *C. gracilis* > *T. pseudonana* > *S. costatum*. There is a significant linear relationship between the TAG content of the diet and cyprid energy reserves [49]. Clearly, although *Skeletonema costatum* has been recommended as larval food for barnacle larval culture decades ago [50], it is not a desirable algal species due to its poor nutrient concentration.
2. For barnacle larval culture, food concentrations should be maintained at least $> 10^3$ algal cells mL^{-1} . Nauplius II of *B. amphitrite* cannot survive through successive naupliar stage at *Skeletonema costatum* concentrations $\leq 10^3$ cells mL^{-1} [51] and failed to develop to cypris with a mixture of

algae *Pavlova lutheri*, *Platymonas* sp., and *Thalassiosira pseudonana* at concentrations of $<1 \times 10^5$ cells mL^{-1} [52]. The recorded minimal algal concentration to support larval development of *Balanus amphitrite* was at <300 cells mL^{-1} [53], $<1,000$ cells mL^{-1} [54], and $<3.6 \times 10^3$ cells mL^{-1} .

3. For the tube-building polychaete *Hydroides elegans* larvae culture, *Isochrysis galbana* appears to be better algal feed than the others. At concentrations $<10^3$ cells mL^{-1} , $>35\%$ larvae survived through the 10-day experiment but lost their ability to become competent. The concentration of 10^5 cells mL^{-1} was the optimal for growth, development, and larval physiological condition for attachment and metamorphosis [55].
4. A mixture of algal food often supports a better growth and development of performance of these test organisms.
5. Temperature, salinity, and other culture variables have profound effects on larval growth and development, and competency to attach and metamorphose [49, 56].

14.5.2.2 Larval Culture

Acorn barnacles are common sessile intertidal organisms and also among the major hard foulers. As barnacles secrete glycoprotein glue to cement themselves permanently onto hard substrates [57], they form surface structures that are very difficult to be removed. Accumulation of those structures can clog water intakes of nuclear power stations, desalination systems, and pipelines or create substantial drag in moving vessels. The damage caused by fouling barnacle has been documented for many centuries and is the major task of antifouling control. Therefore, larvae of barnacles have been logically used in antifouling bioassay for many decades.

As sessile barnacles can be found in almost all surfaces (both hard, such as rocky shore, and soft surfaces, such as the skin of sharks and whales, trunks of mangrove trees, and the floating algal blades and wooden boards), the adaptive power for living in diverse environments is very high in this group of organisms. Of course, there are also many barnacle species worldwide, providing diverse choice of barnacle species as test organisms [58, 59]. Nevertheless, the life cycle of most barnacle species is similar, and the most common barnacle species used in laboratory bioassay is *Balanus (Amphibalanus) amphitrite*. Therefore, in this chapter, we will use this species as a model organism to introduce larval development and culture methods.

Like other acorn barnacle species, *Balanus amphitrite* (Darwin) adults are hermaphroditic (meaning the same individual have both sexual organs) but can hardly carry out self-fertilization. Since they live in calcareous plates (there are six plates in general, but for some species, those plates may merge) cemented to the surface, adults can only cross-fertilize with their neighbors with their long penis (modified cirri). Fertilized eggs are developed inside the body in the base and hatch into nauplius I stage, which is characterized by one bright red eye but without a thorax or abdomen [60]. Nauplius I larvae are released from the adults into the water column and are nonfeeding organisms; they often molt into nauplius II larvae

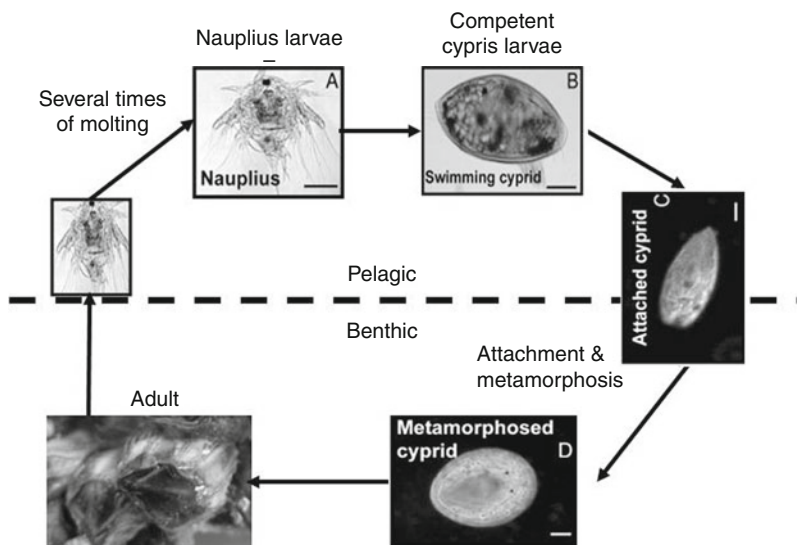


Fig. 14.28 Life cycle of *Balanus amphitrite*. Nauplius I larvae begin their life cycle by being released from adults into the water column. They molt into nauplius II a few hours later and feed on plankton. They continue to molt into nauplius III, IV, V, and VI larvae within 3–4 days. Cypris larvae actively search for a suitable place to settle with modified antennules. When they have found a suitable place, they attach and secrete a glue. Attached cypris larvae molt into young juvenile within a few hours

within a few hours and begin to feed on both phytoplankton and zooplankton right after completing the molting process. Nauplius II larvae molt into nauplius III, IV, V, and VI larvae within 3–4 days in *B. amphitrite* (Fig. 14.28), but may take weeks to months to complete those moltings in other barnacle species. The nauplius VI larvae molt into cypris that are nonfeeding larvae again. Cypris stage may last hours and days, again depending on the species. Cypris larvae often actively search for a suitable place to settle with modified antennules. When they find a suitable place, they attach using their antennules and secrete a glycoprotein glue. Before the glue/cement hardens, the cypris still has the ability to detach itself from the surface. However, as soon as the cement solidifies, attachment becomes irreversible. The attached cypris molts into a young juvenile within a few hours. There is substantial evidence that young cypris larvae have a high discriminating power on assessing surface suitability based on texture [61], wettability [62], color, chemistry, the presence and absence of a natural profilm or the composition of the microbial community structure of the biofilm [63–68], chemical cues of conspecific species, and flow dynamics [50, 69, 70]. However, aged cypris larvae (naturally and artificially) often become less selective to settling sites and tend to settle on any available surface, and this is linked to an exhaustion of energy reserves in cypris larvae [48, 49, 56, 71–73].

To develop larval culture of *B. amphitrite*, adults collected from the field or kept in the laboratory but fed well with newly hatched *Artemia* sp. are used for

experiments. The brood stocks can be induced to release nauplius I larvae by changing the water and stimulating by light-shock. Alternatively, the egg lamellae of individual adults containing late stage developing embryos can be dissected and placed in 0.5 L of seawater. Nauplius I larvae are hatched during the 1-day incubation at room temperature. If they are healthy, they should be able to molt into nauplius II within 2–3 h. Please keep in mind that brood stock can be kept in aerated seawater at room temperature (ca. 24°C). If adults are well fed with newly hatched *Artemia* sp. larvae daily and, in some cases, supplemented with the diatom *Skeletonema costatum*, they shall be able to release nauplius I larvae every few days. This allows laboratories far from coastal areas to maintain reproductive barnacle populations for the antifouling bioassay.

Newly molted Nauplius II larvae are attracted to a point-source light and can be directed for collection with a pipette under a dissecting microscope. Planktotrophic nauplius II larvae are cultured at a density of 2 larvae mL⁻¹ in 0.22- μ m-filtered natural seawater at 30 ppt salinity (FSW) using *Chaetoceros gracilis* Schutt as the ideal food source (although the diatom *Skeletonema costatum* has been used by many laboratories, it has been proven to be a relatively poor diet for barnacle larval culture) [56]. Nauplius II larvae develop through planktotrophic nauplius III, IV, V, VI and then molt to a nonfeeding cyprids in several days (depending on the rearing condition). During the rearing period, successive algal food is added to each culture beaker (ideally at least twice per day), and seawater in culture beakers is changed daily by filtration or siphoning. Crystamycin (22.5 mg mL⁻¹, Penicillin G, and 37.5 mg mL⁻¹ Streptomycin sulfate) shall be added to the culture beaker to inhibit bacterial growth. Previous studies indicated that addition of the above antibiotics in the culture medium has no adverse effect on barnacle larval development [74]. The culture is maintained at 24°C under a 12 L:12D photoperiod until all larvae became cyprids. The naupliar stages of *Balanus amphitrite* can be identified and described [75] under a compound microscope at 24-h intervals. Freshly molted cyprids or aged cyprids can be used for antifouling assays.

H. elegans (Fig. 14.29) is a gregarious calcareous tube-building polychaete that occurs in tropical and subtropical waters. This animal causes a serious biofouling problem in the Pearl Harbor, Sydney Harbor, and Southern parts of the Chinese coast (including Hong Kong) as juveniles and adults secrete calcified tubes that jam pipelines of the cooling systems of power stations, buildings, submarines, clog nets and cages of mariculture, forming a high biomass on submerged surfaces and on the surfaces of farmed animals such as abalones and pearl oysters. In Hong Kong, during the spring and summer months, fish farmers need to clean their nets and cages that are heavily fouled by *H. elegans* every other week. Unfortunately, it is always very difficult to remove calcified worm tubes on fish nets. Therefore, this species is considered one of major foulers in tropic and subtropical regions and has been used as an antifouling target in a number of research laboratories [76, 77]. *H. elegans* in fact is a small animal (only about 2 cm long of soft body in 2–6 cm long of calcified tube); however, it only takes about 1–2 weeks for a juvenile to develop into a sexually mature adult that can release several thousand small eggs (about 50–65 μ m in diameter). The males and females release their gametes into the

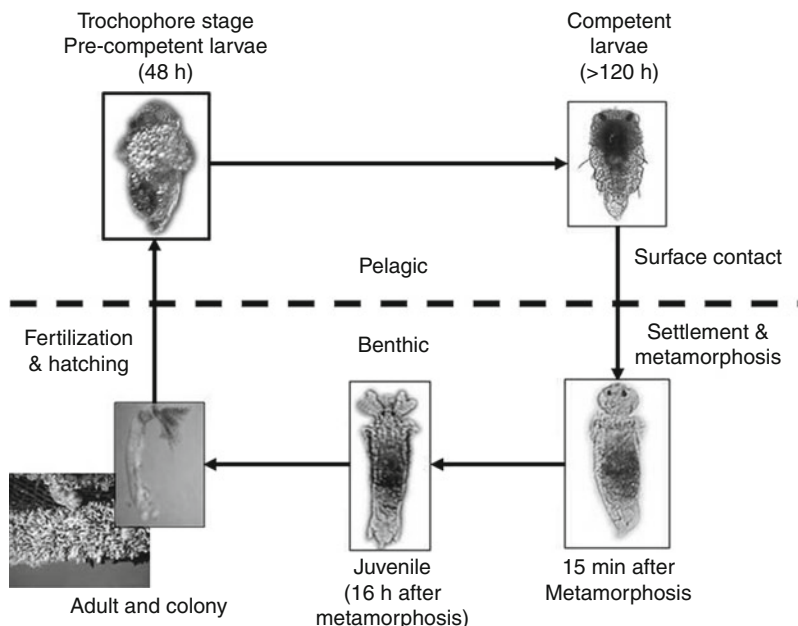


Fig. 14.29 Life cycle of *Hydroides elegans*. Gametes are released into the water column, and fertilized eggs can hatch into young trochophores within 24 h. Four to five days later, trochophores complete attachment and metamorphosis within a time span of 9–12 h

water column, and the fertilized eggs can hatch into young trochophores within 24 h. With sufficient food supply, trochophore can develop into competency to attach and metamorphose within 4–5 days. It takes settling larvae only 9–12 h to complete attachment and metamorphosis. The same adult can release mature gametes every 7–10 days with a life span of about 8–10 months. This animal has almost all the required characteristics for a laboratory test animal, such as short generation time, fast growth, high fecundity, repeat spawning ability, ability to reproduce all year round, and ease of culturing (for both larvae and adults) [55, 76–79].

The development of larval culture can follow the protocol outlined in Fig. 14.30. Freshly collected adults should be used immediately or be brought to the laboratory and kept in water tables supplied with filtered flow-through seawater (if possible) or in the aquarium filled with filtered seawater. Adult females and males are carefully isolated from their neighbors (could be *H. elegans* or *Bugula neritina*) under a dissecting microscope and placed in separate 5-mL Petri dishes. Individual adults are forced to release their gametes when their tubes are gently broken with a dissecting needle or fine forceps [55, 78, 80]. Female bodies are often orange in color (due to the presence of yolky eggs), while males are often milky white. Matured females release eggs of similar size and bright orange in color and spherical in shape. When females are not ready to spawn or not in good condition but forced to release their eggs, these are often pale in color and in different sizes and shapes, which should not be used for developing larval culture. High-quality

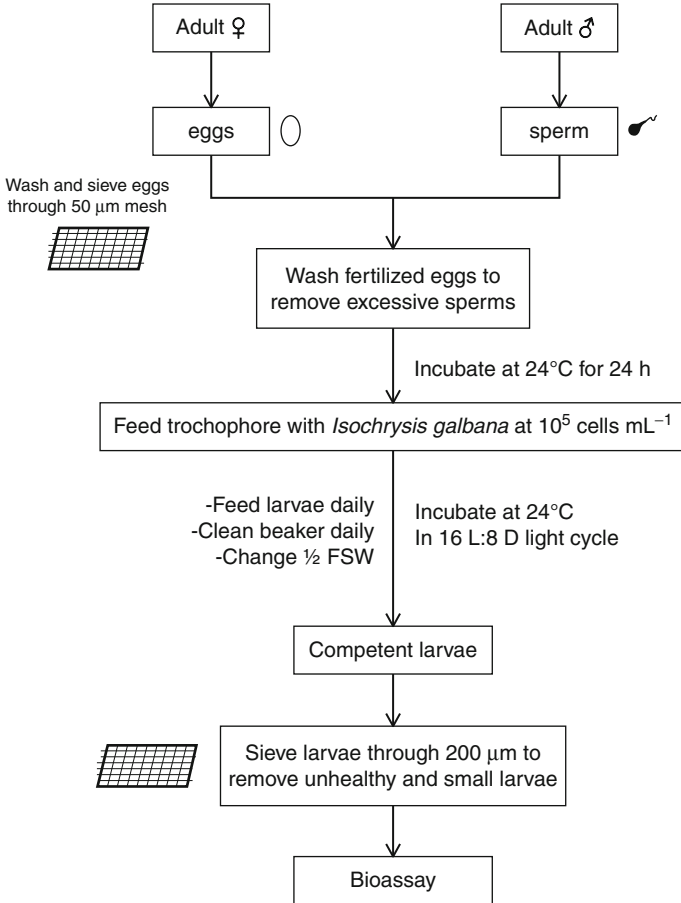


Fig. 14.30 Larval culture of *Hydroides elegans* for bioassay

eggs from several females are pooled together, sieved through a 35- μm mesh (to eliminate small eggs that are often unhealthy) using autoclaved 0.22- μm filtered seawater, and placed in 150-mL Erlenmeyer culture beaker. A few drops of highly concentrated sperm (from several males) are added into the beaker and well mixed with the egg suspension to allow fertilization to take place. As fertilization rate is near maximal in this species over a remarkably wide range of sperm concentrations (approximately 10^5 – 10^8 cells mL^{-1} – even at 10^3 sperm mL^{-1} at least 60% of eggs are fertilized) [81], there is no real need to monitor sperm concentration. After a few minutes, the fertilized eggs are filtered through a 35- μm mesh submerged in autoclaved filtered seawater to decant excess sperm, and transferred to 1 liter culture beakers containing 0.22- μm filtered seawater. The culture beakers are kept at 25°C under a 12 L:12D photoperiod in a growth chamber. After 20 h, the hatched trochophore larvae are transferred to clean beakers containing 0.22- μm filtered seawater. Larvae are fed with the flagellate *Isochrysis galbana* (Tahitian

strain) at a concentration of $1-2 \times 10^5$ cells mL⁻¹ in batch culture. Before algal food is added to the culture, the algal culture is centrifuged to remove algal culture media and algal pellets are resuspended in 0.22- μ m filtered seawater. Larval culture is maintained under the same culture conditions for 3–4 days. The larval culture is transferred to a clean culture beaker and fed daily, by filtering or pipetting. When most of the larvae reach competency to attach and metamorphose, the culture is filtered through a 150- μ m mesh to eliminate small larvae before being used for the antifouling bioassay.

Larval competency to attach and metamorphose must be tested before larvae are used for antifouling bioassays since competency affects bioassay results drastically. Competence can be assessed by pipetting a 24 subsample of larvae into a solution of 10^{-4} M IBMX in seawater. Replicates consisting of 10–15 larvae are placed in six-cell tissue culture wells containing 5 mL of treatment solution and incubated at 22°C on a 15 h light:9 h dark photoperiod. The status of larvae in experimental dishes is determined using a dissecting microscope at 24 h after initiation of an assay. Larvae that can attach to the culture well, produce a tube, and grow tentacles are considered to have undergone normal metamorphosis, while unattached and swimming or crawling larvae are considered to be unmetamorphosed [80]. Once at least 90% of subsampled larvae become competent to metamorphose in response to IBMX, the remaining larvae can be used for antifouling bioassay.

Alternatively, larval competency can be tested by using well-developed natural biofilms as positive cues. However, due to variation in the bioactivity of natural biofilms developed under different conditions, reproducibility of a bioassay may not be as good as using IBMX as the inducer.

The cheilostome bryozoan *Bugula neritina* (Linne) (Fig. 14.31) is one of the most abundant fouling organisms [82]. It is widely distributed in subtropical and temperate marine waters [83], but its population peaks at different months in different locations. As this species releases larvae that are competent to attach and metamorphose within minutes without the need of an inducer [84], it has been widely used as a test organism in antifouling bioassays [85]. Laboratory cultures can be developed to provide a consistent supply of raw materials for drug screening.

To prepare larvae for bioassay (Fig. 14.32), fresh colonies are brought to the laboratory and transferred to plastic mesh cages submerged in fresh seawater tanks in the dark overnight with aeration. Colonies are placed in 4-L beakers containing filtered seawater in the early morning and placed directly under an artificial light source. Adults usually release brooded larvae in response to light shock; larvae are attracted to the beam of the supplementary light source and can be easily transferred to test vessels using a pipette. The metamorphosis can be divided into two phases [86, 87]. The first phase is drastic and quick; metamorphosis initiates when the swimming larvae attaches to the substratum, with concomitant morphogenetic movements including eversion of the internal sac, retraction of the apical disk and involution of the corona, and formation of the precursor to the cystid and polypide [86, 87]. The second phase of metamorphosis is more gradual, ranging in duration from 36 to 48 h, and includes complete degradation of larval tissues and substantial morphological reorganization.

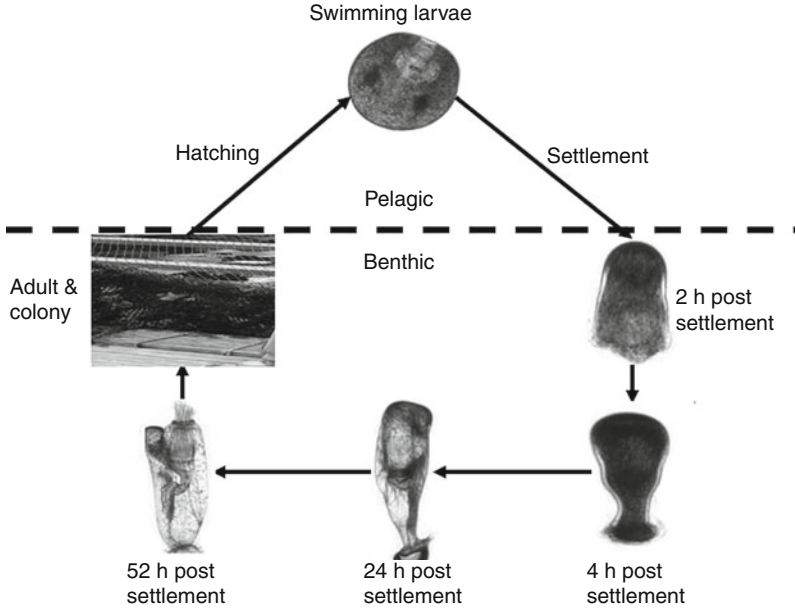


Fig. 14.31 Life cycle of *Bugula neritina*, consisting of a swimming larval stage and a sessile juvenile and adult stage

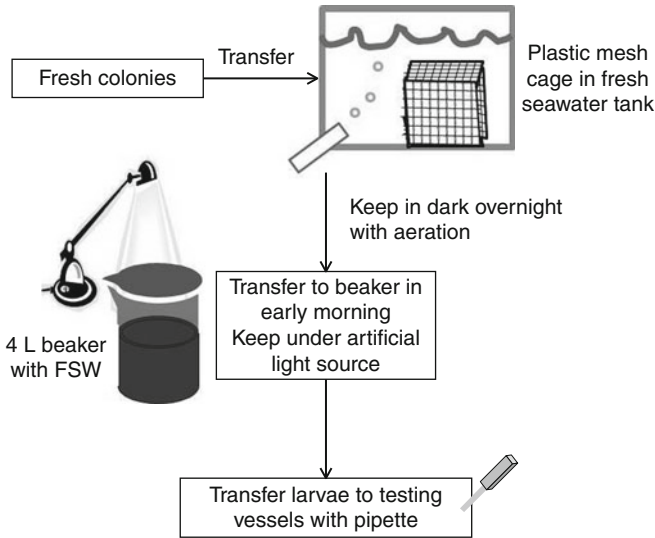
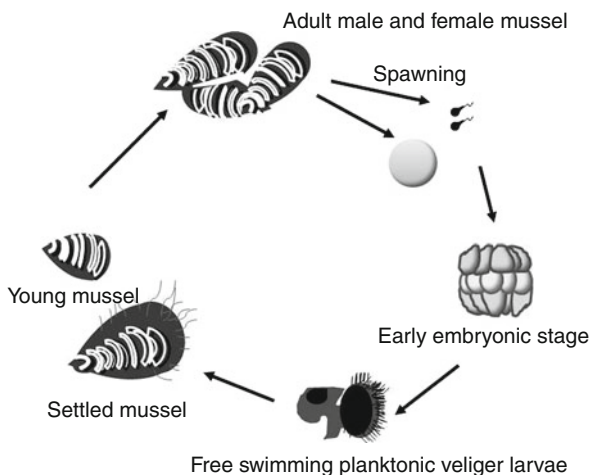


Fig. 14.32 Larval culture of *Bugula neritina*, which can be developed in the laboratory to provide a consistent supply

Fig. 14.33 Life cycle of the common mussels. Gametes are released and fertilized in seawater, and hatch into trochophore larvae that quickly develop into free-swimming planktonic veliger larvae in 1–2 days. Veliger larvae feed on plankton and develop into pediveliger larvae in 1–4 weeks before developing competency to attach and metamorphosis. This figure was adapted from Bord Iscaigh Mhara (1990) <http://www.piscestt.com/FileLibrary%5C12%5CMussel%20Culture.PDF>



Mussels are major foulers in aquatic environments. Small (0.63–3.8 cm long) freshwater zebra mussels (*Dreissena polymorpha*) (Fig. 14.33) fouling caused possibly the largest economic loss in Europe and North America in human history by a single fouling species (http://en.wikipedia.org/wiki/Zebra_mussel) as they clog water intakes of municipal water supplies and hydroelectric companies, and block pipelines in many freshwater environments such as the Great Lakes area. Meanwhile, marine mussels such as *Mytilus* spp. and *Perna* spp. are found all around the coasts in the world. The history of biofouling problems caused by these species is as long as that of harvesting them for human consumption or for fishing bait (for catching crabs, lobsters, and fishes). Mariculture industries of marine mussels have been developed [88] in almost all the coastal countries, and mussel farming can be traced back to thousands of years ago. These bivalves are often the dominant organisms on the shores of oceans and seas.

Mussels are dioecious bivalves and highly prolific bivalves. Individual females can produce millions of eggs a year. The matured female gonads are often reddish orange in color while the male yellowish cream or milky white. The major spawning season peaks in the spring or early summer, but for some mussel species, there may be a second spawning season in late fall (which is never as extensive as the spring one). During the spawning season, the males and females shed their gametes into the seawater where fertilization takes place. Spawning is often synchronized in a mussel population to maximize the fertilization rate and can be triggered by various factors. The fertilized eggs hatch into young trochophore larvae that quickly develop into free-swimming planktonic veliger larvae in a day or two. Veliger larvae remain in the water column, feed on phytoplankton, and develop into pediveliger larvae in 1–4 weeks, depending on species, water temperature, and availability of food until they reach competency to attach and metamorphose. Competent larvae become negatively phototactic and sink to the bottom and search and attach on a suitable surface by secreting byssus (proteinous substances).

During the metamorphosis process, the larval organs such as velum (swimming organs) are shed or adsorbed, meaning that animals are no longer able to swim with ciliated swimming organs. However, similar to other marine bivalves, determination of complete metamorphosis in the mussel is often difficult. Therefore, in most bioassays using mussel larvae as test organisms, we use larval attachment and loss of swimming organs as the end point. In addition, for mussel species, young juveniles may deattach themselves and ride on water currents by secreting mucous threads in order to relocate their site for permanent settlement. This ability/characteristic has also been used for antimussel attachment assays in antifouling screening.

Freshly collected adult mussels are brought to the research laboratory and carefully cleaned by removing all encrusting epifaunal organisms on individual shells. Large individuals with wider shells are selected and kept in flow-through seawater tables temporarily. Spawning is induced by injecting 2 mL 0.5 M KCl into the mantle cavity of each mussel and allowing them to stand out of water at room temperature for 1 h before immersion into 1- μm -filtered, UV-light-irradiated seawater (FSW) in individual glass or plastic beakers at room temperature [89]. Spawning can also be induced by thermal shock (transferring mussels between temperatures of approximately 10°C and 25°C at hourly intervals [90]) or by air drying the mussel in cold and dark environmental chambers and then submerging in warm seawater at hourly intervals. If these methods do not induce spawning, both male and female gonads can be dissected from healthy mussels. After checking the eggs' size and shapes, as well as sperm swimming ability under a microscope, gametes can be used for larval culture (personal experience).

Freshly released/obtained eggs and sperm are mixed at 100 and 200 sperm egg⁻¹ ratio to allow fertilization to take place [91] in 1 L glass beakers containing 0.22- μm filtered seawater. Fertilization success is checked by subsampling mixed gametes to check for polar bodies in the fertilized eggs under a microscope. Cultures with high fertilization rates and normal embryo development (>80%) are used. The fertilized eggs suspension is transferred to a small aquarium containing 0.22- μm filtered seawater and held undisturbed until the formation of trochophore larvae (may take 24–72 h, depending on species and culture temperature). Trochophore larvae at a density of 100–200 larvae mL⁻¹ are transferred to a clean aquarium by either siphoning or filtering (to decant unfertilized eggs and unhealthy embryos), and the larval condition is monitored by examining subsamples of larvae under the microscope. If a high rate of abnormality is detected, the entire larval culture should be abandoned [92] (Fig. 14.34). Larvae are fed with either individual species or a mixture of microalgae *Isochrysis galbana*, *Chaetoceros* spp., or other available algal species at a concentration of 10⁵ cells mL⁻¹ [92, 93]. The larval feed is added, and at least 1/3 of the seawater in the culture container is replaced with fresh 0.22- μm filtered seawater by siphoning daily. Debris and deposits on the bottom of the culture are also removed by siphoning. The larval culture is transferred to a clean culture container every 2–3 days (to avoid biofilm formation on the container walls) by siphoning the culture over a 45- μm mesh sieve. Development and growth of larvae are inspected under the microscope to detect any abnormality every 2–3 days until all of the larvae reach competency to attach and metamorphose.

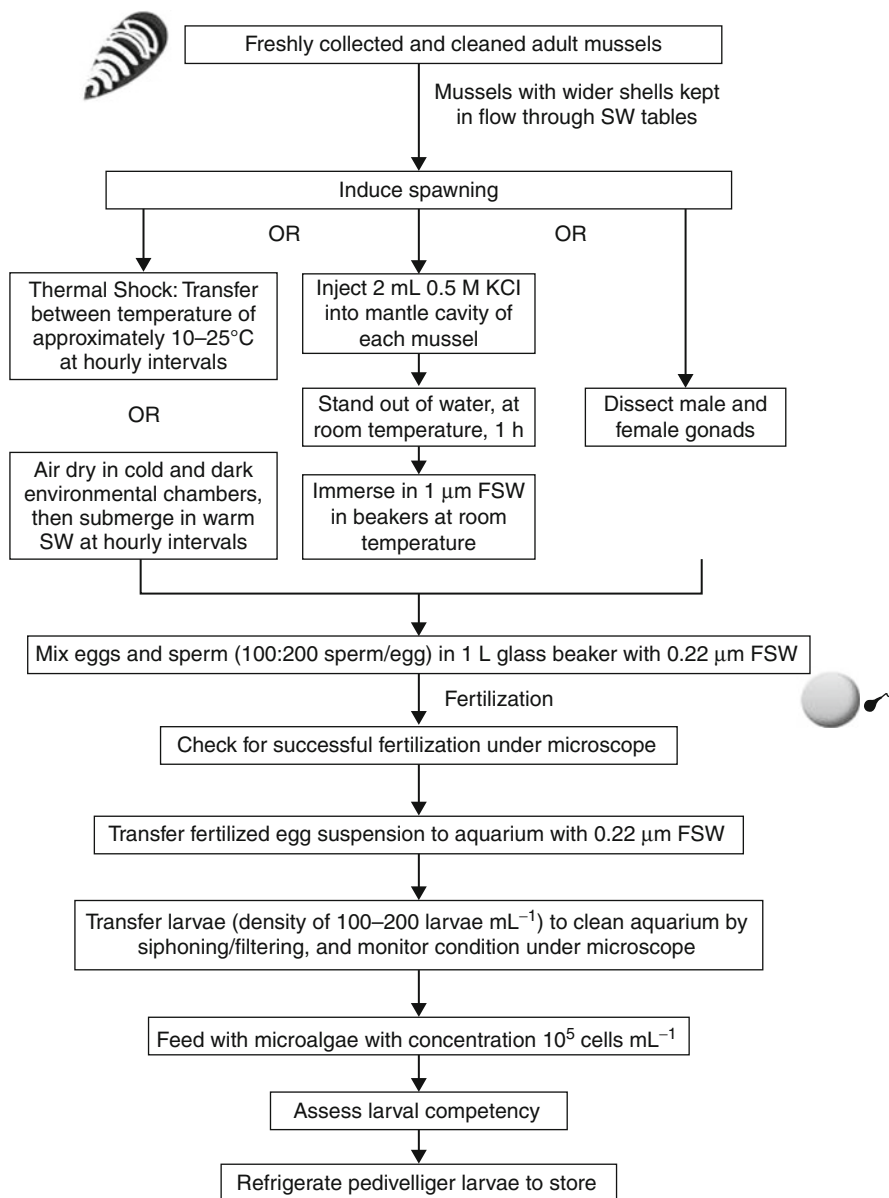


Fig. 14.34 Larval culture of mussels

Larval competency can be assessed by a slightly modified methodology from [94]. Briefly, after larvae reach pediveliger stage, 20–30 larvae are transferred in 5 mL to Petri dishes containing elevated KCl concentrations in seawater to assess metamorphic competence daily. The optimal concentration of excessive KCl

to induce mussel larvae to settle varies (10–50 mM above ambient) from species to species and needs to be determined carefully. There should be at least five to six replicate dishes. All individuals exposed to KC1 are checked to determine for the presence of gill filaments and shell brims.

Refrigeration of pediveliger larvae of the mussel for various periods has been examined and suggested to be a good way to store competent larvae for up to 1–3 months for antifouling bioassay purposes [95].

14.5.3 Antifouling Assays Using Larvae of Major Fouling Organisms

When using invertebrate larvae as test organisms in antifouling bioassays, various end points have been used, including swimming speed, swimming behavior (mode of locomotion and phototaxis, response to flow), survival, but most importantly, the attachment rate and metamorphosis rate. While in most cases, larval attachment and metamorphosis are treated as a single end point, that is, larval settlement, there have also been cases to treat larval attachment and metamorphosis as distinctive and distinguishable processes.

Regardless of what end points are recorded and what larval species are targeted, the following important quantitative indices are used: LC_{50} and EC_{50} , and the ratio of these two.

1. LC_{50} refers to the lethal compound concentration where 50% of the targeted organisms die within a given period of time, which can range from minutes to several days, depending on the bioassay protocol and test organisms.
2. EC_{50} refers to the concentration that leads to 50% inhibition of a particular biological activity, such as settlement in antisetlement screening assays.
3. A theoretical ratio of LC_{50} and EC_{50} data implies the possible relationship between toxicity and the inhibition of performances. When this ratio is small (close to 1.0 or below 1.0), it suggests that the compounds/extracts may act on test organisms through toxic mechanisms, while a large ratio (such as >15) indicates that the substance may act in a less or nontoxic manner. Therefore, this ratio is commonly used to guide the screening for antifouling compounds. A sensible strategy for screening for antifouling compounds looks for substances of low or negligible toxicity that inhibit larval settlement of major foulers, since these compounds may have a better chance to get through more rigid environmental regulation in the future.

Because larval settlement is not only affected by many exogenous factors such as substratum type, rugosity, light, surface films, host inductance but also by indigenous ones such as genetic differences, physiological conditions, and sensory perception between larval batches, it requires substantial background research before one species can be adopted for antifouling screening bioassays. This may well explain why only a few larval species have been routinely used over the last several decades, although many species have been tried or suggested for antifouling bioassay. Keeping this in mind, we will describe testing protocols only for the species introduced above.

14.5.3.1 Using Barnacle Larvae as Test Organisms

Range-finding assays (Fig. 14.34) [96]: To define a possible functional range (regardless of EC_{50} or LC_{50}), a preliminary bioassay on cyprid settlement can be carried out using 24-well polystyrene plates (Falcon, USA), although the results of this type of assay are hardly ever seen in publication. The pure compounds or chemical extracts are dissolved in dimethyl sulfoxide (DMSO) and added to autoclaved FSW to yield final concentrations ranging from very low (around $\mu\text{g mL}^{-1}$) to very high ($200 \mu\text{g mL}^{-1}$). Cyprids (10 ± 2 individuals) are added to each well with 1 mL of the test solution. In total, there are 8 test solutions of target compounds or extracts, plus wells containing FSW and wells containing FSW with DMSO serving as two types of negative controls. Each treatment should have two replicates. The plates are incubated at 28–30°C for 24 h in an environment with a 15 h:9 h L:D photoperiod. After incubation, the wells are examined under a dissecting microscope. Cyprids that do not move with their appendages extended or do not respond when touched with a dissecting needle are counted as dead, while those unattached/swimming ones are counted as unsettled. The assay is terminated by adding two to three drops of 10% formalin to each well. All of the unattached larvae are washed away with deionized water, while attached juveniles are enumerated [59]. The percentage of larval

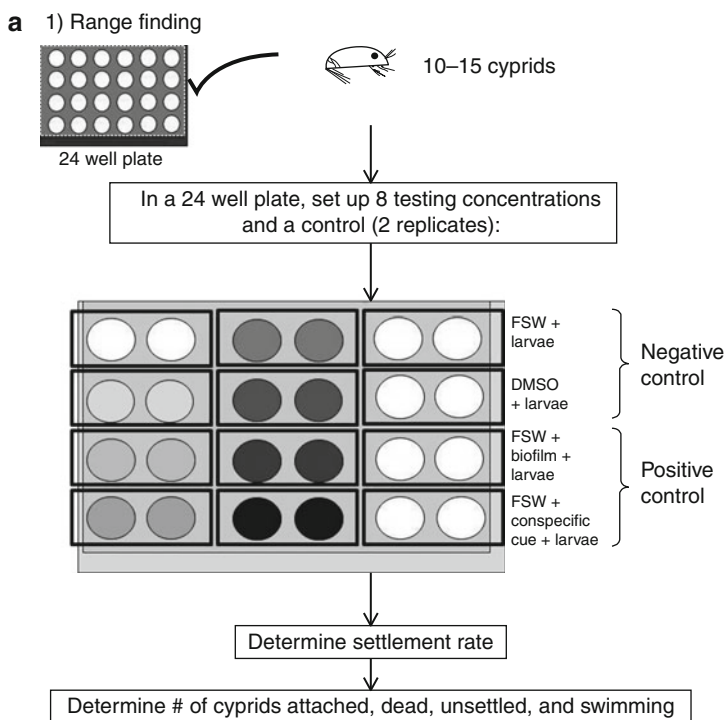


Fig. 14.35 (continued)

b 2) Narrow range for determination of EC_{50} and LC_{50} , 5-6 replicates

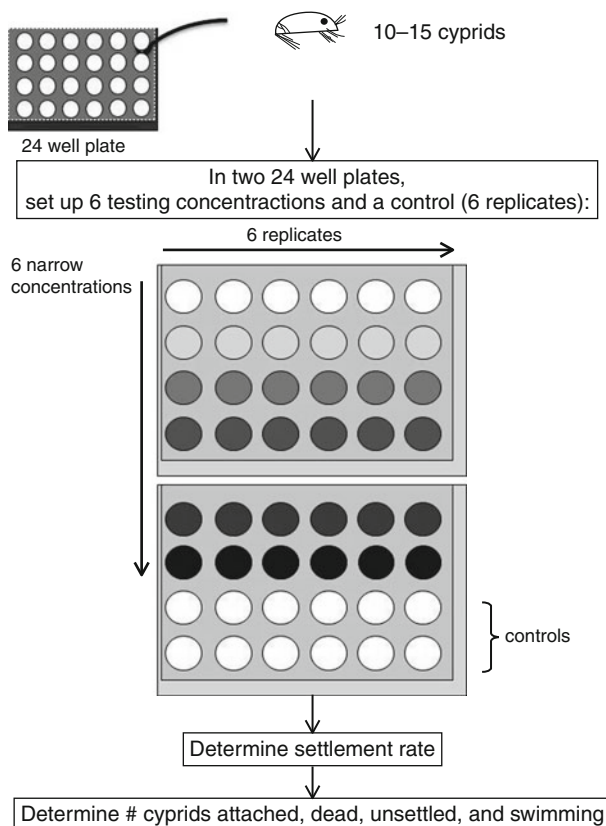


Fig. 14.35 Range finding assay for antifouling compounds, in order to define a possible functional range of cyprids. Abbreviations: LC_{50} lethal concentration (the concentration causing death of 50% of the group of test organisms), EC_{50} effective concentration (the concentration inducing an effect on half of a group of test organisms, and in this case, the effect would be settlement)

settlement is determined by counting the number of settled individuals under a dissecting microscope and expressed as a proportion of the total number of larvae in the well. The therapeutic ratio (a comparison of the amount of an antifouling compound/extract that inhibits 50% larval settlement to the amount that causes 50% larval death) (LC_{50}/EC_{50}) is roughly estimated (Fig. 14.35).

Following up range finding assays, the bioassay is repeated with six test concentrations within a relative narrow range. For each treatment, there should be at least five to six replicate wells. The therapeutic ratio is calculated in order to determine the effectivity of the antifouling compound against larval settlement. The EC_{50} (with 95% confidence interval) for settlement inhibition is estimated by probit analysis counts of a log dilution series of the test compound.

14.5.3.2 Using *Hydroides elegans* Competent Larvae as Testing Organisms

Fifteen competent larvae are placed into each of the experimental dishes. Experiments are conducted for 24 h at 24°C under continuous illumination, and then swimming and settled larvae are counted under the microscope. A larval bioassay is conducted with five to six replicates in multiwell polystyrene dishes (#3047, Falcon, USA). AFSW-filled dishes are used as the negative controls, while the phosphodiesterase inhibitor 3-isobutyl-1-methylxanthine (IBMX, Fluka Ltd.) is commonly used as an artificial stimulator (as the positive controls) for larval attachment at 10^{-4} M in AFSW [81]. Otherwise, dishes with well-developed natural marine biofilms are used as the positive controls (because larvae often settle well in response to well-developed natural biofilms). After this period of time, swimming, settled and dead larvae are counted under a dissecting microscope. LC_{50} and EC_{50} of the test compound or extract are determined according to the same method described in the barnacle larval settlement assays (Fig. 14.36).

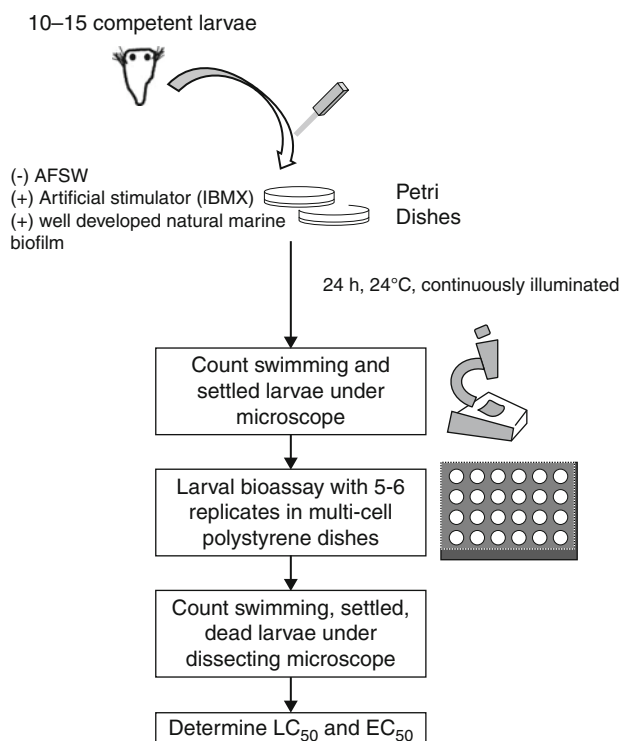


Fig. 14.36 *Hydroides elegans* as test organism for extracts or compounds. Abbreviations: (–), negative control; AFSW autoclaved filtered seawater, (+) positive control, IBMX 3-isobutyl-1-methylxanthine (a phosphodiesterase inhibitor that is used as an artificial stimulator for the positive control)

14.5.3.3 Using *Bugula neritina* Larvae as a Test Organism

Approximately 20 newly released larvae (i.e., within 15 min) can be sterilely added to each well of a 24-well polystyrene plate containing 1 mL of the test solution per well. Five replicates per treatment are used. Wells containing only filtered seawater with DMSO serve as the controls (Fig. 14.37). The plates are incubated at 27°C for 1–3 h, and the percentage of larval settlement is determined by counting the settled, live larvae under a dissecting microscope. Results are expressed as a proportion of the total number of larvae in the well. EC_{50} (inhibits 50% of settlement of larvae in comparison with the control) and LC_{50} (the concentration at which 50% of larvae were dead in comparison with the control) levels of pure compound or extract are calculated by using the Probit software [97–99].

14.5.3.4 Using Mussel Larvae and Juveniles as Test Organisms

Since larval culture of mussels is often time-consuming and challenging (in maintaining very healthy larval culture and assessing competency to attach and metamorphose as well as in determining the completion of metamorphosis), this larval settlement bioassay is becoming less popular. Instead, young juveniles collected from natural environments are more commonly used in antifouling bioassay.

Mussel larval settlement and metamorphosis assay [100, 101] (Fig. 14.38): Prior to the antifouling bioassay, 5-mL Falcon Petri dishes are allowed to develop natural biofilms in seawater tables supplied with flow-through seawater. Twenty competent pediveliger larvae of mussels are added into each 5-mL Petri dish (Falcon, USA) containing 5-mL FSW as the positive controls or 5 mL of test

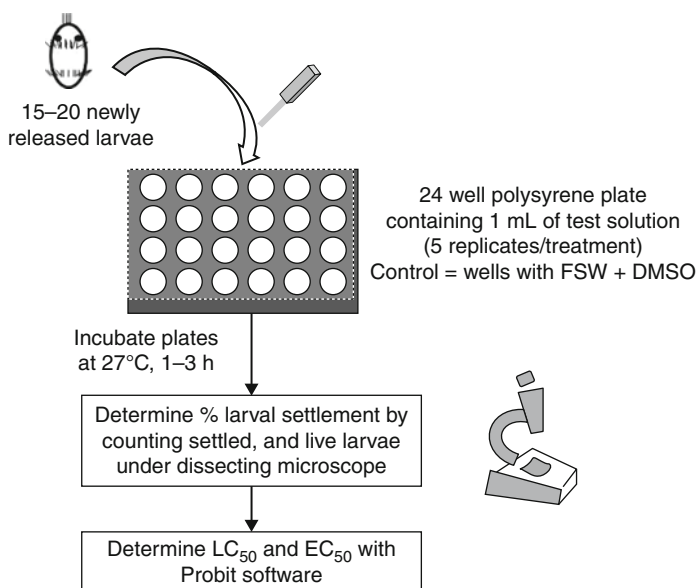


Fig. 14.37 Using *Bugula neritina* as test organisms

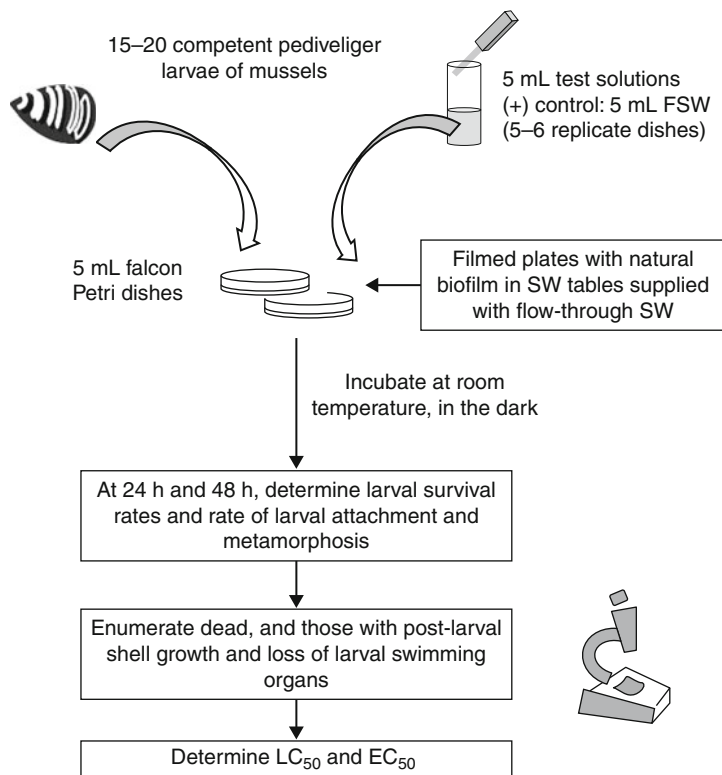
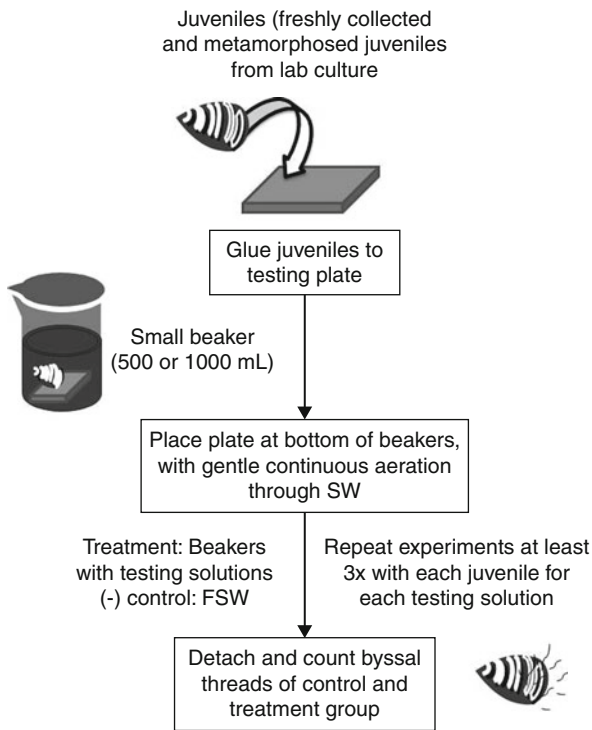


Fig. 14.38 Mussel larval settlement and metamorphosis assay. This figure is adapted from Dobretsov and Qian [100]; Bao et al. [101]

solutions as the treatment. In case that natural biofilm development becomes rather difficult or bioactivity of natural biofilms for inducing mussel larval settlement is unstable or too low, competent larvae are treated for 10–20 min with elevated KCl solution at an optimal concentration defined in the competency assay described in the larval rearing section, prior to being added into each Petri dish uncoated with natural biofilms. All of the Petri dishes are incubated at room temperature in the dark, and at least five to six replicate Petri dishes are used for each treatment. Larval survival rate, as well as the rate of larval attachment and metamorphosis, is determined under a microscope after 24 and 48 h from the commencement of the experiment by counting the number of dead individuals (mortality) and the number of individuals with postlarval shell growth and loss of larval swimming organs. LC_{50} and EC_{50} are calculated according to the methods described in the previous section.

Free single mussel assay A (modified from Etoh et al. [102]) (Fig. 14.39): Freshly collected from field and metamorphosed juveniles from laboratory culture are glued to the test plate using nontoxic ‘crazy glue’ (or other glues). The plate is placed at the bottom of a small beaker (500–1000 mL) containing seawater with continuous but gentle aeration and left for 4 h. Beakers containing test solution are used as treatment,

Fig. 14.39 Free single mussel assay. This figure is adapted from Etoh et al. [102]

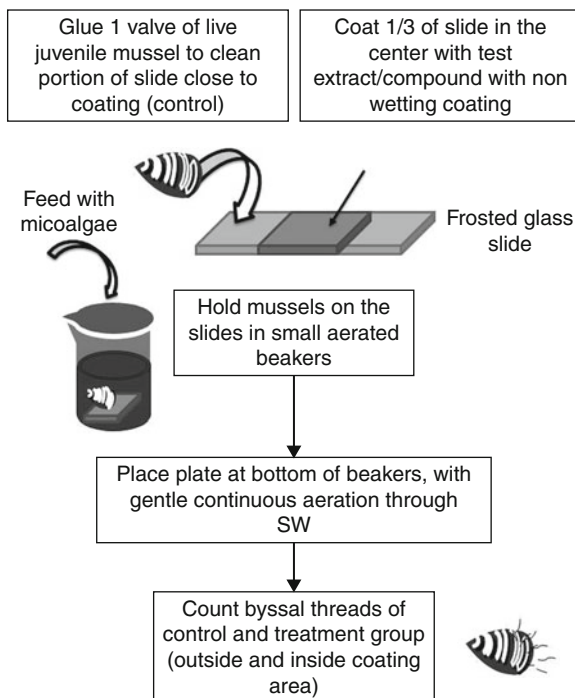


while ones with fresh filtered seawater serve as the negative controls. After 4 h, a number of byssal threads produced by each juvenile are counted by detaching threads one by one. The experiments are repeated at least three times with each juvenile for each test solution (to save juveniles and chemicals). The number of byssus produced by each mussel in both the treatment and controls is calculated and compared.

Juvenile byssus threads assays [103, 104] (Fig. 14.40): The byssal thread bioassay is developed and extensively used by Japanese scientists. In the laboratory bioassay, 1/3 of the center of clean frosted glass slides are coated with test extract or compound alone or extract/compound with nonwetting coating (EXTRUDETTM). One valve of a live juvenile mussel is glued to the clean portion of the slide close to the coating. Mussels on the slides are held in small aerated beakers for 1–10 days and fed with microalgae. The number of the byssal threads attached outside and inside the coating area of each mussel is counted at the end of experiment and is compared to that in the controls (area without extract or compound coating). A compound or extract would be considered as active (antifouling) if >90% of the byssal threads are found outside of the areas.

A similar system has been used for field antifouling bioassays in Japan [103]. A piece of cardboard (Webron, Tokusyu Seishi Co., Ltd., Japan) is trimmed into 50 × 1 cm strips, washed with methanol, and dried before use. The front side of the cardboard (40 cm²), except for both ends, which is used for attachment, is coated with a test compound or extract dissolved in 0.5 mL of organic solvent (mainly

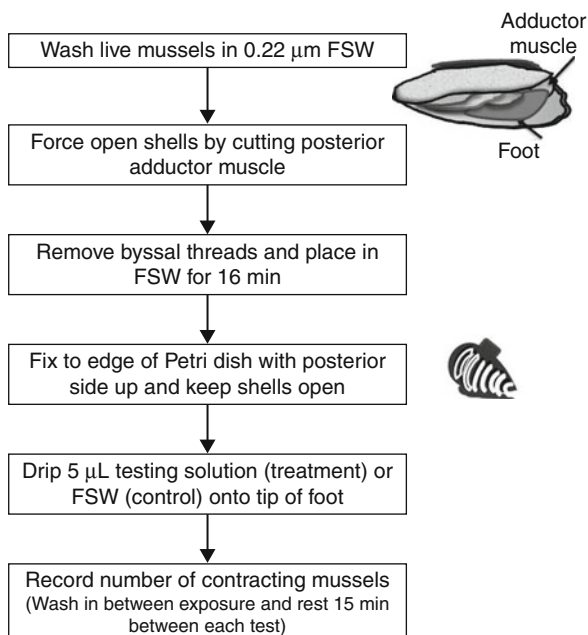
Fig. 14.40 Juvenile mussel byssal thread assay. This figure is adapted from Ina et al. [103], and Sera et al. [104]



MeOH), using an absorbent cotton ball. The blank plate is prepared by the same procedure described above. After the solvent is evaporated, both plates are arranged in a line fixed tightly on an exclusive stand without wrapping. Ten test mussels are fixed around each zone. Each plate is set at the bottom of an experimental aquarium with running seawater, which is covered to create dark conditions. After 3 h, the number of byssuses attached outside the coated zones and total number of byssuses of each mussel is determined. The number of inactive (dead) mussels is also recorded. Antifouling activity is determined as a percentage at each concentration of the test compound or extract as follows: number of byssuses \times 100 (%).

Mussel foot contraction assay [105] (Fig. 14.41): This type of bioassay is not commonly used as observation of behavior may not be as easy as counting settlement, metamorphosis, or byssal thread production. Yet, it provides an other means of bioassay screening. Briefly, live mussels are first washed in 0.22- μ m filtered seawater, and then mussel shells are forced open by cutting the posterior adductor muscle. After removal of byssus threads, the mussels are placed in filtered seawater for 15 min. Each mussel is then fixed to the edge of a Petri dish with the posterior side up by using a holder or glued while their shells are kept open to expose their foot. For the control, 5 μ L of FSW is dripped onto the tip of the foot gently (try not to physically stimulate the foot). Only mussels that do not respond to FSW drips should be used for follow-up experiments. To test antifouling compounds, 5 μ L of test solution (of compounds or extract) is gently dripped onto the mussel foot following the same method as in the controls. If the mussel contracts in a few

Fig. 14.41 Mussel foot contraction assay, as an alternative to observing settlement, metamorphosis, or byssal thread production. This figure is adapted from Hayashi and Miki [105]



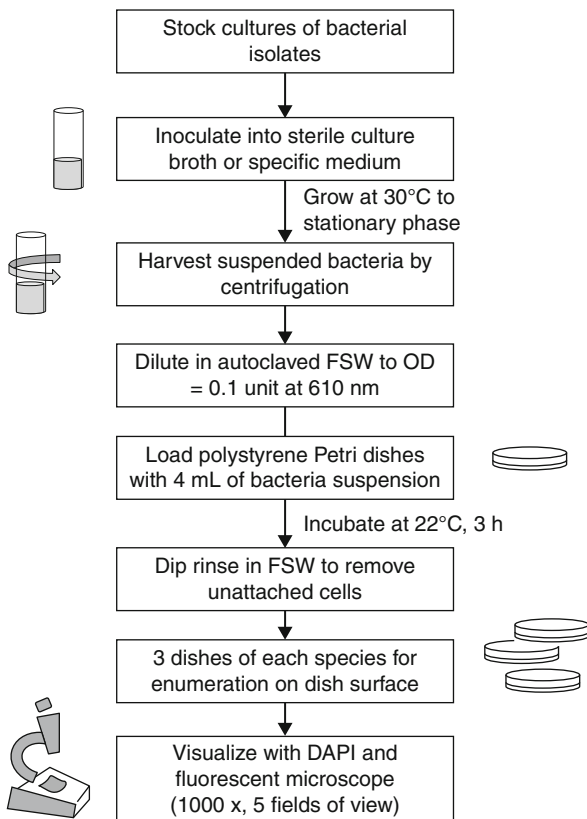
seconds, this is considered as a response. The number of responding mussels is recorded. In this type of assay, the same group of mussels can be reused. To do so, the mussel feet are gently washed with filtered seawater immediately after observation of their responses to chemical exposure. The animals should be allowed to rest in filtered seawater for at least 15 min before the next round of testing. The concentration of the test solution can be raised from the point of dripping the ASW as control until all the mussels show a reaction. The responses of the mussels are indicated by percentages at each concentration of test solution, calculated as number of reactive mussels/ (number of reactive mussels + unreactive mussels) \times 100 (%).

14.5.3.5 Antilarval Settlement of Bacterial and Diatom Films

Besides testing bioactivity of chemical extracts or pure compounds from marine macroorganisms and microbes, antilarval settlement of biofilms developed from monospecies of bacteria or multispecies of bacteria is often the first step in screening for bioactive bacteria and diatoms, which leads to subsequent isolation and purification of antifouling compounds from bioactive strains and species (methods described in early section). Therefore, here, we introduce the general protocol for antilarval settlement of bacterial and diatom films, using larvae of *B. amphitrite*, *H. elegans*, and *Bugula neritina* [85, 97, 106] (Fig. 14.42).

Development of bacterial film: Start with stock cultures of bacterial isolates from the Marine Bacteria Culture Collection. All bacteria are inoculated into sterile culture broth [0.5% (w/v) peptone, 0.3% (w/v) yeast extract in sterilized filtered (FSW)] or specific medium (for some unique species and grow at 30°C to the

Fig. 14.42 Development of biofilms, for subsequent screening of bacteria and diatoms for antifouling compounds. Abbreviations: *OD* optical density



stationary phase [106]. Suspended bacteria are then harvested by centrifugation and diluted in autoclaved FSW to an optical density of 0.1 unit at a wavelength of 610 nm (using a spectrophotometer of TechComp, China). Polystyrene Petri dishes (# 1006, Falcon, USA) are loaded with 4 mL of the bacterial suspension and incubated for 3 h at 22°C to allow bacteria to attach and form consolidated biofilms. Thereafter, the dishes are dip-rinsed in FSW to remove unattached cells before being used for larval settlement assays. For each bacterial species, three dishes are diverted for the enumeration of bacteria on the dish surface. Falcon dishes or glass slides (used as microscopic slides)($n = 3$), are formalin-fixed (4% in FSW), rinsed with distilled water, and stained with the DNA-binding fluorochrome 4',6-diamidino-2-phenylindole (DAPI) (Fluka Chemie AG, Switzerland) [107] at $0.5 \mu\text{g mL}^{-1}$ for 5 min. Stained substrata are wet-mounted on a fluorescence microscope (Zeiss Axiophot, Germany), and bacterial cells are recorded at $1000\times$ magnification in five fields of view chosen randomly ($\lambda_{\text{Ex}} = 359 \text{ nm}$, $\lambda_{\text{Em}} = 441 \text{ nm}$). Data is given as means \pm SE of 5 replicates.

Development of diatom biofilms: Diatoms from the culture collection are cultivated in aerated 400-mL Erlenmeyer culture flasks according to the procedure of Harder et al. [15]. When visible diatom films have developed in the flask,

the monospecific diatom suspensions are transferred to experimental Petri dishes (Falcon, USA) and incubated for 24 h to allow diatoms to attach and develop films on the substrata. These prepared Petri dishes are then washed carefully in FSW. Three dishes are fixed with a 5% solution of formalin in seawater and used for diatom counts using the same methods for determining bacterial density.

Development of natural biofilms: Natural biofilms (NBF) are developed by exposing Falcon Petri dishes to surface sea waters for 5 days before using them for larval bioassays.

Larval settlement bioassays on filmed surfaces: Newly released *Bugula neritina* larvae (i.e., within 15 min) or newly molted barnacle cyprids (obtained as described in earlier session) are used in bioassays without any further treatment. For *Hydroides elegans* competent larvae, they are treated with IBMX according to methods described in the *H. elegans* larval settlement assay prior to be added to filmed Petri dishes. Ten to twenty larvae are added to each filmed Petri dish (either with bacterial film, diatom film, or natural biofilm) in 4 mL of sterile-filtered (0.22 μm) seawater (FSW). Petri dishes without biofilms and containing sterile filtered seawater are used as controls. There should be at least five replicate dishes per treatment. Bioassay conditions for each larval species should follow the protocols described in previous session. At the end of bioassay, the number of attached juveniles is recorded and bioactivity of the biofilm is determined by the settling rate in each treatment in comparison with that in the control.

14.6 Methods of Antifouling Compounds Test

After a potent antifouling compound is identified, the chemical needs to be incorporated into a marine coating (basic coating with or without other biocides) and tested in both laboratory and field assays. Both static panel immersion testing (D3623) and dynamic testing (ASTM D 4938 & 4939) are conducted according to the protocols detailed by the American Society for Testing Materials (ASTM 1998). As recommended, field testing must be conducted in a heavily fouled marine environment, typically a port area, and left for periods of time to determine the degree of resistance provided by the test coatings against attachment of hard (barnacles, oysters) and soft (algae, seaweeds, sponges, etc.) fouling. The details will not be discussed in this chapter.

14.7 Mode-of-Action of Antifouling Compounds

Up to now, very little has been done on the mode-of-action of antifouling compounds at the molecular level while the effects of compounds on behavior and physiology (often indicated by enzymatic activities) of settling propagules of macrofouler have been investigated sporadically. In comparison, more work on the effects of compounds on bacteria and biofilm formation has been carried out because more biological information (genomics, proteomics, transcriptomics, and metabolomics) on

microbes is available. Here we will discuss the general procedures on how to investigate the effects of antifouling compounds on gene and protein expression in settling larvae of marine invertebrate foulers. We hope more work in this area of research will shed light on the molecular mechanisms and targets of antifouling compounds, which will be important for designing biofouling control strategies.

14.7.1 Effects of Antifouling Compound on Gene Expression

To investigate the possible effects of antifouling compounds on settling larvae of marine invertebrate foulers at the gene level, *the first step* is to select target gene(s). The ideal candidate genes should be the ones with (1) known functions in other model organisms (since up to now, there is hardly any solid evidence on the function of any genes in larval settlement and metamorphosis of marine fouling organisms) and (2) full length of the gene sequence (well-matched and informative). However, if we know a given protein is involved in regulating larval settlement and metamorphosis, we can also design primers for the target genes even before we obtain full length sequences of the relevant genes (Figs. 14.43, 14.44).

The second step is to design primers for the candidate genes with Primer Express software (Version 1.0, PE Applied Biosystems, Foster City, CA) for real-time PCR. All primer sets should have a calculated annealing temperature of $\geq 58^{\circ}\text{C}$ (nearest neighbor method), and the PCR products can be easily amplified. Internal controls need to be selected for Quantitative Real-time PCR reaction, and we found that QuantumRNA™ 18s internal standards primers (Ambion Inc., Austin, TX) can serve as internal controls.

The third step is to challenge competent larvae (which are prepared according to methods described in previous sections) with an antifouling compound at a given

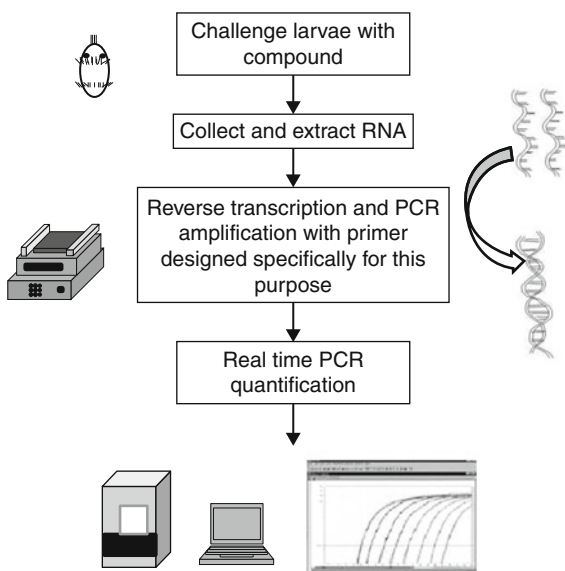


Fig. 14.43 Real-time PCR detection of gene expression

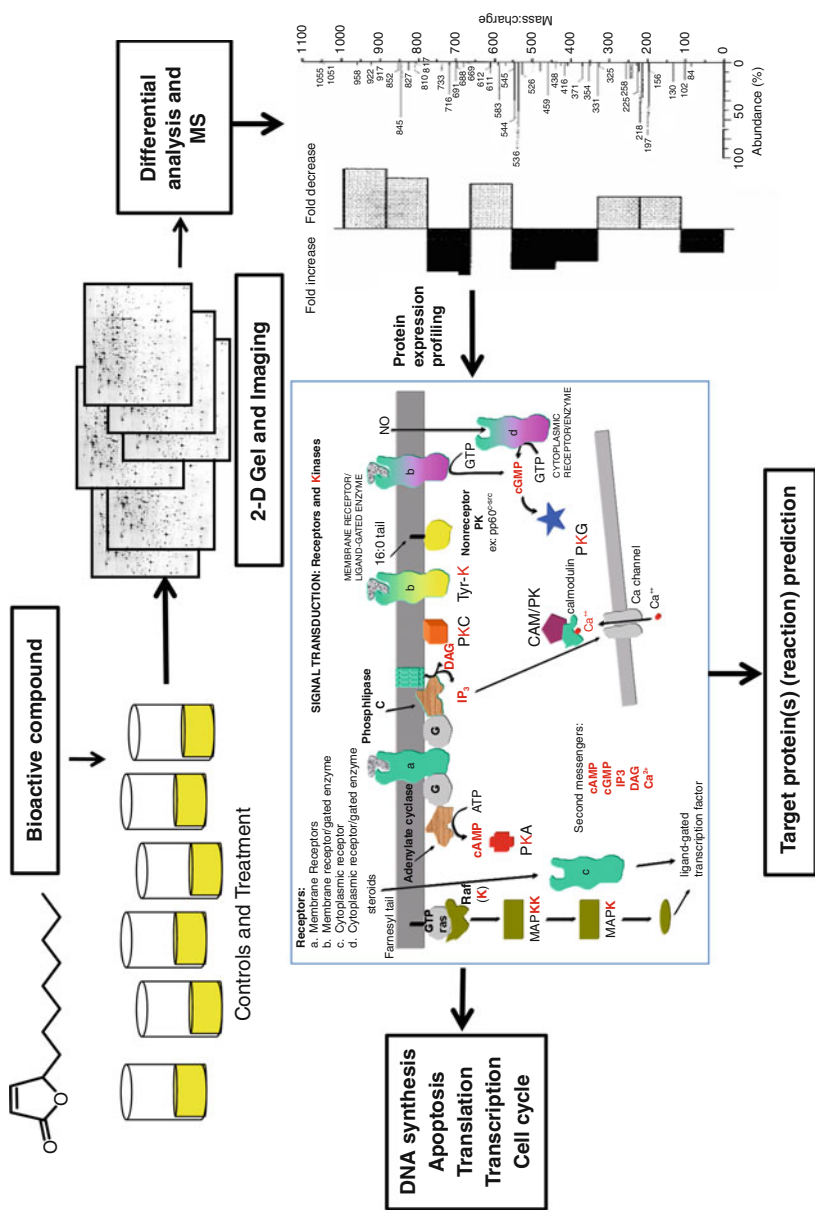


Fig. 14.44 Proteomics is a new technology used to study the mode of action of compounds. For example, signal transduction involves receptors and kinases, resulting in various processes in a cell such as DNA synthesis or translation

concentration and for a given duration (both need to be optimized). Competent larvae without being challenged with the antifouling compound are induced and/or allowed to settle normally and are used as the negative control.

The fourth step is to extract RNA from the control larvae and treated larvae. A sufficient number of larvae in both treatment and control groups are homogenized in TRIzol reagent. The total RNA of each sample is extracted according to the manufacturer's instructions and can be quantified with a GeneQuant Spectrophotometer. RNA samples are treated with RNase free DNase I to eliminate possible trace amounts of genomic DNA contamination immediately prior to proceeding with cDNA synthesis. First-strand complementary DNA can be synthesized from total RNA samples using M-MLV Reverse Transcriptase (USB Corporation, Cleveland, OH) with (N)₆ random primers (TaKaRa, Dalian, China). Briefly, N₆ random primer primed first-strand cDNA can thus be synthesized in a total volume of 20 μ L containing 2 μ g of total RNA [108].

The fifth step is to conduct qRT-PCR. The PCR reactions normally take place in 96-well microtiter plate wells in reaction volumes of 25 μ L with SYBR Green Master Mix at the optimal concentrations of specific primers, using an ABI Prism 7000 Sequence Detector or similar Real-time PCR. Reaction conditions should be predetermined and optimized for particular genes and then programmed in the PCR machine. For each bioassay, there should be at least three replicates, tested cDNA samples and the controls. Specificity of PCR amplification of each pair of primers is confirmed by analyzing PCR products through agarose gel electrophoresis and dissociation curve analysis. Differences in gene expression can then be calculated by the comparative Ct method that compares test samples to a calibrator sample and uses results obtained from a uniformly expressed control gene to correct for differences in the amount of RNA present in the two samples being compared to generate a Δ Ct value. The formula used for fold difference calculation often sets for $2^{-\Delta\Delta Ct}$, where the value of Δ Ct is the difference in Δ Ct values obtained with calibrator and test samples.

14.7.2 Effects of Antifouling Compound on Protein Expression

Studying the effects of antifouling compounds on protein expression is challenging since this requires technology and high-tech instrumentation for protein extraction, purification, separation, and identification. However, this area of research may provide us with a better success rate in identifying the targets of antifouling compounds, which can be very important in developing antifouling strategies. Here, we introduce 2-DE-based proteomic techniques for reference (gel-free proteomics requires substantial LC-MS/MS machine times) [109–111] (Figs. 14.45, 14.46).

The competent larvae are challenged with antifouling compounds at a given concentration and for a period of time (to be optimized for a particular species), and larvae without compound treatment serve as the negative controls [109–111]. After treatment, larvae are collected and placed in lysis buffer, frozen in liquid nitrogen for 5 min, and then stored at -70°C until use. In solution, IEF fractionation

followed by narrow-range 2-DE can substantially improve the proteome coverage. Briefly, the frozen larval samples are added with lysis buffer (7 M urea, 2 M thiourea, 4% CHAPS, 40 mM dithiothreitol (DTT)), homogenized, and then subject to sonication. Protein samples are centrifuged to remove insoluble materials, followed by acetone precipitation (5 volume of precooled acetone). Protein samples are pelleted and resuspended in 0.5-mL IEF fractionation buffer (7 M urea, 2 M thiourea, 4% CHAPS, 40 mM dithiothreitol (DTT), and 1% 3–10 ampholytes). An RC/DC protein assay is conducted, and around 2 mg per sample is taken and then adjusted to 3.25 mL using the IEF fractionation buffer. The electrophoresis of the protein sample solution is analyzed with a Zoom IEF fractionator at constant power (2 W) and limiting current (2 mA) using six isoelectric partition membranes. A 16- μ L aliquot of each fraction is checked for fractionation efficiency

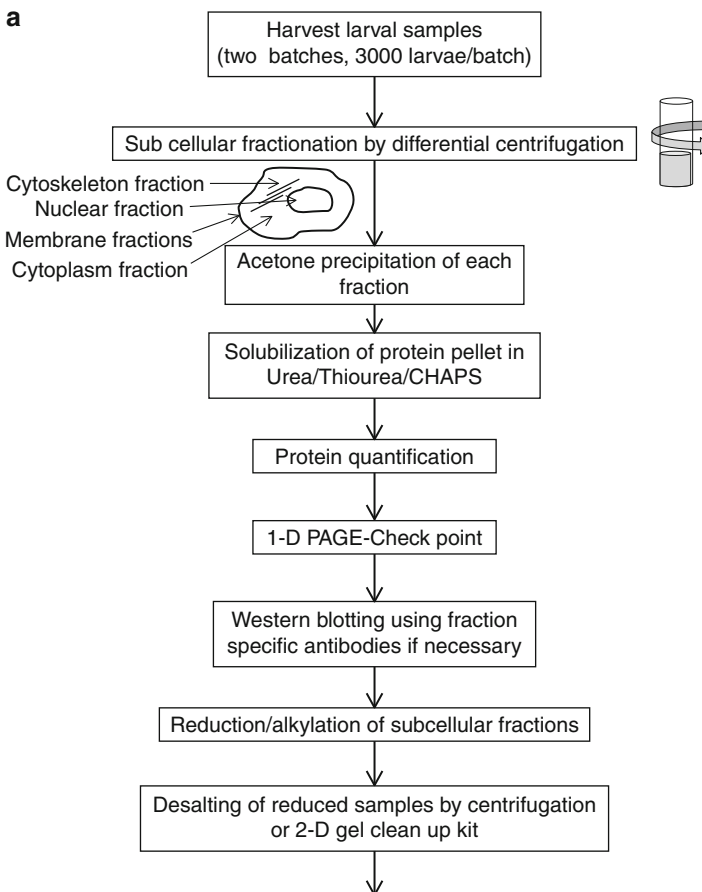


Fig. 14.45 (continued)

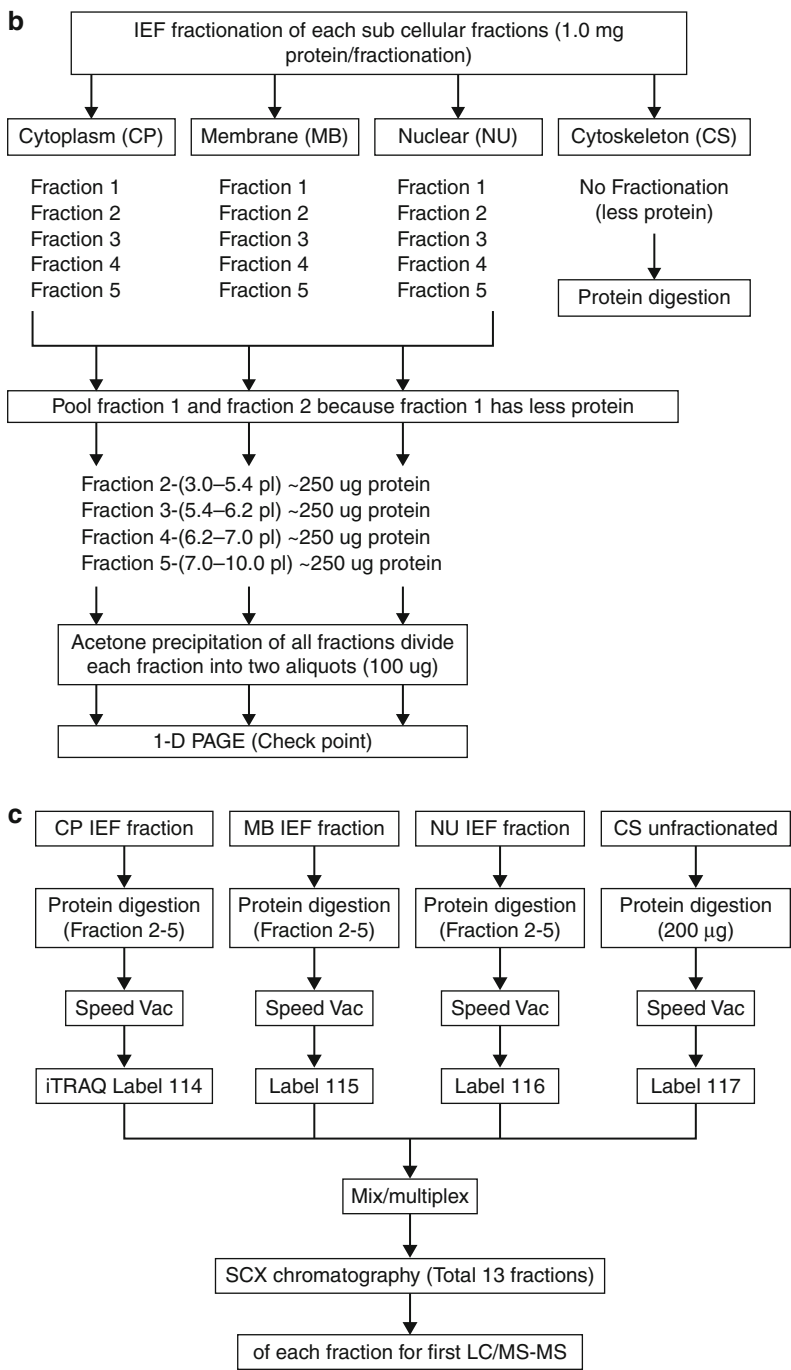
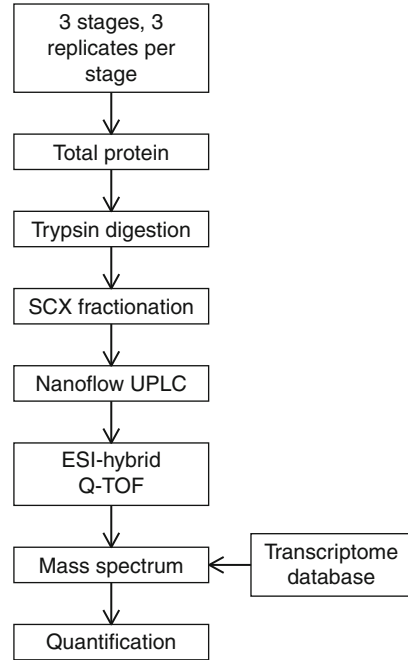


Fig. 14.45 (continued)

Fig. 14.46 Shotgun proteomic study of marine organisms. Abbreviations: *Nanoflow UPLC* nanoflow ultra performance liquid chromatography, *ESI-hybrid*, energy storage inverter, *Q-TOF* quadrupole-time of flight, ESI-hybrid



with SDS-PAGE. Zoom IEF fractions are precipitated in acetone and dissolved in 300- μ L rehydration buffer (7 M urea, 2 M thiourea, 4% CHAPS, 1% DTT, and 0.5% IPG buffer). The solution is sonicated for 10 min twice, incubated at room temperature for 1 h, and centrifuged at 12,000 rpm for 10 min. IPG strips (*e.g.*, *pH* 3.0–7.0) are rehydrated with sample solution overnight at 20°C with 50 mA current for 14 h and subjected to IEF using a Protean IEF Cell. IEF is performed under the following conditions: 250 V for 20 min, 1,000 V for 2 h, and with a gradient of 10,000 V for a total of 60,000 Vh. After IEF, the second dimension is performed at 20°C at a maximum of 24 mA per gel for approximately 8 h until the bromophenol blue reaches the bottom of the gel. All gels are fixed in 50% methanol and 10% acetic acid overnight, stained for phosphoproteins and total proteins, and imaged on a Typhoon trio imager. The scanned gels can be analyzed using the PDQuest software (version 8.0; Bio-Rad) according to the protocol provided by the developer. Spots on ProQ Diamond stained gels are matched to SYPRO Ruby



Fig. 14.45 Proteomic analysis of *Bugula neritina*. Abbreviations: *CHAPS* 3-[93-cholamidopropyl]-dimethylammonio]-1-propanesulfonate, a detergent, *1-D PAGE* one-dimensional polyacrylamide gel electrophoresis, *SCX chromatography* strong cation exchange chromatography, *iTRAQ* isobaric tag for relative and absolute quantification, *CP IEF* cytoplasm isoelectric focusing, *MB IEF* membrane isoelectric focusing, *NU IEF* nuclear isoelectric focusing, *CS* cytoplasm, *LC/MS-MS* liquid chromatography–mass spectroscopy

image replicate groups. The quantitative detection of changes in phosphoprotein and total protein abundance are set at a threshold of more than 1.5-fold. The number of spots that are significantly different between the controls and treatments is identified and compared (Student's *t* test, $p < 0.05$).

2-DE is stained with Coomassie Blue G-250. Differentially expressed phosphoproteins and protein spots are excised, and the excised gel pieces are destained with 50% MeOH/50 mM NH_4HCO_3 , dehydrated with 50% acetonitrile (ACN) twice, and then 100% ACN. The gel pieces are dried by vacuum centrifugation for 30 min. The completely dried gel pieces are added with 20 μL of 12.5 $\text{ng } \mu\text{L}^{-1}$ trypsin (Promega, USA) in 10 mM NH_4HCO_3 /10%ACN, and digestion proceeds at 37°C for 16 h. The peptides are extracted following the protocol described in Thiagarajan et al. [110] and analyzed using an MALDI-TOF/TOF or LC-MS-MS. MS and MS/MS data is combined through the MS BioTools program (Bruker-Daltonics) to search the NCBIInr database using Mascot software (Matrix Science, London, UK), and protein identification is conducted according to the method specified in Qian et al. [111].

14.8 Conclusions

Screening for low-toxic and nontoxic antifouling compounds from marine organisms will remain at the frontier of research for the coming decades until a suite of very effective and environmentally friendly marine natural products are identified, commercialized, and applied as routine antifouling agents, due to the practical needs and huge market potential. Bioassay systems will play most critical and vital roles in screening efforts and have to be taken as top priority in antifouling screening research. Ideally, a battery of screening bioassays shall consist of both antimicrofouling and antimacrofouling assays with multiple target species for each group. And certainly, target species shall include both hard foulers and soft foulers.

In reality, to reduce operational costs and save time, high-throughput assays using microtiter plates shall be used as much as possible, particularly for preliminary screening assays, followed by more complex bioassay processes. In the near future, it is expected that molecular biomarkers (genes, proteins, receptors, or receptor system) will provide a better means to design more targeted bioassay systems, which may not only speed up screening process but also save time needed to conduct an environmental safety and mode-of-action study of identified chemical compounds because the molecular target is already known.

However, to develop a targeted bioassay (using molecular markers), we need to gain a much better understanding of:

1. Molecular mechanisms of spore and larval attachment and metamorphosis
2. Mode-of-action of antifouling compounds against settling propagules (how they act, how long it takes for a compound to reach the target, what they target)
3. Behavior of chemical compounds (synergistic or antagonistic interactions), accumulation, transportation, and transformation

4. Effects of the physical and chemical environment on chemical function, such as water flow dynamics, surface matrix, and pH
5. Effect of biological factors on compound function and behavior, such as biofilm development, microbial interaction and metabolites; responses of fouling organisms to compounds, ontogenetic susceptibility shift, and so on

14.9 Study Questions

1. Why do we need to screen for antifouling compounds from marine organisms?
2. What kind of compound would be an ideal antifouling compound with market potential in the future, why?
3. What are the pros and cons of using marine microbes as the source of antifouling compounds?
4. What characteristics would make a species desirable for antifouling bioassays?
5. Why do we need to study the mode of action of antifouling compounds?

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Chemically Mediated Competition and Host–Pathogen Interactions Among Marine Organisms

15

Marc Slattery and Deborah J. Gochfeld

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Abstract

Competition and pathogenesis are two important ecological processes in marine ecosystems. Competition defines interactions between individuals relative to the acquisition of limiting resources. This process includes the act of fouling, but for the purposes of this chapter, we will focus largely on competitive interactions between macroorganisms. Pathogenesis is the initiation and progression of

M. Slattery (✉)

Department of Pharmacognosy, The University of Mississippi, Oxford, MS, USA
and

National Center for Natural Products Research, The University of Mississippi, Oxford, MS, USA
e-mail: slattery@olemiss.edu

D.J. Gochfeld

National Center for Natural Products Research, The University of Mississippi, Oxford, MS, USA
e-mail: gochfeld@olemiss.edu

a disease in a host organism, and it has become recognized as an increasingly important process in marine ecosystems, particularly in the face of accelerating climate change and stress from anthropogenic stressors. There is fairly solid evidence that these processes can be mediated by allelochemicals and antimicrobials, respectively. Yet unequivocal proof that natural products are acting in an ecologically relevant manner, *in situ*, represents a major experimental challenge for marine ecologists. The goal of this chapter is to (1) provide an overview of these ecological processes, (2) single out particularly successful research techniques relative to these processes, and (3) distinguish marine natural products that have been identified as defenses against competitors and pathogens. This chapter will focus on sessile invertebrates and plants since their mechanisms for defending themselves against competition and pathogenesis are more likely to include the production of natural products. To date, there are several examples of extracts from marine plants and invertebrates that have demonstrated allelopathic and antimicrobial activity using a diversity of experimental methodologies. Highlighted are examples of metabolites shown to play a role in allelopathic interactions with algae, soft corals, and sponges, as well as compounds that display antimicrobial activity in algae, soft corals, and sponges.

15.1 Competition

Competition can be one of the most significant ecological processes in the structure and function of terrestrial and aquatic communities [1]. Competition is typically associated with the acquisition of limiting resources such as space, light, and/or food [2]. In marine communities, competition can be particularly intense between benthic organisms that are attached to the substrate, including algae, sponges, hard and soft corals, and tunicates. Competition has been further characterized as either occurring through contact with another organism (= “direct”) or as occurring across a distance (= “indirect”) [3]. In marine communities, indirect competition is often mediated through overgrowth/shading [4, 5], but it can also involve the use of toxic natural products [6]. Rice [7] first coined the term “allelopathy” to generically include any instance in which a natural product (= “allelochemical”) is released into the environment by an organism, where it either harms or aids another organism in the vicinity (i.e., a potential competitor). While this definition has been further refined with time, a persistent concern is proving whether allelopathy actually occurs in nature [8].

Allelopathic interactions in marine communities include the production of antifoulants that limit overgrowth and thus access to various resources, primarily by microorganisms; this is the subject of a separate chapter in this text (see ► [Chapter 14](#)). In addition, allelopathic interactions can occur between benthic macroorganisms via direct contact, when the allelochemicals are surface-bound, or via indirect interactions, when the compounds diffuse through the water column to a distant competitor. Despite reasonable field observations supporting potential allelopathic interactions,

there are few unequivocal experimental studies of chemically mediated competition in marine communities and even fewer that have characterized the natural products responsible. Here, we will provide an overview of those studies relative to several important sessile organisms and use the results to comment on the technical challenges of assessing allelopathic interactions in marine communities.

15.1.1 Algae

Macroalgae are important components of most marine ecosystems and are often effective competitors against other organisms. Phase shifts from coral- to algal-dominated communities throughout the Caribbean during the 1980s demonstrate the delicate competitive balance between these key constituents [9, 10]. For example, when the dynamics of space utilization by brown and red seaweeds and the coral *Oculina arbuscula* were examined at 12 reef habitats in North Carolina, across a 25-m-depth gradient, there was a strong negative correlation between algae and coral cover that appeared to be mediated by light preference of these taxa and by algal inhibition of coral recruitment [11]. Manipulative grazer exclusion/nutrient addition experiments further demonstrated that competition with seaweeds, through shading and scour, limits the distribution of corals on these temperate reefs. This study provides an excellent example of the subtle competitive interactions between algae and corals and the complexity of experimental design requisite to tease apart these factors.

Few studies have provided evidence for allelopathy in macroalgae; three important cases are reviewed here. Kuffner et al. [12] examined larval recruitment of the hard coral *Porites astreoides* and the gorgonian *Briareum asbestinum* in the presence of five species of algae and three species of cyanobacteria. The authors performed field surveys of three reefs in the Florida Keys to ascertain benthic cover of algae, cyanobacteria, sponges, corals, and suitable settlement substrata to assess potential competitors to larval coral recruits. They then constructed replicate larval recruitment chambers [12] that contained conditioned tiles (= control), tiles with an artificial aquarium plant (= mimic), or tiles with one of the algal or cyanobacterial species that were deployed in the field or in an aquarium. One hundred coral larvae were introduced to each chamber and allowed to settle for 4–9 days, at which point the percent survival, percent recruitment, and locations on the tiles were recorded. Their results demonstrated that all but one species of algae caused avoidance behavior or inhibition of recruitment by *P. astreoides* larvae and that *Lyngbya confervoides* and *Dictyota menstrualis* caused significant larval mortality. *Lyngbya majuscula* similarly reduced recruitment and survival of *B. asbestinum* larvae. Recent work has demonstrated that extracts of *D. pulchella* and *D. pinnatifida* affect larval survival of *P. astreoides* (V. Paul, personal communication 2009). While an actual allelochemical compound has not been isolated to date, given field data on the distributions of these algae and cyanobacteria, this research indicates that allelopathy may perpetuate current phase shift

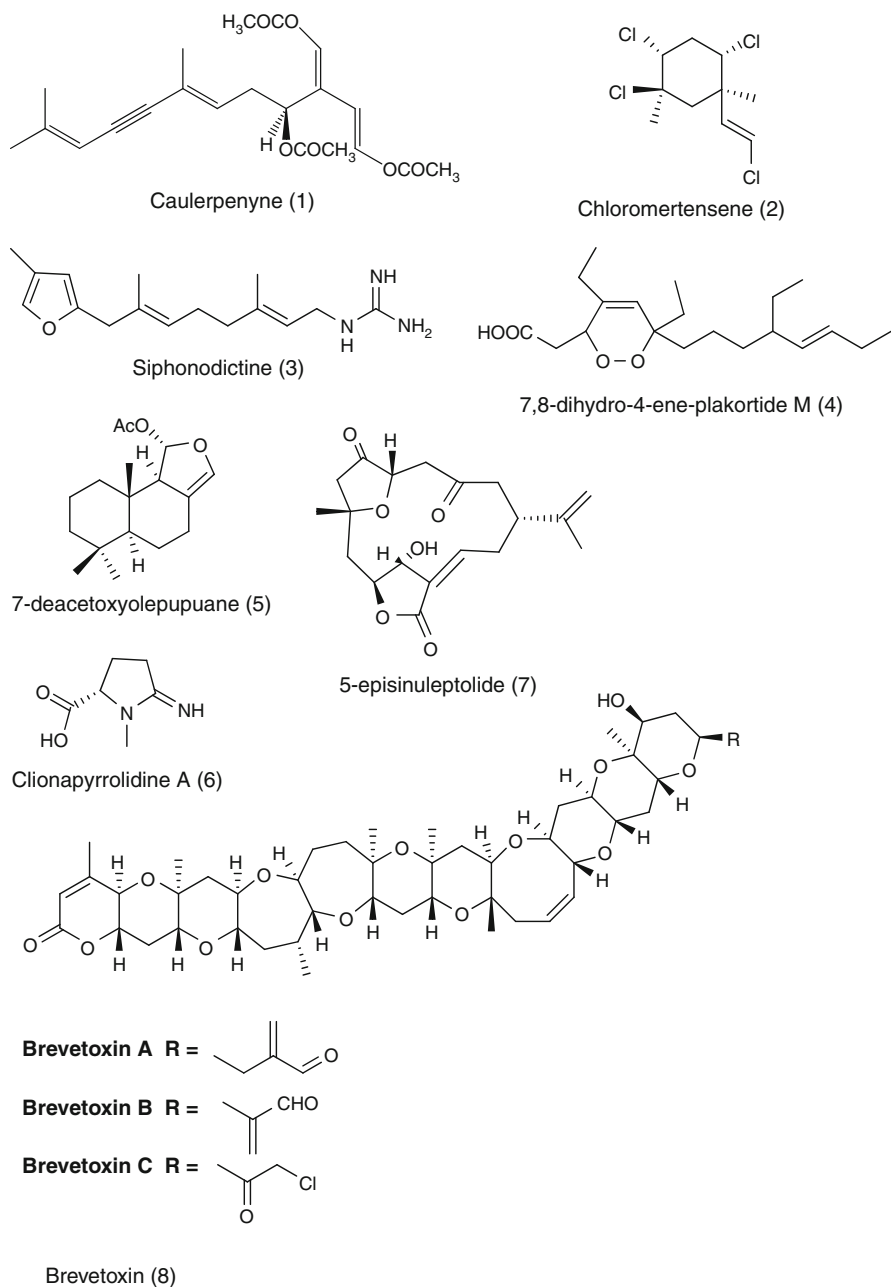


Fig. 15.1 Allelopathic natural products isolated from marine organisms

conditions on tropical reefs by inhibiting the ability of corals to settle and become established.

The Australian seaweed *Caulerpa racemosa* var. *cylindracea* has become invasive in the Mediterranean Sea where it has caused significant changes to the benthic communities [13] and physiological stress to the native seagrass *Cymodocea nodosa* [14]. Crude extracts of the invasive alga at 100 ppm and three known pure compounds at 10 and 1 ppm were exposed to leaf fragments of *C. nodosa* for 6 days under controlled laboratory conditions [15]. The leaf fragments were analyzed daily using pulse amplitude modulated (PAM) fluorometry to assess optimal quantum yield ($= F_v/F_m$), which can be considered a proxy for chlorophyll *a* content [16]. Only the crude extract and caulerpenyne (Fig. 15.1:1) at 10 ppm were found to significantly depress quantum yield and therefore photosystem function. While this study provides preliminary evidence for a *C. racemosa* allelochemical that inhibits the native seagrass *C. nodosa*, it suffers from many of the arguments used to criticize allelopathy [8]. Specifically, there is no supporting evidence from field manipulations to demonstrate that an allelochemical was responsible for the stress to *C. nodosa*, and if present, whether the metabolites were waterborne or surficial. There is also no analytical evidence to demonstrate that the compounds were tested at ecologically relevant concentrations; the activity at 10 ppm may be meaningless if caulerpenyne occurs at levels closer to the inactive 1 ppm. Finally, the absence of activity in two other compounds isolated from *C. racemosa*, and the lack of a bioassay-guided isolation approach, does not rule out additional additive and/or synergistic allelopathic compounds.

More compelling with respect to allelopathy in algae is the work of de Nys et al. [17]. They observed varying degrees of tissue necrosis in the sponge *Dictyoceratida* sp. the gorgonian *Isis* sp., and the soft corals *Sinularia cruciata*, *S. flexibilis*, *S. polydactyla*, and *Clavularia* sp. near the red alga *Plocamium hamatum* on the Great Barrier Reef, Australia. When in contact with the green alga *Chlorodesmis fastigata*, these species did not exhibit tissue necrosis. To assess potential allelopathic activity of this alga, the authors performed two manipulative field experiments. In the first experiment, they placed *P. hamatum* in contact and noncontact settings (5 and 30 cm distance) with the soft coral *S. cruciata*, and they tagged/monitored unmanipulated field “controls” to rule out handling effects; necrosis was assessed at 24 h, 48 h, and 14 days. The second experiment controlled for mechanical abrasion due to contact, by “painting” the algal metabolite chloromertensene (Fig. 15.1:2) onto artificial aquarium plants at a concentration of 2%, which is within the reported range of the metabolite in natural populations [18]. In both cases, contact with the metabolite resulted in tissue necrosis within 48 h, which provided strong evidence for allelopathic inhibition of the soft coral due to the algal monoterpene. However, the authors note that this response was not as extreme as when the soft corals were in contact with the algae, suggesting that there might be other important allelopathic compounds. In contrast to the study by Raniello et al. [15], this study was grounded in solid field observations and manipulative trials. However, the inclusion of a crude extract treatment would have been useful in this study.

15.1.2 Sponges

The functional roles of sponges on reefs, and their numerical dominance, make them some of the most important benthic taxa [19, 20]. In addition, sponges are one of the best-studied models in marine chemical ecology [21], producing a diversity of natural products [22]. Like algae, sponges must protect themselves from competition at the microscale (i.e., epibiosis) [23] and at the macroscale. Although there are more examples of allelopathy by sponges than by algae, many of the methodological challenges faced by phycologists exist for sponge researchers as well. There have been several field studies related to the distributions of marine invertebrates and sponges that demonstrate competitive dominance by chemically defended species [24, 25] or inhibition of settlement and/or metamorphosis near these species [26, 27]. One of the first attempts to address allelopathy on coral reefs focused on the sponge *Aka* (= *Siphonodictyon*) sp. from Palau [28]. This sponge burrows into coral heads leaving only an osculum, surrounded by dead coral tissue, to filter seawater for nutrients. The authors isolated the compound siphonodictine (Fig. 15.1:3) from the sponge and tested its effect at 10 ppm and 100 ppm in seawater in laboratory assays with the coral *Acropora formosa*. Within 30 min, they observed toxin-like effects of respiratory depression and tissue necrosis for the low and high doses, respectively. While these data are intriguing from the anecdotal point of view, this study suffers from methodological details. For example, the original field observations were made on the massive coral *Montipora* sp.; staghorn corals like *A. formosa* do not suffer from infestation by this burrowing sponge. Also, ecologically relevant concentrations of the metabolite were never tested, nor were concentrations within sponge mucus, which was identified as the likely “delivery system” of the compound. This is a model species that would benefit from a revised study using a more robust experimental design.

More recently, the crude extracts of 20 Caribbean sponges were tested against 3 species of Caribbean sponges that are fast overgrowers (*Tedania ignis*, *Lissodendoryx isodictialis*, and *Haliclona hogarthi*) and the extract of the North Carolina sponge *Aplysilla longispina* against the colonial tunicate *Diplosoma listerianum* [29]. The authors developed a novel assay approach that placed overgrowth species in the center of a 15 × 15 cm acrylic plate surrounded on opposing sides by either control or extract-treated Phytigel™ (see [29]). This provided the overgrowth sponges with the potential for lateral growth in any direction over a 3-week period, and it allowed the researchers to ascertain whether extract-treated gels were avoided (= allelopathic). Their results showed that only 7 of the 20 Caribbean sponge extracts inhibited overgrowth, while 3 sponges promoted overgrowth, and the rest had no effect. A separate test demonstrated that extracts of a subset of these sponges were stable in the gels for up to 3 weeks, so the authors concluded that their results indicate that allelopathy among sponges may not be widespread. Nonetheless, they do acknowledge that specifics of each of these extracts tested may account for false negatives in their dataset, and this study should be considered a conservative estimate of the degree of allelopathy in Caribbean sponges. This holistic project clearly demonstrates the potential

importance of allelochemical-mediated competition among sponges, and it should prove useful for testing hypotheses based on field observations and relative to the isolation of specific allelopathic compounds.

Porter and Targett [30] focused more specifically on a single species of Caribbean sponge, *Plakortis halichondroides*, and its interaction with the coral *Agaricia lamarcki*, in St. Croix, US Virgin Islands. Field surveys indicated that this sponge is common between 20 and 30 m depth, and when it occurs in contact with a coral, the coral exhibits signs of physiological stress about 40% of the time. Moreover, 14 species of coral, representing 8 of the 9 Caribbean coral families, were overgrown and killed by this sponge. The authors tested 11 hypotheses related to competition-mediated physiological stress as measured through changes in biomass and oxygen flux. They conducted manipulative field experiments including (1) noncontact scenarios, (2) contact with sponge exudate only, (3) direct contact with the sponge for 24 h, and (4) direct contact with the sponge for extended periods. The latter three treatments resulted in a significant depression of zooxanthellae density, chlorophyll *a* concentrations, and nitrogen mass, relative to controls. Likewise, oxygen flux, representative of net photosynthesis, was also depressed under “contact” conditions. This bleaching response approximated the observed responses of natural field interactions, and the fact that a physiological response could be generated by contact with the sponge exudate alone provided compelling evidence for an allelochemical. Interestingly, in a study of sponge-dominated marine caves in the Bahamas, *P. halichondroides* was separated from other species by clear substrate [31]. The water surrounding these sponges contained the metabolite 7,8-dihydro-4-ene-plakortide M (Fig. 15.1:4), and at ecologically relevant concentrations, this compound killed cells of a potential sponge competitor *Oscarella* sp. in the laboratory. *Plakortis* spp. produce many compounds of similar structure to 4, so it is possible that this or a related compound was responsible for coral tissue necrosis in the study by Porter and Targett [30].

To date, the strongest evidence for allelochemical interactions amongst sponges was generated on Guam, USA, where frequent overgrowth of the sponge *Cacospongia* sp., by the sponge *Dysidea* sp., was observed [32]. This overgrowth often resulted in *Cacospongia* sp. tissue necrosis but not reduction in the defensive metabolites of this species. The authors suspended natural concentrations of crude extracts from *Dysidea* sp. in agar solidified onto window screen and cable-tied these strips to branches of the *Cacospongia* colony in the field. Control strips were similarly prepared, but they contained the carrier solvent only, and these were attached to a neighboring branch of the same colony [32]. Approximately 80% of the tissue under the extract-treated agar strips was necrotic after 1 week, while necrosis under control strips was negligible. In a similar assay using the *Dysidea* metabolite 7-deacetoxyolepupane (Fig. 15.1:5) at ecologically relevant concentrations, they also observed a significant treatment response, but the tissue necrosis was only about half that of the crude extract, suggesting that there may be additive effects. The metabolite yields of *Dysidea* in contact with either *Cacospongia* or rock substrate did not differ, indicating that competition does not induce the production of the allelochemical. This study went on to assess the effects of

Cacospongia extracts on *Dysidea* metabolite production, but it found no significant differences between control and treatment groups. It also demonstrated that the allelochemical (Fig. 15.1:5) functions as a feeding deterrent compound against the predatory angelfish *Pomacanthus imperator*. This study is a solid model for future studies of allelopathy in marine systems; the use of field observations to generate testable hypotheses has produced a complete picture of the chemical interactions between two competitive species. The sole flaw of this study, the lack of a bioassay-guided approach to isolate additional allelopathic compounds, actually highlights a challenge faced by researchers studying competition in marine ecosystems. These processes tend to be quite slow, so viable bioassays might occur over temporal scales measured in weeks. To sequentially follow multiple chemical fractions, in a replicated manner, could literally take years of fieldwork. Thus, researchers often have to rely on a “best guess” based on the activity of related molecules and/or the concentration relative to the dry mass of the organism. Nonetheless, two recent papers have reduced the time needed to run an allelopathic assay. Sponge allelopathy against the coral *Diploria labyrinthiformis* was assessed using extracts incorporated into Phytigel™ molds [33]. Nine common bioactive Caribbean sponges were extracted, and volumetric equivalents were mixed into the gels and fixed to the surface of corals for 18 h. They used PAM fluorometry to assess impacts to symbiotic zooxanthellae photosystem function, which was indicative of stress. Although allelopathic metabolites were not identified, this process offers promise for future studies assuming the response to the allelochemicals is manifested in zooxanthellae productivity. A similar bioassay procedure was used to assess allelopathy by the burrowing sponge *Cliona tenuis* against the hard coral *Siderastrea siderea* [34]. They were able to follow a bioassay-guided approach to the bioactive compound clionapyrrolidine A (Fig. 15.1: 6) by limiting exposures to 24 h. While this paper lacked the field detail of the study by Thacker et al. [32], it demonstrates the apparent toxicity of their allelochemical and the potential implications for competition research.

15.1.3 Hard Corals

Scleractinian (= “hard”) corals are the primary reef-building components of tropical marine hard-bottom communities, and as such, they are often in contact and potentially in competition with other community constituents. Hard corals are known to utilize overgrowth, extracoelomic digestion, and/or “sweeper tentacles” to gain a competitive edge [4, 35], but at least two studies have addressed potential allelopathy in this group of benthic invertebrates. Competitive hierarchies between hard and soft corals were examined on the reefs of southern Taiwan [36]. The investigation was restricted to the study of natural interactions totaling 1,168 pairwise contacts characterized by either (1) the production of a dead margin, (2) overgrowth without tissue necrosis, or (3) stand-offs which lacked necrosis and overgrowth. Results of this broad field survey indicated that soft corals were typically subordinate to the scleractinians in this competitive network. Nonetheless,

the author noted at least eight interactions that appeared to represent allelopathy, and in all of these cases, soft corals were dominant to their hard-coral competitors. Allelopathic competition in the coral *Tubastraea faulkneri* was also studied on the Great Barrier Reef, Australia [37]. This laboratory-based study assessed the toxicity of *T. faulkneri* extracts against 12 species of scleractinian larvae at standard concentrations ranging from 10 to 500 $\mu\text{g ml}^{-1}$. These experimental concentrations were estimated to be 100–5,000 times lower than tissue levels. Larval mortality varied between the coral species, and there was no toxicity to conspecifics. Four indole alkaloids were isolated from *T. faulkneri*, but these were not assayed for allelopathic activity. Based on these data, the authors conclude that these compounds are released into the water column to prevent larval recruitment in the vicinity of *T. faulkneri*. While both these studies provide useful preliminary information, neither offers unequivocal proof that hard corals control competitors using allelochemical compounds.

15.1.4 Soft Corals

Like sponges, soft corals have also been the subjects of much interest relative to their chemical ecology, including studies regarding their competitive abilities [38]. Much of that work occurred on the Great Barrier Reef where soft corals are a spatial dominant of the benthic communities [39] and often interact with other soft and hard corals [5]. Some of the earlier experiments that addressed potential allelopathic effects of these soft corals were based on field observations of movement away from a competitor, stunted growth, tissue necrosis, and/or mortality. In some cases, there were responses in the absence of physical contact, suggesting that waterborne allelochemicals may have been involved [40]. However, field manipulations of soft corals into contact interactions suffered from poor experimental design. Specifically, the use of multiple contact treatments against individuals prevents attribution of the observed necrotic effects [41]. More recently, the role of local environmental factors on the competitive ability of two soft corals, *Clavularia inflata* and *Briareum stechei*, and a hard coral, *Acropora longicyathus*, was examined in all pairwise interactions [42]. These manipulative field experiments involved transplanting between an inshore and a midshelf reef, with appropriate back-transplant and nonhandled controls. Competitive endpoints included overgrowth, tissue bleaching and necrosis, and whole colony mortality. Their results at the inshore site gave a dominance pattern of *Briareum* > *Clavularia* > *Acropora*, while the midshelf site exhibited a reversal of dominance between *Clavularia* and *Acropora*. The authors hypothesized that nutrient enrichment, lower light, and predation at the inshore site may be responsible for the soft coral superiority there. While allelopathy was not specifically addressed in this well-designed field study, the responses observed argue for terpene-mediated competitive dominance and for future studies focused on this question. Later experiments by this group were designed to assess the mechanistic processes by which soft coral allelochemicals impact hard coral competitors. Toxic diterpenes were exuded into

the water column by the soft corals *Sinularia flexibilis* and *Lobophytum hedleyi* at concentrations of 5–20 ppm [43]. They found that at concentrations higher than 5 ppm, branchlets of the hard corals *Acropora formosa* and *Porites cylindrica* expelled their zooxanthellae and nematocysts. The authors concluded that these responses would reduce the corals' abilities to obtain nutrients and defend themselves, respectively, thus lowering their fitness in highly competitive environments. While the ecological relevance of the allelochemical concentrations might be questioned, this study nonetheless provides compelling insights into the mechanism of action of putative allelopathic metabolites.

Competition is not limited to interactions between disparate groups of organisms. Competitive dominance of the hybrid soft coral *Sinularia maxima* × *polydactyla* was observed over its parents *S. maxima* and *S. polydactyla* on the reefs of Guam [44]. A significant decline in the parent soft coral populations was noted over a period from 1994 to 2003, associated with an increase in the hybrid population. To determine whether contact-mediated competition might account for the differences in population dynamics, they assessed the outcome of 124 interactions between the hybrid and either parent in the field. After 3 weeks, 80% of these interactions resulted in tissue necrosis on the parent species (i.e., hybrid dominance), while 20% of the interactions were not resolved. A field assay, similar in technique to that described by Pawlik et al. [33], was conducted on these soft corals. However, tissue necrosis was used as an endpoint after 3 weeks of exposure to extract-containing gels. The parent soft corals and the hybrid all produced extracts that exhibited some degree of tissue necrosis to congeners, but not to conspecifics. Necrosis induced by the hybrids was on the order of 40–60% of the exposed tissue, while the parent extracts induced only 5–10% tissue necrosis. The length of this assay made it impractical to conduct a bioassay-guided isolation of the hybrid allelochemical. Nonetheless, recent assays with the isolated metabolite, 5-episinuleptolide (Fig. 15.1:7), indicate that this compound is partially responsible for the bioactivity attributed to the hybrid extract (Slattery, 2005).

Like tropical reefs, Antarctic benthic communities are also space limited and therefore highly competitive [45]. The soft coral *Alcyonium paessleri* appears to use contact-mediated allelopathy to compete with at least one space dominant sponge in McMurdo Sound [46]. Replicate soft corals and sponges were cemented individually into small flower pots and then moved to the field in contact and noncontact situations for 1 year. Tissue necrosis was not observed when *A. paessleri* was placed in contact with conspecifics, the soft coral *Clavularia frankliniana*, or four common sponges. However, a fifth sponge, *Mycale acerata*, exhibited significant tissue necrosis when in contact with *A. paessleri*. Interestingly, this sponge was a competitive dominant to the sponge *Kirkpatrickia variolosa* [45], which was a competitive equal to *A. paessleri* [46], suggestive of the competitive hierarchy feedback loops proposed by Jackson and Buss [6]. While a putative allelochemical from *A. paessleri* was not identified, it is possible that the cytotoxic metabolite 22-dehydro-7 β -hydroxy-cholesterol (which was a negative olfactory cue for soft-coral predators) might also have allelopathic properties. This compound, along with three other waterborne sterols, was collected in situ near *A. paessleri* colonies using

60 cc syringes [47]. A more elegant allelochemical collection device was developed and tested on soft coral exudates; this apparatus has the potential to further studies of allelopathic compounds released into the water column [48].

15.1.5 Others

Among the most obvious sessile invertebrates on tropical and temperate reefs are the colonial tunicates, and these individuals are often competitive dominants to other groups of benthic organisms [49]. Tunicates typically produce important natural products with defensive properties [22, 50], particularly related to the prevention of surficial fouling [51, 52]. However, most studies associated with tunicate-macroorganism competition seem to indicate that this process is mediated by overgrowth, not allelopathy [53, 54]. On Caribbean coral reefs, the zoanthid *Palythoa caribaeorum* is a dominant member of the benthic community. With some of the fastest growth rates (2.5–4.0 mm/day) recorded for anthozoans, this organism overgrows virtually every other benthic invertebrates, placing itself at the top of the competitive hierarchies in these communities [55]. This species also produces a diversity of natural products, including palytoxin; however, the use of these as allelochemicals has not been evaluated. In contrast, soft bottom communities are often dominated by infaunal worms, including the terebellid polychaete *Thelepus crispus*. This species produces brominated aromatic metabolites that deter the recruits of competitive nereid polychaetes *Nereis vexillosa* [56]. Moreover, these compounds are nonpolar and thus likely remain in the sediment around the polychaete burrows for long periods of time.

Two additional papers demonstrate the complexity of competitive interactions within marine ecosystems. Up to this point, all of the examples of interactions have focused on macroorganisms in benthic communities. While antibiotic-mediated competition between microbes is relatively well accepted [57], the question of competition between microbial and animal decomposers for benthic food falls represents a unique approach to studies of allelopathy [58]. The authors used traps baited with either fresh or microbe-laden (= 48 h colonization in flowing seawater) carrion to assess attractiveness to scavengers; the former bait was 2.6 times more attractive to scavengers. The stone crab preferred the frozen carrion 2.4 times more often than the microbe-laden carrion. In addition, organic extracts of microbe-laden carrion contained noxious extracts that repelled many of the scavengers in the system. While this paper failed to identify the specific metabolites produced by the microbes, this unique field and laboratory study demonstrated a previously underappreciated ecological interaction.

Allelochemical-mediated competition within planktonic communities has also been studied [59]. Specifically, the authors studied the dinoflagellate *Karenia brevis*, which is responsible for monospecific blooms that cause red tide conditions in the Gulf of Mexico. They compared the growth of *K. brevis* with 12 co-occurring phytoplankton species under monoculture and mixed culture laboratory conditions. In nine of the mixed culture conditions, *K. brevis* inhibited growth rates relative to

growth in monocultures, while *Rhodomonas lens* growth was enhanced, and two additional species were unaffected. In a follow-up experiment, the extracellular filtrates of *K. brevis* were collected, extracted, and introduced to monocultures of the competitive phytoplankton. Six of the nine species were inhibited by the filtrate and lipophilic extracts of *K. brevis*, supporting an allelopathic mechanism for bloom characteristics. In the final competition experiment, ecologically relevant concentrations of brevetoxin (Fig. 15.1:8) were introduced to monocultures of the competitive phytoplankton. This compound only caused weak inhibition in one species, *Skeletonema costatum*, although it did induce autoinhibition in *K. brevis*. This study demonstrated appropriate methodologies for dealing with allelopathy in planktonic organisms, and it provides compelling evidence for multiple allelochemicals within *K. brevis* that likely act somewhat selectively and/or in an additive manner.

15.2 Pathogenesis

In contrast to competition, the importance of pathogenesis as an ecological phenomenon within marine ecosystems has only recently received much attention. In recent decades, reports of diseases affecting populations of marine organisms have increased dramatically worldwide [60–63]. This is especially true for corals, but diseases also threaten algae, seagrasses, sponges, gorgonians, molluscs, crustaceans, sea urchins, fishes, and marine mammals [61, 64]. Not only is the rate at which emerging diseases are being discovered escalating but also the number of host species and geographic ranges of diseases has also been increasing. Diseases affecting natural populations threaten biodiversity, resilience, and the ecological balance of communities, as well as the ecological services they provide to humans [65].

Mass mortalities resulting from infectious disease outbreaks (epizootics) have resulted in major changes in community structure of marine ecosystems in recent years. For example, during the 1980s, a waterborne disease of the long-spined sea urchin *Diadema antillarum* spread rapidly throughout the Caribbean, reducing the abundance of this important herbivore by nearly 99% on most Caribbean reefs [66]. This keystone species served a major ecological role by removing macroalgae from Caribbean reefs, and in its absence, algae overgrew reef surfaces and inhibited the survival and settlement of corals, resulting in a phase shift from coral-dominated to algal-dominated reefs Caribbean-wide [9]. This alteration of community types has remained stable for nearly three decades. Unfortunately, at the time, our knowledge of marine diseases was relatively minimal and the pathogen was never identified, nor were appropriate samples collected and preserved for future analysis.

Why have diseases increased to such unprecedented levels? Increased anthropogenic stress in near-shore environments, overfishing, and environmental conditions associated with global climate change have all been implicated as contributing to increased disease levels [60, 61, 67–69]. It is unknown whether the emergence of these diseases is due to the introduction of novel pathogens [61, 70], changes in virulence or range of existing pathogens [71–73], or changes in host susceptibility

[60, 74]. Overall declines in coral reef communities may also play a role, as reduced species and genetic diversity due to declining population sizes may increase susceptibility to emerging infectious diseases [75]. Understanding diseases in marine ecosystems is increasingly important given that a large proportion of the world’s population lives near the coast; this need is particularly acute where societies are closely tied to and depend upon coral reefs for their economic and social well-being.

15.2.1 Coral Diseases

Due to their high profile in the public eye, diseases of scleractinian corals are by far the best described in the marine environment, and new diseases are reported with increasing frequency in an expanding number of hosts on a global scale [63, 76, 77]. Coral disease has emerged as a serious threat to coral reefs worldwide and a major cause of reef deterioration [67, 78]. Although our understanding of coral diseases still lags far behind those of terrestrial wildlife, several lessons can be learned from research accomplishments to date, so we will use this important marine functional group as a case study for disease dynamics and resistance mechanisms.

15.2.1.1 Pathogenesis

Disease transmission, onset, and progression are the result of complex interactions between the host, environment, and pathogen, and all must interact in a precise way for disease to occur. For example, in *Vibrio*-induced coral bleaching, the mere presence of the *Vibrio* bacterium associated with the coral host is not sufficient to cause disease. Adhesion and ingress of the bacterium into the coral also requires elevated seawater temperatures [79]. Thus, understanding coral disease dynamics is difficult due to this complex interplay between both abiotic and biotic interactions. Moreover, just like in human host–pathogen transmission, additional species may act as vectors of disease in marine environments [80].

The frequent association of abundant *Vibrio* spp. with diseased coral tissues has led some researchers to question whether they act as primary pathogens for certain diseases or whether they are more opportunistic, colonizing previously compromised hosts [81, 82]. *Vibrio* spp. are abundant and relatively nonselective, so they could be opportunistic [83], but so far, no evidence directly supports this hypothesis, and there is no evidence from molecular screening studies that *Vibrio* spp. found associated with diseased tissues are pathogenic, or that only compromised hosts are infected.

15.2.1.2 Etiology

Nearly 30 coral diseases have been described from reefs across the world in recent years [77, 78], although only a handful of causes (etiologies) have been elucidated. To date, Koch’s postulates have only been fulfilled for five coral diseases (see Table 15.1). Koch’s postulates represent the gold standard for the verification of

Table 15.1 Etiology of coral diseases for which Koch's postulates have been fulfilled

Disease	Species affected	Geographic region	Pathogen	Vector	Bioactive extracts/ compounds tested
White band disease-II	<i>Acropora</i> spp.	Caribbean	<i>Vibrio charchariae</i> (= <i>V. harveyi</i>) [192, 200]	–	–
White plague-II	30+ hard coral	Caribbean	<i>Aurantimonas coralicida</i> [201]	–	Pathogen tested against extracts from 18 Caribbean corals ([202], Gochfeld, unpublished data 2009) and three Hawaiian corals [117]
White pox disease	<i>Acropora palmata</i>	Caribbean	<i>Serratia marcescens</i> * [94]	–	Pathogen tested against extracts from 18 Caribbean corals ([202], Gochfeld, unpublished data 2009) and three Hawaiian corals [117], mucus and bacteria from <i>Acropora palmata</i> [122]
Aspergillosis	10+ gorgonian	Caribbean	<i>Aspergillus sydowii</i> [70, 181]	African dust, or terrestrial runoff [182, 183]	Pathogen tested against extracts from Caribbean gorgonians [135, 136, 185, 188], mild activity against julieannafuran from <i>Gorgonia ventalina</i> [71]
Bacterial bleaching	<i>Oculina patagonica</i>	Mediterranean	<i>Vibrio shilonii</i> (= <i>V. shiloi</i>) [203, 204]	Fireworm <i>Hermodice carunculata</i> [205]	Pathogen tested against extracts from 18 Caribbean corals ([202], Gochfeld, unpublished data 2009) and three Hawaiian corals [117]
Bacterial bleaching	<i>Pocillopora damicornis</i>	Indo-Pacific	<i>Vibrio coralliilyticus</i> [109]	–	Pathogen tested against extracts from 18 Caribbean corals, ([202], Gochfeld, unpublished data 2009) and three Hawaiian corals [117]

(continued)

Table 15.1 (continued)

Disease	Species affected	Geographic region	Pathogen	Vector	Bioactive extracts/ compounds tested
White syndrome	20+ hard coral	Indo-Pacific	Two new <i>Vibrio coralliilyticus</i> strains + four other <i>Vibrio</i> spp.* (Note: different pathogens affected different coral species) [83]	–	–

*Tested at concentrations exceeding those likely to be found in the marine environment

Koch's postulates represent a procedure proposed by Robert Koch in the late 1800s [206] to verify that a presumed microbial pathogen is the actual cause of a particular disease. Under these rules:

- The putative pathogen must always be found associated with a particular disease.
- The putative pathogen must be isolated from the disease state and grown in pure culture under laboratory conditions.
- The pure culture of the putative pathogen must reproduce the disease when inoculated into or onto a healthy organism.
- The putative pathogen must be reisolated from the newly diseased organism and identified as the same putative pathogen.

Satisfaction of Koch's postulates is difficult under the best of circumstances, but particularly so when the host is a marine organism since (1) less than 1% of known marine microbes have been successfully cultured under laboratory conditions. For the most part, we do not understand the specific biotic and abiotic conditions to which these organisms are exposed, and these conditions have rarely been successfully duplicated in the laboratory. (2) For a particular microorganism to cause pathogenesis to a particular host, additional factors may be required, such as the presence of specific other microorganisms (e.g., as in the polymicrobial black band disease), aspects of seawater chemistry, temperature, light, or metabolites produced by the host, symbiont, or microbial associates. (3) In most cases, even those for which Koch's postulates have been performed, the natural mode of infection of a pathogen is not known; hence, exposing the intact healthy host to a slurry of bacteria in an aquarium may have little relevance to the real world. (4) Likewise, the concentration of pathogen used for inoculation in laboratory experiments may be far greater than a host would ever be exposed to in nature. (5) Pathogenesis may only occur when a host's immune system is already compromised by other pathogens or other types of environmental stressors, following predation or another type of injury, or when the host's physiological condition is more susceptible (e.g., during periods of rapid growth or reproduction). (6) Natural transmission of the pathogen may require an intermediate host or vector rather than through the water column. (7) Reisolation of the pathogen from the site of the new infection cannot necessarily prove whether the pathogen was not there prior to inoculation or occurred in the surrounding water. (8) Marine invertebrates, particularly sponges and corals, are relatively simple organisms. The signs or symptoms that can be seen (at least by the human eye) are relatively few but may in fact represent responses to many different types of conditions, pathogens, or other stressors. Therefore, even if a putative pathogen is identified using Koch's postulates, it does not mean that only that pathogen is responsible for a particular response. More than one pathogen may cause the same response in a given host. (9) Through host–environment interactions, it is highly likely that pathogens may cause different signs or symptoms in different individual hosts or in different species of hosts.

disease etiology; however, fulfilling Koch's postulates requires the ability to culture the pathogen in the laboratory, which may not be possible for many marine diseases [84]. Several other hurdles in the characterization of disease etiologies exist [85]. For example, corals can only exhibit a limited range of symptoms that a human observer can visually identify; therefore, it is likely that multiple types of etiologies may result in the same signs in a coral. The converse is also a problem; any given pathogen or abiotic stressor may cause multiple signs in corals. This could vary depending upon the coral host genotype, zooxanthellae clade, associated microbial community or interactions among any of these factors.

In the past five years, numerous new coral diseases have been described, particularly from the Indo-Pacific region, and our knowledge of their etiologies has advanced rapidly. Three new diseases were reported from the Great Barrier Reef, Australia [86]: skeletal eroding band caused by the protozoan, *Halofolliculina corallasia*; a ciliate disease called brown band disease; and white syndrome, a collective term for disease resulting in tissue loss. White syndrome infections in certain coral species in Palau, the Great Barrier Reef, and the Marshall Islands were found to be caused by six different strains of pathogenic *Vibrio* spp. [82]; these pathogens were shown to cause infection and were identified at the site of infection using molecular methods.

Other etiologies are more difficult to confirm. Dark spot syndrome (DSS) in corals from American Samoa and Hawaii was found to be associated with endolithic fungi [87]. This was also found to be the case for DSS in the Caribbean coral *Siderastrea siderea* but other unidentified endolithic organisms were found associated with DSS in *Agaricia* sp. [88]. Due to the endolithic nature of these fungi, fulfilling Koch's postulates is unlikely. A new bacterial strain *Thalassomonas loyaeana*, isolated from white plague in *Favia fava* from the Red Sea, was found to infect the coral in laboratory experiments, but only in the presence of a filterable factor in the water, and reisolation of the pathogen was not performed [89, 90]. Black band disease (BBD), the first coral disease reported, consists of a polymicrobial consortium, the components of which may vary with environmental conditions [91]; due to this variability, it will likely be impossible to fulfill Koch's postulates for all possible combinations.

15.2.1.3 Geographic Variability

In the Caribbean, coral disease has been implicated as a major factor contributing to the decline of coral reefs, resulting in apparent ecological phase shifts from coral- to algal-dominated ecosystems [9, 76]. An outbreak of white band disease in the 1980s killed acroporid corals throughout the Caribbean [92, 93], and an outbreak of white pox disease in the Florida Keys reduced the cover of the dominant *Acropora palmata* by over 70% between 1996 and 2002 [94]. Until recently, Indo-Pacific corals were believed to be relatively immune to disease; however, it is now apparent that coral diseases are major problems on Indo-Pacific reefs as well [77]. Although coral disease research in the Indo-Pacific is in its infancy, there are clear signs that diseases are emerging as a serious threat to these reefs. For example, a substantial increase in white syndrome has been observed on the Great

Barrier Reef [86]. Coral diseases have also been reported from Philippines [95], American Samoa [96], Marshall Islands [83], Marianas Islands [97], main Hawaiian Islands [98], and even from comparatively pristine areas such as the Northwestern Hawaiian Islands [99] and Palmyra Atoll [100].

15.2.1.4 Environmental Stressors

Natural and anthropogenic stressors have been implicated in the increased incidence and prevalence of marine diseases. Climate change, particularly elevated seawater temperature, may influence pathogenesis, either by reducing coral resistance or by increasing the growth and virulence of coral pathogens [60, 68, 72, 101]. For example, there is a significant relationship between the frequency of warm temperature anomalies and outbreaks of white syndrome on the Great Barrier Reef [102], and an outbreak of white plague following a thermally induced bleaching event on reefs in the US Virgin Islands caused an average of 51.5% loss in coral cover [103]. BBD also appears to be affected by water temperature, with distinct seasonal increases in disease prevalence on both Caribbean and Indo-Pacific reefs [104, 105]. Bacterial bleaching of *Oculina patagonica* is restricted to summer temperatures [106]. However, not all coral diseases are affected by thermal stress. For example, although there was seasonality in the prevalence of DSS in the Bahamas, this seasonality was not directly related to seawater temperature [107]. Nonetheless, the virulence of certain pathogens does increase at higher temperatures [72, 108, 109], and elevated temperature as expected with climate change predictions may facilitate the expansion of a pathogen's ecological niche [73].

Anthropogenic impacts on coastal areas are increasingly reducing the water quality on coral reefs, with evidence of direct negative impacts on coral health and of interacting effects with pathogens. Experimental studies have demonstrated that nutrient enrichment significantly increases coral mortality and the severity of yellow band disease [110], as well as the rate of progression of BBD [111], and addition of dissolved organic carbon caused coral pathologies similar to band diseases [112]. Correlative data suggest that disease prevalence increases with exposure to anthropogenic stressors, including nutrients [74, 113]. Both BBD and white plague type II were significantly more prevalent on reefs closest to sewage effluent in the Virgin Islands [114]. However, the high prevalence of coral diseases at relatively pristine sites [99, 100, 107, 115, 116] argues against a direct role of human disturbance in all diseases. In addition to nutrients, sediment from terrestrial runoff may serve as a potential reservoir for opportunistic pathogens of corals [77].

Sewage can also bring human enteric pathogens into the sea [94]. These organisms can survive in the ocean, have been isolated from the surfaces of corals, and should therefore be considered potential pathogens to marine organisms. Protection from these potential pathogens may be particularly important in near-shore habitats that might be more susceptible to leaching or spills. In assays testing the antibacterial activity of three Hawaiian corals, the highest levels of inhibitory activity were against the human enteric bacteria *Serratia marcescens*, *Clostridium perfringens*, and *Yersinia enterocolitica* [117]. *Clostridium perfringens* and

other enteric bacteria have been found within the surface mucus layers of several species of corals in the Florida Keys [118]. Since coral diseases have typically been reported more frequently from reefs with higher levels of human activities, these fecal pathogens may represent risk factors associated with coral disease.

15.2.1.5 Susceptibility

Differential susceptibility to disease has consistently been found among coral genera. In the Caribbean, the genus *Acropora* is selectively targeted by certain diseases [76], and in the Indo-Pacific, disease prevalence appears to be greatest among acroporids, poritids, and pocilloporids [86, 95, 99]. Intraspecific variability has also been observed, with diseased colonies found immediately adjacent to unaffected conspecifics [107, 117]. The fact that affected genera, species, or colonies (individuals) occur adjacent to unaffected ones indicates a high degree of variability in resistance to infection. Whether they originate from the host coral, zooxanthellae symbionts, or microbial associates, differences in levels of defenses within and between coral species and colonies and from different locations may help explain patterns of disease occurrence on reefs.

15.2.1.6 Resistance

Corals employ a suite of defense mechanisms to rid themselves of sediment, settling organisms, and potential pathogens, including mucus, phagocytic cells, enzymes and other proteins that are upregulated in response to various stressors, and antimicrobial chemical defenses [64, 76, 117, 119, 120]. Differences in types and levels of defense vary among genera, species, and even at the level of the individual colony [117]. These differences might enable particular populations, species, or genotypes to have an advantage over others in resisting invasion by pathogens [121]. To date, few studies have specifically examined mechanisms of defense against pathogens, yet an understanding of mechanisms of disease resistance in corals is essential to our understanding of patterns of disease prevalence and virulence.

It has been suggested that coral mucus-associated bacteria may act as a first line of defense in the protection of corals and may help prevent infection by occupying niches on the coral surface and tissues and/or by producing antimicrobial compounds, possibly as allelopathic defenses against potential competitors [120, 122–124]. These natural microbial communities preferentially utilize carbon sources in the mucus for their own metabolism [125]. Natural coral-associated bacterial communities have been shown to change in response to environmental stress, including pathogenesis. For example, there was a shift in the mucus-associated bacterial community on *Acropora palmata* following bleaching; there was a decline in the natural complement of bacteria, many of which exhibited antibacterial activity and an increase in *Vibrio* spp. [122]. It was concluded that this could indicate an environmentally induced shift away from beneficial bacteria in the healthy host, and that variability in the protective qualities of coral mucus could allow the emergence of disease. In addition, chemical compounds produced by corals or their microbial

associates can also function as attractants to certain bacteria [117], which may represent a mechanism by which pathogenesis is initiated or by which the natural coral-associated microbial community can be maintained.

Chemical defenses in sessile soft-bodied organisms provide protection from predators, competitors, pathogens, and fouling organisms [126–129] and are necessary for the survival of these species. Site-specific variability in chemical defenses may result from a variety of abiotic and biotic factors, including light [130, 131], temperature [132], predation pressure [133, 134], competition [125], or pathogens [71, 117, 135, 136]. By comparison with the soft-bodied invertebrates, there have been fewer investigations of chemical defenses in scleractinian corals. This is likely due to a combination of conservation concerns, since most corals are listed as threatened or endangered species in many countries, and the technical difficulties of working with scleractinian corals. The presence of antimicrobial chemical defenses has been proposed as a potential mechanism of disease resistance in scleractinian corals [76, 119], but few studies have tested this directly.

In one of the earliest studies on coral chemical defenses, antimicrobial activity was documented in aqueous extracts of at least one colony from 37 of 55 species of Australian corals [137]. In another study on Australian corals, extracts from 100 coral species inhibited the growth of a marine cyanobacterium, and extracts from eight species inhibited the growth of marine bacteria [138]. These studies used the standard disk diffusion assay to assess the presence of antimicrobial activity. In this assay, a lawn of the test microbe is grown on an agar plate, and extract is added to a paper disk, which is placed on the lawn. Antimicrobial activity is observed as a zone of inhibition surrounding the disk in which microbial growth was inhibited. Although still widely used, and one of the only assay options for extracts with limited solubility in aqueous growth media, this assay has limitations. First, it requires that the extract be able to diffuse out of the disk and into the growth media at a rate that is uniform and relevant to microbial growth. Second, assay duration needs to be carefully considered since initial inhibition may be masked by later growth. Third, the concentration of extract added to the disks likely has little relevance to the concentration found in the organisms themselves. These two studies also assessed antimicrobial activity using a single standard concentration of extract, but neither compared this to the concentration of extracts in the corals themselves.

Coral eggs have also been evaluated for the production of antimicrobial chemical defenses, but extracts of eggs from only one out of 11 coral species inhibited growth of only three out of 94 bacterial strains [139]. The Indo-Pacific coral, *Pocillopora damicornis*, rapidly (1 min) produced antibacterial activity in response to mechanical stress [140]. They added cultures of *Vibrio coralliilyticus*, the pathogen that causes bacterial bleaching in *P. damicornis*, to seawater in which a coral had been stressed, and the released antibacterial activity in the seawater killed the pathogen. Of the several bacterial strains tested, the greatest antibacterial activity was observed against this natural pathogen. The Caribbean coral *Siderastrea siderea* also exhibits antibacterial activity against ecologically relevant marine bacteria using the disk diffusion assay [107]. More recently, a liquid growth assay was used to demonstrate that aqueous extracts from several species of

Caribbean corals, and three species of Hawaiian corals exhibit antibacterial activity against a panel of bacteria including known coral pathogens, potential pathogens from human waste, and bacteria isolated from the surfaces of Hawaiian corals [117]. This assay was performed in 96-well plate format, and natural concentrations of extracts were added to wells of bacterial cultures to assess their ability to inhibit bacterial growth. To date, the only natural products isolated from hard corals known to have antibacterial activity to potential ecologically relevant bacteria (i.e., anthropogenic *Escherichia coli*) are montiporic acid A and B [141]. Interestingly, the former compound performs multiple ecological roles, also acting as a feeding attractant to the coral specialist mollusc *Drupella* sp. [142].

Selectivity is a hallmark of antimicrobial activity in corals [107, 117, 137, 140]. This selectivity may be adaptive if it facilitates the development or maintenance of the coral's natural microbial community. Instead, selection to inhibit only those organisms that might be detrimental to coral health should be favored. The presence of antimicrobial activity in various coral extracts suggests that corals may be able to regulate, to some extent, the microbial communities that are associated with their surfaces.

Antibacterial activity also varies by coral condition. Concentrations of specific chemical components in extracts from *Siderastrea siderea* vary with tissue condition (healthy colonies vs. healthy and diseased tissues on colonies with DSS), reflecting changes in levels of infection of individual colonies [107]. When healthy tissues on colonies of *Montipora capitata* affected by *Montipora* white syndrome (MWS) were compared to those from their nearest healthy neighbors (controls), control extracts exhibited significantly greater antibacterial activity against *Yersinia enterocolitica*, and there was a trend toward this pattern against six other bacterial strains, suggesting that higher levels of antibacterial activity in control corals may protect them from pathogens and may help explain why these colonies remain disease free on a reef with other infected colonies [117]. Within colonies affected by MWS, diseased tissues had significantly greater antibacterial activity against *Aurantimonas coralicida*, and there was a trend toward this pattern against five other bacterial strains. This could result from induced defenses in diseased tissues in response to pathogen challenge.

15.2.2 Algae/Seagrass Diseases

Seagrass pathogenesis causes dramatic and long-lasting effects within regional ecosystems. An outbreak of eelgrass wasting disease nearly eradicated populations of the eelgrass *Zostera marina* from North America and Europe in the 1930s, with periodic recurrences in the intervening decades [143]. The zoosporic fungus *Labyrinthula zosterae* was identified as the etiologic agent of this disease [144], and an unidentified congener has been attributed to the mortality of the seagrass *Thalassia testudinum* [145]. *Labyrinthula* spp. are ubiquitous in coastal marine habitats, but only periodically do they become pathogenic, and the reasons for this are not clear, but they may be associated with other environmental stressors reducing overall seagrass health, and therefore resistance.

Marine algae are also susceptible to disease. Red spot disease affecting the commercially important Japanese kelp *Laminaria japonica* is the result of a bacterial infection, although the identity of the pathogen remains in question [146]. The kelp *Nereocystis luetkeana* suffers from a bacterial infection known as white rot disease, caused by *Acinetobacter* sp. [147]. “Raisin disease” in *Sargassum* spp. is caused by a fungal infection of *Lindra thalassiae* [148], and other fungal infections have afflicted the commercially cultivated red algae *Porphyra* spp. in Japan [149]. Coralline algae are also susceptible to disease. The most common, coralline lethal orange disease, affects a diversity of crustose coralline algal species worldwide; to date, the bacterial pathogen has not been identified [150]. A coralline white band syndrome also affects coralline algae in the Caribbean, causing extensive mortality [151].

Antimicrobial activity is widespread in marine plants. Using a combination of disk diffusion assays and liquid growth assays to test extracts from 49 Caribbean marine algae and three seagrasses for antimicrobial effects against five ecologically relevant marine microbes, 90% of extracts were active against at least one microorganism, and 77% of extracts were active against two or more [152]. In the same assays, comparable levels of activity were observed among 54 species of Indo-Pacific marine algae and two species of seagrasses [153]. A more targeted assessment of antifungal activity in seagrasses from Florida demonstrated that four out of five species selectively inhibited the growth of fungi, including the seagrass pathogen *Lindra thalassiae* [154]. In addition to identifying antifungal activity in whole tissues and organic extracts, this study demonstrated that oxidative stress signaling pathways are also incorporated into the seagrasses’ defense against fungal infection [154].

Phenolic metabolites (including condensed tannins) represent the major group of secondary metabolites in seagrasses, and their proposed ecological activities include antipredator and antimicrobial defenses [155]. Infection by the pathogen *Labyrinthula zosterae* induces an increase in phenolic production in *Zostera marina*, even in areas distant from the site of infection, suggesting that the induced response is systemic [156]. In particular, caffeic acid (Fig. 15.2: 9) increases in response to infection with *L. zosterae* and exhibits antimicrobial activity against the pathogen [157]. Gallic acid (Fig. 15.2: 10) concentration increased by 250% following infection by *L. zosterae*, but its ability to inhibit the growth of the pathogen has not yet been established [156]. In the seagrass *Thalassia testudinum*, there is also evidence that phenolic levels increase in blades infected with the pathogen *Labyrinthula* sp.; however, this does not appear to be induced by the infection per se. Instead, this was considered pseudoinduction, a result of compounds accumulating in a localized region of the blade as the lesion inhibited the flow of resources within the blade [145]. Thus, unlike induced responses to pathogenesis, changes in levels of phenolics in *T. testudinum* in response to infection are unlikely to be adaptive [145]. In addition to phenolics, *T. testudinum* produces the flavone glycoside 7-O-beta-D-glucopyranosyl-2"-sulfate (Fig. 15.2:11), which provides antifungal protection [158].

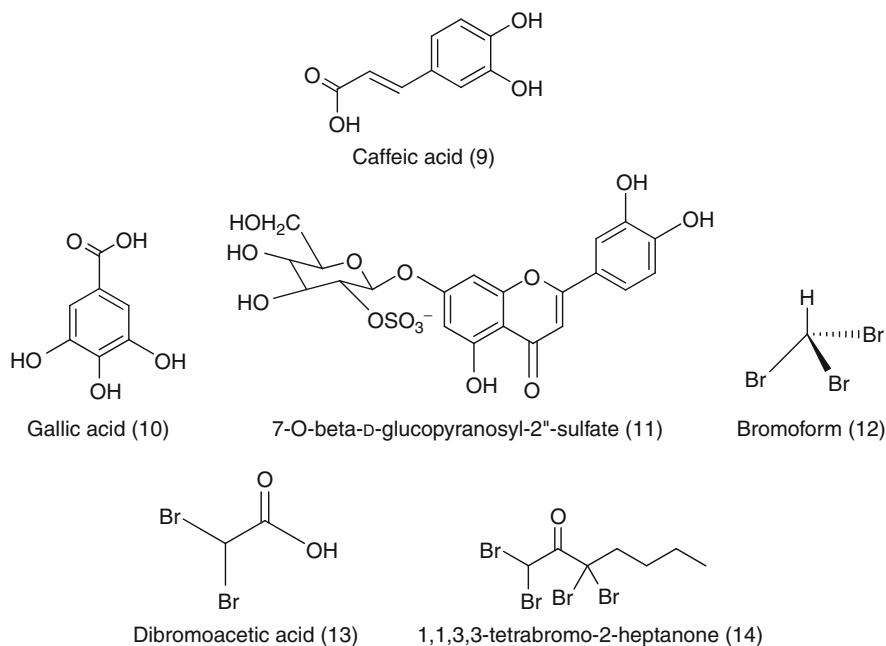


Fig. 15.2 Antimicrobial natural products isolated from marine algae and seagrasses

The red alga *Asparagopsis armata* exhibits antibacterial activity against ecologically relevant *Vibrio* spp. and biomedical bacteria [159]. In this species, the antibacterial compounds are bromoform (Fig. 15.2:12) and dibromoacetic acid (Fig. 15.2:13), both of which are released into the water column and may thereby interact with bacteria prior to settlement [159]. When *A. armata* is cultured in media without bromine, higher densities of epiphytic bacteria grew on algae that did not produce these brominated compounds. The low level of fouling observed on the Swedish red alga *Bonnemaisonia hamifera* is due to the antibacterial compound 1,1,3,3-tetrabromo-2-heptanone (Fig. 15.2: 14), a poly-halogenated 2-heptanone [160]. This compound was tested at natural surface concentrations against 18 bacteria isolated from red algae and exhibited selective antibacterial activity. In addition, when applied to gels and deployed in the sea, natural surface concentrations of this compound reduced overall bacterial growth relative to controls [160]. The red alga *Delisea pulchra* produces halogenated furanones, which, at natural concentrations, prevents surface bacterial colonization by inhibiting bacterial quorum sensing [161].

15.2.3 Sponge Diseases

In contrast to corals, diseases of sponges were documented as early as the 1930s, when disease outbreaks devastated the commercial bath sponge industry in the

Caribbean and later in the Mediterranean [162]. In the past few years, reports of sponge diseases have reemerged across the globe. In only a few cases have the etiologic agents been identified. Tissue necrosis in *Geodia papyracea* from Belize resulted from the sponge's own symbiotic cyanobacteria multiplying faster than the host could control their numbers under thermal stress [163]. A spongin-boring alpha-proteobacterium was identified as the etiologic agent of disease in *Rhopaloeides odorabile* from the Great Barrier Reef through the fulfillment of Koch's postulates [164]. Various other bacteria [165], including those that specifically attack structural spongin fibers [166], fungi [167], and cyanobacteria [168], have also been postulated as sponge pathogens, although these have not been confirmed. Recently, the disease *Aplysina* red band syndrome (ARBS) was described from the Bahamas, where it affected approximately 10% of *Aplysina* spp. rope sponges [168]. This disease manifests as a red band composed of filamentous cyanobacteria surrounding a necrotic lesion that becomes colonized with algae. ARBS is easily transmitted via sponge–sponge contact. ARBS reduces sponge growth and weakens the sponge skeleton, which often breaks at the site of the lesion.

Sponges produce a diversity of secondary metabolites that play important roles in their survival [32, 127, 169] and provide an impressive source of pharmacologically active molecules [170–172]. Some of these compounds are believed to be produced de novo by the sponges themselves, while others are now recognized to be products of microbial symbionts [173]. Sponges naturally host diverse microbial communities, consisting of symbionts, opportunists, and pathogens [174]. Most of the early studies on sponge antimicrobials used biomedical models (i.e., human pathogens) to assess potential antimicrobial activity of sponge extracts or metabolites, and numerous compounds with pharmaceutical interest have been identified. More recently, assays evaluating potential ecological roles have been developed, and these have used microorganisms isolated from marine sources, usually the sponge itself, the water column, or the surfaces of nearby biotic or abiotic substrata. Clearly, these assays have more relevance in terms of the efficacy of antimicrobial activity against potential pathogens to which the sponge would naturally be exposed. The greatest number of studies has assessed the antifouling effects of sponge metabolites (discussed in ► Chapter 14), but the prevention of microbial fouling of the sponge surface is of course relevant to the protection of the sponge from pathogenesis as well.

Antimicrobial activity of sponge extracts is widespread, both taxonomically and geographically [175]. Fewer studies have characterized individual metabolites that act to inhibit marine microbes specifically. Extracts and pure compounds from several species of Caribbean sponges were assessed for their ability to inhibit attachment of *Vibrio harveyi*, a ubiquitous marine bacterium, to agar blocks [176]. Since attachment is a primary step in settlement, this process is critical to both fouling and pathogenesis. Eighty-one percent of the sponges tested, and six compounds isolated from four different sponge species inhibited *V. harveyi* attachment at natural or lower concentrations [176]. Extracts from a subset of these sponge species were also tested for their effects on the growth and attachment of

24 marine bacterial isolates from the sponges' natural habitat [169]. Using the disk diffusion assay, only four of these extracts inhibited microbial growth. One isolate from the surface of the sponge *Agelas conifera* exhibited increased attachment but reduced growth when exposed to the extract from that sponge [169]. Using bioassay-guided isolation of the extract from *Aiolochoxia crassa*, ianthellin (Fig. 15.3: 15) was identified as a metabolite that inhibited attachment, while a bromotyrosine derivative (Fig. 15.3: 16) inhibited bacterial swarming, a mechanism by which bacteria colonize a surface [169]. In a study of Red Sea sponges, the disk diffusion assay was used to characterize the effects of sponge extracts on the growth of several ecologically relevant bacteria [177]. Eight of the 11 sponge extracts inhibited bacterial growth, and bioassay-guided isolation of the active compounds from *Amphimedon viridis*, the sponge with the greatest activity, yielded a mixture of two pyridinium alkaloids, halitoxin (Fig. 15.3: 17) and amphitoxin (Fig. 15.3: 18). This mixture exhibited selective activity against seawater isolates, whereas isolates from the sponge itself were not inhibited. Interestingly, the surface of *A. viridis* appeared to be free of bacterial fouling, suggesting that bacteria in the water column are unable to colonize the surface of *A. viridis*, whereas bacteria associated with the sponge may be actively selected by the fact that they are immune to the sponge's chemical defenses. Following wounding, an activated defense in *Aplysina aerophoba* catalyzes the production of the antibacterial compounds aeroplysinin-1 (Fig. 15.3: 19) and dienone (Fig. 15.3: 20) to concentrations known to be active; this response might protect injured cells that may have an increased probability of penetration by potential pathogens [178].

The location of metabolites within the sponge may provide clues as to their potential utility as antimicrobial defenses under natural conditions, as well as to their biosynthetic origin. In one of the few studies to address these issues, a variety of techniques were used to demonstrate that oroidin (Fig. 15.3: 21) and sceptrin (Fig. 15.3: 22) were affiliated with sponge rather than bacterial cells in *Agelas conifera* and indicated that sponge spherulous cells were responsible for production of these metabolites [179]. Natural concentrations of extracts caused polyp retraction in the coral *Madracis mirabilis*, and the pure metabolites exhibited antimicrobial activity and feeding deterrence [179]. Tissue wounding increased the concentration of these metabolites, both of which were also found to be released into the water column. The antimicrobial brominated compounds arothionin (Fig. 15.3: 23) and homoaerothionin (Fig. 15.3: 24) in *Aplysina fistularis* are also exuded into the water column and are believed to play a role in inhibiting surface fouling [180]. The ability of antimicrobial compounds to be released into the water column in the vicinity of the sponge surface, or at least to be bioavailable on the sponge surface, is likely crucial to their efficacy in preventing pathogenesis. Novel methods to measure these compounds, which likely occur in very dilute concentrations, are clearly needed. Solid-phase microextraction (SPME) fibers may provide one method to detect minute concentrations of specific types of metabolites over very fine spatial scales.

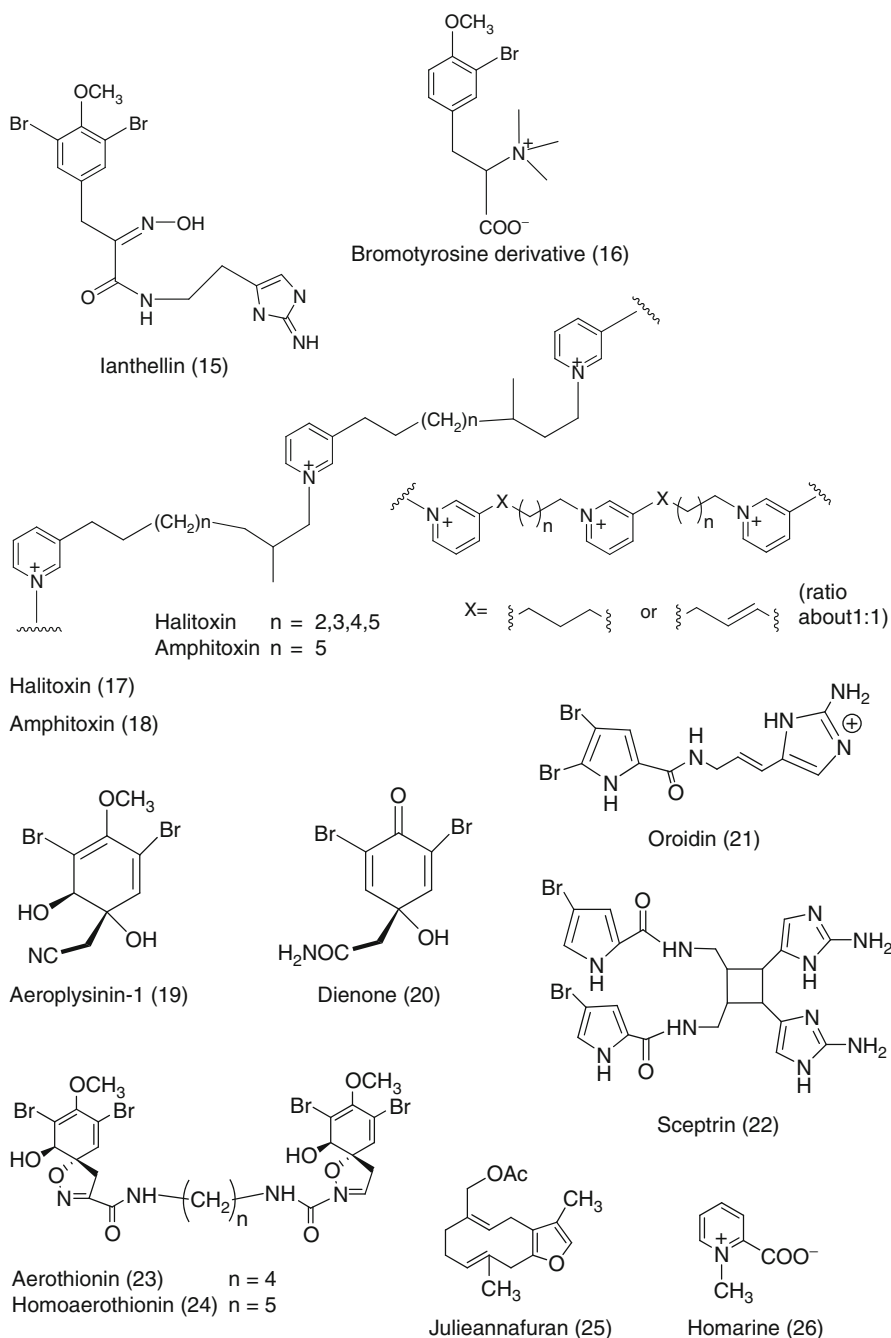


Fig. 15.3 Antimicrobial natural products isolated from marine invertebrates

15.2.4 Soft Coral/Gorgonian Diseases

One of the most extensively studied marine diseases is Aspergillosis, a disease affecting Caribbean gorgonian corals. Aspergillosis is caused by the terrestrial fungus *Aspergillus sydowii* [181], which finds its way onto Caribbean reefs via dust storms from the Sahara Desert and in sediment that runs off of land as a result of human activity [182, 183]. A Caribbean-wide outbreak of Aspergillosis resulted in extensive mortality of the sea fans *Gorgonia* spp. [183, 184]. Both waterborne and physical transmission of Aspergillosis have been demonstrated [183]. Secondary metabolite production by *A. sydowii* isolated from diseased sea fans may be associated with pathogenicity, but this has not yet been verified [183].

Temperature increases activation of certain host immune responses (e.g., oxidative enzymes and cellular immunity), suggesting that gorgonians may increase resistance to disease when faced with warming climatic conditions [68]. However, elevated temperature has been shown to reduce the efficacy of chemical defenses against the fungal pathogen *A. sydowii* [185], suggesting perhaps a trade-off in immune responses under different environmental conditions. Reduced variability in levels of disease resistance on reefs with higher levels of Aspergillosis suggests selection for disease resistance [136], and it has been proposed that resistance in the remaining population of sea fans following the Caribbean-wide Aspergillosis epidemic may explain the recent decline in prevalence of this disease [186].

Extracts from many Caribbean gorgonian species have antimicrobial activity [187], and several inhibit spore germination of *Aspergillus sydowii* [135, 188]. The immune system of the Caribbean Sea fan, *Gorgonia ventalina*, has been studied extensively, and antifungal compounds are one of several immune mechanisms employed in response to Aspergillosis infection. These antifungal compounds are found in higher concentrations in infected sea fans and may be induced by infections with Aspergillosis [135, 136, 189]. Differences in levels of antifungal chemical defenses have been linked to both interspecific [190] and intraspecific [191] variability in susceptibility to Aspergillosis. Intraspecific variability in antifungal activity occurs at the level of the individual sea fan, with elevated levels of antifungal activity in the vicinity of the lesion itself [135], as well as among reefs, which may explain some of the geographic variability observed in the prevalence of this disease [136, 191]. To date, there have not been any bioassay-guided attempts to identify antifungal compounds. In contrast with changes in antifungal activity, there was an indirect effect of pathogenesis on chemical defense: infected sea fans produced significantly reduced concentrations of the feeding-deterrent compound julieannafuran (Fig. 15.3: 25), thereby increasing the susceptibility of diseased corals to predation [71]. Bacteria isolated from the surfaces of gorgonians also produce antibacterial defenses [192] and could thereby be participating in the host's defense against pathogenesis.

Alcyonacean soft coral extracts from the Antarctic [193], Red Sea [194], and Indo-Pacific [195] also exhibit widespread antimicrobial activity. Some of this activity is associated with waterborne molecules released from the surface of the coral that inhibit bacterial attachment [47, 195]; one such molecule is the highly polar homarine

(Fig. 15.3:26; [47]). These studies used a variety of methods to obtain the waterborne molecules, including the use of syringes to sample water at different distances from soft corals in situ [47], and “conditioning” seawater in the laboratory by placing soft corals into individual containers and sampling the water therein [195].

15.2.5 Tunicate Diseases

Of the invertebrates, tunicates possess the most complex cell-based immune system, while still maintaining a cell-free immune response, which includes the production of antibacterial peptides and other antimicrobial secondary metabolites [64, 196]. Like other sessile marine organisms, the antifouling properties of tunicate extracts and secondary metabolites have been widely studied [51, 197]. With regards to antimicrobial activity that might aid in preventing pathogenesis, tunicate compounds have been evaluated predominantly against potential human pathogens, and a diversity of proteins and other metabolites has been considered as viable leads for pharmaceutical research (e.g., [172]). For example, when extracts from the tunicate *Ecteinascidia turbinata* were injected into the American eel, *Anguilla rostrata*, suffering from a bacterial infection, the extract increased antibody titers and survival [198], confirming a diversity of mechanisms of action for tunicate antibacterial defenses. In a rare example of ecological relevance, the chemical inhibition of bacterial settlement was compared with antibacterial toxicity in Mediterranean tunicates, and it was concluded that while these two processes were likely complementary, they were controlled by different metabolites [199].

15.3 Conclusions

Marine communities worldwide face unprecedented variation due, in part, to climate change and anthropogenic stressors. While the importance of predation to the structure and function of these communities has long been accepted, it is increasingly clear that competition and pathogenesis will play significant roles in the near future. Reduced biodiversity in marine communities will likely lead to greater competition for limiting resources; this should favor selection of species with allelopathic compounds. These compounds might act to prevent fouling organisms or macroorganisms from overgrowing surface tissues via contact-mediated (“direct”) processes. Alternatively, the more proactive (“indirect”) approach of releasing allelopathic compounds into the water column where they can act at a distance will also be beneficial. The significant impact of pathogenesis on marine communities has been recognized for at least three decades. In that time, more species have been affected, with increasing frequency, and over broader spatial scales. Antimicrobial compounds often represent the most targeted defense system of the organisms that produce them as they often exhibit selective activity against particular species. These disease resistance mechanisms exhibit similar variability among individuals within a population, as innate immunity does for human hosts exposed to pathogenic microbes.

To date, there is good evidence to support allelopathy and antimicrobial activity in marine algae and invertebrates. More challenging is the use of bioassay-guided isolation of the putative marine natural products involved in competitive and pathogenic interactions. Competitive processes are often characterized by interactions that occur over spatial scales of weeks to months, too long and costly for bioassay-guided procedures. However, recent elegant experimental designs with algae, sponges, and soft corals have led to the identification of allelopathic compounds of ecological relevance. In contrast, whereas pathogenic interactions might occur over a time span of several hours, many marine microbes are at present “unculturable,” and for those, performing ecologically relevant antimicrobial assays in a laboratory setting will be impossible. Nonetheless, the molecular biology revolution has provided important insights into putative pathogens and mechanisms of infectivity. There have also been some successes isolating bioactive antimicrobial natural products from seagrasses, algae, sponges, and soft corals. Future studies of competition and pathogenesis in marine communities should focus on the role of bioactive natural products and include the experimental lessons reviewed here.

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Stephen H. Wright, Andrea Raab, Jörg Feldmann, Eva Krupp, and Marcel Jaspars

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Abstract

This chapter covers the unique ability of marine invertebrates to bioconcentrate transition metals by up to 8 orders of magnitude above background concentrations. A brief introduction deals with the bioinorganic principles of the subject matter and the natural concentrations of metals in the environment. Next, previous metal surveys of marine invertebrates and the potential reasons for hyperaccumulation are discussed, and this is followed by a section on previously

S.H. Wright (✉) • A. Raab • J. Feldmann

Marine Biodiscovery Centre, Department of Chemistry, University of Aberdeen, Old Aberdeen, Scotland, UK

e-mail: a.raab@abdn.ac.uk, j.feldmann@abdn.ac.uk

E. Krupp

Department of Chemistry, Marine Biodiscovery Centre, University of Aberdeen, Old Aberdeen, Scotland, UK

e-mail: e.krupp@abdn.ac.uk

M. Jaspars

Department of Chemistry, Marine Biodiscovery Centre, University of Aberdeen, Aberdeen, UK

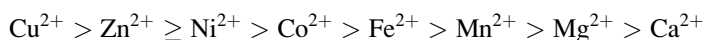
e-mail: m.jaspars@abdn.ac.uk

isolated marine natural product – transition metal complexes. Studies on marine natural product complexation using physical methods are described in the context of their binding specificity and affinity. Many of these studies were conducted to try and discover potential functions for the marine natural product – transition metal complexes. Methodological aspects to discover new complexes of this type are discussed, especially hyphenated techniques utilizing elemental and molecular mass spectrometric methods. A final section proposes a rational way to uncover new marine natural product – transition metal complexes and potential methods to determine their function in nature.

16.1 Introduction

A number of metal ions are essential to life. This includes the bulk ones such as sodium, potassium, magnesium, and calcium used for osmotic balance and in the formation of biomaterials. In addition, there are trace metal ions that are critical in metalloenzymes and cofactors in enzymes and proteins [1]. Most of these are found in the first transition period such as vanadium, manganese, iron, cobalt, nickel, copper, and zinc. It is recognized that certain transition metals usually fulfill certain roles in metalloenzymes, for instance, zinc is often involved in hydrolysis enzymes and copper in oxidation enzymes [1]. An important role for metals is in oxygen transport, which in many animals is carried out by hemoglobin, containing an iron-porphyrin cofactor, and in crustaceans by the copper-containing protein, hemocyanin. An imbalance in the metal concentrations in most organisms will lead to disease or failure to thrive, and therefore, maintenance of metal homeostasis is vital to an organism's survival. For this reason, all life has developed sophisticated mechanisms for the acquisition, storage, and utilization of metal ions as well as elegant methods to keep the concentrations within an acceptable and healthy range. Metal uptake is affected by a number of factors, including speciation, chelation, pH, temperature, salt concentration, and redox potential, as well as age, sex, and physiology of the organism, yet levels are exquisitely controlled in healthy organisms [2].

The main barrier to metal uptake is the hydrophobic cell membrane, and two key mechanisms exist for internalizing biologically important metal ions (Fig. 16.1) [3]. The first is via the use of an energy pump which actively transports M^{2+} into the cell. The second is of more relevance here and involves the use of a transport ligand, often known as an ionophore, or siderophore when it is iron specific (L_t in Fig. 16.1). The ligand L_t complexes to M^{2+} , which is either in a hydrated form or in equilibrium with an external ligand L_e . Thus, the stability constant of L_t must be greater than that of L_e for the transport ligand to be effective. It must be remembered that for divalent metal ions, the stability of complexation to flexible ligands is essentially independent of the ligand and follows the Irving–Williams series shown below and that this may affect which metal is bound by such an ionophore [1].



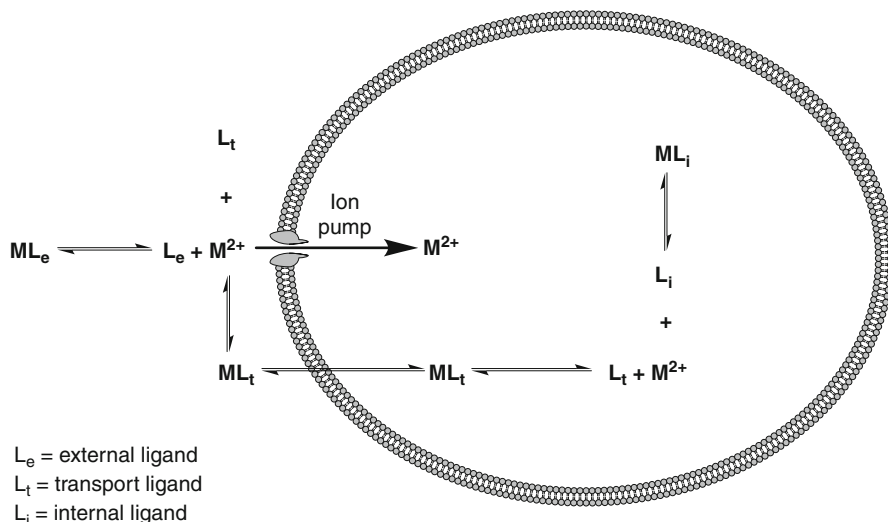


Fig. 16.1 Different routes by which a divalent metal can be taken up into a cell across the membrane [3]

The formation of an ionophore–metal complex generates a concentration gradient of the metal ions across the membrane despite the cell’s already high internal metal concentration. Once inside the cell, the metal ions are bound strongly to internal ligands (L_i in Fig. 16.1) which cannot diffuse out of the cell, thus forming a kinetic trap so that there is little transport of the metal out of the cell. This implies that the stability constant of L_i must be greater than that of L_t for this to occur. There are many examples of ionophores and siderophores which allow transmembrane transport of vital metal ions.

Measurements of the concentrations of these essential metal ions in the earth’s crust show that the bulk metal ions (Na, Mg, K, Ca) are present in high amounts, in the order of moles per kg (Fig. 16.2). The trace transition metal ions are present in much lower concentrations, ranging from 10^{-2} – 10^{-3} mol/kg, excepting Fe, which is present at about 1 mol/kg. The biological availability of these metals in the crust is much lower than these reported concentrations as they are often not in a form that is accessible to organisms that need them. In the marine environment, the situation is different with the bulk metal ions 1–3 orders of magnitude less concentrated in open-ocean seawater and the trace metal ions, present at 10^{-9} – 10^{-10} M concentrations, 7–10 orders of magnitude lower than in the earth’s crust [4]. On the continental shelf, these values are slightly higher due to the input from terrestrial runoff and rivers. In the open ocean, the major input of trace metal ions is dust deposition from the atmosphere with a minor contribution from hydrothermal vents. These low concentrations are worsened by the fact that these metal ions are not present in seawater as hydrated ions, but may be complexed to an organic ligand, or present inside an organism, with some studies reporting that greater than 99% of certain

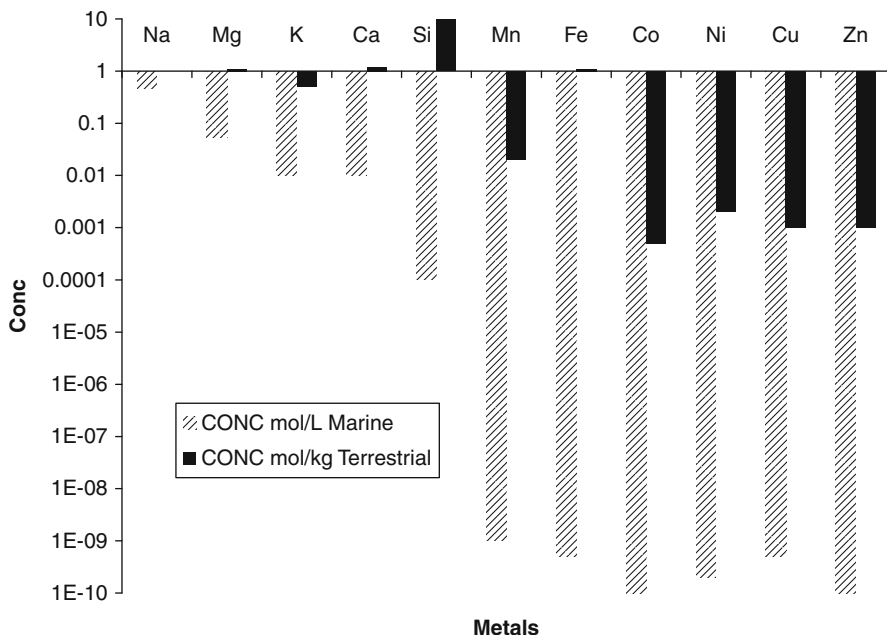


Fig. 16.2 Comparison of biologically important metal ions in marine and terrestrial environments (oceanic seawater and the earth's crust)

trace metal ions are complexed (e.g., Fe, Cu) [5]. Nutrient cycling for these metal ions is very fast compared to the bulk metal ions, exemplified by residence times of tens to hundreds of years compared to millions of years for the bulk ions. Essential nutrient ions also show a characteristic depth profile, with a very low concentration at the surface where it is heavily utilized by life in the photic zone, and then increasing to an asymptote at greater depth [4].

Given these high pressures for such vital, essential resources, marine organisms must have evolved unique mechanisms for acquisition, sequestration, and utilization of trace elements. Most research in this area has been carried out for open-ocean planktonic microorganisms which are responsible for most of the Earth's primary productivity (photosynthesis). It is known that in certain regions of the world's oceans, this productivity is limited by the scarcity of essential ions, particularly iron, and this may have an impact on the Earth's climate [6]. Iron acquisition by siderophores produced by marine microorganisms involves a number of very elegant mechanisms, and these compounds show some of the highest iron affinity constants ever recorded [7]. Very little is known about the way that marine macroorganisms, particularly invertebrates, carry out these essential functions, despite the fact that some marine invertebrates, such as sea squirts, hyperaccumulate certain metals. For this reason, this chapter will be limited to the

current understanding of the role of small molecule natural products in the complexation of metal ions in benthic, sessile marine invertebrates and will exclude the vast body of knowledge on marine microbial siderophores and ionophores.

16.2 Metal Surveys of Marine Invertebrates

For nearly a century, it has been known that there are extraordinary concentrations of vanadium in the blood cells of some ascidian species [8]. Only now are the processes becoming clearer by which this hyperaccumulation of vanadium is achieved by a factor of 10^7 over seawater [9]. The functional role of the vanadium to the ascidian is still undefined, and the necessity for the reported 0.35 M concentrations of vanadium in certain types of ascidian blood cells is unclear [9]. Speculation is rife with suggestions as to its true function from acting as an oxygen store [10] to playing a role in antifouling [11], but neither of these has been substantiated to date.

These findings spurred a great deal of research in the 1980s and 1990s on the possible mode of complexation of vanadium, which was proposed to be by the small molecule tunichromes (e.g., **1**), but cytochemical studies report that high concentrations of vanadium and the tunichromes do not appear in the same blood cell types [12]. Recent work shows that the vanadium is coordinated by amine nitrogen of the unusual 10.5 kDa peptide vanabins from *Ascidia sydneiensis samea*, which contain an unusual fold and nine disulfide bridges [9].

Besides vanadium, little has been reported on the complete metal complement of ascidians or other sessile marine invertebrates such as sponges, soft corals, or echinoderms. Studies reporting concentrations of other metals in sessile marine invertebrates are very limited, and many of these are collected for ascidians in Monniot's 1978 review [13]. This reports elevated concentrations of a number of transition metals in ascidian tissues, but often gives no exact concentrations or how these were measured. However, for iron, it gives a concentration of 5,100 ppm in *Pyura stolonifera*. Reports of lower iron concentrations are more common and often co-occur with elevated vanadium concentrations [8]. Some other metal concentrations that are provided in the Monniot review have been summarized in Table 16.1 [13]. For other metals that are not included in the table, either these are not significantly elevated (Sr, Zn, Sc, Eu, Th) or the concentrations are not provided explicitly (Co, Cu, Zr, Mo).

Our recent preliminary work on ascidians from the Great Barrier Reef using inductively coupled plasma mass spectrometry (ICP-MS) on $\text{HNO}_3/\text{H}_2\text{O}_2$ digests of the whole organism tissues shows a range of metals at concentrations significantly above the local seawater levels (Table 16.2). In particular, vanadium, iron, and arsenic were observed at high concentrations. Iron was observed at around 100 ppm or greater in 6 of the 11 organisms, while vanadium showed the highest concentrations of all the metals analyzed. The concentrations of iron ranged within $1\frac{1}{2}$ orders of magnitude, while the concentrations of vanadium were highly variable,

Table 16.1 Reported concentrations of metals in ascidians from Monniot et al. [13]

Organism	Metal	Concentration
<i>Ciona intestinalis</i>	Sn	$10^6 \times$ seawater conc.
<i>Microcosmus sulcatus</i>		
<i>Styela plicata</i>		
<i>Ciona</i> sp	Mn	120 ppm
<i>Eudistoma Ritteri</i>	Ti	1,512 ppm
	Cr	144 ppm
<i>Pyura stolonifera</i>	Fe	5,100 ppm
<i>Molgula manhattensis</i>	Nb	25–98 ppm
<i>Styela plicata</i>	Nb	250 ppm
	Ta	540 ppm

ranging across 5 orders of magnitude from being almost absent (0.2 mg/kg) to reaching part-per-thousand levels (2,050 mg/kg). The variability did not seem to correlate with taxonomic groups, with two species of *Didemnum* accounting for the extremes of the observed vanadium concentrations and members of two families accounting for the highest concentrations. Comparing the measured concentrations with the reported oceanic concentrations (Table 16.2) [14] of a range of metals gives the indicative bioconcentration factors shown in Fig. 16.3. The range of bioconcentration factors ranges over 7 orders of magnitude with the highest values observed for Fe (1.6×10^7), Mn (2.2×10^6), and V (1.0×10^6). Biologically important metals are highly concentrated which suggests active acquisition is occurring, but also nonessential metals such as Cd and U are being concentrated by 3–4 order of magnitude. Clearly, much more work is required to fully appreciate the extent of metal concentration by ascidians, including the range of metals and the bioconcentration factors.

These surveys can mark the beginning of investigations into possible complexation of the accumulated metals by secondary metabolites. A total metals analysis of the organic extract of the organism can guide the search for chelating agents. For example, the high iron present in the organic ($\text{CH}_2\text{Cl}_2/\text{MeOH}$) extract of *Eudistoma gilboviride* (Fig. 16.4) led us to discover Fe^{II} chelates that comprised 0.4% w/w of the extract [15]. This study is described in more detail later in the chapter.

Apart from the Monniot review and our own work reported above, we have been unable to locate more recent broad studies encompassing other sessile marine invertebrate phyla reporting on the concentrations of a range of metals in environmentally noncontaminated environments. Filter-feeding invertebrates, mainly sponges, have been used as bioindicators for metal pollution; however, this represents the organisms' responses to high metal loads and not their native state. The Mediterranean sponge *Crambe crambe* was shown to accumulate Cu and Pb, and could be regarded as a useful bioindicator for these metals [16]. A 12-year longitudinal study on twelve metals in the Mediterranean sponge *Spongia officinalis* showed spatial and temporal variation in their concentrations indicating a significant reduction in heavy metals after a sewage plant came

Table 16.2 Preliminary investigation of metal concentrations in 11 ascidians from the Great Barrier Reef and oceanic concentrations [14] of those metals presented in ppm (mg of metal per kg of organism, dry weight or mg per kg of seawater). Values are measurements of single $\text{HNO}_3/\text{H}_2\text{O}_2$ digests of ground whole dry organism

Species	sp	<i>Apidium</i>	<i>Didemnum</i>	<i>Didemnum</i>	<i>Didemnum</i>	<i>Polysyncrator</i>	<i>Didemnum</i>	<i>Polycarpa</i>	<i>Didemnum</i>	<i>Didemnum</i>	<i>Lissoclinum</i>	Oceanic metal
		sp 1	sp 2	sp 3	sp	sp	sp 4	sp	sp 5	sp 6	<i>patella</i>	concentrations
Li	0.9	1.8	1.4	2.1	2.7	1.2	0.5	1.5	0.3	0.3	1.6	1.8×10^{-1}
V	31	970	2050	82	0.7	0.9	0.7	6.2	0.2	0.7	0.4	2.0×10^{-3}
Cr	0.7	9.0	4.2	1.7	1.4	2.8	7.4	5.4	1.0	1.2	0.8	2.1×10^{-4}
Mn	1.3	43	19	3.4	2.5	8.7	11	19	1.3	0.9	3.1	2.0×10^{-5}
Fe	52	480	270	220	29	160	97	100	14	14	43	3.0×10^{-5}
Co	0.3	0.8	0.3	0.3	0.2	0.3	0.2	0.3	0.1	0.2	0.1	1.2×10^{-6}
Ni	1.5	7.3	3.0	3.3	0.9	1.9	3.6	5.6	2.0	1.8	1.7	4.8×10^{-4}
Cu	5.9	4.7	5.2	7.1	0.8	3.2	1.5	1.5	1.5	1.6	4.1	1.5×10^{-4}
Zn	23	24	8.2	20	7.1	7.0	0.2	5.7	0.1	0.3	4.3	3.5×10^{-4}
As	8.9	9.5	11	120	1.6	8.7	4.6	1.5	6.0	4.5	6.7	1.2×10^{-3}
Se	1.0	1.8	1.6	4.9	0.2	1.1	1.0	2.1	0.3	0.2	0.7	1.6×10^{-4}
Rb	1.1	1.6	2.5	3.5	0.5	1.5	1.9	2.2	0.3	0.5	2.4	1.2×10^{-1}
Mo	0.6	1.6	1.6	1.7	0.2	1.0	0.7	4.6	0.5	0.4	0.3	1.0×10^{-2}
Cd	0.2	0.2	0.7	1.6	0.2	1.1	0.5	0.2	0.0	0.2	0.5	7.0×10^{-5}
Ba	5.2	5.6	6.3	1.1	9.2	6.3	8.6	7.2	4.9	10	3.4	1.5×10^{-2}
U	3.4	1.6	2.5	1.5	0.2	3.1	1.8	0.9	2.9	3.9	1.8	3.2×10^{-3}

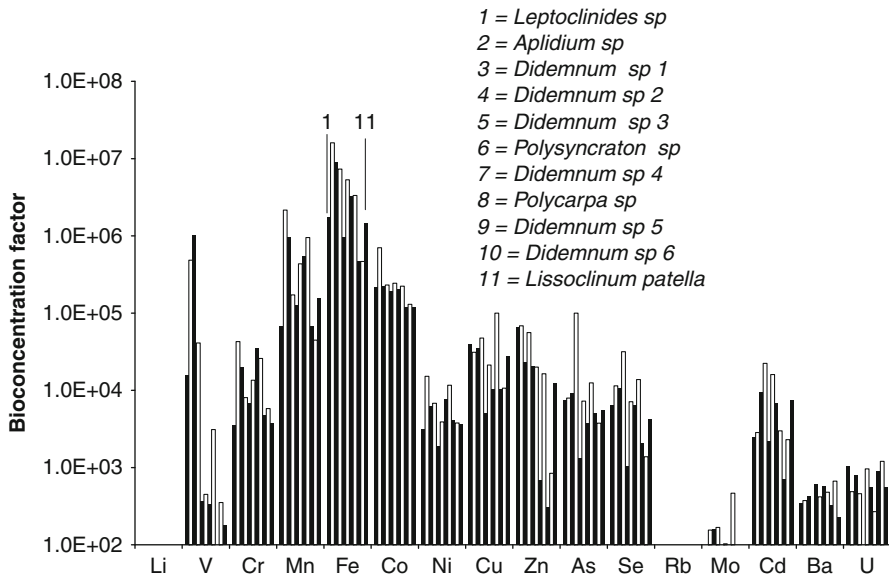


Fig. 16.3 Indicative bioconcentration factors for 11 ascidians from the Great Barrier Reef using information given in [Table 16.2](#)

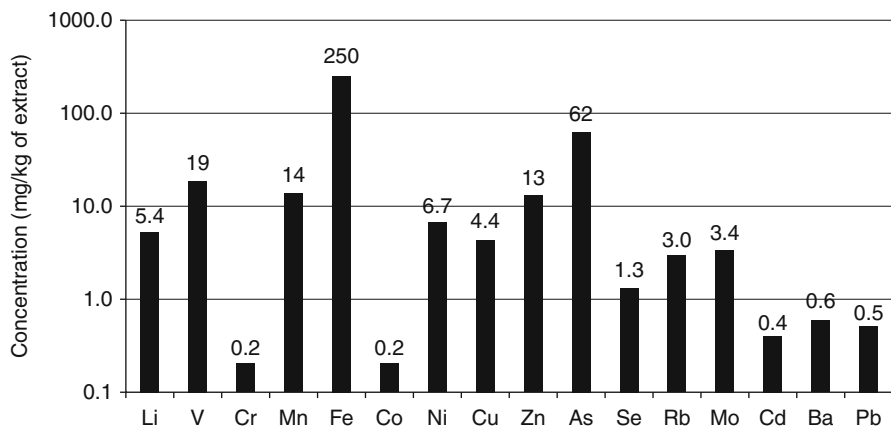


Fig. 16.4 Concentration (mg/kg) of a selected range of metals in the organic extract of the Great Barrier Reef ascidian *Eudistoma gilboviride*. Values are results of an $\text{HNO}_3/\text{H}_2\text{O}_2$ digest of a $\text{CH}_2\text{Cl}_2/\text{MeOH}$ extract of the dried organism. Metals that were analyzed but present at less than 0.05 mg/kg are not shown (Be, Ga, Ag, Te, Tl, Bi, and U) [15]

into operation [17]. One final report is worthy of note. The deepwater sponge *Tedania charcoti* collected in Prydz Bay, Antarctica, was shown by ICP-atomic emission spectroscopy to have extraordinary levels of Cd (15,000 ppm) and Zn (5,100 ppm) [18].

16.3 Why Do Marine Invertebrates Concentrate Metals?

Concentration of metals by up to 7 orders of magnitude from seawater by these invertebrates is a significant feat, and it is assumed that a number of specialized metal ligands and metal transport proteins are involved in this process, such as the vanabins mentioned previously. Internal transport proteins have been well defined in other organisms such as transferrin and ferritin for iron and the amino-terminal Cu and Ni binding motif in a number of Cu and Ni transport proteins [1]. The involvement of natural small molecule organic ligands has often been speculated (i.e., L_t in Fig. 16.1), but there is little concrete evidence that these are involved in the uptake and possible storage of nutrient metals for marine invertebrates, as has been shown for bacterial siderophores and ionophores [1]. A small number of marine natural products have been isolated complexed to transition metals, and a variety of roles have been speculated for the metal in these complexes [19].

The most obvious role of marine invertebrate compounds with the potential to complex metals is that they sequester metals for the organism's metabolism (i.e., L_t or L_i in Fig. 16.1). Some of the known compounds will be catalogued in the next section, but proof of their function as siderophores or ionophores in the producing organism is still lacking. An indication that marine siderophores differ from their terrestrial counterparts is exemplified by alterobactin (**2**), isolated from the open-ocean marine bacterium *Alteromonas luteoviolacea*, which has one of the highest stability constants ever reported [7]. This compound is secreted in response to low iron environments and complexes iron via the catecholate and β -hydroxyaspartate moieties.

It is possible that metal complexation is a way to imbue the natural product with biological activity and thus allow it to play a role in preventing predation and fouling, but this has not been shown conclusively so far. Some invertebrate marine natural products may complex a redox-active metal to confer reactivity to the ligand-metal complex. A terrestrial example is the anticancer agent bleomycin, derived from the microbe *Streptomyces verticillus*, which requires the presence of Fe(II) or Cu(I) and molecular oxygen to enable sequence-selective DNA binding and cleavage [20]. This hypothesis has been tested for very few marine natural products, the most significant of which is the copper-mediated nuclease activity of tambjamine E (**3**) isolated from the ascidian *Atapozoa* sp. [21]. It appears that a 2:2 complex of **3** with Cu(II) in the presence of oxygen, but in the absence of an external reducing agent, gives rise to stoichiometric DNA cleavage via a mechanism involving a reactive oxygen species. The pyridoacridine alkaloid ascididemnin (**4**) from the ascidian *Didemnum* sp. looks like a suitable candidate for binding to transition metals, especially Cu(II), and it was initially suggested that the mechanism by which it induced topoisomerase-II-mediated DNA cleavage involved a ascididemnin-Cu complex which was capable of generating reactive oxygen species [22]. However, the presence of Cu was shown not to be required and reactive oxygen species are produced by direct reduction of the iminoquinone moiety.

It is possible that the presence of a nonredox active metal in a complex with a marine natural product confers a preferred bioactive conformation to the complex. A protein example of this is the ubiquitous calmodulins, which change conformation upon binding to Ca, thus allowing the complex to bind to specific proteins and elicit a specific response [23]. A final suggestion is that the metal ions are necessary for templating the biosynthesis of macrocyclic ligands, but there has been no direct evidence for this hypothesis although there is some synthetic evidence that the presence of metal ions may assist such reactions [24].

The examples already discussed show that certain functional groups (e.g., hard/soft ligands) and molecular features (e.g., macrocycles, structural constraints) are often encountered in organic metal ligands. Learning from the metalloproteins, the presence of residues such as histidine, methionine, cysteine, tyrosine, aspartic and glutamic acid, and their derivatives in a natural product may suggest that the compound is involved in metal binding. Care needs to be taken that the coordination environment these represent is taken into consideration. Typical functional groupings found in siderophores and ionophores such as catecholates, hydroxamates, and β -hydroxyaspartates also imply a role of the compound in metal complexation. Complexation sites such as those present in heteroaromatics such as **3** and **4** are also very suggestive of a role in metal complexation. A number of moieties expected in metal-complexing natural products have been summarized in Fig. 16.5. More difficult to predict are conformations of macrocycles which present carbonyl, amide, or other functional groups in a coordination environment ideal for metal binding.

Based on such principles, a large number of marine metabolites are proposed to function as metal ligands; however, only very few cases have been substantiated. Most of the structural types that are suspected of being able to complex to metal ions have been catalogued in the influential review by Michael and Pattenden [19]. Rather than duplicating this information, we will give a brief survey of the structural classes which have proposed complexing abilities, followed in the next section by those in which either the metabolite was isolated as a metal complex or for which complexation studies have been carried out.

We have already seen examples in which obvious chelating functionalities are present such as the tunichrome **1** which contains three trihydroxyphenylalanine-derived substructures [8]. There is now evidence that these compounds are not involved in the complexation of vanadium, but it is possible that they are involved in the complexation of iron [12]. Similar moieties, in this case a dihydroxyphenol in addition to two β -hydroxyaspartates, are present in **2**, which has been shown to be a strong iron-complexing agent [7]. Tambjamine **3** has characteristic pyrrole functionality which predisposes it to bind to copper [21]. Ascididemin **4** has a bipyridyl “bay” region, which again makes it a likely candidate for complexing to transition metals, but the initial isolation study showed it did not complex iron(II) [25]. The eudistomins from *Eudistoma* sp. (e.g., **5**) have long been suspected of

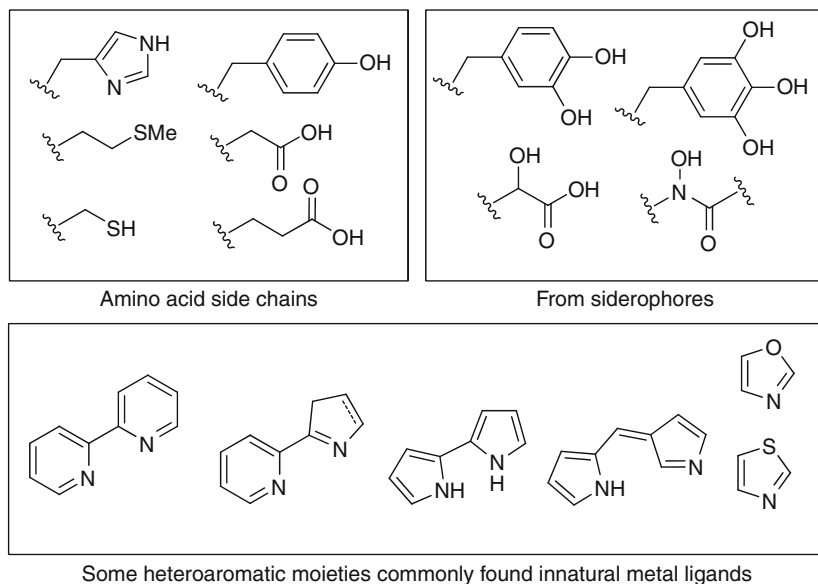
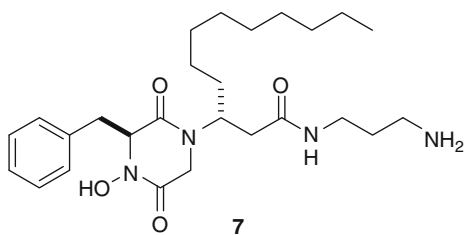
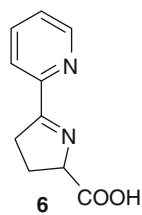
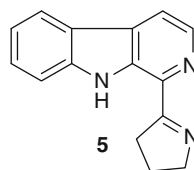
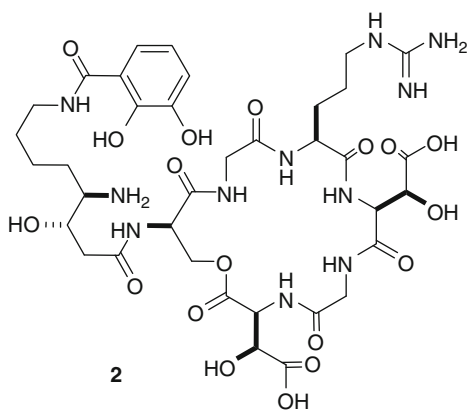
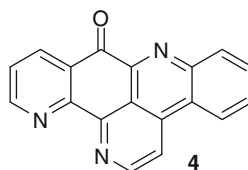
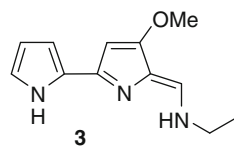
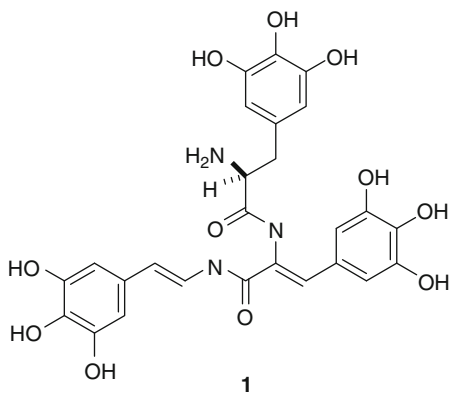
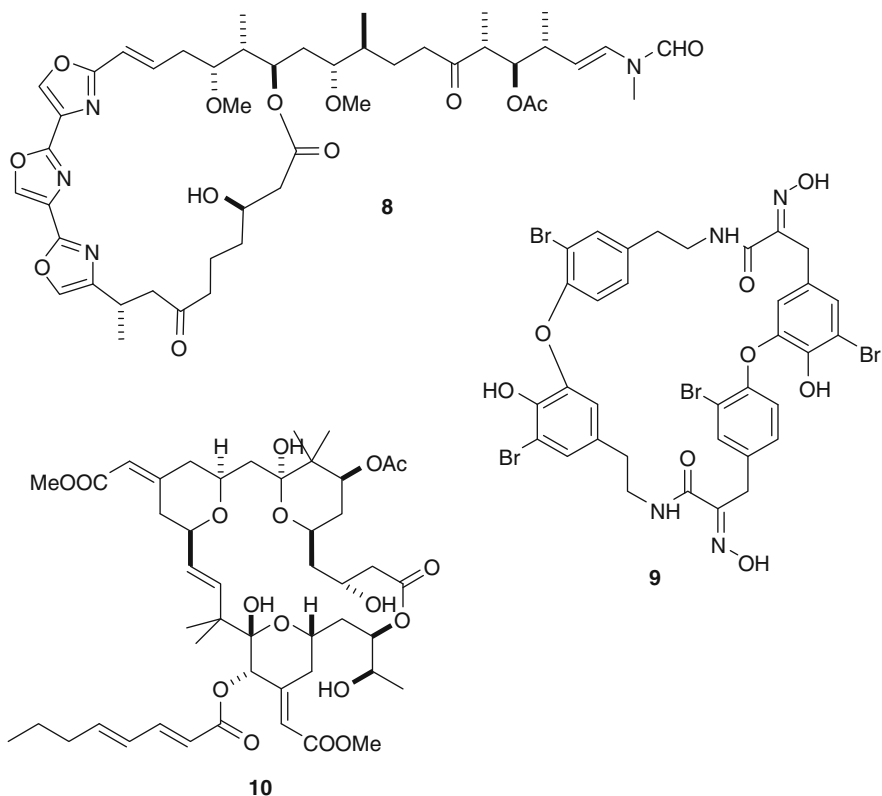


Fig. 16.5 Functional groups often encountered in natural metal ligands

being capable of chelating iron [26], due to their resemblance to the Fe(II) chelator pyrimine (**6**) isolated from a *Pseudomonas* sp. [27]. Etzionin (**7**) isolated from an unidentified Red Sea ascidian [28] contains a hydroxamate functionality as well as a terminal amine, and the combinations of these moieties are reminiscent of the potent siderophore deferoxamine [29]. Compounds containing small heterocycles (e.g., oxazoles, oxazolines, thiazoles, thiazolines) are often suspected of being capable of chelating metals. One such example is ulapualide (**8**), isolated from the nudibranch *Hexabranchnus sanguineus*, containing an array of three oxazoles. A molecular mechanics study was carried out with **8** complexed to a dummy metal ion and was used to predict its relative stereochemistry [30]. This structure also typifies the large macrocycles with a wealth of chelating functionality which make them appear ideal candidates for metal complexation. Other macrocycles such as the oxime-containing iodotyrosine-derived bastadins from the sponge *Ianthella basta* (e.g., **9**) [31] are also suspected of complexing metals, but there has been no definitive proof. Similarly, polyether macrolides such as the bryostatins derived from the bryozoan *Bugula neritina* (e.g., **10**) apparently display a perfect coordination environment for the binding of metals, but this has not been substantiated despite being suggested when its structure was first reported [32].





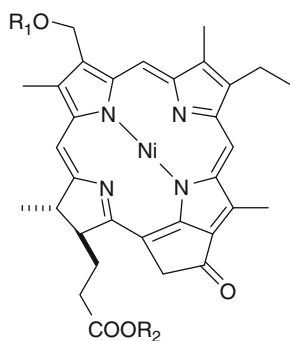
16.4 Marine Natural Products Isolated Containing Metals

A survey of the literature and databases reveals very few marine invertebrate natural products which have been isolated as metal complexes. Compared to the last comprehensive survey by Michael and Pattenden which highlighted compounds **11–13**, only a few more complexes have been reported (**14**, **16**) [19]. In addition to this, a few marine microorganism-derived metal complexes have been isolated, but these are beyond the scope of this review. Of the previously reviewed compounds, the nickel-containing porphyrin tunichlorin (**11a**) was originally isolated from the Caribbean ascidian *Trididemnum solidum* [33] and again later from the South Pacific Ocean sea hare *Dolabella auricularia* [34]. Subsequently, a large

number of acyl tunichlorin analogues (**11b**) were isolated from *Trididemnum solidum* where the acyl chains ranged from C_{14:0} to C_{22:6} [35]. Zinc complexes have been isolated from calcareous sponges; the first one was the clathridine–zinc complex (**12**) isolated from the Mediterranean sponge *Clathrina clathrus* [36]. A second zinc-complexing compound was isolated from a Fijian *Leucetta* sponge, the zinc complex of isonaamidine C (**13**) [37].

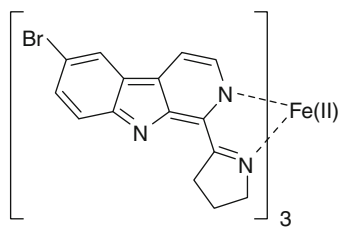
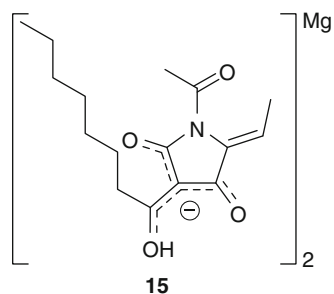
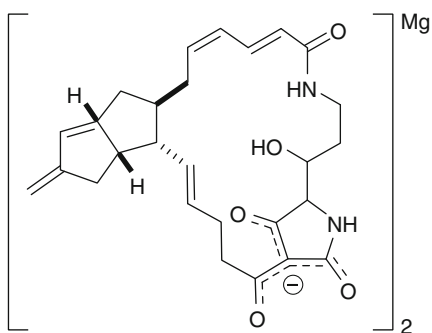
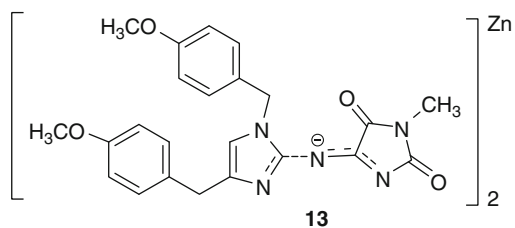
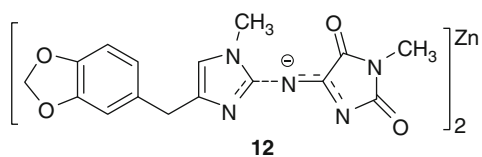
The unique geodin A, a macrocyclic polyketide lactam tetramic acid, was isolated as its magnesium complex (**14**) from the Australian sponge *Geodia* sp. [38]. The 2:1 complex was originally observed by mass spectrometric methods, and the stoichiometry was confirmed by atomic absorption spectroscopy. Geodin A is related to the tetramic acid magnesidin A (**15**) produced by the marine *Vibrio gazogenes*. Magnesidin A (**15**) was isolated as its magnesium complex but was found to be unstable to chromatographic methods using TFA [39]. This raises the point that although a marine natural product may exist as a metal complex in vivo, the extraction and isolation procedures may destroy the complex. The complexes reported above have all been stable to the work-up and chromatographic conditions, but it is likely that many others do not survive. Additional evidence for this comes from the existence of several zinc-free clathridines and naamidines from calcareous sponges, which may have been present as their zinc complexes in vivo but are destroyed during extraction and isolation procedures. To take this into account, we developed an isolation procedure using size exclusion chromatography which was mild enough to enable weak complexes to survive the purification process [15]. Application of this methodology, which is described in detail in Sect. 16.6, enabled the recovery of the 3:1 eudistomin–iron complex (**16**) from the Australian ascidian *Eudistoma gilboviride*, whose metal complement we had previously determined (Fig. 16.4). The methodology also enabled us to calculate that 0.4% of the organic extract of the organism was composed of the complex **16** and its analogues and that this represented 75% of the total lipophilic iron found in *E. gilboviride* and therefore a significant proportion of the organism's total iron content [15]. In addition, a reexamination of the crude extract by UV spectroscopy indicated that complex **16** was indeed present at this stage of the isolation procedure. It is possible that the formation of this complex is an artifact of sample preparation, but its concentration and presence in the original extract seem to suggest that it plays an important role in the organism's physiology as iron chelator. As mentioned previously, the eudistomin core structure (**5**) resembles the known iron chelator pyrimine (**6**) which also forms a 3:1 complex with iron(II) [27]. Further studies with pyrimine (**6**) showed that its complexes with Cu(II), Fe(II), and Mn(II) acted as efficient superoxide dismutase mimetics, with Cu(II) giving the best results [40]. It is possible, therefore, that the role of complex **16** in *E. gilboviride* is for the

removal of reactive oxygen species which may be generated in the high light environment it inhabits.



11a $R_1 = R_2 = H$

11b $R_1 = \text{acyl}, R_2 = H \text{ or Me}$



16.5 Marine Natural Product Complexation Studies

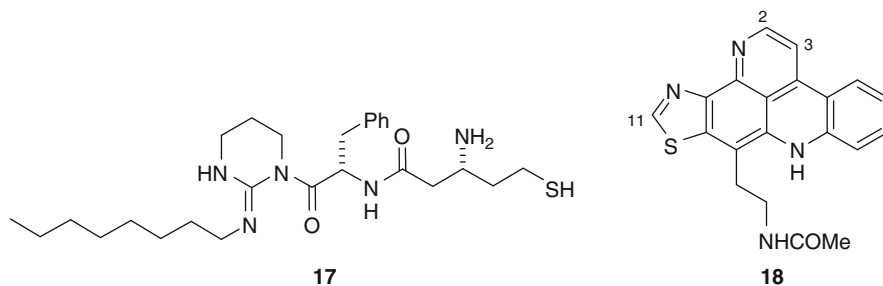
In the preceding sections, we have seen a limited number of authentic complexes isolated from marine invertebrates and some speculation based on the combined functionality and conformation of a molecule presenting a coordination environment suitable for complexing metals. The eventual aim of any studies based around determining metal chelation by marine natural products is to predict their function and hence their benefit to the producing organism. The nuclease activity determined for the copper complex of tambjamine (**3**), mentioned above, may indeed be its natural function, and it may thus act as a means of chemical defense. Similarly, the potential role of the eudistomin–iron complex **16** as a superoxide dismutase appears to make sense in its normal environment, yet neither of the assertions regarding these complexes' native function is easy to confirm.

As a first step toward understanding the function of marine metabolite–metal complexes, the basic structural and physicochemical parameters need to be determined. Several research groups have tried to confirm suspected complexation ability of marine natural products using spectroscopic and other methods. A useful parameter in such work is the binding selectivity for a particular metal ion, and then its binding affinity must also be measured. The ligand atoms involved in the complexation must also be determined so that the complete coordination environment and eventually the full three-dimensional structure of the complex in the solid or solution state should be solved. In this section, we will discuss illustrative examples of how combined physical, spectroscopic, and theoretical methods can be used to confirm the metal-complexing ability of some of the suspected ligands derived from marine invertebrates.

The simplest studies just involve one or two techniques to determine the metal complexation ability of a potential ligand, and this was the case for the highly unusual peptide caledonin (**17**), isolated from the New Caledonian ascidian, *Didemnum rodriguesi* [41]. The structural features of **17**, a penicillamine-like β -amino acid at one end and a hydrophobic chain at the other, made the investigators suspect that it was involved in metal ion transport across membranes. ^1H NMR titration studies of **17** with Zn(II) resulted in a 2:1 ligand to metal complex which was confirmed by mass spectrometric studies. Changes in the ^1H NMR spectrum on complexation to Zn(II) suggested that the terminal thiol and amino groups were involved in the binding.

Kuanoniamine D (**18**) contains a bipyridyl-type “bay” chelating functionality, and this was investigated in more detail using a variety of techniques and a range of metals which provided evidence for the formation of 2:1 ligand–metal complexes [42]. ^1H NMR titrations increasing the amount of ZnCl_2 showed line broadening of the signals at H2, H3, and H11 in **18** which sharpened and remained unchanged once a 2:1 ratio was attained. Kuanoniamine D fluoresces with λ_{ex} 350 nm and λ_{em} 524 nm, and the emission peak was greatly attenuated upon addition of excess Zn(II), Fe(II), and Cu(II) and was completely quenched on addition of Co(II). Fluorescence titrations could therefore be used to confirm the ligand to metal

ratio for Cu(II) and Co(II) in the complex and determine stability constants of $2.5 \times 10^{10} \text{ M}^{-2}$ for Co(II) and $1.3 \times 10^{10} \text{ M}^{-2}$ for Cu(II).



The original isolation paper of ascididemin (**4**) indicates that it does not bind to iron(II) [25]. The compound was subsequently reisolated from a *Lissoclinum* sp., measurements of the metal content in the ascidian extract showed elevated levels of several transition metals (Cu, Zn, Fe), and the mass spectrum showed an isotope pattern consistent with a 4-CuOAc complex, which suggested that **4** might complex copper [43]. As ascididemin is fluorescent (λ_{ex} 219 nm, λ_{em} 295, 334 nm), a fluorescence quenching study was carried out (Fig. 16.6), and the fluorescence quenching mechanism and efficiency were evaluated. This showed that the fluorescence quenching efficiency is significantly greater for the Cu(II) complex than the Co(II) or Ni(II) ones.

An early complexation study was initiated by the realization that the cyclic depsipeptide jaspilakinolide (Fig. 16.7a, **19**), isolated from the Fijian sponge, *Jaspis* sp., resembled several other depsipeptide ionophores such as the enniatins [44]. Consequently, Inman and coworkers conducted ^1H NMR titrations of a 200-mM solution of **19** in CD_3CN with Li^+ , Na^+ , and K^+ . Only Li^+ generated significant changes in the spectrum, which were used to calculate a binding constant of 60 M^{-1} for the 1:1 complex of **19** with Li^+ . Significant conformational changes were observed via the change in a number of coupling constants, implying changes in dihedral angles of **19**. A molecular mechanics study using explicit Li^+ revealed a conformation consistent with these dihedral angles that allowed the carbonyls at C1, C10, and C14 to bind to the Li^+ with reasonable Li–O bond lengths, and that Li–O distance was too long for the carbonyl at C17. A more recent study took a different approach and first determined the solution conformation of **19** in CD_3CN using NOE-restrained molecular dynamics calculations (Fig. 16.7b) [45]. This was followed by the determination of the solution structure of 16 mM **19** in CD_3CN in the presence of 1 equivalent of Li^+ which was modeled using NOE restraints without the use of an explicit Li^+ . Again, large changes in the conformation on formation of a 1:1 ligand to metal complex were evident, as is clear from the resulting minimum energy structure represented in Fig. 16.7c. This conformation appeared very different from that determined in the earlier study [44], perhaps as an effect of the much lower concentration employed in the more recent study [45].

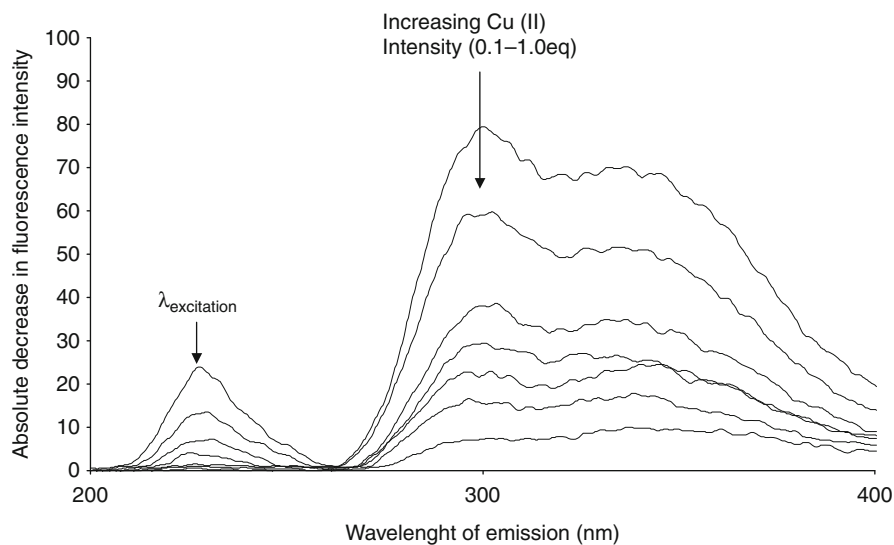


Fig. 16.6 Titration of ascididemin (**4**) with increasing amounts of Cu(II) monitored by fluorescence spectroscopy showing fluorescence quenching with increasing amounts of Cu(II). Excitation wavelength set at 219 nm and emission monitored at 295 and 334 nm

A full conformational search without NOE restraints in the presence of explicit Li^+ found a low-energy conformation that was similar to the solution conformation in Fig. 16.7c. An overlay of the calculated and experimentally determined chelating structures is shown in Fig. 16.7d. This then suggests that at this concentration, the Li^+ binds outside the macrocycle, involving the carbonyls at C14 and C17, and the π -electrons of the β -tyrosine. A comparison of these two studies thus casts light on another difficulty, that weak complexes such as this may display different modes of coordination depending on the concentration.

The cyanobactins, exemplified by the patellamides, **20**, and westiellamide, **21**, are posttranslationally modified ribosomal cyclic peptides containingazole moieties isolated from cyanobacteria. The patellamides, **20**, were originally isolated from the ascidian *Lissoclinum patella* but were subsequently shown to be produced by the symbiotic cyanobacterium *Prochloron didemni* [46, 47]. One study showed elevated levels of copper and zinc in the tissues of *Lissoclinum patella* [48], adding ecological significance to the previously observed crystal structure of ascidiacyclamide **23** with two equivalents of copper and a bridging carbonate (Fig. 16.8a, b) [49]. These authors studied these complexes by a number of techniques and found that in the solid state the $\text{Cu}\cdots\text{Cu}$ distance was 4.43 Å, whereas a separate study showed this to be 3.7 Å in solution using EPR measurements coupled with molecular simulations [50]. The key findings of many studies, by a number of authors using a range of techniques, including mass spectrometry,

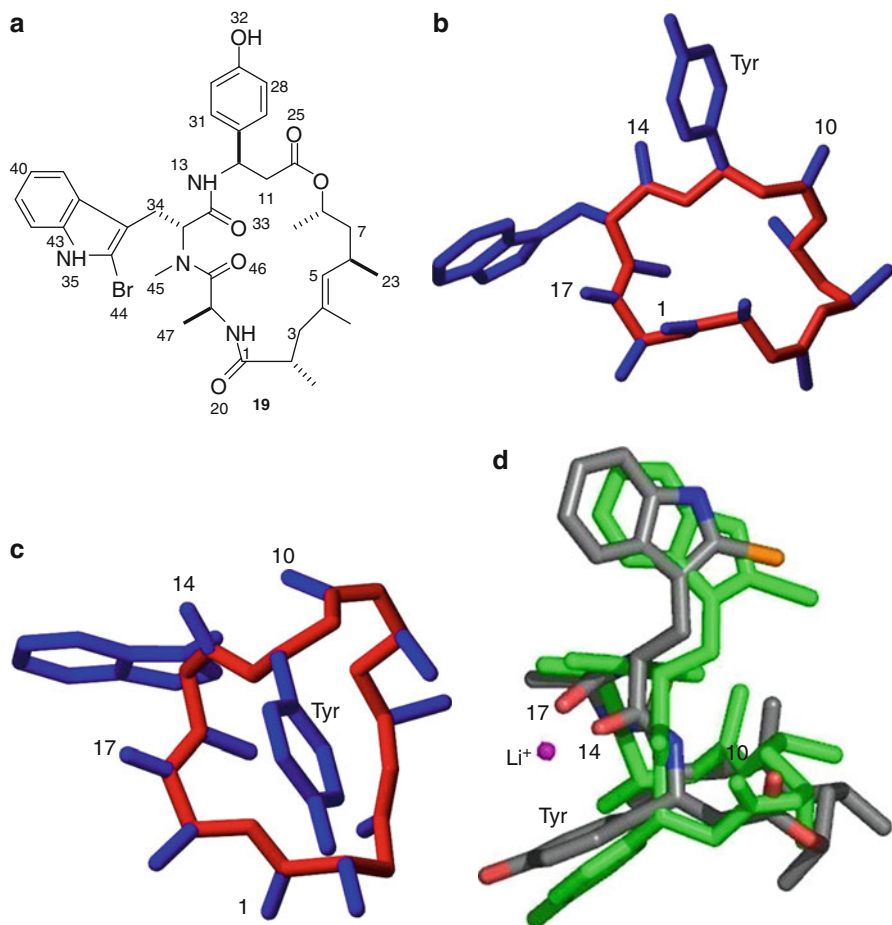
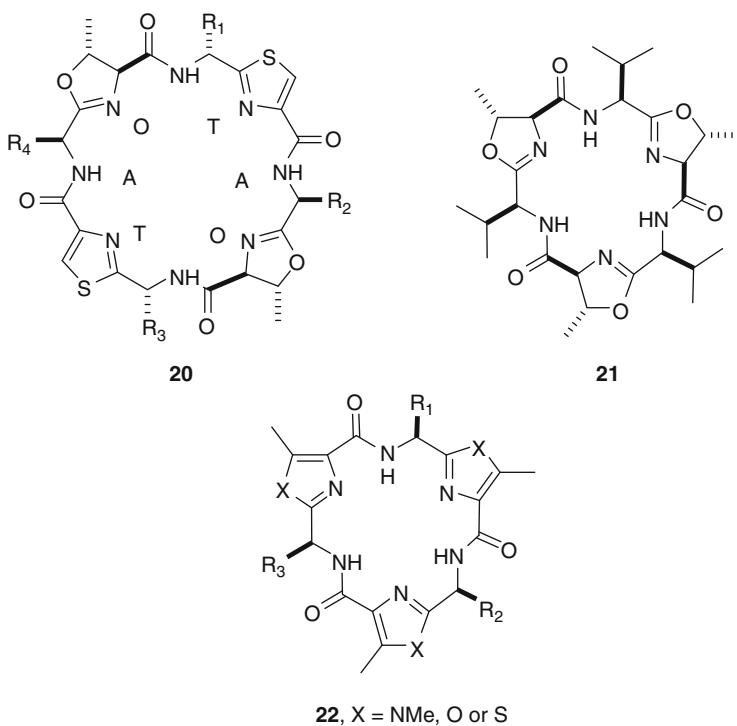


Fig. 16.7 (a) Structure of jaspakinolide; (b) NOE-restrained molecular dynamics structure of jaspakinolide in CD₃CN; (c) NOE-restrained molecular dynamics structure of jaspakinolide with 1 equivalent of Li⁺ in CD₃CN; (d) Overlay of the structure in (c) with a Li⁺ docked minimized jaspakinolide obtained by conformational searching

ultraviolet, circular dichroism, NOE-restrained molecular dynamics calculations, and magnetic susceptibility have been recently summarized [24]. This intensive research was prompted by Hawkins' original suggestion that the patellamides (20) could complex two equivalents of copper via the thiazole (T), amine (A), and oxazole (O) nitrogens, as later confirmed by many of these studies.[26] A cooperative binding mechanism was demonstrated in which the binding of one Cu(II) ion unfolded the patellamide molecule to present a second TAO-binding site ready to accept the second Cu(II) ion (Fig. 16.8c) [51]. The presence of elevated

levels of copper in *Lissoclinum patella* and the ideal coordination environment presented for the complexation of two Cu(II) ions suggested that this complex played an important role in the ecology of the organism, whereas the role of a Zn–patellamide complex was deemed less important due to the lower stability of the complexes formed [48, 51]. The distance between the two copper centers in the patellamide–dicopper complexes tantalizingly suggested that they might have a role in activating dioxygen, similar to the dicopper proteins, but this has not been verified to date [52].



The study of westiellamide (**21**) was initiated by the unusual sandwich complex generated with four Ag(I) ions (Fig. 16.8d) [53]. The near-planar structure of **21**, upon complexation with Ag, is modified by the rotation of the oxazoline rings perpendicular to the macrocycle, with the coordination environment for the fourth Ag(I) ion generated by the carbonyl groups pointing toward the center of the sandwich. A detailed study of these complexes of **21** and analogues **22** has been published recently, showing that the compounds are highly preorganized for Cu(II)

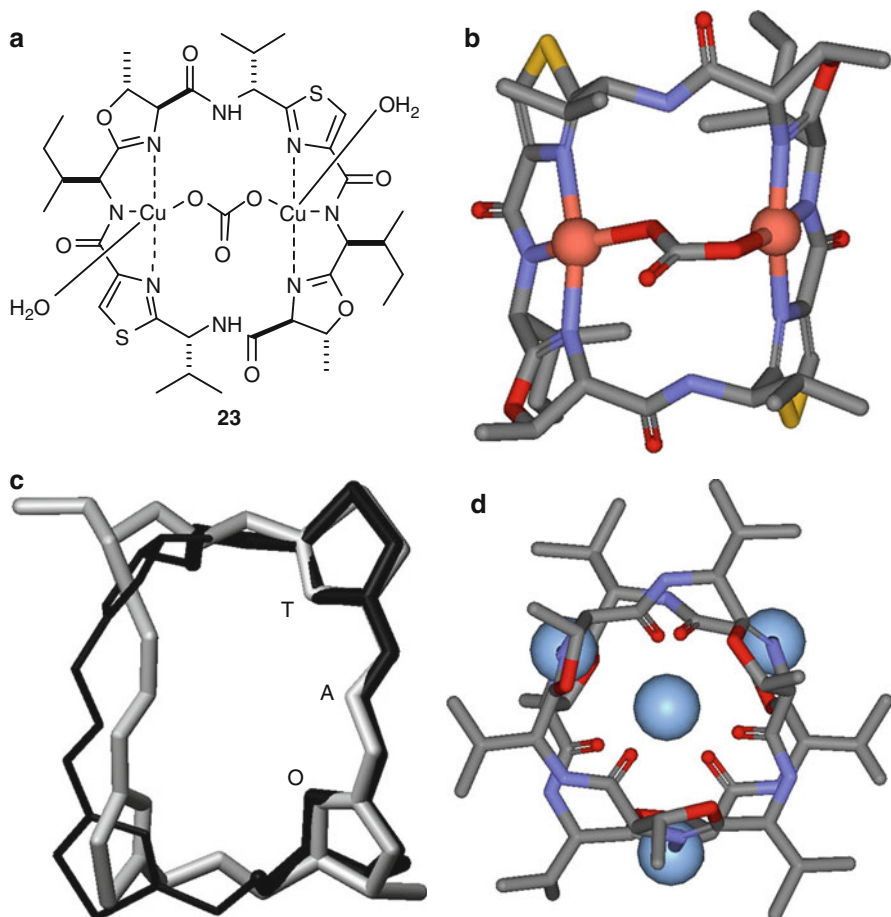
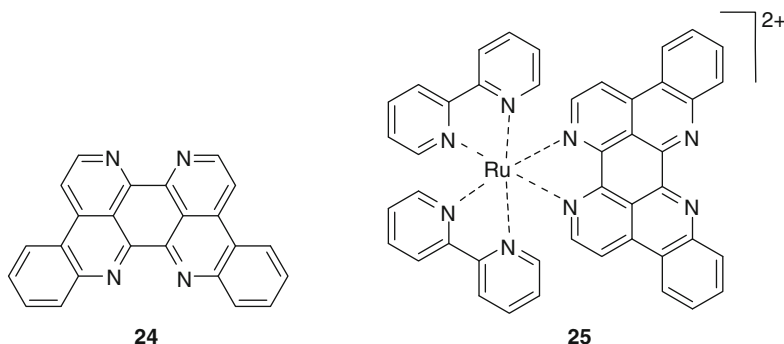


Fig. 16.8 (a) Ascidiacyclamide– Cu_2CO_3 structure. (b) Crystal structure of the ascidiacyclamide– Cu_2CO_3 complex, Cu depicted as spheres. (c) Overlay of the patellamide C–Cu NOE-restrained molecular dynamics structure (*black*) with the ascidiacyclamide crystal structure (*gray*) showing the TAO nitrogens in the correct configuration to accept the second Cu ion. (d) Sandwich complex of two westiellamide molecules with four Ag ions, Ag depicted as spheres

coordination [54]. These examples show that although some of these complexes may form with biologically relevant metals, in other cases, novel complexes can be formed using other metal ions. Such is the case for eilatin (24), isolated from the Red Sea ascidian *Eudistoma* sp. which forms complexes with ruthenium and two

bipyridyl units (**25**) [55]. These complexes have anti-HIV activity in vitro by binding to DNA and RNA.



16.6 Methods to Identify Metal Complexes from Marine Invertebrates

From the preceding discussion, it is clear that metal-complexing agents from marine invertebrates are underinvestigated. The complexes that have been studied, either isolated as complexes, or ligands studied in the presence of metals show excellent selectivity, high affinity, and some fascinating biological activities. For this reason, efficient methods for the recovery of intact complexes or potential ligands need to be developed. Much work has been done on developing rapid colorimetric methods for the discovery of iron ligands such as the chrome azurol S (CAS) assay [56], but there is a dearth of similar assays for other metals of interest in addition to which a more general method, able to cope with a range of metals, would be preferable.

The method of choice for the detection of trace elements in solution is ICP-MS (inductively coupled plasma mass spectrometry), an elemental mass spectrometric technique, which is able to detect most elements in solution below concentrations of 1 ng/mL (ppb). The method is not only sensitive but also has the ability to detect multiple elements simultaneously which enables the screening of extracts or acid-digested tissues for a series of elements of interest. These can be the classical transition elements: metalloids such as arsenic and selenium, and nonmetals such as bromine, iodine, phosphorus, and sulfur. Hence, the ICP-MS analysis of extracts from marine organisms can quickly establish which samples contain significant quantities of elements of interest.

ICP-MS uses a hard ionization source that completely destroys, atomizes, and ionizes every compound, so with this technique, it is intrinsically impossible to determine intact molecules. However, when chromatographic separation in the form of HPLC (high-performance liquid chromatography) is interfaced to ICP-MS, molecular information can be gained indirectly; different molecules

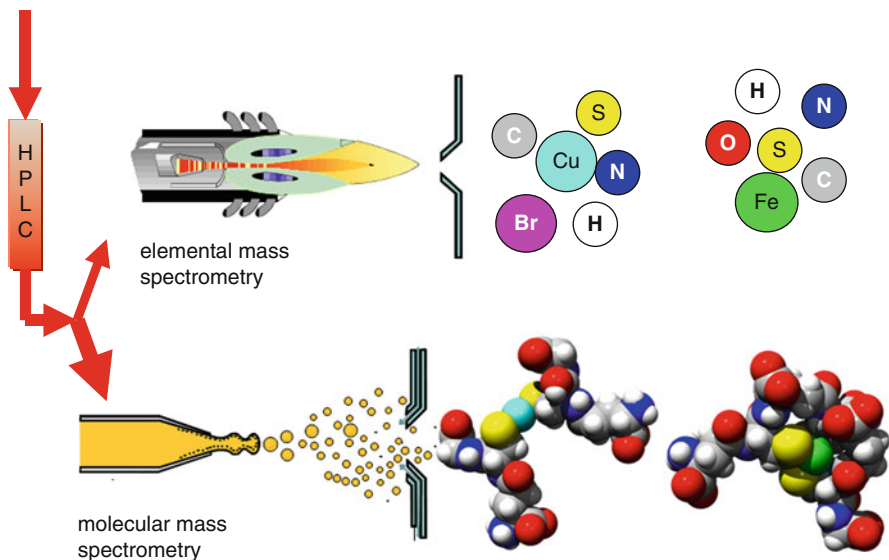


Fig. 16.9 HPLC hyphenated simultaneously to ICP-MS and ES-MS to identify and quantify metal complexes in extracts of biological marine specimens

containing trace elements are separated by HPLC, and element-specific detection is achieved with ICP-MS. The molecular identification relies on retention time comparison with standard compounds. This technique can also be used to screen for unknown compounds and can give information whether or not different compounds containing a certain element occur in a sample extract. However, HPLC-ICPMS alone cannot identify novel compounds where no standard compound is available. For molecular identification of unknown compounds in a sample extract, molecular mass spectrometric methods such as electrospray ionization mass spectrometry (ES-MS) are needed. Electrospray is a soft ionization technique that is able to ionize molecules, complexes, and even unstable compounds without fragmentation. When HPLC is interfaced to ES-MS, compounds can be separated and detected, but it is very difficult to identify the metal-containing species from an ES mass spectrum. Here, the combination of ICP-MS and ES-MS has proven ideal for the detection of labile metal compounds in complex extract matrices. The combination of both MS detectors capitalizes on their complementary analytical features, and recently HPLC has been coupled simultaneously to both detectors. [Figure 16.9](#) illustrates this innovative arrangement of interfacing HPLC in parallel to ICP and ES mass spectrometers.

All metal compounds in an extract can be detected simultaneously, and elemental as well as molecular information can be collected. While the ICP-MS identifies the “needle in the haystack” by giving direct information about the retention time of the molecules containing the element of interest (which could be characteristic for the ligand such as bromine in **9** and **16** or for the complexed metal-like zinc in **12**

and **13** or iron in **16**), ES-MS provides molecular information in the same time window. This enables the identification of traces of metal complexes in a crude biological extract, without having a standard at hand. This system is especially useful for the identification of target species with unknown elemental composition and structure and which are potentially labile during chromatography. Since only one chromatographic system is used, the system can be tailored for the identification of certain complexes. This has been demonstrated for the identification of labile arsenic and mercury phytochelatin complexes, which were separated on a reverse-phase column in a methanol/formic acid mobile phase [57, 58].

However, the major disadvantage of all MS-based techniques is that they have to be linked to chromatography or capillary electrophoresis. Ion-exchange chromatography and capillary electrophoresis typically use buffers with high aqueous content, which are not generally suitable for natural products due to solubility issues. Reverse-phase HPLC is the most commonly used form of LC-MS for analysis of natural products, but it tends to result in dissociation of all but strong chelates. To enable LC-MS of even weak natural product chelates, we investigated size-exclusion chromatography (SEC) with a natural product friendly solvent system. Contrary to other forms of chromatography, SEC involves minimal interaction between the analytes and the stationary phase, which helps to prevent dissociation of metal complexes. We combined the use of a poly(methyl methacrylate) SEC-HPLC column with a methanolic buffer. However, analyte interactions with residual hydrophilic sites on the stationary phase resulted in chelate dissociation and excessive retention. Through much trial and error, we developed a buffer (50 mM trimethylamine carbonate, pH 8.8) that was able to prevent the dissociation of weak chelates [15]. Although some chelates were still strongly retained on the column, these could be eluted with 100 mM formic acid in methanol with minimal complex dissociation.

This SEC-HPLC method was coupled to both ICP-MS and ES-MS to investigate organic extracts of ascidians for chelates. As previously mentioned, cyclic peptides produced by the ascidian *Lissoclinium patella*, such as the patellamides (**20**), are able to chelate copper with stability constants in the region of 1×10^4 – 3×10^5 [48, 59, 60]. These copper complexes were successfully observed using SEC-HPLC-ICP/ES-MS in an extract of *L. patella* that had been spiked with copper. The unspiked extract of *L. patella* was also analyzed by this method, but no complexes were observed, which suggested that these cyclic peptides were not complexed to copper in the organism.

Many novel natural product chelates that exist undetected may be discovered by SEC-HPLC-ICP/ES-MS. A crude extract of *Eudistoma gilboviride*, in which we had discovered high levels of iron (Fig. 16.4), was analyzed using this method. Peaks in the ES mass spectrum were detected that coeluted with Fe peaks in the ICP-MS chromatogram (Fig. 16.10). Despite only using low resolution ES-MS, we were able to identify complexes of Fe(II) with eudistomin H (**16**) and its analogues. The incorporation of high-resolution ES-MS would enhance this method's potential for discovery of novel chelates manifold. While the presence of these novel Fe(II)–eudistomin chelates were identified in the organic extract, the question remains as

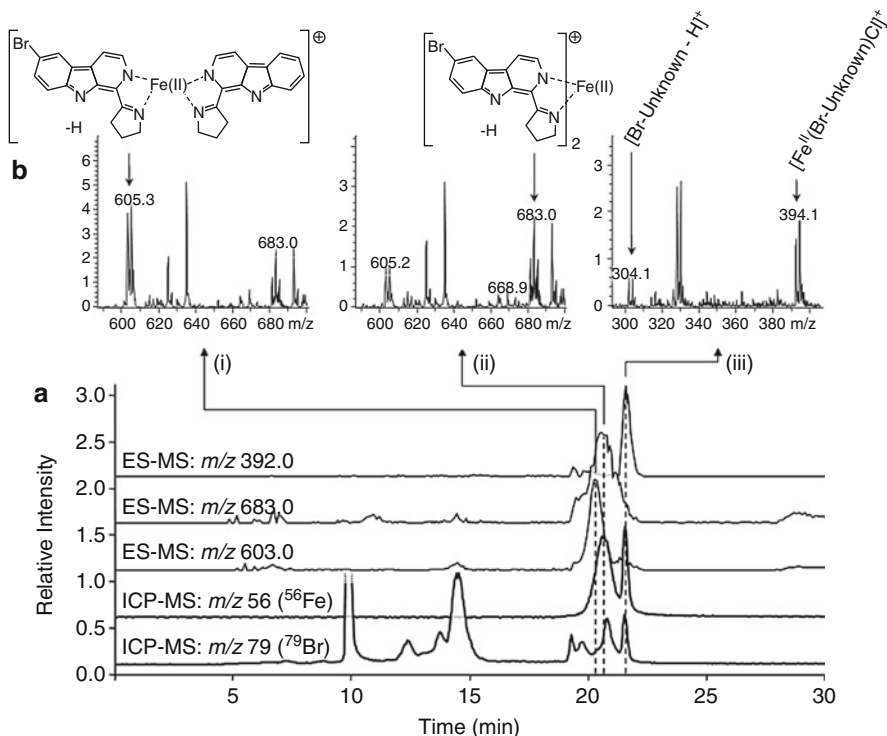


Fig. 16.10 Iron(II) complexes identified in a organic extract of the ascidian *Eudistoma gilboviride* by size exclusion chromatography coupled in parallel to ICP-MS and ES-MS. (a) Selected ICP-MS (Fe, Br) and ES-MS (603, 683, 392 m/z) extracted ion chromatograms. (b) Mass spectra and identifications for peaks at 20.5, 20.8, and 21.6 min [15]

to whether they were present in the organism itself or were formed during the extraction process.

If the metal complexes dissociate during chromatographic separation, other methodologies which do not rely on separation techniques have to be employed, such as electrochemical (EC) detection. These techniques are usually applied to aqueous solutions but have a potential to be used for nonaqueous extracts. EC techniques can thus detect complexes with different stability constants by tuning experimental parameters and can distinguish between free metal ions, labile metal complexes, and inert stable complexes. Although it cannot directly identify the molecular structure of the complex, it is possible to determine the conditional stability constant of the complex. So far, no study has been published which applied EC techniques for the identification of metal complexes in biological extracts. Although EC methods are well-established methods in oceanography, the reason why these are not widely used for the analysis of metal-containing natural products might be the severe matrix problems when they are used in nonaqueous solution.

In order to overcome this problem, and to guarantee the integrity of the metal complex during analysis, direct analytical methods need to be employed which do not rely on the extraction step in the first place, methods that can be used to determine whether a complex is actually present in the organism itself. These are elemental and molecular imaging methods. One type of analysis is based on the absorption of synchrotron radiation. In particular, X-rays generated by tuneable synchrotron radiation can be applied to the specimen, and the absorption is then recorded as a function of the energy. X-ray absorption near edge spectroscopy (XANES) and extended X-ray absorption fine structure (EXAFS) give information about the element and the redox state as well as the bond length to the ligands. For example, it is possible to identify whether arsenic is trivalent or pentavalent and whether it binds to ligands via oxygen or sulfur using the fresh specimen without any extraction steps. EXAFS analysis is often only used for the identification of the redox state of the metal. For example, the identification of the different redox ions in different ascidians (*Ascidia ceratodes* and *Ascidia nigra*) gave evidence of subgeneric differences and was the basis for further investigations to identify vanadium(IV)-binding proteins in ascidians [9, 61].

The drawback of these synchrotron radiation (SR)-based methods is that they cannot be used as routine analysis for screening analysis since beamtime at a synchrotron is limited and very expensive. SR methods can reveal whether any novel metal complexes are disintegrated or formed de novo during the sample preparation and the analysis. The complementary use of XANES/EXAFS methods compared to MS-based methods has never been applied to the identification of novel marine products, but was successfully employed for the identification of arsenic complexes in plants [62].

Another approach is to analyze marine organisms directly using elemental and molecular imaging techniques. Micro-XANES analysis makes it possible to record an element spectrum on a spot the size of 100 μm . Rastering the target in the laser beam enables the construction of an image which contains semiquantitative data of the element distribution in the organism with additional information of its redox state or binding ligands. This can be used to identify the organ in which the most interesting metal complexes are located. Where synchrotrons are not available, other laboratory-based techniques such as LA-ICP-MS (laser ablation ICPMS) can be used for generating elemental maps of the organism. For this analysis, it is necessary to produce thin sections, by microtoming, of the organism, and by interrogating it with a laser beam of variable energy, the material is ablated and transported into the ICP-MS. Multielement maps can be constructed on specimen size up to 10 cm^2 with a spatial resolution as low as 10 μm .

Although these techniques give vital information about the spatial distribution of metals and metalloids, no metal complexes can be identified. Hence, again molecular information is a necessary addition to the elemental mapping. In recent years, new surface molecular imaging methods have been developed which can assist to gain information on small molecules and metal chelates. After a surface application of a matrix of easily ionizable substances, soft ionization of the molecules can

easily transfer the charge to molecules to form molecular ions which can be transported into a mass spectrometer for analysis. This technique is called MALDI-TOF-MS (matrix-assisted laser desorption ionization time of flight mass spectrometry). This method has recently been used to identify secondary metabolites produced by marine cyanobacteria and sponges [63]. The newest development is the use of DESI (desorption electrospray ionization) MS for the localization of natural products directly on the marine organism without applying any matrix on the surface) [64].

If elemental and molecular imaging techniques are used with adjacent thin sections of one organism, metal and ligand maps can be matched and superimposed using image manipulation techniques. This has never been demonstrated with marine organisms, but its potential was demonstrated when it was successfully used to identify metal–protein complexes in a liver abscess [65].

In summary, a variety of analytical methodologies can be used for screening analysis of metal-containing natural products in extracts. To choose the best methodology, readers may refer to a recent review which critically appraises different methodologies for the determination of trace element compounds in biological samples [66].

16.7 Conclusion – A Proposal for a Structured Search for Marine Natural Products Containing Metals

Besides developing the tools to more efficiently discover complexes and ligands from marine invertebrates, it is also worth thinking carefully about how a constructive search for these might be structured. There are some structural features and general considerations which are important when looking for complexes and ligands from marine invertebrates, and these could form the search parameters for a directed search.

The first parameter to consider is the metal content of the invertebrate tissues and organic extracts. A high concentration of metals in the organic extract suggests that they are complexed by an organic ligand. Interest in the eudistomins (e.g., **5**) was aroused by the high content of Fe in the extract of *Eudistoma gilboviride* (Fig. 16.4), which led to the discovery of the eudistomin–iron complex **16** [15]. Therefore, the screening of the organisms to look for transition metals (e.g., Mn, Fe, Co, Ni, Cu, Zn, Mo) in organic extracts will be very productive, but as has been discussed before, few studies have addressed this.

In assessing compounds with potential metal-complexing properties, structural features of known compounds can be very suggestive of good metal ligands. Initially, this may include looking for hard/soft ligands, groups which are involved in metal binding in metalloproteins such as histidine, methionine, cysteine, tyrosine, aspartic and glutamic acid, as well as the coordination environment these present (Fig. 16.5). Additionally, we can look for typical functional groupings found in siderophores and ionophores such as catecholates, hydroxamates, and

β -hydroxyaspartates as well as those present in heteroaromatics (Fig. 16.5). If we are considering the functions of these complexes, such as the generation of reactive oxygen species by the tambjamine (**3**)–copper complex, then the metal center should be coordinatively unsaturated to allow a substrate to bind.

Cyclic compounds have a greatly reduced conformational space compared to acyclic compounds, often allowing them to present ideal coordination environments for metal complexation. This, together with constraining features such as azole rings and prolines, should be given priority as search parameters. Other features such as disulfide bridges also reduce the conformational space accessible.

If we are considering the potential biological functions of these metal complexes, we should look for groups with potential for involvement in redox processes. Some of the compounds have signatures implying the possibility of redox involvement such as disulfide bridges. Similarity to known metalloprotein active sites may also be considered an important search parameter to ascribe a function to a complex, such as the similarity of the patellamide dicopper complexes (Fig. 16.8a, b) to dicopper proteins. A similarity search according to substructures is likely to be less successful than a similarity search based on key coordinating atoms in the active site. One final feature to look out for is protection of the coordination environment by lipophilic groups which might be important for controlling substrate access.

These search parameters, when combined, may lead to the discovery of a number of exciting new complexes from marine invertebrates with associated biological functions and potential for medical or biotechnological applications.

16.8 Study Questions

1. Suggest reasons why marine invertebrates might hyperaccumulate metals. What evidence is there to support each theory?
2. Many marine natural products contain functionality that suggests an ability to complex transition metals. What functional groups and structural features might be important in complexing transition metals? From the marine natural product literature or databases, identify four such structures and propose which metals they might bind to and why.
3. Which physical methods might you use to determine the binding specificity and affinity of marine natural products for transition metals?
4. If you were presented with an organic invertebrate extract that was identified as containing high levels of zinc, what steps would you take to isolate and determine the structure of the zinc complexed to the marine natural product?
5. Draw a flowchart explaining the steps that need to be taken to carry out a structured search for marine natural product metal complexes. You should explain the choice of your steps and the methods to be used at each stage.

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Part 4

Biosynthesis of Marine Natural Products

Angelo Fontana, Emiliano Manzo, M. Letizia Ciavatta, Adele Cutignano, Margherita Gavagnin, and Guido Cimino

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Abstract

This chapter deals with feeding experiments in biosynthetic studies of secondary metabolites from marine organisms. The evolution of the field is traced through a critical report of both review papers published from the 1980s and selected studies published in the latest years. The progress in the methodologies, from simple modification of advanced precursors, through incorporation of substrates with radioactive or stable isotopes, to recent extensive use of molecular genetic techniques, served as a main guideline for the preparation of this overview. Finally, after a section dedicated to the methodologies, the biosynthesis of

*The chapter is dedicated to the memory of Prof. Constantinos Vagias, valuable friend and talented scientist.

A. Fontana (✉) • E. Manzo • M.L. Ciavatta • A. Cutignano • M. Gavagnin • G. Cimino (✉)
Istituto di Chimica Biomolecolare – Consiglio Nazionale delle Ricerche, Via Campi Flegrei,
Pozzuoli (Naples), Italy
e-mail: afontana@icb.cnr.it, emiliano.manzo@icb.cnr.it, letizia.ciavatta@icb.cnr.it,
adele.cutignano@icb.cnr.it, margherita.gavagnin@icb.cnr.it, guido.cimino@icb.cnr.it

oxylipins from diatoms and propionates from Mediterranean sacoglossans, recently conducted in the authors' institute, will be discussed with more detail.

17.1 Introduction

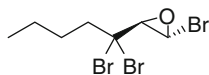
Biosynthesis (bios = life and synthesis = building up) concerns the biochemical process by which simple substrates (e.g., acetate) are converted to complex molecules in living organisms. The subject matter, which has historically occupied a key role in the Chemistry of Natural Products, deals with the biochemical transformations committed to production of a metabolite and also offers unique clues on the regulation of these processes and their relationships with the general metabolism in living organisms. Recently [1], the extensive use of molecular genetic methods opened new and surprising perspectives in this field. However, feeding experiments with labeled precursors continue to offer the basic information to construct a correct biosynthetic pathway. The history of the biosynthesis on marine natural products is quite recent. The first comprehensive review on this topic appeared only in 1983 [2]. It could be interesting to report some words used by the editor to introduce this chapter in the preface of the book: "Our scanty knowledge of living habits of marine organisms and to their adaptation to laboratory conditions has hampered biosynthetic research of marine metabolites. It is hoped that this chapter will stimulate others to venture in this *mare incognitum*." The suggestion was accepted by many scientists, and several overviews [3–9] have recorded the progressive growth from the infancy to the adult age of this research activity. A number of overviews deal with biosynthesis in selected organisms: mollusks [10], dinoflagellates [11], and opisthobranchs [12]; others are dedicated to the biosynthesis of selected classes of compounds: sterols [13], polypropionates [14], algal oxylipins [15], macrolides [16], and isocyanides [17].

In this chapter, we will try to delineate through a critical reading of these reviews the main biosynthetic route in marine natural products covered by using feeding experiments. Recent investigations completed in the last 4 years and some selected studies mainly carried out in the authors' institute will be described with more detail. Finally, for nonexpert readers, a short section, Sect. 17.5, is dedicated to technical issues related to administration and detection of labeled precursors in biosynthetic studies.

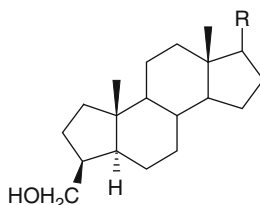
17.2 Main Steps in the History of Feeding Biosynthetic Experiments in Marine Organisms

The chapter by Barrow [2] reports the first biosynthetic experiments on marine organisms. Feeding experiments with a simple labeled precursor, [1-¹⁴C]acetate, indicated that in the sponge *Microciona prolifera* the unusual fatty acids with chain lengths of C₂₄ to C₂₈ are obtained by a chain elongation from C₁₆

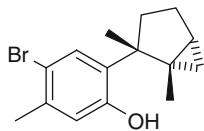
precursors [18]. A polyketide pathway was also detected in the red alga *Bonnemaisonia nootkana* [19] for *trans*-1,3,3-tribromo-1-heptene oxide (**1**). The majority of the feeding experiments reported by Barrow were realized with advanced precursors committed to transformations in the side chains and the polycyclic core of dietary sterols in sponges and also in the skeleton of halogenated sesquiterpenoids of the sea hare *Aplysia californica*. A selected example is the administration of [4- 14 C]cholesterol to sponge *Axinella verrucosa* to prove the biosynthesis of the hydroxymethyl carbon of 3 β -hydroxymethyl-A-norsteranes (**2**) from C-3 of cholesterol by contraction of the ring A followed by bond formation between C-2 and C-4 [20], whereas doubly labeled precursor with tritium at positions 3 and 4 proved the loss of 3 α and 4 β hydrogen atoms [21]. Feeding experiments with tritiated laurinterol (**3**) established the conversion of the algal metabolite **3** into aplysin (**4**) by the opisthobranch *A. californica* [22]. Barrow pointed out the necessity of avoiding conclusions supported only by preliminary evidence: "It seems unwise to speculate and postulate novel chemistry on the basis of feeding experiments," and concluded his chapter with the prophetic expectation for a larger use of stable isotopes in the coming years.



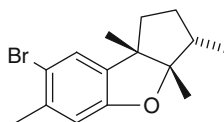
1 *trans*-1,3,3-tribromo-1-heptene oxide



2 3- β -hydroxymethyl-A-norsteranes



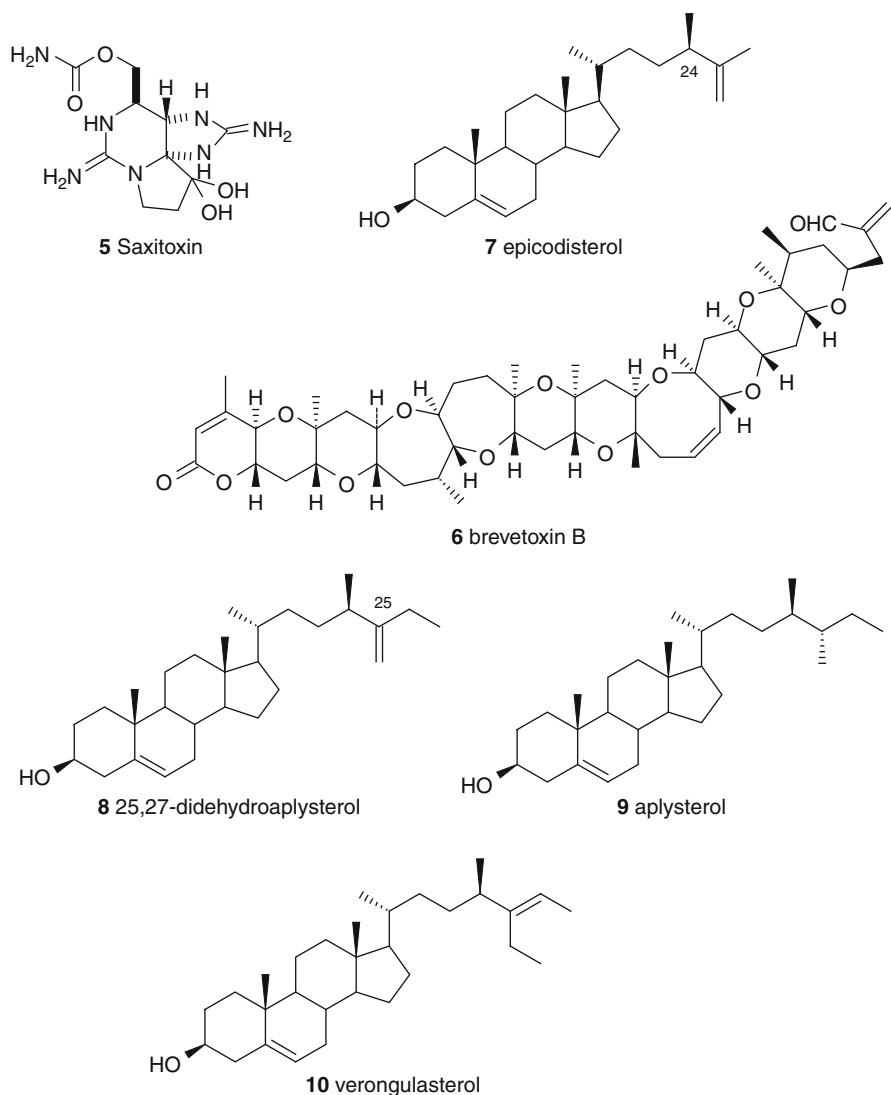
3 Laurinterol



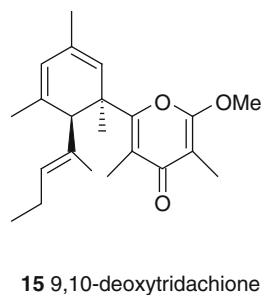
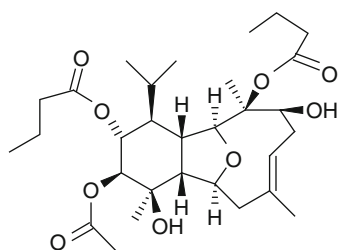
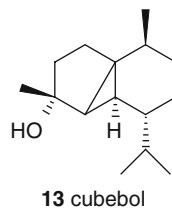
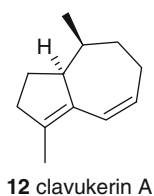
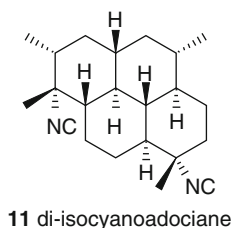
4 Aplysin

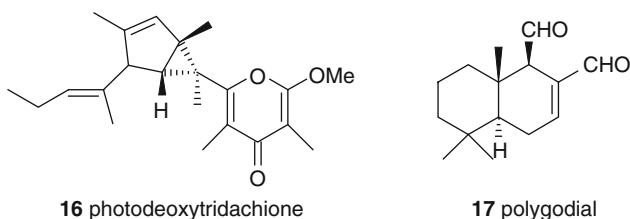
The subsequent reviews by Mary Garson [3, 4] underline the extraordinary development of biosynthetic studies in the late 1980s. These studies embraced the main marine phyla, although stable isotopes were seldom utilized. Most of the general comments reported in these articles are still relevant today. The authors' attention is especially focused on the technical difficulties in biosynthetic experiments with marine organisms, as well as on the potential role of symbiotic microorganisms as true producers of the investigated metabolites. The biosynthetic studies are envisaged as a very promising tool to overcome the uncontrolled harvest of bulk quantities of marine organisms according to a rightful respect of environmental and ecological arguments. The reviews mostly report studies on

microorganisms. Of particular interest is the discussion of the biosynthetic studies [23, 24] on the dinoflagellate toxins saxitoxin (5) in *Gonyaulax tamarensis* and brevetoxins, e.g., brevetoxin B (6), in *Gymnodinium breve*. In line with Barrow, great relevance is given to Djerassi's investigation on the ability of sponges to modify dietary metabolites and, in particular, the side chain of sterols. In this frame, epicodisterol (7), but not its 24-epimer, was identified as precursor of 25,27-didehydroaplysterol (8), aplysterol (9), and verongulasterol (10) in *Aplysina fistularis* [25].

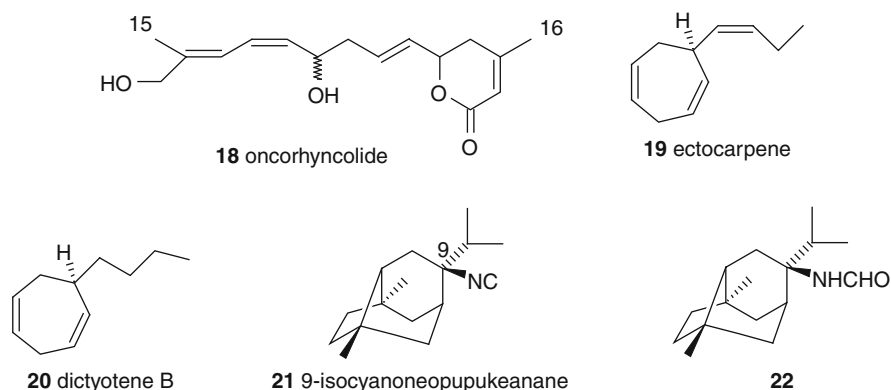


The first rigorous evidence of incorporation of cyanide into a diterpenoid skeleton was obtained studying an *Amphimedon* sponge [26, 27]. Some words on the methodology adopted during this experiment are necessary. The feeding experiments with sodium [^{14}C]cyanide started in small aquaria (6–10 dm³) then the sponge was transplanted to a fixed grid in the sea for almost 30 days. Clear incorporation was detected in both the isocyanide groups present in diisocyanoadociane (**11**). This research opened the way to relevant studies that will be successively discussed. Biosynthesis of terpenes from soft corals has been proven by feeding *Heteroxenia* sp. with [1- ^{14}C]acetate and [2- ^{14}C]mevalonate and detecting clear incorporation into the two terpenoids clavukerin A (**12**) and cubebol (**13**) [28]. The Kuhn–Roth degradation of the labeled mevalonate samples indicated isotopic scrambling due to acetate incorporation after degradation of mevalonate. In the same paper, feeding experiments with [2- ^{14}C]acetate led to radioactive enrichment of the diterpenoid **14** from *Alcyonium molle* due to labeling of the acyl substituents. The result underlines the technical constraint of feeding experiments with radioactive tracers, as well as the risks of putting forward hypotheses based only on this technique. Biosynthesis de novo of 9,10-deoxytridachione (**15**) and photodeoxytridachione (**16**) in the sacoglossan mollusk *Placobranchus ocellatus* was inferred by use of [^{14}C]bicarbonate [29]. In addition to historical value, this paper is a milestone that underlined for the first time the potential of opisthobranchs as candidates for biosynthetic studies. In confirmation of Ireland and Scheuer's insight, the biosynthesis of the terpene skeleton of the defensive allomone polygodial (**17**) was for the first time proved by direct injection of [2- ^{14}C]mevalonate in opisthobranchs of the genus *Dendrodoris* a few years later [30].



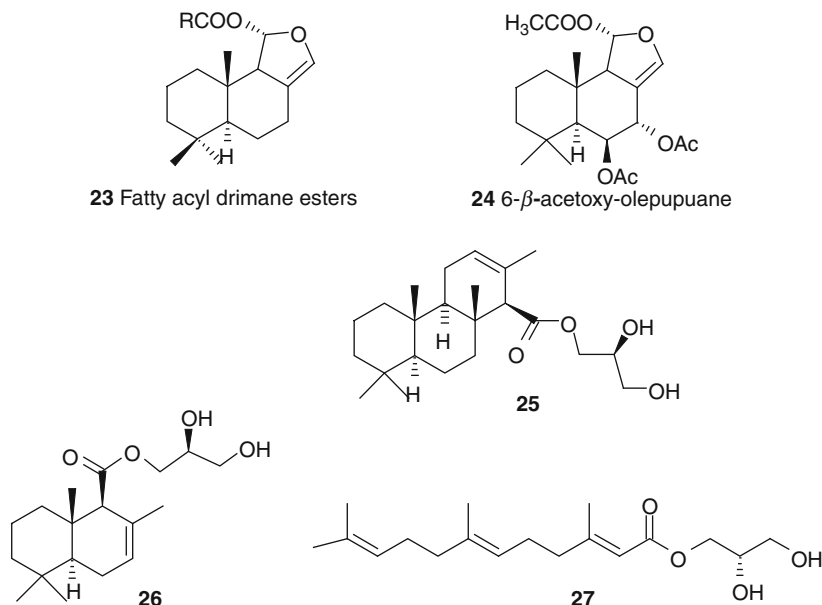


Garson's second review [4] reports the introduction of the use of stable isotopes in biosynthetic experiments with marine organisms. An outstanding example is the study of the bacterial metabolite oncorhyncolide (**18**) through incorporation of seven intact acetate units in the alkyl chain and labeling of carbons 15 and 16 from C-2 of two other acetate units [31]. Biosynthesis of cyanobacteria and dinoflagellate toxins was the subject of different investigations that generally improved the knowledge of these processes. Of particular interest was the study of the volatile pheromones, ectocarpene (**19**) and dictyotene B (**20**), involved in sexual reproduction of brown macrophytic algae (Phaeophyta). Fortuitously, the same metabolites are also produced in the terrestrial plant *Senecio isatideus* by cyclization and decarboxylation of (3*Z*, 6*Z*, 9*Z*)-dodeca-3,6,9-trienoic acid and (3*Z*, 6*Z*)-dodeca-3,6-dienoic acid, respectively, starting from natural C₁₈ [32]. By analogy, the same biochemical pathway was suggested for the algal pheromones. However, feeding experiments with deuterated substrates proved that arachidonic acid is the real precursor of dictyotene B (**20**) in the alga *Ectocarpus siliculosus*. The origin of the pheromones from eicosanoids in algae was confirmed by further studies [33]. The use of doubly labeled [¹³C, ¹⁵N] cyanide established the incorporation of intact C–N bond in the sponge metabolite 9-isocyanoneopopukeanane (**21**) [34]. On the basis of the large coupling constant ($J_{15\text{N}-13\text{C}}$ 13 Hz), hydrolysis of compound **21** to the corresponding formamide **22** was also suggested.



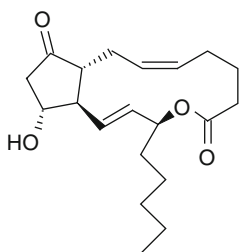
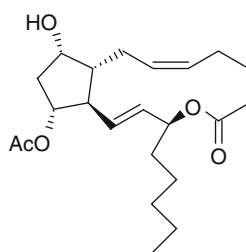
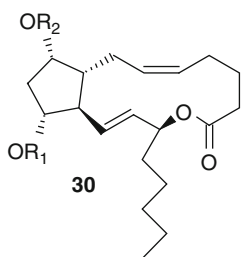
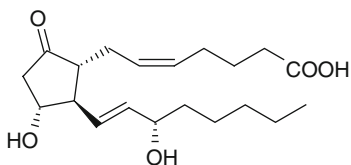
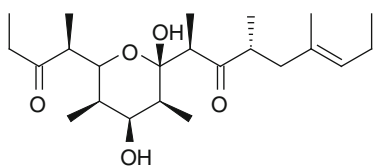
Structural analogies between products from microorganisms, coelenterate, and tunicates were discussed in support to the role of symbionts in the synthesis of the secondary metabolites isolated from the invertebrates. Nevertheless, most of these correlations appear to be only speculative and are not supported by following studies. Much attention

is dedicated to the biosynthesis in mollusks, especially nudibranchs. These invertebrates are apparently vulnerable, the mechanical protection of the shell being completely absent. The animals have replaced the physical protection with a complex defense strategy that also involves the use of chemicals mostly sequestered from the diet. However, in a few examples, the defensive allomones are produced *de novo* by the mollusks [35–37]. Feeding experiments with [2- ^{14}C]mevalonate proved biosynthesis of drimane sesquiterpenoids **17**, **23**, and **24** in the Mediterranean *Dendrodoris limbata* and *Dendrodoris grandiflora* [38–41], as well as of terpene part of glycerides **25–27** in the Canadian *Archidoris montereyensis* and *Archidoris odhneri* [42, 43].

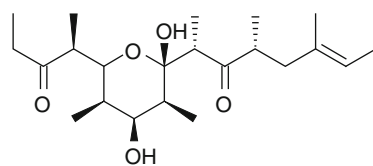


Feeding experiments established the origin of prostaglandin-1,15-lactones from arachidonic acid in the nudibranch *Tethys fimbria* [44–48]. This mollusk adopts a very effective defensive strategy known as autotomy. The nudibranch lives hidden in the sand and, when molested, detaches some dorsolateral appendages named cerata which continue to wriggle for many hours, distracting the predators. The key product is the defensive allomone PGE₂-1,15-lactone (**28**) that is found only in cerata and mucus. Synthesis of this molecule involves formation of PGF_{2 α} -11-acetate-1,15-lactone (**29**) in the mantle. By transesterification, **29** is also the likely precursors of the corresponding 9- and 11-fatty acyl esters (e.g., **30**) in the reproductive glands. Compound **28** is transformed into the corresponding PGE₂ (**31**) that is suggested to induce the contractions of the detached cerata. Another interesting study reported by Garson is that on pulmonate mollusks of the genus *Siphonaria* [49, 50]. Feeding experiments with [1- ^{14}C]propionate led to establish the *de novo* synthesis of very unusual polypropionates: denticulatin A (**32**), denticulatin B (**33**), siphonarins A (**34**), and siphonarins B (**35**). The structural analogy with actinomycete metabolites raised the suspicion that the true producers of marine

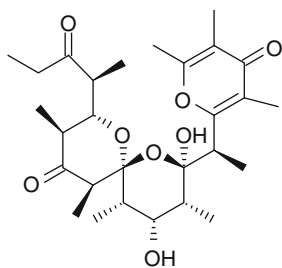
polypropionates could be bacterial symbionts. All these experiments were realized with intact organisms by direct injection of the precursor. This methodology displays a clear advantage from avoiding the dilution of the precursor in the seawater, although the complexity of mollusk physiology and the body barriers sometimes hamper the distribution of the metabolite into the mollusk organs.

28 PGE₂-1,15 lactone29 PGF_{2α},11-acetate-1,15 lactoneR1= H, R2=fatty acyl or
R1= fatty acyl, R2=H31 PGE₂

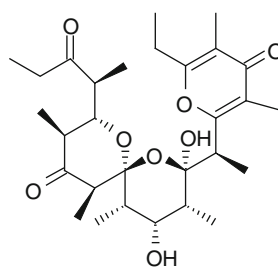
32 denticulatin A



33 denticulatin B

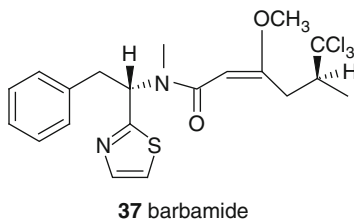
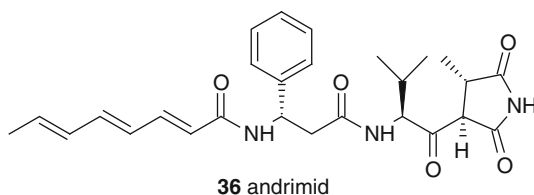


34 siphonarin A



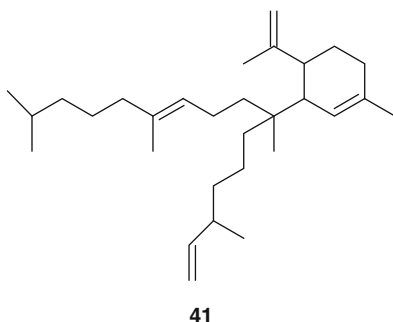
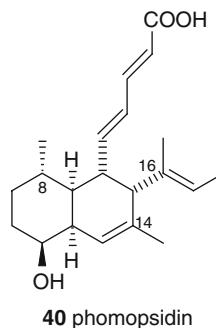
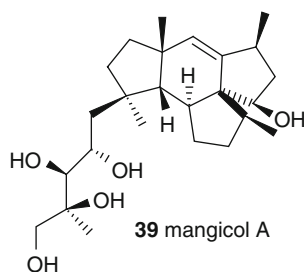
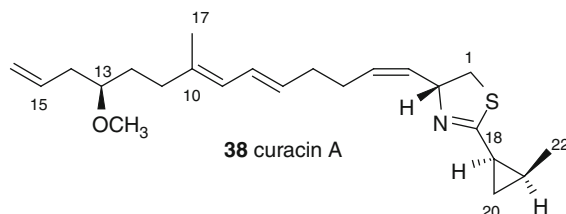
35 siphonarin B

Through three excellent chapters, Moore realized a comprehensive overview on marine biosynthesis covering the literature until the end of 2004 [5, 8, 9]. The first report takes into consideration 10 years (1989–1998) of studies on microorganisms and macroalgae. It proves the enormous development of the use of stable precursors fostered by the progress of NMR and MS instrumentations and the first application of molecular genetic techniques. Particularly active was Andersen's group, which, for example, investigated the biosynthesis of the antibiotic andrimid (**36**), a metabolite produced by the bacterium *Pseudomonas fluorescens* isolated from an unidentified Alaskan tunicate [51]. Experiments with C-13-labeled acetate gave incorporation of intact C₂ units in the acyl chain and in the unusual acylsuccinimide moiety. The experiment also proved the acetate origin of the methyl substituent on the heterocyclic ring, thus suggesting that the succinimide of andrimid derived from a mixed process with acetate and amino acid. Biosynthetic studies in cyanobacteria and dinoflagellates targeted complex polyethers, macrolides, and also small molecules like barbamide (**37**), a halogenated molluscicidal metabolite of *Lyngbya majuscula* [52]. Well-designed experiments with differently [¹³C]-labeled L-leucines proved that chlorination exclusively occurs at the *pro-S* methyl group of leucine. The issue of the true producers of marine natural products is an old one, but remains of current interest. In this review, more than 20 metabolites from sponges and tunicates are suggested to be microbial products on the basis of structural analogies.

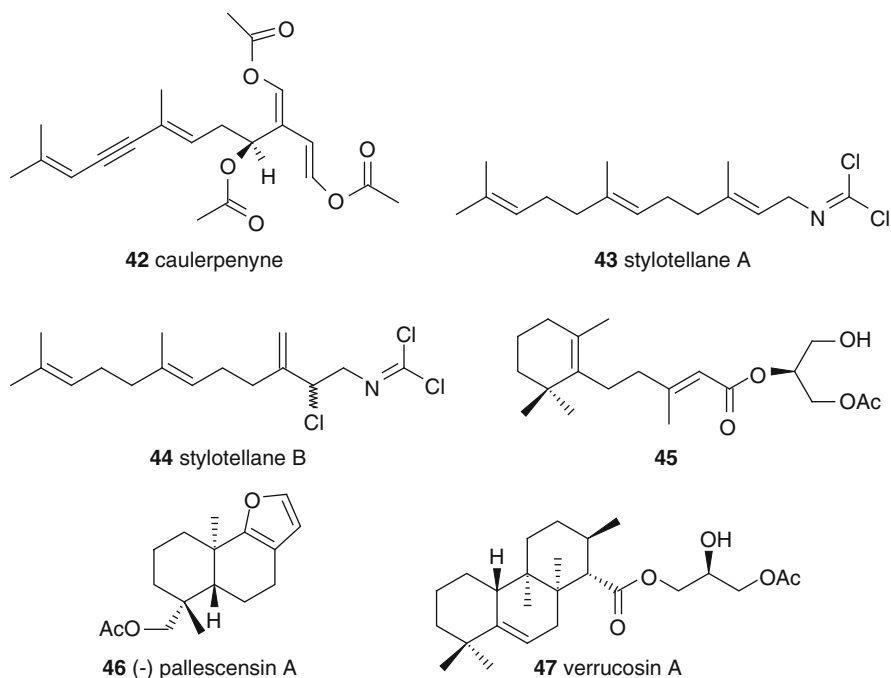


Moore's second review is dominated by the rise of the molecular techniques. This topic is treated with more detail in another chapter of this book. The majority of the overviewed studies are, according to the previous reports, on bacteria, cyanobacteria, and dinoflagellates. A good example is the biosynthesis of curacin A (**38**) [53]. Curacin A was isolated from a Curaçao strain of the marine cyanobacterium *Lyngbya majuscula* and is a potent antiproliferative and cytotoxic agent against many cancer-derived cell lines. Rigorous biosynthetic experiments demonstrated the incorporation of eight intact C₂ units (18/19, 21/22, 4/5, 6/7, 8/9, 10/11, 12/13, 14/15) and the origin of C-16 and C-20 from C-2 of two further acetate units. The methyl groups at C-10 and C-13 incorporated [methyl-¹³C]methionine, whereas the O-13 derived from the oxygen of an acetate unit. These results suggest that the polyketide pathway starts

from cysteine units, and then, after elongation with eight acetate units, a terminal dehydrative decarboxylation leads to the double bond at carbons 15, 16. Surprisingly, the origin of the terminal 5 carbons (from C-18 to C-22) is not isoprenic but is obtained by a Claisen acetyl acetate/acetate condensation. The first biosynthetic studies on marine fungi were also reviewed. Feeding experiments with [^{13}C]acetate proved a mevalonate pathway (MVA) for the sesterterpene mangicol A (**39**) [54] from a *Fusarium* marine fungus, whereas phomopsidin (**40**) from a marine-derived *Phomopsis* fungus incorporated nine intact acetate units and three methyls (at carbons 8, 14, and 16) from L-[S- ^{13}C]methionine [55]. The review also reports some biosynthetic studies on oxylipins and highly branched isoprenoids (HBIs) from diatoms. The first topic will be treated with more particular in one of the following sections of this chapter. Feeding experiments with [1- ^{13}C]acetate [56, 57] on the planktonic diatoms *Rhizosolenia setigera* and *Haslea ostrearia* provided evidence that the terpenoids (sesterterpenoids, sterols, and phytol) from the *H. ostrearia* were biosynthesized following the methylerythritol (MEP) pathway, whereas the branched triterpenoid (**41**) in *R. setigera* was obtained by the MVA pathway that leads first to geranyl pyrophosphate and geranylgeranyl pyrophosphate and then to their coupling.



The last review by Moore [9] deals with the biosynthesis of marine secondary metabolites in marine macroorganisms, especially on oxylipins and halogenated monoterpenes from macroalgae were reviewed. Administration of $[1-^{13}\text{C}]$ acetate and $[^{13}\text{C}]\text{CO}_2$ to the invasive alga *Caulerpa taxifolia* established synthesis of the sesquiterpene caulerpenyne (**42**) from the methylerythritol-4-phosphate (MEP) pathway [58]. The studies on sponges were mainly directed toward the metabolic relationships between sponges and their symbionts through the cellular localization of the secondary metabolites. Feeding experiments with $[^{14}\text{C}]$ -labeled cyanide and thiocyanate clarified the origin of the dichloroimine moiety of two metabolites, stylotellane A (**43**) and B (**44**), isolated from the tropical sponge *Stylotella aurantium* [59, 60]. A relevant part of this review considers again the biosynthesis of opisthobranch products by injection of precursors labeled with stable isotopes. The methodology introduced by Andersen's and Faulkner's groups [61] established the origin of the terpenoids **25**, **27**, and **45** through the mevalonate (MVA) pathway in *A. montereyensis*, *A. odhneri*, and *Sclerodoris tanya*. Analogously, feeding experiments [62] with $[6-^{13}\text{C}]$ glucose and $[^{13}\text{C}_2]$ acetate proved the MVA pathway for the drimane esters **23** and (–)-pallescensin A (**46**) present in *Doriopsilla areolata*, which confirmed the results previously obtained by radioactive precursors [63]. Interestingly, related sesquiterpenoids showing an enantiomeric ring junction of the decaline are also present in a *Dysidea* sponge which could be included in the diet of the mollusk [64]. Feeding experiments with $[6-^{13}\text{C}]$ and $[5-^{13}\text{C}]$ glucose yielded low but complementary labeling that strongly supported the MVA origin of the terpene part of verrucosin A (**47**), a toxic glyceride of the nudibranch *Doris verrucosa* [65].



This 30-year ride among the main biosynthetic studies on marine natural products reveals the outstanding and independent contribution of many groups from all over the world for the progress of the field. After the pioneering and stylish studies with radioisotopes, the introduction of stable isotopes has led to a tremendous advancement in the knowledge of biosynthetic mechanisms. As Moore suggested on the verge of the marine genomic era [8], the extensive application of the molecular methodologies is expected to have an even more important impact in deepening our understanding and appreciation for complex marine pathway.

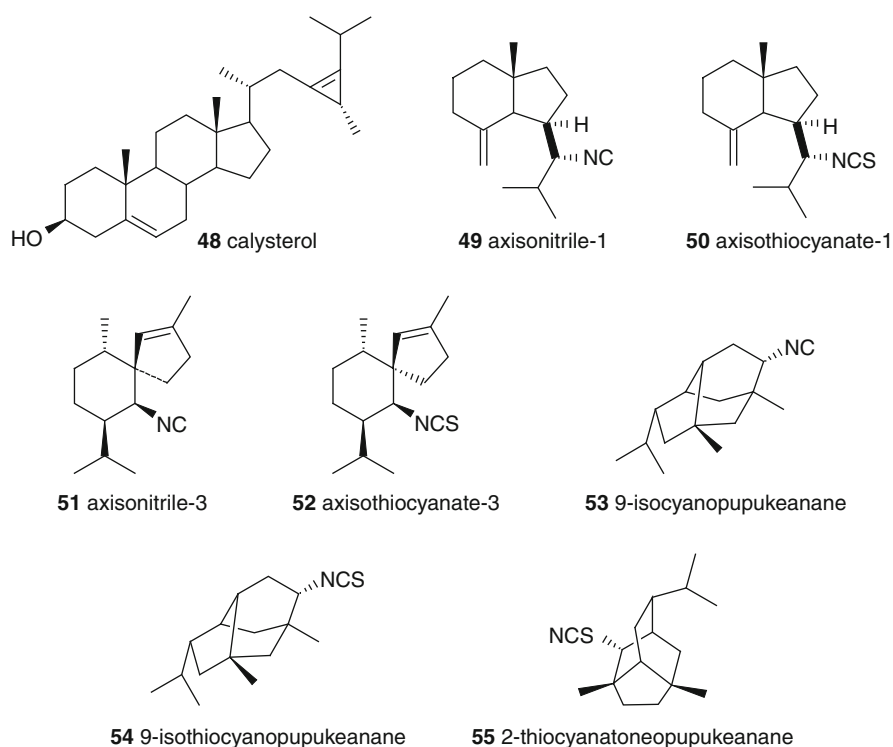
17.3 Main Steps on Selected Biosynthetic Topics

Reports of biosynthetic data on specific topics are extremely numerous. Our selection of the topics discussed in this chapter has been driven by the idea to provide a general view of the biosynthesis by feeding experiments in marine organism.

From the 1990s, a series of review papers have been focused on specific biosynthetic topics. The biosynthesis of marine sterol side chains was overviewed by Giner [66]. The chapter covers the studies on sterols from different organisms even if the major attention was paid to sponges. This primitive group of multicellular organisms displays the richest variety of unusual sterols. The first structural studies led to the characterization of sterols featured by unusual chains, e.g., aplysterol (**9**) [67] and calysterol (**48**) [68], and A-nor and 19-nor nuclei [69, 70]. After the first biosynthetic studies by Minale's group on these compounds [71], a development of the subject was mostly due to the impressive contribution of Carl Djerassi by use of radioisotopes [72]. These studies established the first elucidation of the chemical mechanisms responsible for dealkylation and methylation of the side chain, as well as for the construction of cyclopropyl and cyclopropenyl rings. Giner's overview reports a detailed presentation of the biosynthetic experiments that reveal the ability of sponges to modify dietary sterols but not to carry out *de novo* synthesis.

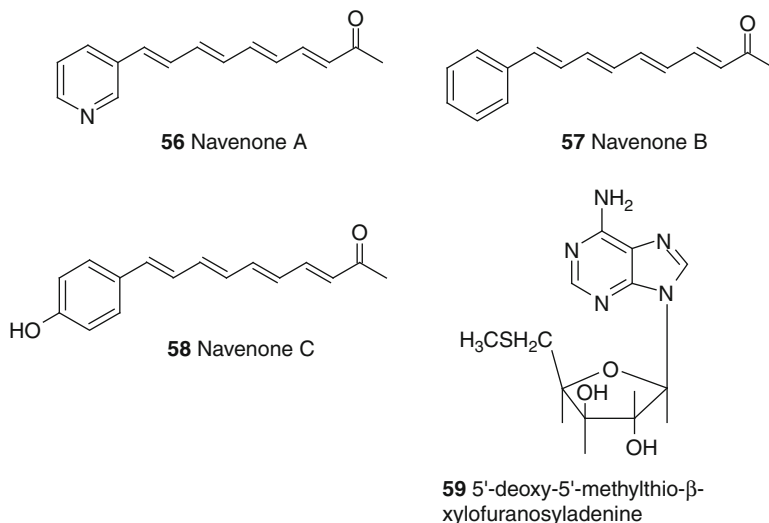
Biosynthesis of marine isocyanides and related natural products was recently reviewed [17], and the relevance of the topic suggests us to discuss the key points. In 1973, Fattorusso's group reported the finding of the first marine terpene isocyanides, axisonitrile-1 (**49**) and axisothiocyanate-1 (**50**), in the Mediterranean sponge *Axinella cannabina* [73]. These compounds exemplify a family of which members have been isolated from other sponges and invertebrates. Generally, isocyanides co-occur with the corresponding isothiocyanates, for example, axisonitrile-3 (**51**) and axisothiocyanate-3 (**52**) [74], and their biosynthetic origin has been for long time a challenging task. The first evidence that sponges are able to link inorganic cyanide to terpene skeletons was obtained by Garson [26]. Feeding experiments with [¹⁴C]cyanide on the sponge *Amphimedon terpenensis* resulted into the incorporation of radioactivity in the diterpene diisocyanoadociane (**11**). Later, the same authors observed that compounds **51** and **52** incorporate both labeled thiocyanate and cyanide in *Acanthella cavernosa* [75]. The sponge was able to interconvert cyanide and isothiocyanate before or after the incorporation in the secondary metabolite. Analogous results were obtained studying the biosynthesis of 9-isocyanopopukeanane (**53**) and 9-isothiocyanopopukeanane (**54**) in

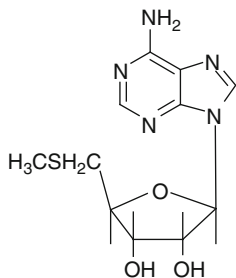
the sponge *Axinissa* n.sp. [76]. In another experiment, in addition to **53** and **54**, inorganic cyanide and isothiocyanate were incorporated into 2-thiocyanatoneopupukeanane (**55**), thus strongly supporting that the conversion precedes synthesis of the secondary metabolite. In the same paper, the authors reported experiments with advanced labeled precursors, [^{14}C]9-isocyanopupukeanane (**53**) and [^{14}C]9-isothiocyano-pupukeanane (**54**), that proved the interconversion of the two compounds and the role of inorganic thiocyanate as former precursor. Nudibranchs belonging to the Phyllidiidae family generally are protected by terpene isocyanides and related metabolites of dietary origin [77, 78]. When the nudibranch *Phyllidiella pustolosa* feeds upon *A. cavernosa* incubated with [^{14}C]cyanide and [^{14}C]thiocyanate, labeled axisonitrile-3 (**51**) and axisothiocyante-3 (**52**) were detected in the mollusk. In control experiments, no incorporation was found after injection of radioactive salts into the mollusk.



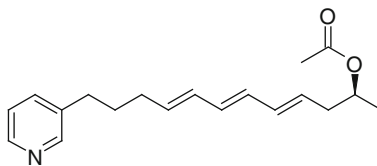
Opisthobranchs are another group of marine invertebrates that has been the subject of numerous biosynthetic studies [10, 12]. In addition to the elucidation of the biochemical pathways, distribution of the labeled metabolites among the different organs and tissues has been envisaged as a tool to investigate the physiology and ecology of these mollusks. Most of these studies concern successive development of the themes discussed in three milestone papers about the biosynthesis of navenones A–C (**56–58**) in cephalaspideans the biosynthesis of 9,10-deoxytridachione (**15**) and photodeoxytridachione (**16**) in sacoglossans [29], and biosynthesis of polygodial (**17**)

in nudibranchs [30]. Relevant exceptions were the above-reported biosynthetic studies on prostaglandin lactones from *Tethys fimbria* [47, 48] and the nucleotide **59** [80], the first naturally occurring analogue of MTA (5'-deoxy-5'-methylthioadenosine, **60**), from the Mediterranean *Doris verrucosa*. Use of stable isotopes has been a crucial factor in the latest investigations with opisthobranchs and has improved our understanding of secondary metabolism in marine invertebrates. Biosynthesis of the alkyl pyridine skeleton of haminol (b61) clearly shows the potential of this approach. Haminol 2 (b61) is the prototype of a family of compounds present in the cephalaspidean *Haminoea*. Its structure is closely related to that of navenone A (b56) but also to the complex architecture of sponge 3-alkypyridines. Feeding experiments with d₄-nicotinic acid, [1-¹³C]acetate, and [1,2-¹³C₂]acetate proved that haminol 2 (b61) is biosynthesized by the mollusk starting from nicotinic acid that is elongated with six acetate units with decarboxylation of the last C₂-unit [81, 82]. In another experiment with the dorid nudibranch *Acanthodoris nanaimoensis*, administration of [1,2-¹³C₂]acetate clarified that the aldehyde group at C-11 of isoacanthodorol (b62) is obtained by shift of C-12 from C-9 to C-11 [83]. In fact, after the injection of the labeled precursor, all carbons of compound b62 exhibited clear incorporation according to a classic mevalonate pathway. Nevertheless, only five intact units were detected, whereas no coupling was observed for C-9 and C-12. The study with stable isotopes ([6-¹³C]glucose, [5-¹³C]glucose, [1-¹³C]acetate, [1,2-¹³C₂]acetate) of the biosynthesis of drimane sesquiterpenoids in porostome nudibranchs was also overviewed. These experiments confirmed the results previously obtained with radiolabeled precursors on compounds b17, b23 and b24 [30, 38] and proved that all these metabolites are biosynthesized according to a classic mevalonate (MVA) pathway. In particular, the clear biosynthesis of 7-deacetoxyolepupane (b63) in the nudibranch *Dendrodoris limbata* is of relevant interest [84]. In fact, compound b63 has also been found in a *Dysidea* sponge [85] that could be included among the preys of the mollusk, but its dietary origin was rigorously ruled out by the clear incorporation of ¹³C in all positions predicted according to a MVA pathway.

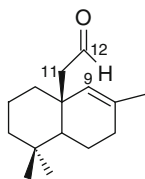




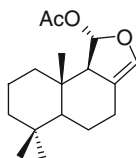
60 5'-deoxy-5'-methylthioadenosine



61 Haminol 2



62 Isoacanthodoral



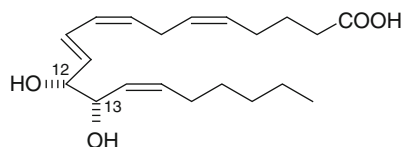
63 7-deacetoxyolepupane

Labeled propionates have been used in the biosynthesis of the sacoglossan metabolites. Polypropionates are very rare in nature. They are unknown in animals, with the surprising exception of some higher marine gastropods (opisthobranchs and pulmonates). Otherwise, their presence is restricted to terrestrial bacteria and fungi, where they are produced through different biosynthetic pathways from propionate or acetate-methionine, respectively. The topic was overviewed in excellent manner by Davies-Coleman and Garson [14] and will be treated with more detail in Sect. 17.7 of this chapter.

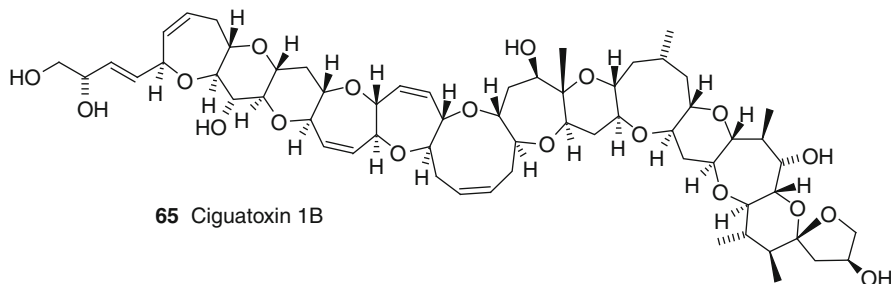
Feeding experiments were extensively applied in the study of oxylipin biosynthesis in algae. The matter was extensively reviewed by Gerwick [15]. The three major groups of macrophytic algae possess unique oxylipins. Generally, red algae (Rhodophyta) metabolize C₂₀ acids by oxidation at C-12; green algae (Chlorophyta), C₁₈ acids, by oxidation at carbons 9 and 13; and brown algae (Phaeophyceae), both C₁₈ and C₂₀, by selective lipoxygenase that recognize (*n*-6) polyunsaturated fatty acids. Experiments led to the understanding of the biosynthesis of vicinal diols like 12*R*,13*S*-dihydroxyeicosatetraenoic acid (**64**) in the red alga *Glacilariaopsis lemaneiformis*. Cell-free preparation of the alga was treated [86] with exogenous arachidonic acid under an atmosphere enriched in ¹⁸O₂. Compound **64** was recovered as methyl ester and exhibited incorporation of ¹⁸O in both hydroxyl groups. Further experiments with advanced precursors [87] established that both oxygen atoms derive from a single molecule of oxygen, concluding that vicinal diols in *G. lemaneiformis* are biosynthesized by sequential action of an arachidonic acid 12*S*-lipoxygenase followed by a hydroperoxide isomerase.

Dinoflagellates possess potent toxins that display at least three different skeletons: polyether ladders (e.g., ciguatoxin 1B, **65**), linear polyethers (e.g., okadaic acid, **66**), and macrolides (e.g., amphidinolide B, **67**). The marine dinoflagellates of

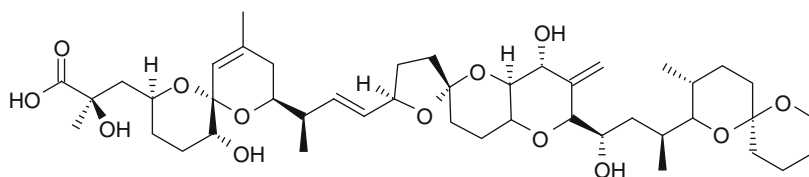
the genus *Amphidinium* produce an impressive series of macrolides, of which biosynthesis has been surveyed by Kobayashi and Tsuda [16]. The incorporation pattern after feeding experiments with $[1,2-^{13}\text{C}_2]$ acetate revealed the acetate origin for all carbons of the macrolides and, in particular, all carbons of the branched methyls were derived from C-2 of acetate and linked either to C-1 of intact acetate or to an isolated C-2 of acetate. The apparent anomaly that the polyketide chain is interrupted by isolated C-2 of acetate units has been justified through an oxidation of C-2 of an acetate unit to α -diketide followed by a Favorskii-like rearrangement that leads to C-1 deletion by elimination of carbon dioxide [88].



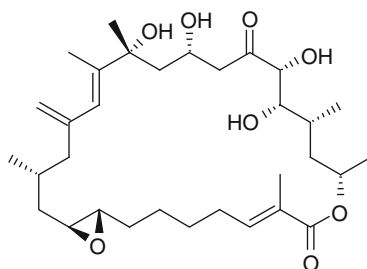
64 12*R*,13*S*-dihydroxyeicosatetraenoic acid



65 Ciguatoxin 1B



66 Okadaic acid



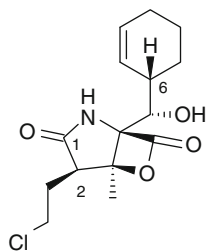
67 Amphidinolide B

17.4 Recent Feeding Biosynthetic Studies

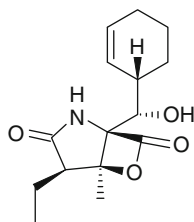
Lately, a variety of biosynthetic researches have been carried out especially in marine microorganisms, algae, and mollusks. Some of these studies are discussed with more detail in this section.

The biosynthesis of salinosporamide A (**68**) was established by Moore's group [89–91]. This work is an excellent example of the importance of rigorous feeding experiments to predict metabolite assembly in biological systems. Salinosporamides (**68–72**) are potent anticancer agents produced by the marine bacterium *Salinispora tropica* [92–94]. They are characterized by a densely functionalized γ -lactam- β -lactone bicycle displaying at C-2 an alkyl substituent sometimes halogenated in ω position. Recently, the salinosporamide family has been enlarged to embrace a related metabolite, cinnabaramide A (**73**), isolated from a terrestrial streptomycete [95]. In consideration of the structural features of salinosporamides A and B (**68** and **69**), coupling of acetate, butyrate, and a nonproteinogenic phenylalanine derivative was predicted as putative biogenesis of both bacterial polyketides. According to this hypothesis, feeding experiments with [1,2- $^{13}\text{C}_2$] acetate led to the incorporation of three intact acetate units in salinosporamide B (**69**) but, surprisingly, only one intact acetate unit in salinosporamide A (**68**). Administration of [U- $^{13}\text{C}_6$] glucose gave enrichment of all carbons of both compounds but showed an enrichment pattern in agreement with the results from the [1,2- $^{13}\text{C}_2$] acetate. The data indicated an apparent divergence in the biosynthesis of the four-carbon fragment bearing the chlorination site, which initially was interpreted as implying the use of tetrose for **68** or butyrate for **69**. Contribution of these building blocks could not be proven, whereas the authors reported the involvement of the unusual chloroethylmalonyl-CoA in **68** and ethylmalonyl-CoA in **69** [91]. Interestingly, these new PKS extender units arose from two different biochemical pathways that fully agreed with the labeling results. The role of ethylmalonyl-CoA as biosynthetic precursor had been previously reported by Kubanek and Andersen in the opisthobranchs *Triopha catalinae* and *Diaulula sandiegensis* (reviewed in ref. [9]). According to this hypothesis, feeding experiments with [1- ^{13}C]propionate in other salinosporamides led to clear incorporation at C-1 of salinosporamide D (**70**) but also at C-12 of salinosporamide E (**71**) [90]. Compound **71** could be obtained by using a pentanoate building block derived from acetate and propionate precursors. Good incorporation was also observed giving pentanoic acid, but better results were obtained with *trans*-2-pentenoic acid, suggesting that α,β -pentenoic carboxylic acids are an advanced intermediate in other salinosporamides. The feeding experiments also ruled out the anticipated function of phenylalanine. In fact, [1- ^{13}C] phenylalanine was not incorporated into **68**, whereas the origin of the aromatic residue from shikimate was verified; after that, C-1, but not C-7, of [1,7- $^{13}\text{C}_2$] shikimic acid (**74**) was assimilated at C-6 of **68** [89]. On this basis, a hybrid polyketide synthase-nonribosomal peptide synthetase (PKS-NRPS) pathway was suggested. This nice work is emblematic to testify the impressive progress in the biosynthesis of marine natural products but also to draw attention on the key role of the feeding experiments with stable isotopes. The information on the exact site of incorporation is extremely

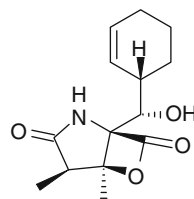
informative and allows the elucidation of the chemical mechanism also in unusual process, such as the rare case of PKS assembly based on pentyl building blocks.



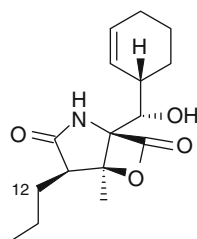
68 Salinosporamide A



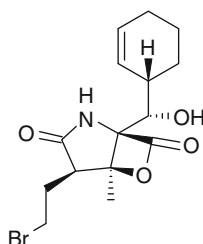
69 Salinosporamide B



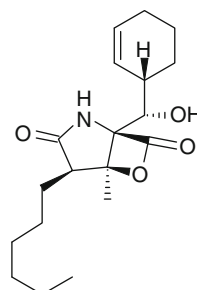
70 Salinosporamide D



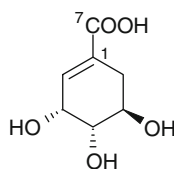
71 Salinosporamide E



72 Bromosalinosporamide



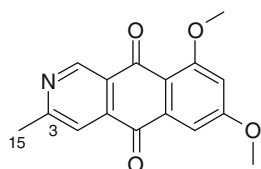
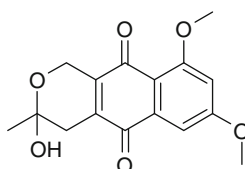
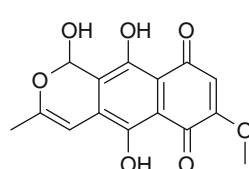
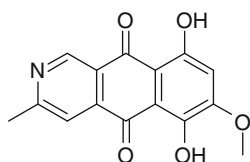
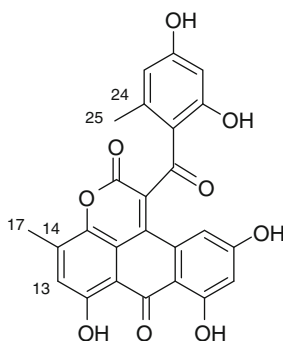
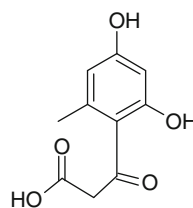
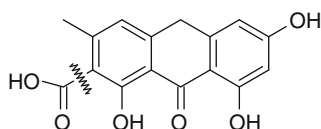
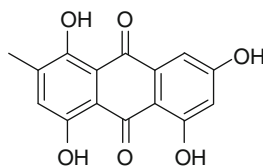
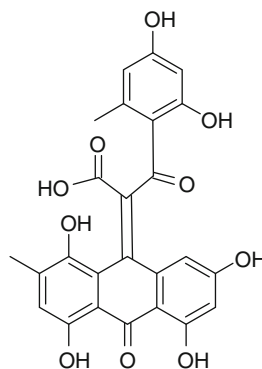
73 Cinnabaramide A



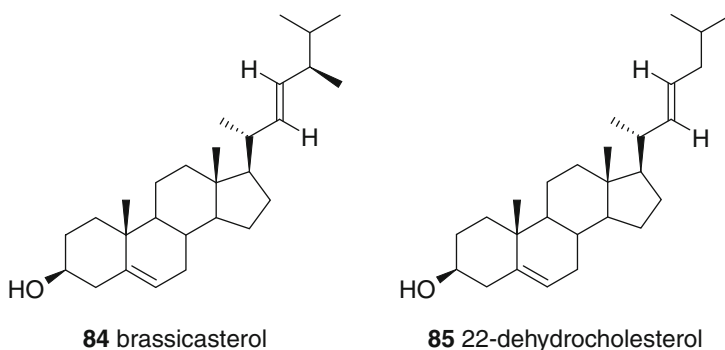
74 Shikimic acid

Biosynthesis in marine fungi is a recent topic in marine science, and a few successful investigations have been reported only in the latest years. Scorpinone (**75**) is a 2-aza-antraquinone present in the fungus *Amorosia littoralis* isolated from marine sediment [96, 97]. Two alternative biosynthetic pathways can be suggested. The first involves a polyketide structure containing seven linear acetate units with subsequent incorporation of a nitrogen atom, the second, six acetate units linked to alanine (N, C-3, C-15) with final decarboxylation. Feeding biosynthetic studies [98] with [2-¹³C]acetate and [1,2-¹³C₂]acetate confirmed the first hypothesis. In fact, seven intact acetate units were incorporated in scorpinone (**75**). The same incorporation was observed in herbarin (**76**), a related co-occurring metabolite previously isolated from the yeast *Torula herbarum* [99]. Herbarin displays a cyclic hemiketal structure where oxygen replaces nitrogen at position 2 of **75**. Herbarin could be the precursor of scorpinone. This hypothesis is well supported by the interconversion in benzene containing excess ammonia between two related metabolites, anhydrofusarubin lactol (**77**) and bostrycoidin (**78**), isolated from terrestrial fungi [100]. Aspergiolide A (**79**) is a novel

antitumor compound produced by the marine-derived filamentous fungus *Aspergillus glaucus* [101]. The clear polyketide pathway was recently investigated by a series of feeding experiments with [1- ^{13}C]acetate, [2- ^{13}C]acetate, and [1,2- $^{13}\text{C}_2$]acetate [102]. All carbons of **79** displayed good incorporation. Twelve intact acetate units were detected, whereas the signal of C-13 showed a single enrichment deriving from C-2 of acetate. The ^{13}C labeling observed for all carbons of **79** excluded the possibility that the polyketide pathway starts from a single acetate unit with subsequent elongation with 12 C_2 extender units and decarboxylation of the last fragment. Actually, aspergiolide (**79**) is biosynthesized starting from two acetate units, C-25/C-24 and C-17/C-14, which are elongated with four and seven C_2 extender units, respectively, giving two intermediates, A (**80**) and B (**81**). Decarboxylation of **81** leads to catenarin (**82**), a polyketide previously isolated from *A. glaucus* [103]. Aldol condensation between intermediate A and catenarin gives the putative intermediate C (**83**), which after an intramolecular esterification forms aspergiolide (**79**).

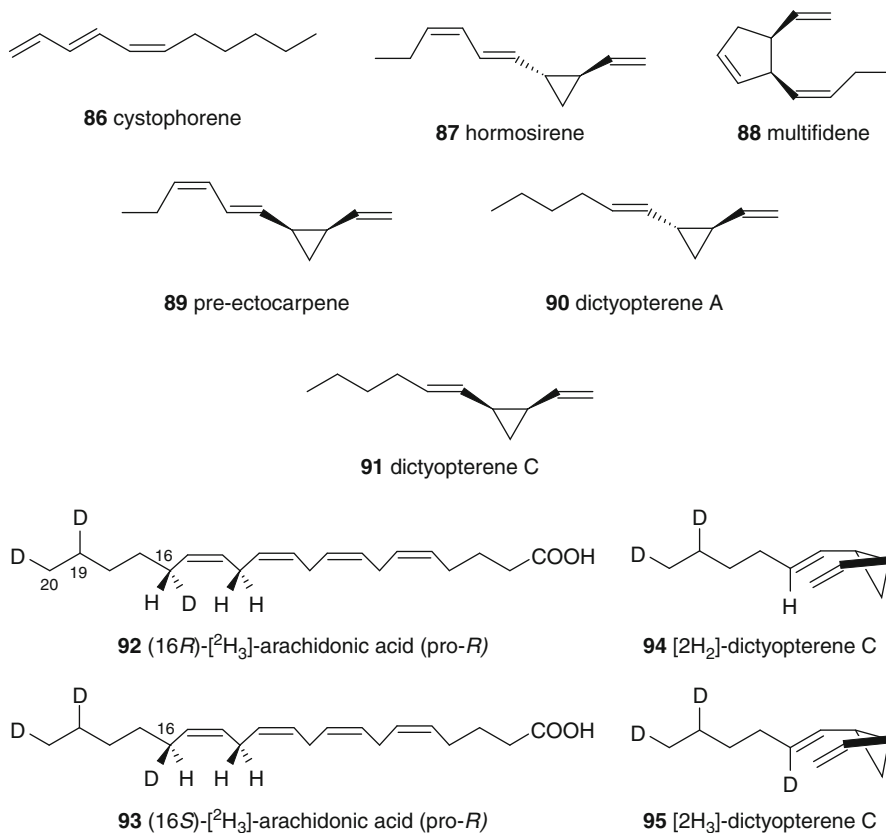
**75** scorpinone**76** Herbarin**77** anhydrofusarubin lactol**78** bostrycoidin**79** aspergiolide A**80** intermediate A**81** intermediate B**82** catenarin**83** intermediate C

An interesting biosynthetic procedure was used by Chu's group for the inspection of two marine heterotrophic dinoflagellates species, *Oxyrrhis marina* and *Gyrodinium dominans* [104]. The authors proved that the two protists are not able to biosynthesize de novo the sterol core, but *G. dominans* can alkylate and desaturate dietary sterols, transforming cholesterol into brassicasterol (**84**) and 22-dehydrocholesterol (**85**). This result, which closely resembles Djerassi's conclusions with sponges, is of great importance for the innovative methodology employed in the work. Advanced precursors were sequestered by the two protists through the microalga *Perkinsus marinus* which is not able to biosynthesize sterols but accumulates them. The microalga was cultured in a medium with [3,4-¹³C]cholesterol and then was offered to the two protists. GC/MS analysis revealed in *P. marinus* the presence of cholesterol and **85**. The same mixture was detected in *O. marina* whereas the sterol pattern of *G. dominans* exhibited the enhancement of compound **85** together with brassicasterol (**84**) and other three unidentified C₂₈, C₂₉, and C₃₀ sterols. The authors also tried to deliver [¹³C]brassicasterol to *O. marina* and *G. dominans* by the same methodology in order to establish whether the two dinoflagellates are able to demethylate the sterol. C-13-labeled brassicasterol (**84**) was produced by the unicellular alga *Rhodomonas salina* cultured in f/2 medium enriched with [¹³C]CO₂. Assimilation of this product into *P. marinus* was unfortunately unsuccessful because of the inability of the microalga to grow in culture medium containing the labeled compound. Because of this, gelatin acacia microspheres (GAMs) containing labeled brassicasterol with dimensions similar to those of *P. marinus* were prepared and delivered to *O. marina* and *G. dominans*. Labeled [¹³C] carbons were detected only in brassicasterol (**84**). On the contrary, *G. dominans* displaying labeled C_{29:1} and C_{30:0} sterols confirmed its ability to alkylate dietary sterols. In this study, the incorporation of labeled substrates was detected only by mass spectroscopy. The feeding methodology is however of great interest, and, whenever associated with analysis by NMR spectroscopy, could be of general application in biosynthetic studies with marine protists.



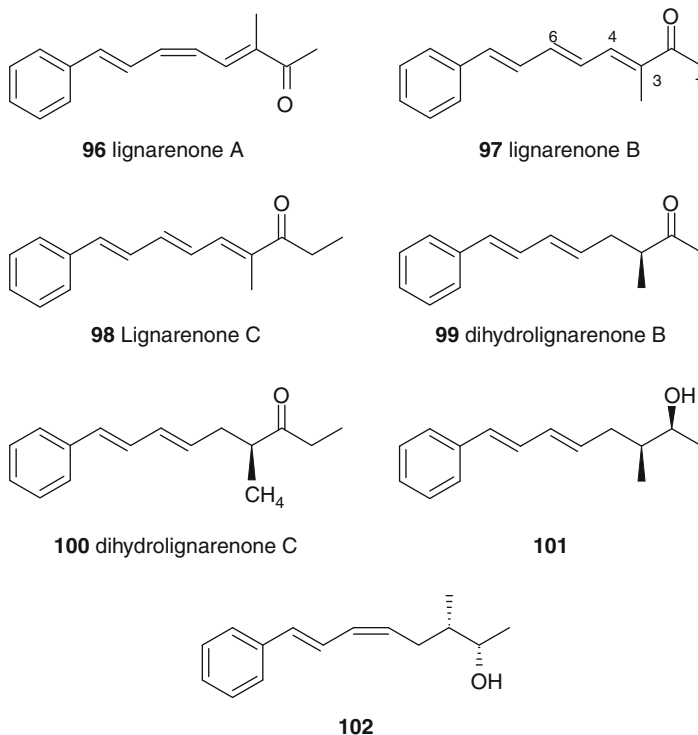
During sexual reproduction, female gametes of brown algae release C₁₁ hydrocarbons that attract their male partners [33]. These compounds show linear and monocyclic structures (**19**, **20**, **86–91**) that derive from the aliphatic terminus of polyunsaturated fatty acids, including arachidonic acid and eicosapentaenoic acid [105]. The mechanistic details of this process have been very recently addressed in the

brown alga *Ectocarpus siliculosus* by Rui and Boland [106]. Algal pheromone production in *E. siliculosus* is particularly interesting since the genuine lipoxygenase product pre-ectocarpene (**89**) is inactivated by a Cope rearrangement to ectocarpene (**19**) (2,000-fold less active than **89**) in a short time [107]. Administration of chirally labeled precursors, (16*R*)- and (16*S*)-[16,19,20-²H₃]arachidonic acids (**92**, **93**), to the culture of the algal gametes gave [²H₂]dictyopterene C (**94**) and [²H₃]dictyopterene C (**95**), respectively, proving in a rigorous manner that cycle formation is associated to loss of the C(16)-H_R. The paper shows also an elegant synthesis of the deuterated substrates by Wittig reaction involving a chirally labeled hexanal.



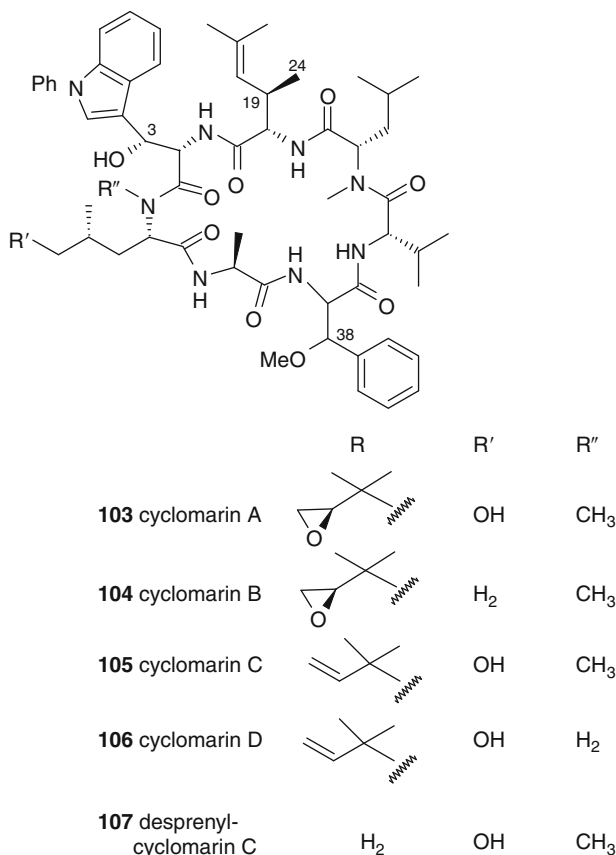
During the last few years, some biosynthetic experiments with stable isotopes were undertaken to study the polypropionate pathway in opisthobranch mollusks. Most of them will be discussed in the last section of this chapter. An apparent propionate unit is also present in lignarenones (**96–102**), aryl-alkenyl metabolites possessed by the cephalaspidean mollusk *Scaphander lignarius* [108, 109]. Feeding experiments with [²H₅]phenylalanine [110] led to a strong incorporation in lignarenone B (**97**), then injecting [1,2-¹³C₂]acetate, two intact acetate units were detected by ¹³C-NMR at carbons 7/6 and 5/4, whereas a clear enhancement was

observed for C-1. No incorporation was recorded at carbons 2/3/8 that, apparently, could belong to a propionate unit. This hypothesis was recently confirmed in the authors' institute [111] by a feeding experiment with [3-²H₃]propionate. In conclusion, benzoic acid is elongated by two extender acetate units, then one propionate unit, and, finally, another acetate unit to give the lignarenones **98** and **100**, whereas the loss of the last carbon leads to lignarenones **96**, **97**, **99**, **101**, and **102**. Probably, an analogue pathway could be suggested for navenone B (**57**) [79].



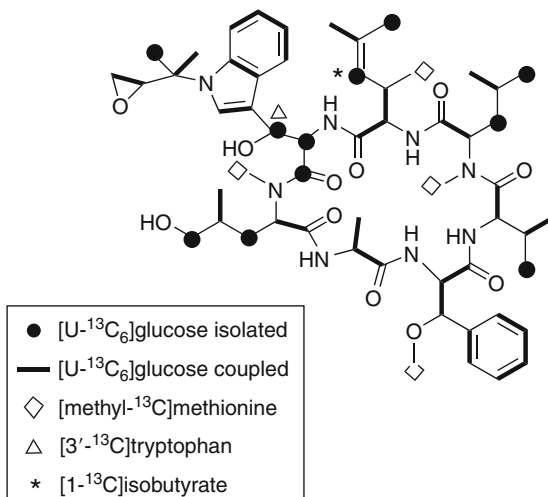
Feeding experiments with stable isotope-containing precursors is an extraordinary tool to investigate the complex mechanistic implications of natural product pathways. Also, as demonstrated by the biosynthesis of salinosporamides [89–91] described above, they represent an essential complement to molecular genomic techniques. In this view, an excellent paper that combines both approaches concerns the biosynthesis of cyclomarins A (**103**) [112]. Cyclomarins A–C (**103–105**) are potent anti-inflammatory marine natural products isolated from an estuarine streptomycete, strain CNB-982 [113]. Cyclomarins A and C were also found in another marine actinomycete, *Salinispora arenicola* CNS-205 from Palau, along with two truncated diketopiperazines, cyclomarinazine A and B, and other cyclomarin derivatives, cyclomarin D (**106**) and desprenyl cyclomarin C (**107**) [114–116]. Cyclomarin A (**103**) is a 21-membered cyclic heptapeptide with five modified nonproteinogenic amino acid residues. The fragments are (1) *N*-(1,1-dimethyl-2,3-epoxypropyl)- β -hydroxytryptophan,

(2) *N*-methyl- δ -hydroxyleucine, (3) alanine, (4) β -methoxyphenylalanine, (5) *N*-methylleucine, (6) valine, and (7) 2-amino-3,5-dimethyl-4-hexenoic acid (ADH).



Feeding experiments with stable isotopes on *Streptomyces* sp. CNB-982 are summarized in Fig. 17.1. Incorporations prove that the moieties 1, 2, and 5 derive from standard amino acids by simple modifications, including oxidation at C-3 and C-38, methylation of two amides and C-38 oxygen, and prenylation at the nitrogen atom of the pyrrol ring. Administration of [*U*-¹³C]glucose also established that the prenyl unit arises, prevalently from mevalonate pathway (MVA) with a minor contribution from the methylerythritol pathway (MEP). Despite incorporation at C-20 from [1-¹³C] isobutyrate, at C-24 by methylation from [methyl-¹³C]methionine, and, finally, at carbons 17–19 from [*U*-¹³C]glucose, the biosynthesis of the 2-amino-3,5-dimethyl-4-hexenoic acid (ADH) fragment was unresolved by the feeding experiments. On the contrary, molecular genetic methods suggested an origin of ADH from isobutyrate, pyruvate, and methionine precursors. In conclusion, this nice work establishes by complementary experiments that cyclomarins are biosynthesized through a nonribosomal peptide synthetase (NRPS) able to link nonproteinogenic amino acids in cyclic peptide products.

Fig. 17.1 Feeding experiments in cyclomarins A [113]



Biosynthesis and molecular genetics of marine natural products from dinoflagellates were also treated in a recent review [117]. Many feeding-based biosynthetic studies have been carried out on the potent paralytic shellfish poisoning (PSP) saxitoxin (**5**) and its analogues that are produced by *Gymnodinium catenatum* and by gonyaulacoid dinoflagellates of the genus *Alexandrium* and *Pyrodinium* [118]. A comprehensive overview of these studies was elaborated by Shimizu [119] which summarized the biosynthesis of saxitoxin (**5**) in eight steps that are summarized in Fig. 17.2: (1) Claisen-condensation between arginine and acetate; (2) a guanidine group is transferred from a second arginine unit to the free amino group of the intermediate B; (3) cyclization leads to the heterocycle D; (4) methylation by *S*-adenosyl methionine (SAM) and desaturation gives the intermediate E; (5) epoxydation; (6) opening of the epoxide to an aldehyde with subsequent reduction; (7) *O*-carbamoylation of the hydroxymethyl side-chain; finally (8) di-hydroxylation completes the biosynthesis. This well-consolidated biosynthetic pathway has been recently [120, 121] revised on the basis of molecular genetic studies. The new biosynthetic pathway is characterized by a different sequence where the SAM-methylation transforms acetate into propionate. Then, the biosynthesis proceeds including substantially the same previously reported biochemical reactions.

All the above-described results open extraordinary new perspectives in the chemistry of marine natural products. Of course, the structural elucidation continues to be the main focus. Then, establishing the structure with extreme rigor and studying its chemical reactivity, the basic biosynthetic steps can be clarified by interdisciplinary studies where the feeding experiments have to be integrated with complementary molecular genetic tools. This approach is also envisaged to boost the development of new drug candidates. However, until now, a crucial point remains undefined. Are symbiotic microorganisms the true producers of many metabolites found in marine macroorganisms? The topic has been treated in Piel's excellent review [122], which in part reanalyzes the remarkable structural analogies among metabolites from sponges and bacteria previously discussed

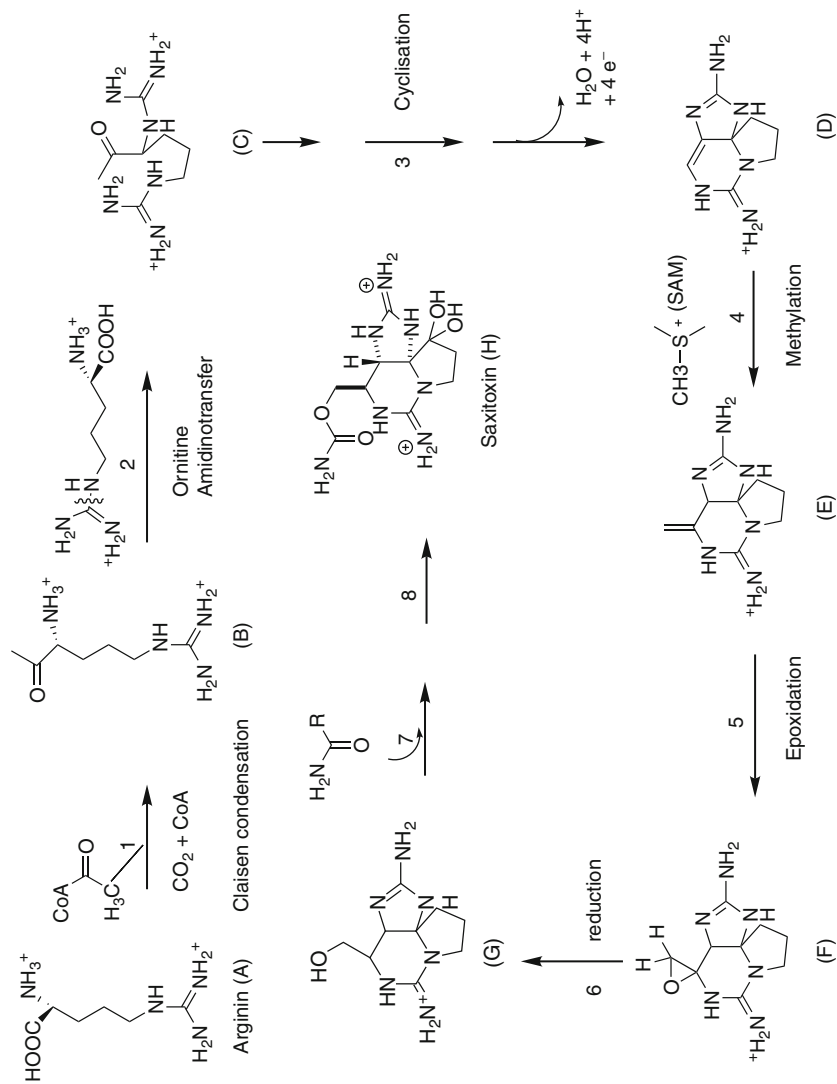
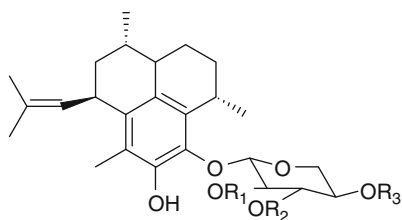


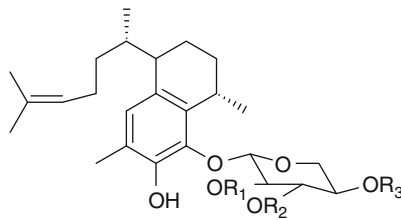
Fig. 17.2 Biosynthetic assembly of saxitoxin [119]

by other authors [5, 123]. Generally, these compounds are polyketides and nonribosomal peptides. Rarely, the isolated symbiotic bacteria preserve the metabolism of the host organism. Analogous conclusions were reported in Li's more recent overview [124] on marine microbial symbionts. These uncultured symbiotic microorganisms are extremely promising candidates for future studies that without disciplinary restriction could gain in importance for biomedical applications.

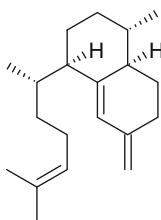
The recent work on the biosynthesis of pseudopterოსins is a step toward this direction. Pseudopterოსins are a family of anti-inflammatory and analgesic diterpene glycosides produced by the gorgonian *Pseudopterogorgia elisabethae* found in a few areas of the Caribbean. After the isolation of pseudopterოსins A–D [125] (**108–111**), many other related metabolites were isolated, including the seco-pseudopterოსins A–D (**112–115**) which display a serrulatane ring system [126]. Separation of the intracellular dinoflagellate symbiont *Symbiodinium* sp. [127] allowed the authors to obtain cultures that incubated with ^{14}C -labeled inorganic carbon and ^3H -GGPP gave radiolabeled **108–111**, thus supporting for the first time the symbiotic origin of pseudopterოსins. Furthermore, feeding experiments with ^3H -GGPP on a cell-free extract of *P. elisabethae* led to radiolabeled pseudopterოსins but also to the isolation of labeled elisabethatriene (**116**) [128]. Radiolabeled assay based on **116** was used to trace the diterpene cyclase activity and to isolate elisabethatriene synthase, a soluble protein that is responsible for the synthesis of serrulatane skeleton [129]. Recently, further mechanistic details with advanced precursors [130, 131] have further embellished this extremely interesting biosynthetic research [132].



108 PsA R1=R2=R3= H
109 PsB R1=Ac, R2=R3= H
110 PsC R2=Ac, R1=R3= H
111 PsD R3=Ac, R1=R2= H
 Pseudopterოსins



112 seco-PsA R1=R2=R3= H
113 seco-PsB R1=Ac, R2=R3= H
114 seco-PsC R2=Ac, R1=R3= H
115 seco-PsD R3=Ac, R1=R2= H



116 Elisabethatriene

17.5 Feeding Experiments and Detection Techniques

The experimental verification of a biosynthetic hypothesis requires establishment of the single steps involved in both construction and functionalization of the carbon skeleton. Until the purified enzyme for each biochemical step is available, biosynthetic studies can be carried out by administering a labeled precursor committed to the synthesis of the product of interest. Despite modest incorporations with complex organisms, feeding studies with stable isotopes have made a deep impact on biosynthetic studies in marine organisms, as much as with the terrestrial counterparts [8, 9]. As a matter of fact, since biosynthetic studies in marine organisms started much later than in terrestrial habitat, most of the experiments carried on in marine species have been made using stable precursors. There are a few but historically important exceptions to this assumption. Sponges are envisaged as the most prolific source of secondary metabolites in marine environments [133]. Nevertheless, the biosynthesis of most of these compounds is puzzling and, with the exception of the metagenomic methods [134–137] and exceptional reports of bacterial association [138, 139], their origin is not clearly understood even though many authors are inclined to consider associated or symbiotic microbes as the most likely producers [140, 141]. As reported in the previous paragraphs, sponge sterols have been the subject of numerous studies from Minale's and Djerassi's groups in the 1980s by employing both radioactive labeling and cell-free extracts (reviewed by Djerassi and Silva [72] and Giner [66]). In these studies, incorporation of ^{14}C -, ^3H -, or, less often, doubly ^3H -, ^{14}C -labeled precursors is followed by complicated analysis of the biosynthetic products by chemical degradation. Both carbon-14 and tritium are β -emitting nuclides that can be detected and accurately measured by a β -counter; after that, the weak radiation is converted into light by scintillation liquid. The procedure consists of dissolving the sample in the scintillation liquid and then measuring the level of emitted photons, which indicates the activity of radionuclides. It is usually possible to carry out quantification of samples containing two different isotopes, for example, ^{14}C and ^3H , and it is also feasible to perform analysis on line by intercepting the liquid coming from the chromatographic column of an HPLC instrument. Nevertheless, the technique is destructive, and the indirect measurement of radiation can be drastically reduced (quenching) by chemical and physical factors (e.g., chlorine compounds, colored samples, two-phase solution) that interfere with the counting process.

Simple incorporation of radioactive CO_2 , acetate, or mevalonate in the soluble form of DBED salt has been used to prove the *de novo* origin of polyketide and terpene carbon skeletons in marine organisms. The major impediments in these experiments arise from (1) the very low level of incorporation that follows administration of the labeling and (2) the difficulties of purifying the target compounds at homogeneity. To avoid this latter problem, products are transformed into derivatives of different polarity by simple and predictable chemical reactions. Although the level of radioactivity can be established for each carbon atom of the target

metabolite, this is not possible in most cases, and therefore, feeding experiments with radiolabel are usually little informative about the biochemical pathways leading to the final compound.

On the contrary, if stable-isotope-containing precursors are used, labeling position in target compounds can be detected by mass spectrometry (MS) and nuclear magnetic resonance (NMR). Both techniques are less sensitive than radioactivity-based methods, but allow unambiguous location of labeling without the requirement of degradation or chemical transformation. Furthermore, the astonishing improvements of these spectroscopic and spectrometric techniques in recent years have strongly lowered the limit of application, thus broadening the field of utilization of stable isotopes in biosynthetic studies.

In the past 20 years, single and doubly ^{13}C -labeled substrates have been employed to elucidate biosynthesis of secondary metabolites in algae, bacteria, fungi, and invertebrates from marine environments. In these studies, analysis of the labeled material is usually carried out by NMR [142]. Carbon-13 has a nuclear spin $I = \frac{1}{2}$ that allows the NMR identification of carbon atoms just as proton NMR identifies hydrogen atoms. In nature, the abundance of the isotope is only 1.1%, and therefore, only a few nuclei are observable by NMR in ordinary compounds. On the other hand, since carbon forms the backbones of organic molecules, the possibility of enriching a specific position and of locating the labeling directly is a powerful tool for elucidating the biochemical transformations leading to primary and secondary metabolites. ^{13}C -NMR spectroscopy has also other advantages deriving by the wide chemical shift range and spin–spin correlation due to coupling constant of vicinal or proximal active nuclides. Many common biogenetic precursors like acetate, propionate, mevalonate, glucose, and related compounds are commercially available with 99% ^{13}C enrichment in specific positions. Other precursors can be directly obtained by a number of standard procedures for synthesis of isotopically labeled substrates.

The precursors can be supplied in very imaginative ways that often depend on the organisms. The precursors are usually added to incubation media or aquarium water in feeding experiments with culturable organisms. They also can be administered by injection, using physiological buffer solution or sterile seawater, with macroorganisms. In this last case, a pulsed administration is used to improve the incorporation yields. The duration of the experiments varies from species to species, but usually, they last for 1–2 weeks. At the end of the feeding protocol, the treated organism is extracted and the target compound is purified by classical chromatographic methods. A cell-free system is a widely used tool for studying *in vitro* biological reactions without the complex interactions found in an intact cell. Cell-free systems are prepared after cellular lysis by using either the whole cell lysate or subcellular fractions. This methodology is often utilized when feeding experiments with the whole organism are not practicable or when information on specific biochemical transformations are sought after.

Isotopic incorporation is usually determined by acquisition of ^{13}C -NMR spectrum through comparison of labeled and natural sample of the compound of interest. Labeling is revealed by intensification of the signals due to those carbons

containing ^{13}C nuclide. The higher the enrichment is, the stronger the signal intensification. With precursors enriched at specific positions, the incorporation is restricted to specific carbons as an effect of the biosynthetic pathway. Individual examples are discussed in the paragraphs below, but probably the most clear application of feeding experiments with carbon-13 is given by the use of labeled glucose to elucidate the terpene biosynthesis from mevalonate or methylerythritol pathways [143, 144]. According to the biochemical reactions leading to the isoprene precursors isopentenyl pyrophosphate (IPP) and dimethylallyl pyrophosphate (DMAPP), C-1 of glucose is specifically placed at positions C-2, C-4, and C-5 of IPP and DMAPP by the mevalonate pathway, or at C-1 and C-4 of IPP and DMAPP by the methylerythritol pathway. Consequently, in experiments with $[1-^{13}\text{C}]\text{glucose}$, the backbones of terpenes derived from mevalonate pathway show NMR signals enriched at carbons 2, 4, and 5 of the isoprene units, whereas the enriched signals correspond to the positions 1 and 5 for those compounds produced by methylerythritol pathway (Fig. 17.3).

Biosynthetic studies of molecular backbones arising from rearrangements or cyclization of linear precursors are particularly well pursued by feeding experiments with substrates containing more than one ^{13}C nuclide. In these studies, information is directly deduced from the spin systems of adjacent carbon-13 atoms, which is revealed by splitting of the corresponding signals because of spin coupling. This phenomenon produces multiplets according to the role of multiplicity that also governs proton NMR. The shape of the resulting signals is diagnostic to determine the spin systems and thus to establish the connectivities between the carbons forming the molecular backbone. Although different types of compounds containing more than one carbon atoms have been used, $[1,2-^{13}\text{C}_2]\text{acetate}$ is the most common example of this family of substrates in feeding experiments with marine organisms. In ^{13}C -NMR spectra, the incorporation of intact C_2 -unit deriving from the doubly labeled acetate is revealed by two doublets flanking the central resonances of the natural carbons (Fig. 17.4). The distance from the two lines (coupling constant) is identical for both signals and is a function of stereoelectronic features of the molecule, thus being diagnostic to recognize the carbons even in the presence of other doublets. In a recent advance, ^{13}C - ^{13}C correlation spectroscopy (COSY) has been used to map the coupling carbons in secondary metabolite. Like the corresponding experiment based on ^1H detection, basic ^{13}C resonances appears on the diagonal, whereas interacting carbons are easily identified by cross-peaks symmetrical to the diagonal [110].

Nuclides other than carbon 13 have not been widely employed in feeding experiments with marine organisms. Deuterium-labeled substrates have been recently used in experiments with marine mollusks, bacteria, and microalgae. Detection of ^2H is usually achieved by MS or MS/MS techniques that also allow localization of the label by analysis of the daughter ions. Deuterium atoms, having nuclear spin $I = 1$, can be also detected by NMR, but the resulting spectra suffer of severe line broadening due to the quadrupole moment of the nucleus. Consequently, deuterium NMR has a range of chemical shift similar to proton NMR but with poor resolution that hampers the general application of this methodology. However, comparison with the

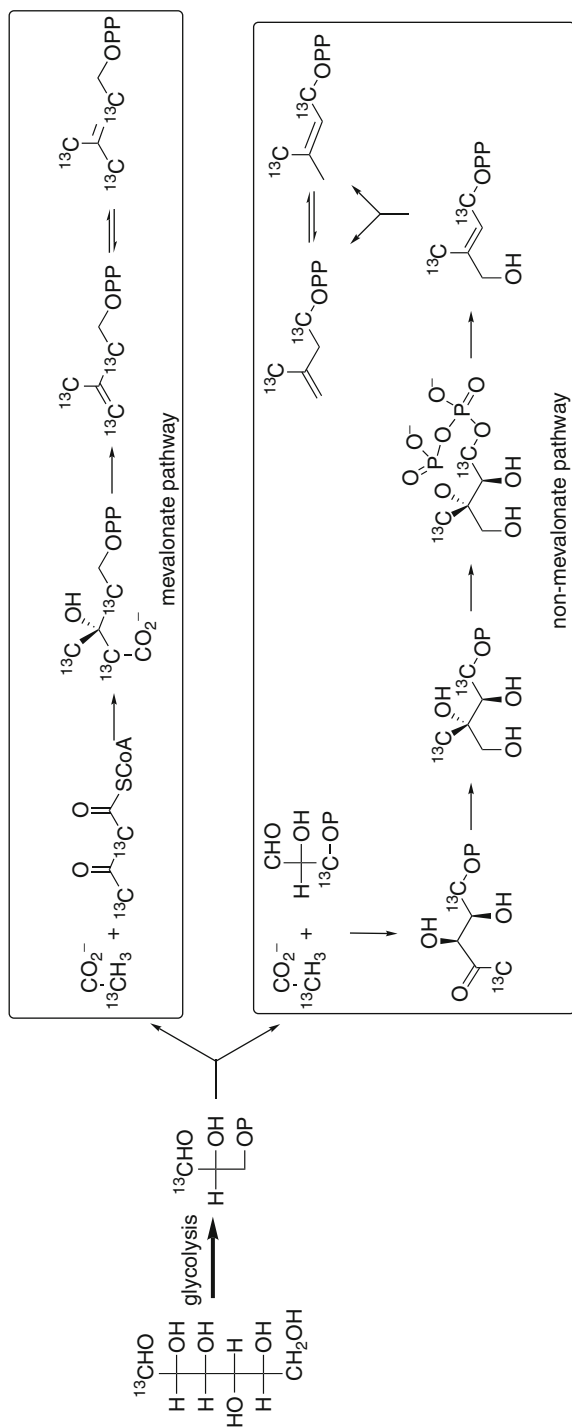


Fig. 17.3 Influence of metabolism due to mevalonate and nonmevalonate pathways on labeling in isoprene precursors, isopentenyl pyrophosphate, and dimethylallyl pyrophosphate. C-13 atoms are shown in the structures

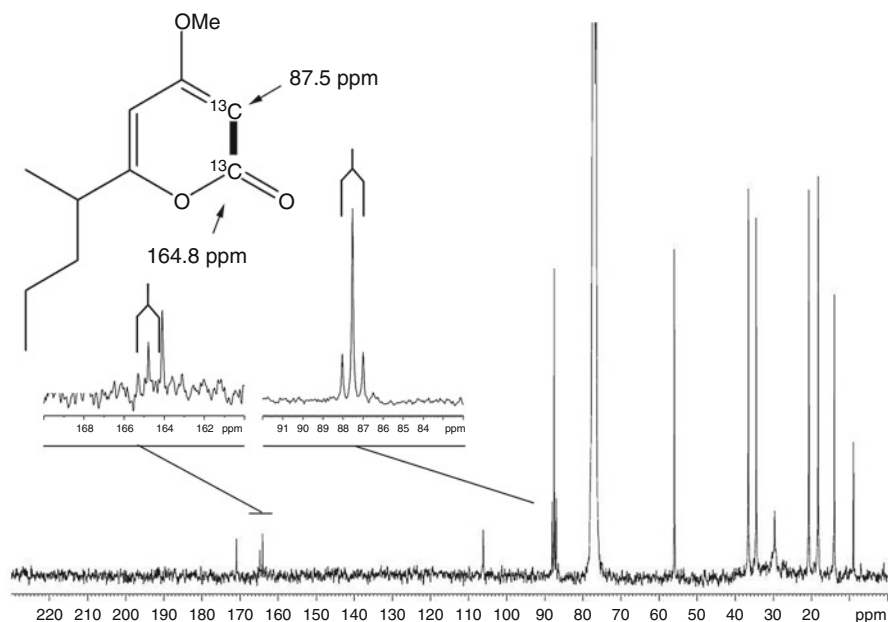


Fig. 17.4 ^{13}C -NMR spectrum of placidene E (**153**) after incorporation of $[1,2-^{13}\text{C}_2]$ acetate. The insert shows the doublet ($J = 78.1$ Hz) flanking the signals of the natural isotopomer

corresponding ^1H -NMR spectrum of the natural compound clearly is usually sufficient to establish which hydrogen has been replaced by deuterium, thus allowing one to determine the main steps of the biosynthetic pathway.

17.6 Lipoxygenase Pathways in Marine Diatoms

Diatom oxylipins embrace a family of lipoxygenase (LOX)-derived fatty acid products reported by independent studies from freshwater and marine genera in the last few years [145–148]. The family consists of (1) breakdown metabolites, such as polyunsaturated aldehydes (PUAs) and ω -oxo-fatty acids, and (2) oxygenated compounds that conserve the original structure of the fatty acid precursor, i.e., hydroxy, keto, oxo, and epoxy derivatives (Fig. 17.5). These metabolites occur commonly and are widely distributed within the diatom lineage; they are characterized by an apparent species specificity that arise from the variability of the oxidation site, the structure of the fatty acids recognized as LOX substrates, and finally, the enzymatic transformations downstream to LOX oxidation [146–150].

Oxylipin pathways are likely encoded by the genome of nearly all photosynthetically active eukaryotes [151], and despite the chemical nature of the individual compounds, the signaling pattern and functional roles are much the same across

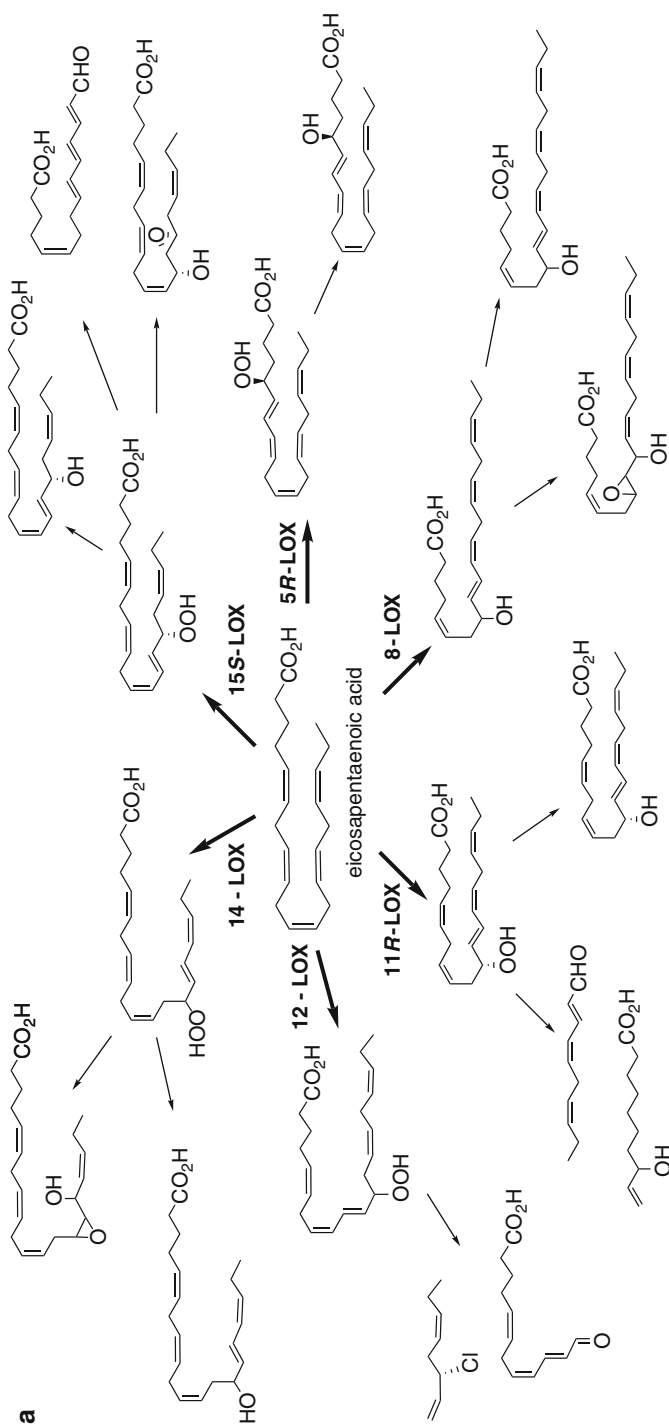


Fig. 17.5 (continued)

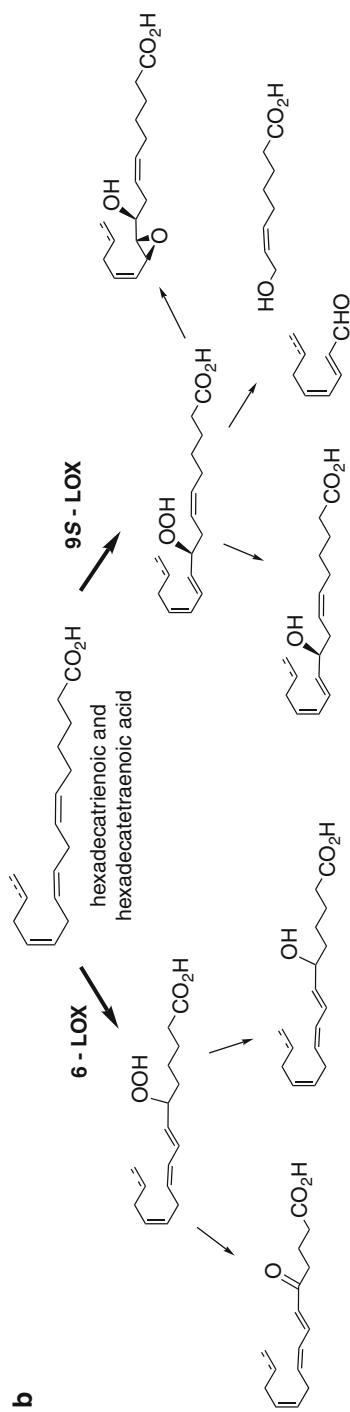
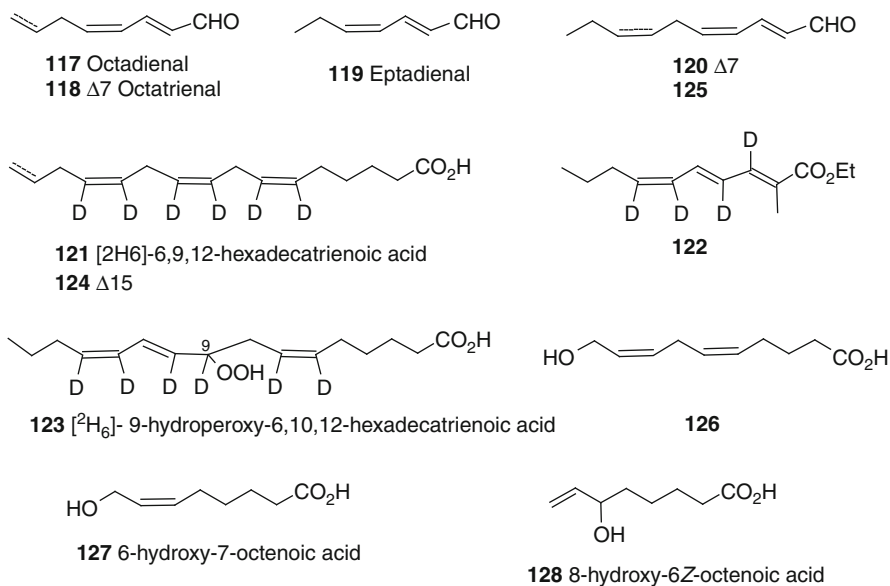


Fig. 17.5 Schematic view of lipoxygenase pathways in marine diatoms. (a) oxylipins from C20-fatty acids, (b) oxylipins from C16-fatty acids. For a discussion of the products, see main text

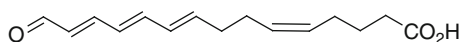
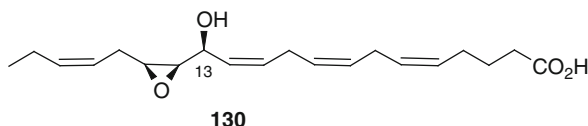
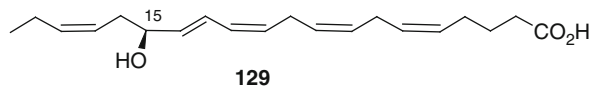
different lineages. In higher plants, where these molecules are mostly synthesized by lipoxygenase (LOX)-dependent oxidation at the 9 or 13 position of C₁₈ polyunsaturated fatty acids [152], oxylipins have played a crucial role in the defense and development [153, 154]. Algal oxylipins [151, 155–157] are mainly synthesized from C₂₀ PUFAs in response to stress conditions or perception of external stimuli as essential intermediates for innate immunity [158, 159]. In diatoms, circumstantial evidence suggests that these molecules are responsible for both the detrimental effects of this lineage on copepod grazers [161], and chemical communication between diatom cells [149, 160–162].

Lipoxygenase metabolism starts with peroxidation of the polyunsaturated fatty acid and formation of a 2,4-pentadienyl hydroperoxide moiety that undergoes spontaneous or enzymatic conversion [163]. Biosynthetic studies in diatoms rely mostly on incubation of labeled fatty acids in cell-free preparation or enzymatic fractions. This approach has been widely used to determine the origin of PUAs (**117–120**), as illustrated for the production of octadienal (**117**) from [6,7,9,10,12,13-²H₆]-6,9,12-hexadecatrienoic acid (**121**) in the planktonic diatom *Skeletonema costatum* (taxonomically reassigned as *Skeletonema marinoi*) [164]. The cells of this microalga were suspended in distilled water and incubated with the labeled acid prepared by deuteration of a polyalkyne intermediate deriving from coupling of propargyl bromide with terminal alkyne in the presence of cesium carbonate [164]. To recover the deuterated derivative of the volatile aldehyde **117**, the rough extracts were derivatized with carbetoxyethylidene-triphenylphosphorane (CET-triphenylphosphorane) to give the stable polyunsaturated ester **122**, which showed a significant M + 4 peaks (natural C₁₃H₂₀O₂⁺, *m/z* 208; labeled C₁₃H₁₆D₄O₂⁺, *m/z* 212) in GCMS. The labeling position of this isotopomer was established by ²H NMR spectroscopy that revealed the exchange of protons with deuterium at C-1 (δ 7.22), C-2 (δ 6.42), C-4 (δ 6.20), and C-5 (δ 5.91) in full agreement with a lyase-dependent breakage of the [6,7,9,10,12,13-²H₆]-9-hydroperoxy-6,10,12-hexadecatrienoic acid (**123**). The subsequent identification of this intermediate by ESI⁺ LC-MS in *Thalassiosira rotula* [146] and the finding of a similar mechanism for the synthesis of octatrienal (**118**) from [6,7,9,10,12,13,15,16-²H₈]-6,10,12,15-hexadecatetraenoic acid (**124**) [165] corroborated the origin of C₈ PUAs from C₁₆ PUFAs. A similar strategy with incubation of *T. rotula* cell free was also used to prove the synthesis of the ω-3 PUAs heptadienal (**119**) and decatrienal (**120**) from eicosapentaenoic acid (EPA) [166]. The enzymatic mechanisms leading to synthesis of **117–120** has been recently suggested as a unique transformation that does not rely to pathways known in other organisms [167]. In *T. rotula*, transformation of d₈-arachidonic acid to deuterated decadienal (**125**), an unnatural analogue of **120**, was complemented by synthesis of [²H₄]-10-hydroxy-5,8-dacdienoic acid (**126**). In full agreement with this result, incorporation of 9,10-[²H₂]-6,10,12,15-hexadecatetraenoic acid led to octatrienal (**118**) together with the isomeric 6-hydroxy-7-octenoic acid (**127**) and 8-hydroxy-6Z-octenoic acid (**128**). Formation of hydroxy acid, such as **126–128**, in lyase process is unusual and

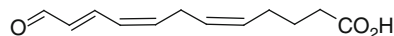
further investigation with [^{18}O]water proved that the alcoholic oxygen derives from the medium, as a result of a carbon-carbon breaking presumably assisted by water.



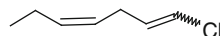
In homogenates of *Chaetoceros socialis*, *Chaetoceros affinis*, and *S. marinoi*, experiments with tritiated EPA also led to specific incorporation into hydroxy, hydroperoxy, and epoxy alcohol derivatives [147]. In *Pseudo-nitzschia delicatissima* (recently reassigned as *Pseudo-nitzschia arenysensis*), eicosapentaenoic acid-dependent 15S-lipoxygenase pathway was responsible for production of oxylipins (**129–131**) along the growth curve, with remarkable changes that are apparently dependent on cellular density. At least one of these compounds, namely (5Z, 9E, 11E, 13E)-15-oxo-5,9,11,13-pentadecatetraenoic acid (**131**), is formed only in the stationary phase immediately before the demise of the culture. Origin of this metabolite was proved by radioactive incorporation after administration of tritiated EPA. No information is hitherto available on the mechanism underlying the lyase activity in *P. delicatissima* [149], but the involvement of an unprecedented cleavage has been proposed for the biosynthesis of the related (5Z, 8Z, 10E)-12-oxo-5,9,11,13-dodecatrienoic acid (**132**) in the diatom *Stephanopyxis turris* [168]. Incubation of this microalga with deuterated arachidonic acid and tritiated 12-hydroperoxy-eicosatetraenoic acid gave incorporation of the labeling in **132** and C_8 chloroalkanes (e.g., **133**). The halogen atoms originate from seawater and are introduced at the same time of the cleavage of the fatty acid hydroperoxide, although it cannot be excluded that the two reactions proceed through two parallel pathways.



131 (5Z,9E,11E,13E)-15-oxo-5,9,11,13-pentadecatetraenoic acid



132 (5Z,8Z,10E)-12-oxo-5,9,11,13-dodecatrienoic acid



133

C₁₆-Fatty acids, such as those incorporated in the synthesis of C₈ PUAs **117** and **118**, are typically components of thylakoid membranes of chloroplasts. Experiments with radioactive tracers [169] and partially purified enzymes [170] suggest that these organelles are the primary source of LOX substrates in diatoms. The activation of the pathway is initiated with the release of free fatty acids by a lipolytic activity that is involved in the hydrolysis of both galactolipids (GLs) and phospholipids (PLs) [169]. The biochemical relationship between these lipidic pools and oxylipins was tested by incubation of ³H-PLs and ³H-GLs in *S. costatum*. Although the specific radioactivity was rather higher in PLs than in GLs, the percentage of radioactivity recovered in heptadienal (**119**) was three times higher after incubation of the sugar conjugates [169]. In a second set of experiments [170], the whole pool of PUAs in *T. rotula* (**117–120**) was obtained from GL incubated with an enzymatic preparation.

17.7 Polypropionates in Sacoglossan Mollusks: When Biosynthesis and Function are Hand in Glove

Polyketides are structurally diverse natural products sharing a common biosynthetic process that relies on a stepwise chain assembly through successive rounds of Claisen-type condensation between an activated malonic acid derivative and an acyl thioester [171]. The family embraces a large variety of bioactive compounds found in many different organisms, from prokaryotes to eukaryotes but seldom in animals. The processive biosynthesis is under control of multicatalytic enzymes, named polyketide synthases (PKS), which are roughly classified as type I, type II, and type III on the basis of the protein architecture.

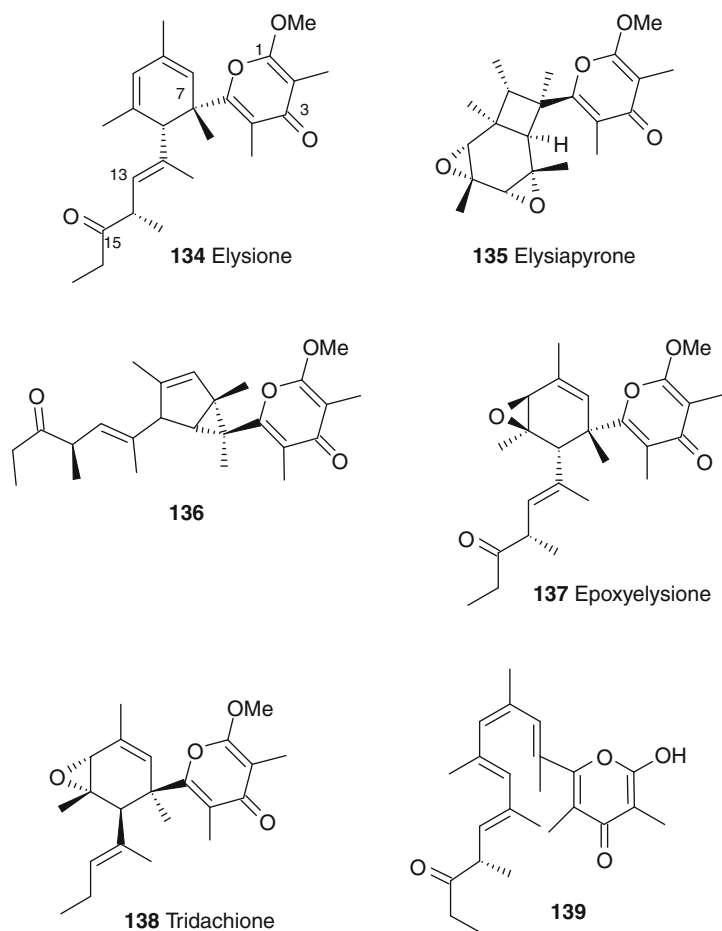
Some opisthobranch gastropods of the order Sacoglossa are able to produce a very specific and rare class of polyketides that, being based on repetition of C-3 units, are collectively named polypropionates. Sacoglossans have also

another unique ability. These marine mollusks derive photosynthetically viable chloroplasts from the algae upon which they feed. The photosynthetic products are transferred from these plastids to mollusk tissues and can sustain the slugs for several months in the absence of a food source [172, 173]. The symbiosis implies a unique exchange of genes between eukaryotic alga and animal [174]. The fixed carbon appears also in secondary metabolites of the mollusks, as first proved by Ireland and Scheuer [29] with incorporation of [^{14}C]bicarbonate into the polypropionates **15** and **16** of the Pacific sacoglossan *Placobranchus ocellatus*. Advanced precursors and chemical transformations involved in the biosynthesis of this family of compounds have been later established in the Mediterranean *Elysia viridis*. Administration of tritiated propionate to seawater gave a clear enrichment of radioactivity in elysione **134** (approximately 37,000 dpm/mg) [175]. To a further study with sodium [$1\text{-}^{13}\text{C}$]propionate, enrichment was in full agreement with incorporation of intact C_3 units in the skeleton of the mollusk metabolite [176]. As such, elysione is suggested to derive from a PKS process based on the repetitive addition of propionate units and final formation of the pyrone ring by spontaneous cyclization occurring after release of the polyketide chain from the thiotemplate [177].

Elysione (**134**) prototypes an impressive number of metabolites including a pyrone ring appended to a range of complex cyclic cores and side chains, which are usually formed by six to eight propionate units [178]. In consideration of the central core, the family embraces at least three structural types featured by cyclohexadiene (e.g., 9,10-deoxytridachione, **15**), bicyclo[3,1,0]hexane (e.g., photodeoxytridachione **16**), and bicyclo[4,2,0]octane (e.g., elysiapyrone **135**) [36, 179, 180]. Photochemical conversion of the propionate skeletons generates 9,10-deoxytridachione (**15**) from photodeoxytridachione (**16**), as well as compound **136** from elysione (**134**) both in vivo and in vitro [29, 176]. The chemical transformation has been extensively proved by synthetic methods, and it is nowadays accepted that the different polypropionate backbones are the result of rearrangement of a common precursor by photochemical or thermal stress [181–186]. On the contrary, exposure of living specimens of *E. viridis* to nonstressing levels of light ($350 \mu\text{E m}^{-2} \text{s}^{-1}$) does not induce detectable rearrangement of the cyclohexadiene skeleton of **134** but decreases the levels of an epoxy derivative named epoxyelysione (**137**). The levels of these pairs of metabolites change in response to light, being the amount of **137** significantly dominant in the dark. The apparent equilibrium between elysione (**134**) and epoxyelysione (**137**) suggests a physiological regulation based on epoxidation or de-epoxidation of the polyketide. Although not tested, a similar process is likely to occur also for 9,10-deoxytridachione (**15**) and tridachione (**138**) of *P. ocellatus* [29] and *Tridachia diomedea* [187]. Since the skeleton rearrangement induced by light overexposure is impossible in absence of the conjugated double bond of the cyclohexadiene core, the reactions of epoxidation/de-epoxidation control the physiological pool of the molecules (i.e., elysione, **134**) in the animal tissue. Because elysione (**134**) and 9,10-deoxytridachione (**15**) are suggested to have a sunscreen role to protect the animals in photophilic environments, the

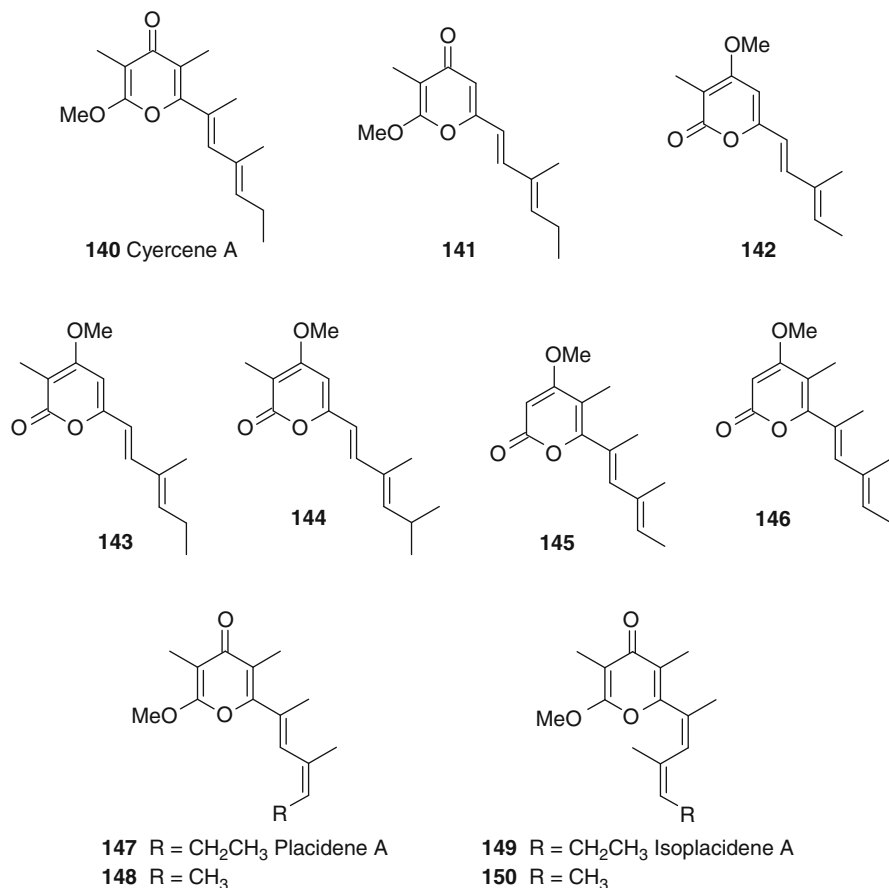
biochemical outcome is a photoprotective process reminiscent of the xanthophyll cycle in higher plants, Chlorophyta and Phaeophyceae [188].

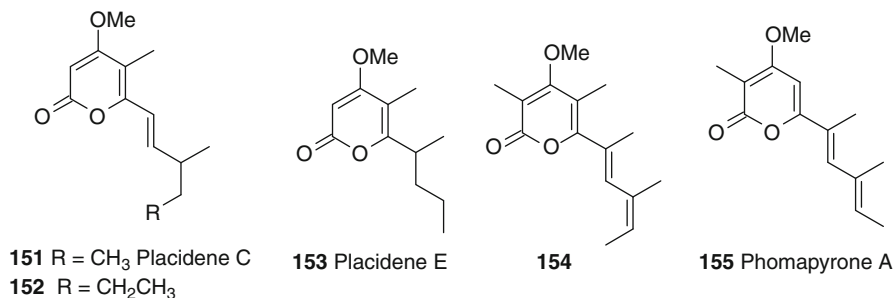
In specimens of *E. viridis* kept in the dark for a few days, a careful analysis led to the identification of a labile product that was not detectable in the animals collected from natural environments. The structural characteristics of this product agreed with a conjugated tetraene polypropionate (**139**) that is likely to represent the primary product of the polyketide biosynthesis in the mollusk [176]. As brilliantly demonstrated by biomimetic synthesis [181–185], the rearrangement of the unstable tetraene **139** followed by pericyclic processes gives access to the impressive molecular variability of mollusk propionates in response to environmental conditions. Since a similar mechanism is also likely to take place for the synthesis of chiral compounds, e.g., 9,10-deoxytridachione (**15**), the reaction of cyclization of the achiral tetraene is suggested to depend on enzymatic catalysis in vivo [176, 180].



Biosynthesis of pyrone propionates, closely related to elysione (**134**), has also been established in other sacoglossans. Injection of $[2-^{14}\text{C}]$ propionate to the Mediterranean molluscs *Cyerce cristallina* and *Ercolania funerea* [189–191] led to selective incorporation in cyercenes (**140–146**), members of a family of putative scavengers that includes also products of the sacoglossan *Placida dendritica* (**147–154**) [192, 193]. A possible interconversion of cyercenes and placidenes has been hypothesized by Zuidema and Jones [192, 193], who proved the biomimetic synthesis of placidene A (**147**) and isoplacidene A (**149**) from cyercene A (**140**) under photochemical conditions.

The structural motif of cyercenes has also been reported in a family of fungal metabolites, including infectopyrone from *Alternaria infectoria* [194], dihydroinfectopyrone and further congeners from *Petriella* sp. [195], nectriapyrone from *Gyrostroma missouriense* [196], stemphyprone from *Stemphylium globuliferum* [197], and phomapyrones D and E from *Leptosphaeria maculans* (asexual stage: *Phoma lingam*) [198].





Biosynthesis of polypropionates in fungi has been recently established on phomapyrone A (**155**) by administration of sodium [2-¹³C]acetate, sodium [1,2-¹³C]acetate, sodium [2-¹³C]malonate, [3,3,3-²H₃]propanoic acid, and L-[Me-²H₃]methionine to cultures of *L. maculans* [198] (Fig. 17.6a). The distribution of labeling indicated the lack of incorporation of propanoic acid and the assimilation of four methionine-derived methyl groups, in agreement with the origin of the polypropionate from methylation of a linear penta-acetate precursor. Similar experiments carried out by injection of sodium [1-¹³C]propionate, sodium [2-¹³C]acetate, and sodium [1,2-¹³C₂]acetate to 64 specimens of *P. dendritica* gave totally different results [199]. In fact, the analysis of the regular skeleton of placidene A (**147**) showed incorporation in carbons derived from C1 of labeled propionate. No carbon of **147** was enriched from labeled acetates that otherwise gave the enrichment of C2-C3, C6-C7, and C10-C11 units of placidene C (**151**) and E (**153**) (Fig. 17.6b) [199].

The experiments with *P. dendritica* proved that the sacoglossan polypropionates are the result of a peculiar biochemical combination of light-dependent reactions and mixed polyketide assembly. The de novo origin of **147** by sequential addition of intact C₃ units to the emerging polyketide underlines a biosynthetic pathway different from that described in fungi, thus implying that the same compound can derive from two different pathways in the two phyla [199]. This is a very important point that suggests a need for caution in speculations about the biogenesis of marine products. Our knowledge of the biochemical transformations in these systems is very inadequate. Frequently, metabolic pathways operating in marine organisms are discussed in relation to terrestrial processes, and assumptions about the origin of marine secondary metabolites, especially from invertebrates, are based on structural similarities to known metabolites of microbial source. The metabolic divergence between fungi and mollusks is in clear contradiction with this line of reasoning. As such, sacoglossan polypropionates represent a very special case that should be adequately considered before one hastily puts forward considerations about the biosynthesis of secondary metabolites especially if derived from marine organisms.

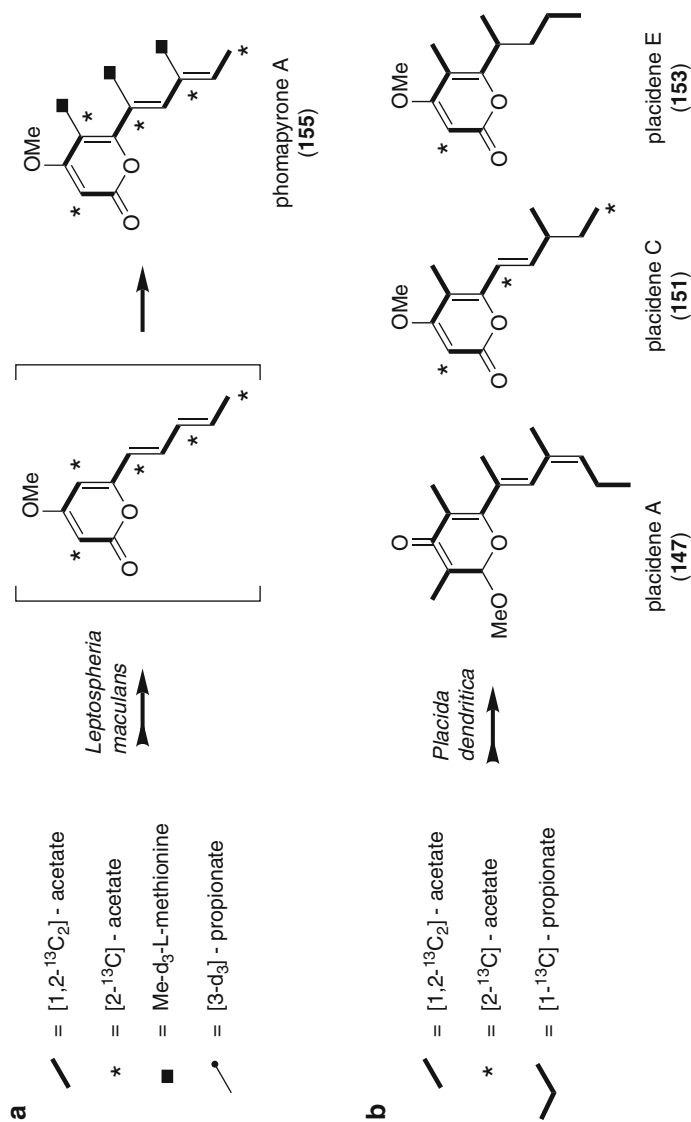


Fig. 17.6 Biosynthesis of polypropionate in the fungus *Leptosphaeria maculans* (a) and the mollusk *Placida dendritica*, (b) The structure in square bracket is a putative intermediate deriving from cyclization of a postulated linear polyketide. There is no evidence that supports the real occurrence of this intermediate

17.8 Conclusions

This chapter has covered feeding biosynthetic studies of the last four decades on marine organisms. The emerging scenario underlines the evolution of the field that has been constantly moving on from the pioneering studies with radioactive tracers to the modern molecular approaches through the use of techniques relying on stable isotopes and enzymatic transformations. Relevance of this research has hitherto concerned (1) the origin of the molecules in relation to the potential role of symbiotic association, (2) the chemistry of biosynthetic reactions as inspiration of synthetic methods in organic chemistry, and (3) the control of the biosynthetic pathways in view of the elucidation of the functional role of the natural products.

In the coming years, full application of molecular techniques to biosynthetic pathways is expected to give access to natural and artificial variants of bioactive products with an unpredictable impact on human medicine. Four decades of studies of marine organisms have led to an extremely rich arsenal of bioactive molecules [133] that, however, have seldom established a position in the drug market [200]. Limiting constraints are for the most part (a) the scarcity of the natural source that reduces the availability of the bioactive molecule and (b) the structural complexity of the bioactive molecules that often hampers their chemical synthesis.

Disclosure of genes coding for the synthesis of these molecules and subsequent engineering of these pathways by heterologous expression is envisaged as a promising way to overcome the present hurdles that limit biotech access to marine natural products and hence open a new era for the development of new drugs. The potentiality of this methodology is underlined by a series of recent papers reporting studies on many marine organisms, including cyanobacteria [201], dinoflagellates [202], marine bacteria [112], and gorgonian symbionts [132]. However, the success of this approach will also depend on the exact knowledge of the biogenesis of secondary metabolites and therefore cannot leave out those biosynthetic studies that are based on feeding experiments.

17.9 Study Questions

1. What is known about the biosynthesis of sponge sterols?
2. Describe the major differences of terpene biosynthesis by mevalonate and methylerythritol pathways.
3. Describe the incorporation of [1-¹³C]glucose into terpenes by mevalonate and methylerythritol pathways.
4. Describe the biosynthesis of pyrone-containing polypropionates in mollusks and fungi.
5. Describe the incorporation of acetate in macrolides of dinoflagellates of the genus *Amphidinium*.
6. How is the presence of β -emitting radionuclides detected in biosynthetic studies?

7. Describe the NMR spectra of molecules after incorporation of singly and doubly labeled ^{13}C -precursors.
8. Which are the arguments for and against the use of radioactive and stable isotopes in biosynthetic experiments?

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David H. Sherman, Christopher M. Rath, Jon Mortison,
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Abstract

Marine natural products are emerging as important sources of new drugs for human health concerns. By understanding the fascinating enzymatic assembly

D.H. Sherman (✉) • C.M. Rath • J. Mortison •
J.B. Scaglione • J.D. Kittendorf
Life Sciences Institute and Department of Medicinal Chemistry, University of Michigan, 210
Washtenaw Ave, Ann Arbor, MI, USA
e-mail: davidhs@umich.edu

lines that generate these molecules, we gain deeper insight into the common mechanisms behind the diversity in structure and biological functions observed in these compounds. Indeed, a better understanding of these pathways could allow improved access to the drugs through heterologous expression or through the use of enzymes as biocatalysts. The mixed nonribosomal peptide synthase/polyketide synthase biosynthetic pathways for the natural products curacin and cryptophycin are explored as case studies in enzymatic diversity. The expanding class of atypical *trans* AT natural products is also discussed. Emerging tools for characterizing these enzymes are also explored.

18.1 Introduction

Natural products have proved to be an exceptionally rich source of small molecule ligands for discovery and analysis of diverse molecular targets relating to human disease. From 1940 to 2006, 47% of approved anticancer therapeutics were natural products or natural product-derived chemical entities [1]. Between 2005 and 2007, 13 natural product, natural product-derived, or semisynthetic drugs have been launched [2]. Natural products may well enjoy a resurgence in drug discovery and development efforts as recent advances such as the ability to engineer and heterologously express biosynthetic pathways may provide effective solutions to current challenges including adequate natural product supplies, improved cost of goods, and effective analogue development.

A significant number of marine natural products contain pharmacological activities that are beneficial to human health. Although there are many examples of terrestrial-derived natural product compounds that are in clinical use, including antibacterial penicillins, cephalosporins, immunosuppressive cyclosporin A, and the cholesterol-lowering HMG-CoA reductase inhibitors best known as the “statins” [3], secondary metabolites from the marine environment are just starting to reach the clinic. These molecules, which have achieved their (largely unknown) endogenous functions over the course of millions of years of evolution, offer chemical scaffolds for development of new analogues with improved or altered biological activity (Fig. 18.1). New bioactive analogues that contain novel structural elements may be generated by both semisynthesis and total synthesis efforts [4, 5].

Indeed, the synthases that produce nonribosomal peptide (NRP) and polyketide (PK) natural products are equally interesting in terms of their application in natural product fermentation and as biocatalysts. The number of natural products that function in biological systems is large but represents only a small fraction of the total possible number of small carbon-based compounds, indicating the importance of stereochemistry and functional groups in natural product functions [6]. Modern synthetic chemistry has encountered significant challenges in preparation of complex, high molecular weight natural products containing a great number of reactive groups and stereocenters for the generation of drug leads in the pharmaceutical industry. Incorporating the use of biocatalysts during natural product synthesis represents a promising strategy for the production of compounds that are a key

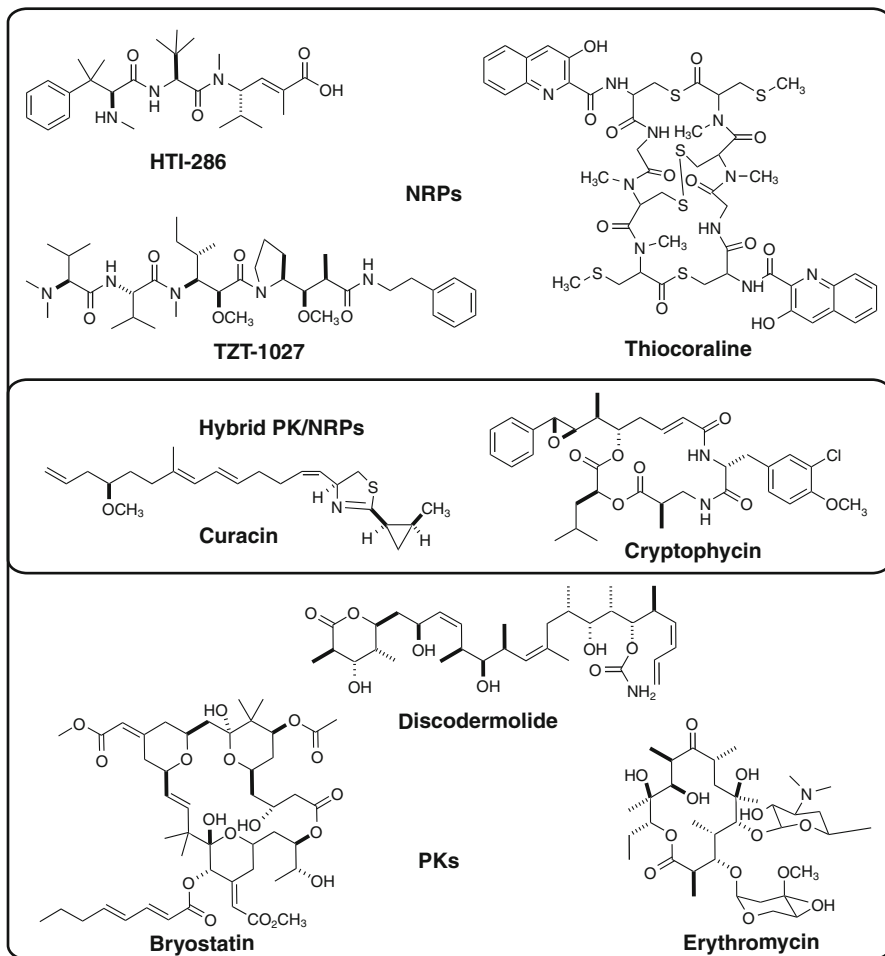


Fig. 18.1 Examples of nonribosomal peptide (NRP), polyketide (PK), and hybrid (PK/NRP) natural products

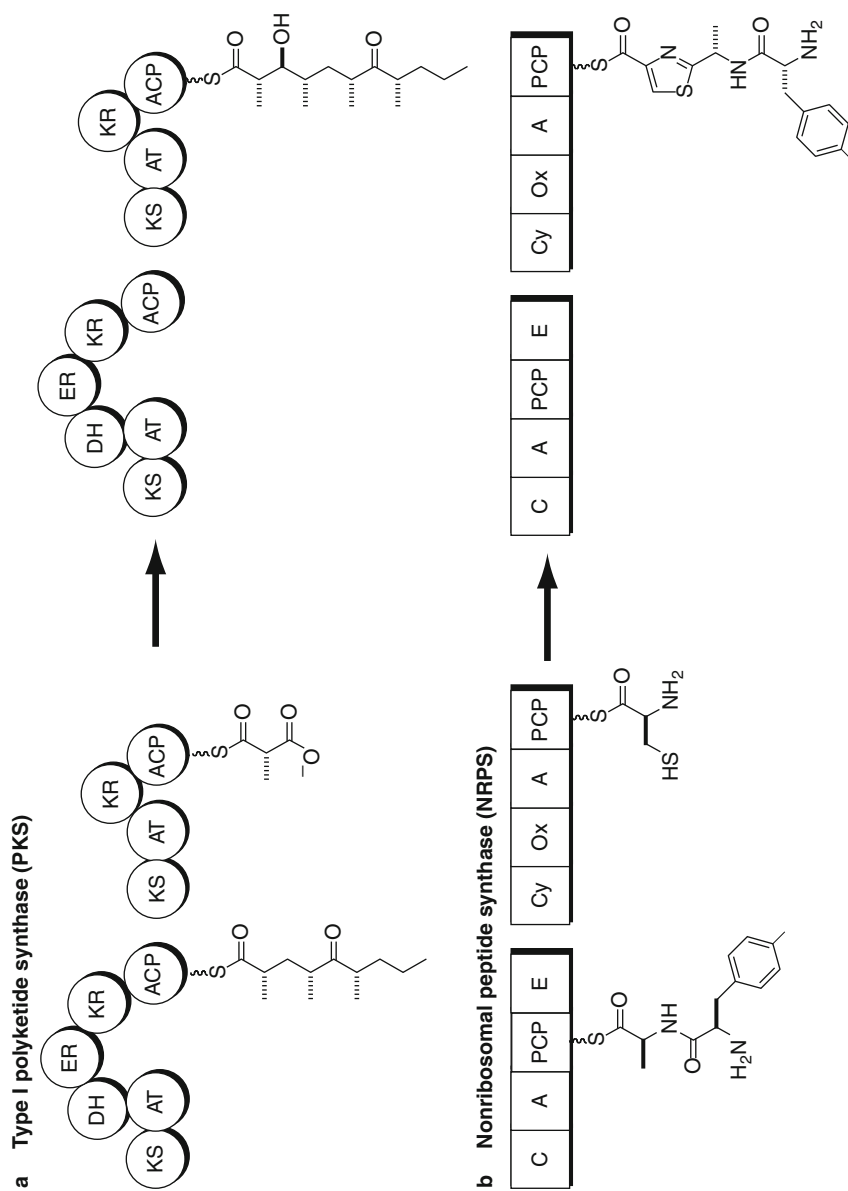
element in pharmaceutical discovery and development efforts [7, 8]. Although enzymes residing in living cells have been extensively used as biocatalysts in the food and beverage industry, isolated enzymes are playing increasingly critical roles in performing chemical transformations on organic compounds for pharmaceutical development [9–12]. Often, these remarkable catalysts are able to perform a wide array of reactions on structurally diverse compounds. Furthermore, enzymes can also selectively catalyze reactions with chiral (enantio-) and positional (regio-) selectivities [12]. With these advantages, enzymes are applied in organic synthesis to avoid tedious protection and deprotection steps commonly required for enantio- and regioselective synthesis. The inherent selectivity of enzymes generates few by-products and provides an environmentally friendly alternative to chemical

catalysts. Enzymes used in organic synthesis include acyl transferases (e.g., lipases, esterases, peptidases, amidases, and acylases), carbohydrate-processing enzymes (e.g., glycosidases, glycosyltransferases), hydrolytic enzymes (e.g., nitrilases, nitrile hydratases), reductases, oxidases and oxygenases, aldolases, and oxynitrilases [9].

18.1.1 Function of Polyketide Synthases and Nonribosomal Peptide Synthetases

Polyketides (PKs), nonribosomal peptides (NRPs), and PK/RP or NRP/PK hybrids represent three large subclasses of highly diverse natural products with various bioactivities [13]. These natural products are generated by large megaenzymes, polyketide synthases (PKSs), and nonribosomal peptide synthetases (NRPSs). Type I PKSs consist of multiple modules, with each module minimally containing three core domains: acyltransferase (AT) domain, ketosynthase (KS) domain, and thiolation (T) domain [also called acyl carrier protein (ACP) domain]. Typically, one type I PKS module catalyzes a single elongation cycle for PK production (Fig. 18.2). During elongation, the AT domain serves as the gatekeeper for specificity, responsible for selecting the appropriate acyl-CoA extender unit (e.g., malonyl-CoA, methylmalonyl-CoA) and transferring the extender unit to the sulfhydryl terminus of the phosphopantetheinyl arm on the T domain [14]. The KS domain catalyzes the decarboxylation of acyl-S-T to generate a carbanion that reacts with the PK intermediate linked to T domain generated in the previous elongation cycle. The resulting α -ketoacyl-S-T becomes the substrate for the next cycle of elongation catalyzed by the subsequent elongation module. In addition to type I PKSs, there are two other classes, type II PKSs and type III PKSs [15]. Unlike the type I class, type II PKSs consist of discrete enzymes that are organized as a multicomponent system [16]. The type III PKSs are distinguished from the others by lack of an AT and T domain. Type III PKS systems typically use CoA substrates (i.e., malonyl-CoA), but there is precedent for their ability to accept acyl-S-T substrates [15, 17].

Similar to the type I PKSs, NRPSs are comprised of multifunctional enzymes that are arranged into modules. Each NRPS module contains three core domains: adenylation (A), condensation (C), and thiolation (T) (also called peptidyl carrier protein [PCP] domain) [18] (Fig. 18.2). The A domain is responsible for selecting and activating the natural or modified amino acid monomer. The activated amino acid monomer is covalently attached via a thioester bond to the cysteamine group of a phosphopantetheinyl arm in the holo-T domain. The condensation (C) domain catalyzes formation of the peptide bond between the amino acid monomer and the peptidyl intermediate tethered to a T domain in an adjacent module. Similar to type I PKS modules, each NRPS module performs a single elongation step of the growing peptidyl chain. In both NRPSs and PKSs, there are several additional domains that contribute to natural product structural diversity. Ketoreductase (KR), dehydratase (DH), and enoyl reductase (ER), and methyltransferase (MT) domains are commonly found in PKS modules, while cyclization (Cy), *N*-MT, and epimerase (E) domains are sometimes embedded within NRPS modules. These additional



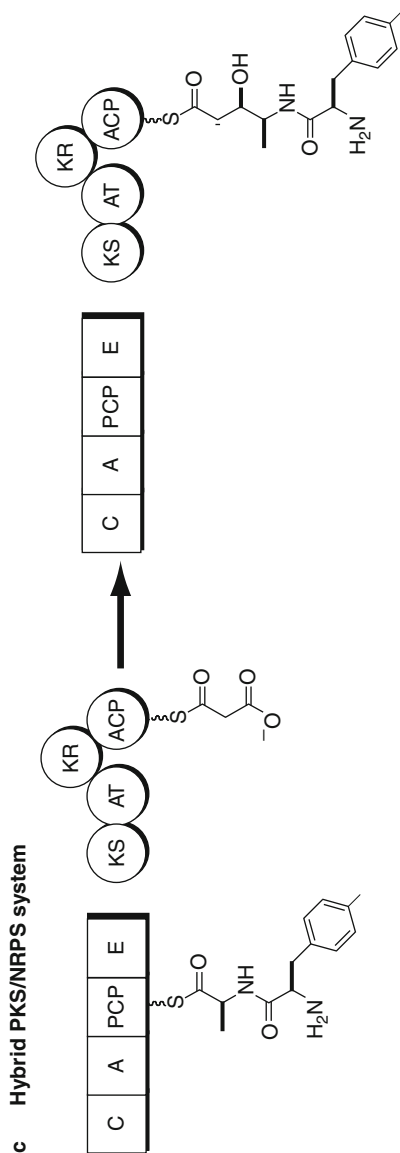


Fig. 18.2 Hypothetical examples of the modular organization in polyketide synthases (PKSs), nonribosomal peptide synthases (NRPs), and hybrid PKS/NRPSs. (a) Two consecutive PKS elongation modules from a hypothetical polyketide biosynthetic pathway that catalyze the elongation of the growing polyketide intermediate by two carbons (from methylmalonyl-CoA), and subsequent β -keto reduction; (b) two consecutive NRPS elongation modules from a hypothetical nonribosomal peptide biosynthetic pathway that catalyze peptide bond formation between the growing peptide intermediate and an activated cysteine residue with subsequent cyclization/oxidation of the incorporated cysteine residue to a thiazole; (c) consecutive NRPS and PKS elongation modules from a hypothetical hybrid nonribosomal peptide/polyketide biosynthetic pathway that catalyze the two-carbon extension (from malonyl-CoA) of the peptide intermediate and subsequent β -keto reduction

domains contribute significantly to the diversity and bioactivity of PKs and NRPs. Thioesterase (TE) domains, typically found at the C-terminus of the final elongation module in both PKs and NRPs, are responsible for terminating biosynthesis. In most cases, TE domains catalyze intramolecular macrocyclization or hydrolysis of the thioester bond between the final T domain and the PK or NRP intermediate [8]. The structures of the nascent PK and NRP products are often further modified through oxidation, glycosylation, acylation, alkylation, and halogenation reactions catalyzed by tailoring enzymes in natural product biosynthetic pathways [19, 20].

In the sections below, a series of marine natural product biosynthetic systems will be described that provide an in-depth overview of genetic and biochemical mechanisms involved in assembly and tailoring of many of these beautifully complex and biologically active molecules.

18.2 Examples

18.2.1 Curacin

18.2.1.1 Isolation and Biological Activity

Curacin A (Fig. 18.3) is a mixed PK/NRP natural product with potent antiproliferative and antimetabolic activity against colon, renal, and breast cancer–derived cell lines [21]. The compound was originally isolated from strains of the tropical marine cyanobacterium *Lyngbya majuscula* discovered in Curaçao by Gerwick et al. [22] and found to possess unusual structural features, including a cyclopropane ring, thiazoline moiety, *cis*-alkenyl group, and terminal double bond. Curacin A has been shown to block cell cycle progression by interacting with the colchicine-binding site on tubulin and inhibiting microtubule polymerization [23]. The clinical development of curacin has been hindered by its high lipophilicity; however, structural analogues having improved water solubility and potency have been recently synthesized to enable continued preclinical studies [24, 25].

18.2.1.2 Gene Cloning, Sequence Analysis

The Gerwick and Sherman laboratories conducted a series of isotope-labeled precursor feeding and NMR studies that established the metabolic origin of all curacin A atoms and their order of assembly [26]. The studies indicated the compound is composed of one cysteine residue, ten acetate units, and two *S*-adenosyl methionine–derived methyl groups, thus suggesting that curacin A was of mixed PKS–NRPS origin. Through the creation and screening of a cosmid library from *L. majuscula* using a general PKS probe, a 64-kb gene cluster containing 14 ORFs was identified. As predicted by the precursor incorporation experiments, the curacin metabolic system (Fig. 18.3) was found to contain nine PKS modules and one NRPS module. Interestingly, this biosynthetic system is unique in that all PKS multifunctional proteins, with the exception of the CurF hybrid PKS/NRPS, are monomodular [26].

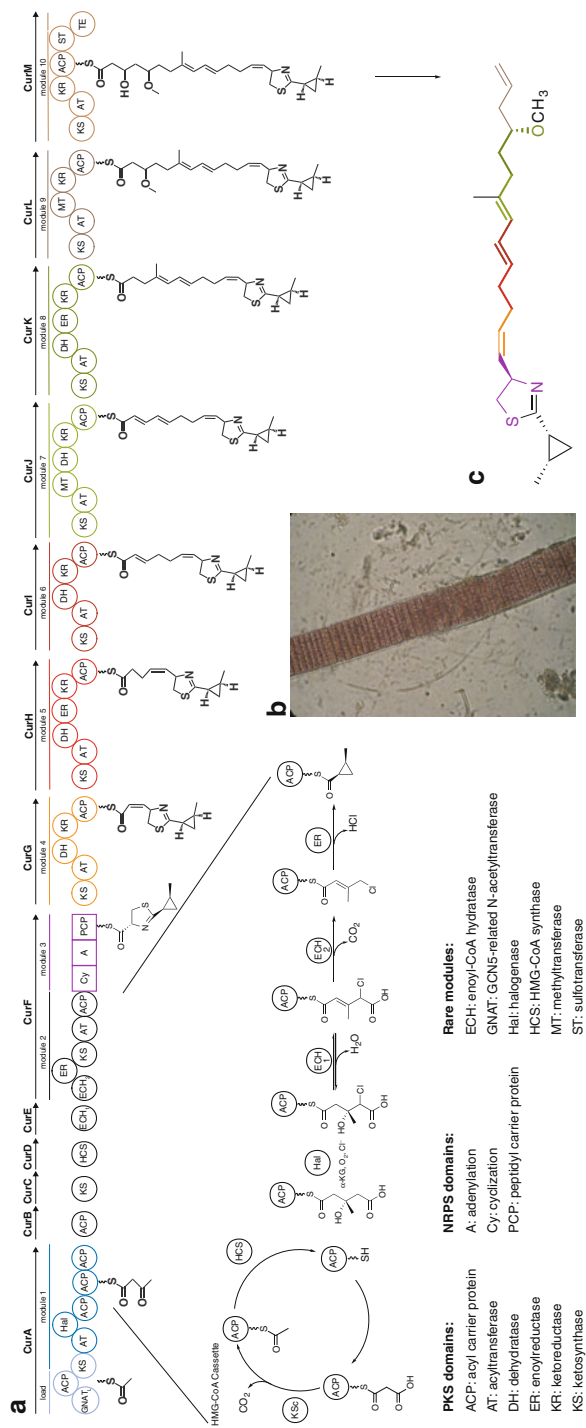


Fig. 18.3 (a) Curacin biosynthesis, (b) producing organism, and (c) structure

Curacin A biosynthesis is initiated by the unique CurA PKS. Bioinformatic analysis of the AT domain located at the amino-terminus of CurA indicated homology with the *N*-acetyltransferase (GNAT) domain, PedI, from the putative pederin gene cluster [26, 27]. Interestingly, a recent study established the role of an astonishing biochemical chain initiation strategy for the loading module of curacin A that involves an unusual tridomain found at the amino-terminus of CurA [28]. This tridomain is comprised of an adapter domain, a GNAT domain, and an ACP domain. In vitro biochemical studies of the isolated tridomain have shown that the GNAT has unprecedented bifunctional activity, as it is capable of first decarboxylating malonyl-CoA to acetyl-CoA and then directing the transfer from acetyl-CoA onto the ACP domain phosphopantetheine arm to produce the acetyl-ACP intermediate [28].

A series of three tandem ACP domains (ACP₃) reside at the C-terminus of the CurA polypeptide that together with four ORFs encoding CurB–CurE, as well as the first two domains of CurF, was predicted to direct formation of the unique cyclopropyl ring in curacin A. Indeed, recent biochemical and structural studies confirmed that the CurE/CurF ECH₁–ECH₂ enzyme pair catalyzes successive dehydration and decarboxylation of (*S*)-HMG-ACP to generate a 3-methylcrotonyl-ACP intermediate for subsequent formation of the cyclopropane ring [29, 30]. Moreover, the CurA ACP₃ domains have been shown to work synergistically, resulting in enhanced catalytic output of the early chain elongation intermediate bearing the cyclopropyl ring [31].

The remainder of the molecule is assembled by seven PKS monomules, CurG–CurM, that catalyze seven successive rounds of condensation with malonyl-CoA extender units. Furthermore, embedded methyltransferase domains in CurJ and CurL are predicted to catalyze transfer of the C-17 and O-13 methyl groups, respectively. Of final interest is the atypical biosynthetic termination mechanism that is predicted to function in both product release and decarboxylative dehydration to form the unusual terminal alkene. Like the majority of other known PK/NRP biosynthetic pathways, the final elongation module of the curacin pathway, CurM, contains a terminal thioesterase domain that was predicted to play a direct role in formation of the terminal olefin. Bioinformatic analysis of the CurM PKS monomule also predicted the presence of a sulfotransferase (ST) domain immediately preceding the TE. ST domains are typically responsible for transferring a sulfonate group from a donor molecule (such as 3'-phosphoadenosine-5'-phosphosulfate, PAPS) to a variety of acceptor carbohydrates, proteins, and other low molecular weight metabolites [32]. Although STs had been previously characterized from both eubacterial and eukaryotic organisms, the presence of an ST domain within a PKS system was unprecedented.

Recent work has revealed the precise functions of the ST and TE domains in terminal olefin formation during termination of curacin biosynthesis (Fig. 18.3). The first step involves ST domain-catalyzed transfer of a sulfonate group (donated by PAPS) to the 3(*R*)-hydroxyl group of the ACP-bound thioester chain, followed by hydrolytic termination of curacin A biosynthesis by the TE to produce the linear free acid bearing a 3(*R*)-sulfate leaving group. High-resolution X-ray crystal

structure analysis of the CurM TE domain provides strong evidence that it catalyzes decarboxylation of the free acid, after which formation of the double bond would be energetically driven by elimination of the sulfate leaving group. Although it is conceivable that upon TE catalyzed hydrolysis, the decarboxylation reaction occurs spontaneously as a result of the presence of the sulfate leaving group at carbon 3, isolation of a substrate mimic bearing these two functional groups indicates that enzyme catalysis by the TE is required. Further efforts to develop this unique polyketide termination mechanism have important implications for facile conversion of fatty acid intermediates into valuable liquid fuels.

18.2.2 Cryptophycin/Arenastatin

18.2.2.1 Isolation and Biological Activity

Cryptophycins, a large class of peptolides, were originally isolated from the cyanobacteria *Nostoc* sp. ATCC 53789 by researchers at Merck as a potent fungicide. A gross structure was proposed, but Merck abandoned the project because the compounds were too toxic to be developed as antifungals [33]. Several years later, interest in the cryptophycins was renewed when a screen of the lipophilic extract of *Nostoc* sp. GSV 224 exhibited potent cytotoxic activity [34]. This activity was attributed to the cryptophycin natural products, which have since been found to have antimetabolic activity and cytotoxicity toward tumor cells in culture, as well as anticancer activity against murine solid tumor models and human tumor xenografts [35–37]. While there are more than 25 naturally occurring analogues (in addition to the nearly structurally identical marine natural product arenastatin [38]), the major compound from both *Nostoc* sp. ATCC 53789 and *Nostoc* sp. GSV 224, cryptophycin 1 (Fig. 18.4), consists of four subunits: hydroxyphenyloctenoic acid (unit A), 3-chloro-*O*-methyl-D-tyrosine (unit B), methyl- β -alanine (unit C), and L-leucic acid (unit D) linked in a cyclic clockwise sequence [34, 39, 40]. Other naturally occurring cryptophycins are analogues that differ from cryptophycin 1 by one or two of these subunits.

Cryptophycin 1 is one of the most potent tubulin destabilizing agents ever discovered, resulting in cellular arrest at the G2/M phase via hyperphosphorylation of Bcl-2, thereby triggering the apoptotic cascade [41]. Cryptophycins are also attractive as chemotherapeutics because they are active against multidrug-resistant tumor cell lines and are not substrates for *p*-glycoprotein pumps [37]. A synthetic analogue, cryptophycin 52 (LY355703), was developed by Eli Lilly & Co. and ultimately reached phase II clinical trials; however, high production costs coupled with dose-limiting toxicity halted its development [42]. In spite of this, a subsequent phase II clinical trial involving patients with platinum-resistant advanced ovarian cancer concluded that the rate of disease stabilization in the absence of adverse events might justify further investigation of cryptophycin 52 [43]. A second generation of cryptophycin 1 analogues with improved solubility properties has been synthesized, and preclinical studies indicate a marked increase in efficacy against a variety of tumors [44].

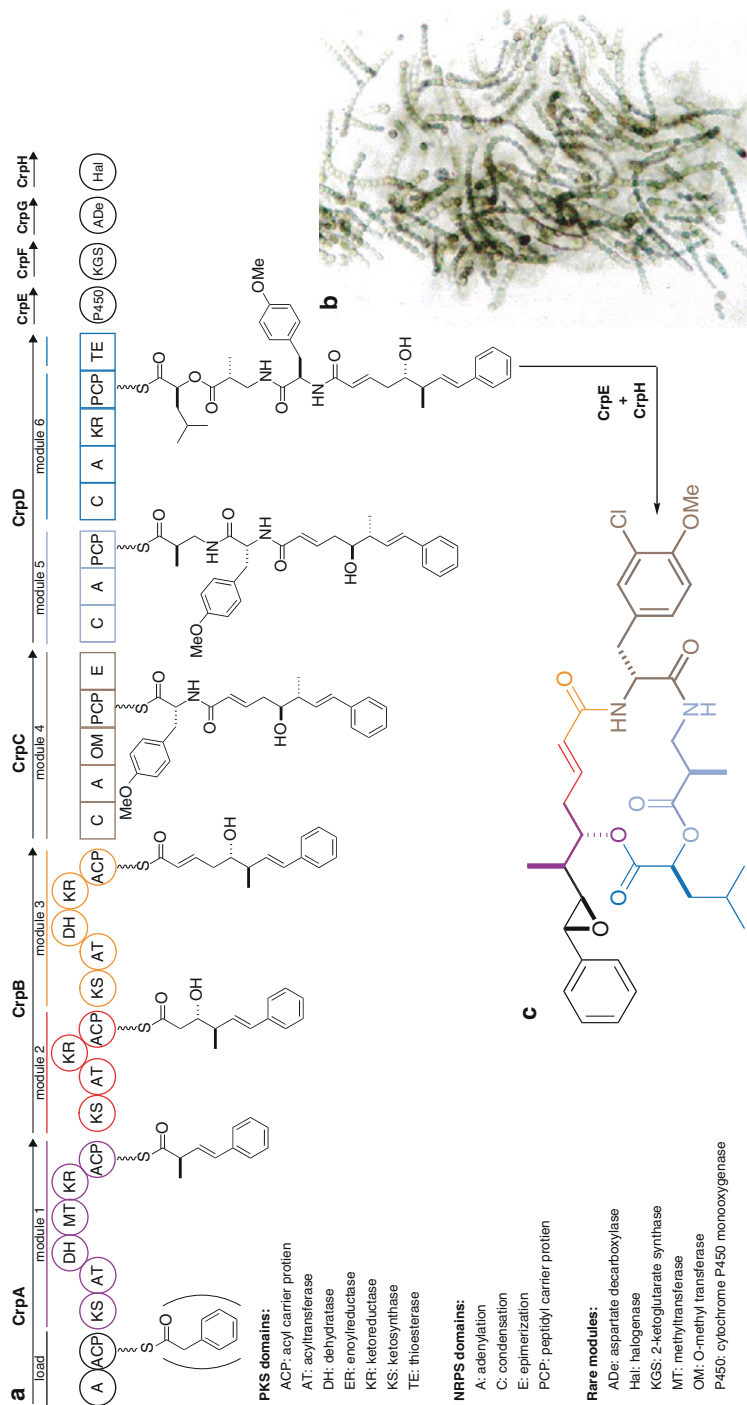


Fig. 18.4 (a) Cryptophycin biosynthesis, (b) producing organism, and (c) structure

18.2.2.2 Gene Cloning, Sequence Analysis

The Sherman and Moore laboratories worked collaboratively to isolate and characterize the cryptophycin gene cluster (Fig. 18.4) using a strategy that relied on comparative metabolomic analysis [45]. In this approach, the A and KS domain sequences of *Nostoc* sp. ATCC 53789 were compared to that of *Nostoc punctiforme* ATCC 29133, a strain that does not produce cryptophycin. This comparative method resulted in the identification of six A domain sequences that were present in *Nostoc* sp. ATCC 53789 but not in *Nostoc punctiforme*. Of these six, a single A domain appeared to be a candidate for the cryptophycin pathway. From this initial lead, the 40-kb cryptophycin biosynthetic gene cluster was identified by cosmid library screening [45].

The cryptophycin gene cluster consists of two modular PKS genes (*crpA* and *crpB*) and two modular NRPS genes (*crpC* and *crpD*). In total, these open reading frames encode seven elongation modules that contain the requisite catalytic domains for assembly of the cryptophycin macrocyclic core structure. In addition, a series of open reading frames, designated *crpE*–*crpH*, are located downstream of *crpA*–*D* and are predicted to encode enzymes that modify the nascent macrocycle to yield cryptophycin 1. These include a cytochrome P450 epoxidase (*crpE*), a putative 2-ketoglutarate-dependent enzyme (*crpF*), an aspartate decarboxylase (*crpG*), and a flavin-dependent halogenase (*crpH*). In addition to characterization of the gene cluster, the Sherman and Moore groups have produced novel cryptophycin analogues by precursor-directed biosynthesis [45]. In vitro biochemical work has also been performed to characterize the TE domain of CrpD [46, 47], the aspartate decarboxylase, CrpG [48], and the P450 epoxidase, CrpE [49]. These studies have unveiled the genetic blueprint of cryptophycin biosynthesis in *Nostoc* sp. ATCC 52789, thereby providing access to a set of catalytic tools for chemoenzymatic construction and modification of new cryptophycin analogues.

18.3 Trans AT Domain Pathways – A Rich Source of Unusual Biochemistry

18.3.1 Trans AT Hybrid PKS/NRPS Systems: An Introduction

One emerging subclass of hybrid PKS/NRPS pathways is the “*trans* AT” hybrid biosynthetic systems. Rather than containing embedded AT domains within their PKS modules, the *trans* AT systems feature a separately encoded, discrete AT domain that is responsible for loading ACP domains with the appropriate CoA substrate (Fig. 18.5). Interestingly, remnants of embedded ATs are found within *trans* AT hybrid pathways and have been proposed to act as “AT docking domains,” or recognition elements, thus providing evidence of an evolutionary link between the two types of pathways [50]. This subclass of natural product synthase serves as an example of the great diversity in pathway architecture represented by these systems.

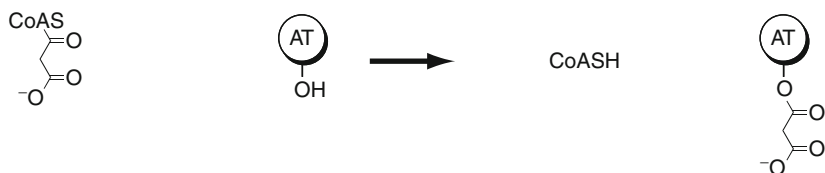
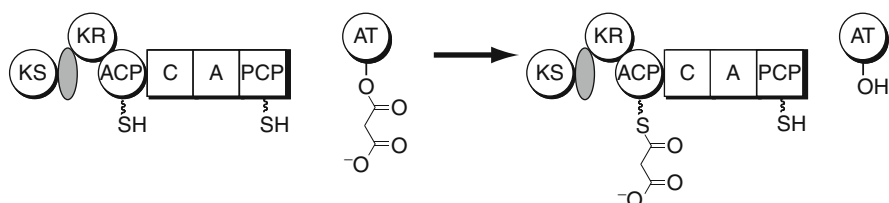
a Loading of *trans*-AT domain**b Transthioesterification of ACP domain**

Fig. 18.5 A schematic of a *trans* AT reaction scheme utilizing a hybrid PKR-NRPS biosynthetic module. (a) Loading of malonyl-CoA onto the AT active site serine; (b) transfer from *trans* AT to the phosphopantetheine arm of the PKS module ACP

Aspects of known NRPS/PKS *trans* AT hybrid biosynthetic pathways including products, pathway organization, in vitro and in vivo biochemistry, biological roles, and potential for future engineering efforts will be explored within this section. For further information, the reader is directed toward one of the many reviews that have been recently published on closely related topics. These include: hybrid NRPS/PKS pathways in general [14, 51], developing molecular tools to engineer these systems [52], compounds derived from marine invertebrates and bacteria [53], symbiotic bacteria-produced secondary metabolites [54, 55], and absence of colinearity including skipping and iteration [56].

18.3.2 Known *Trans* AT Hybrid PK/NRP Pathways

Over the past several years, *trans* AT hybrid biosynthetic pathways have been discovered in a wide range of bacterial species (summarized in Table 18.1, Fig. 18.6). Moreover, in several cases (e.g., onnamide, pederin, bryostatin, and rhizoxin), the bacterial species is engaged in important symbiotic relationships with multicellular hosts. These symbiotic relationships often complicate the identification of the species of origin of the hybrid PK/NRP natural product. With few exceptions, such as those involved in the biosynthesis of mycosubtilin and albicidin, the majority of *trans* AT hybrid pathways are predominantly composed of PKS elongation modules. In fact, it should be noted that *trans* AT pathways that are entirely comprised of PKS modules have been characterized: CpPKS1 [57], mupirocin [58], macrolactam [59], difficidin [60], and bryostatin [61, 62].

Table 18.1 Known hybrid PKS/NRPS *trans* AT pathways. The known hybrid *trans* AT PK/NRP products are listed above by bioactivity, with bacterial class and bionomical. For symbiont products, the host organism is also designated. Protein and gene abbreviations are noted along with PKS and NRPS module composition

Name	Activity	Bacterial class	Producing bacteria	Host	Designation	PKS	NRPS
Albicidin	Cytotoxic	γ -Proteobacteria	<i>Xanthomonas albilineans</i>	N/A	Alb/alb	3	7
Chivosazol	Cytotoxic	δ -Proteobacteria	<i>Sorangium cellulosum</i>	N/A	Chi/chi	16	1
Disorazol	Cytotoxic	δ -Proteobacteria	<i>Sorangium cellulosum</i>	N/A	Dis/dis	10	1
Leinamycin	Cytotoxic	Actinobacteria	<i>Streptomyces atroolivaceus</i>	N/A	Lnm/lmn	7	2
Onnamide	Cytotoxic	Unknown		Sponge: <i>Theonella swinhoei</i>	Omn/onn	?	?
Pederin	Cytotoxic	γ -Proteobacteria	<i>Pseudomonas aeruginosa</i>	Beetle: <i>Paederus</i> sp.	Ped/ped	9	2
Rhizoxin	Cytotoxic	Betaproteobacteria	<i>Burkholderia rhizoxina</i>	Fungi: <i>Rhizopus microsporus</i>	Rhi/rhi	11	1
Antibiotic TA	Antimicrobial	δ -Proteobacteria	<i>Myxococcus xanthus</i>	N/A	Ta/ta	11	1
Bacillaene	Antimicrobial	Bacilli	<i>Bacillus subtilis</i>	N/A	Pks/pks	13	2
Lankacidin	Antimicrobial	Actinobacteria	<i>Streptomyces rochei</i>	N/A	Lkc/lkc	5	1
Mycosubtilin	Antimicrobial	Bacilli	<i>Bacillus subtilis</i>	N/A	Myc/myc	1	7
Virginiamycin M	Antimicrobial	Actinobacteria	<i>Streptomyces virginiae</i>	N/A	Vir/vir	8	2
Thailandamide A		Bacilli	<i>Bacillus thailandensis</i>	N/A		16	1

18.3.3 Biological Activity and Structure of *Trans* AT Hybrid PK/NRPs

PKS/NRPS-derived natural products that are assembled from *trans* AT biosynthetic pathways can be broadly classified as either antimicrobials or cytotoxic chemotherapeutics based on their biological activity (Table 18.1, Fig. 18.6). Certain antimicrobial compounds, such as albicidin and mycosubtilin, have well-defined activities while others, such as bacillaene, chivosazol, and lankacidin, have yet to be rigorously characterized in terms of biochemical targets. Given their ability to cause damage to rapidly growing cells, leinamycin, onnamide, and disorazol each has potential as an anticancer therapeutic. As discussed above, many hybrid PK/NRP natural products have demonstrated clinical utility; however, with the exception of antibiotic TA, none of the compounds are derived from *trans* AT hybrid PKS/NRPS pathways.

18.3.4 In Vivo Analysis of *Trans* AT Hybrid PK/NRP Systems

To date, at least 13 *trans* AT hybrid PK/NRP biosynthetic pathways have been described in the literature (Table 18.1, Fig. 18.6). Intriguingly, aside from the presence of the *trans* AT domain, each of these pathways displays multiple deviations from the typical PKS/NRPS modular organization and composition. In fact, only five of these pathways are colinear with genetic organization, as is typically observed in bacterial PKS or NRPS systems. Module splits, whereby the domains of a single module are divided among multiple polypeptides, are frequently observed within *trans* AT hybrid pathways. 3-Hydroxy-3-methylglutaryl synthase (HMGS) cassettes are also commonly found in these biosynthetic pathways. These cassettes are responsible for the insertion of β -branch points into the middle of the growing polyketide chain [63]. Repeated “tandem” domains and unusual or uncharacterized enzymatic domains are also often present in biosynthetic pathways that employ *trans* AT domains [56]. Additional nonstandard features, such as iteratively acting modules or inactive modules, can often be inferred from the chemical structure of the natural product.

Putative *trans* AT biosynthetic pathways can be linked to a specific natural product through comprehensive bioinformatic analysis which is used to determine domain compositions and predicted acyl [64] or peptidyl substrate [65] incorporation of AT or A domains, respectively [66]. However, in nonlinear pathways, or in pathways that skip or iterate elongation modules, these predictions are challenging and can be misleading. Pathway assignment is typically obtained through genetic disruption and complementation. For example, if the inactivation of a key biosynthetic gene results in a nonproducing phenotype, the pathway/product link is verified. However, this genetic approach is not a viable option for bacteria that are not culturable in the laboratory (often the case for symbionts) or for microorganisms that are not amenable to genetic manipulation. In such cases, the final proof may require complete pathway reconstitution in a heterologous host – a task not yet accomplished for any symbiont pathway. Alternatively, detailed biochemical

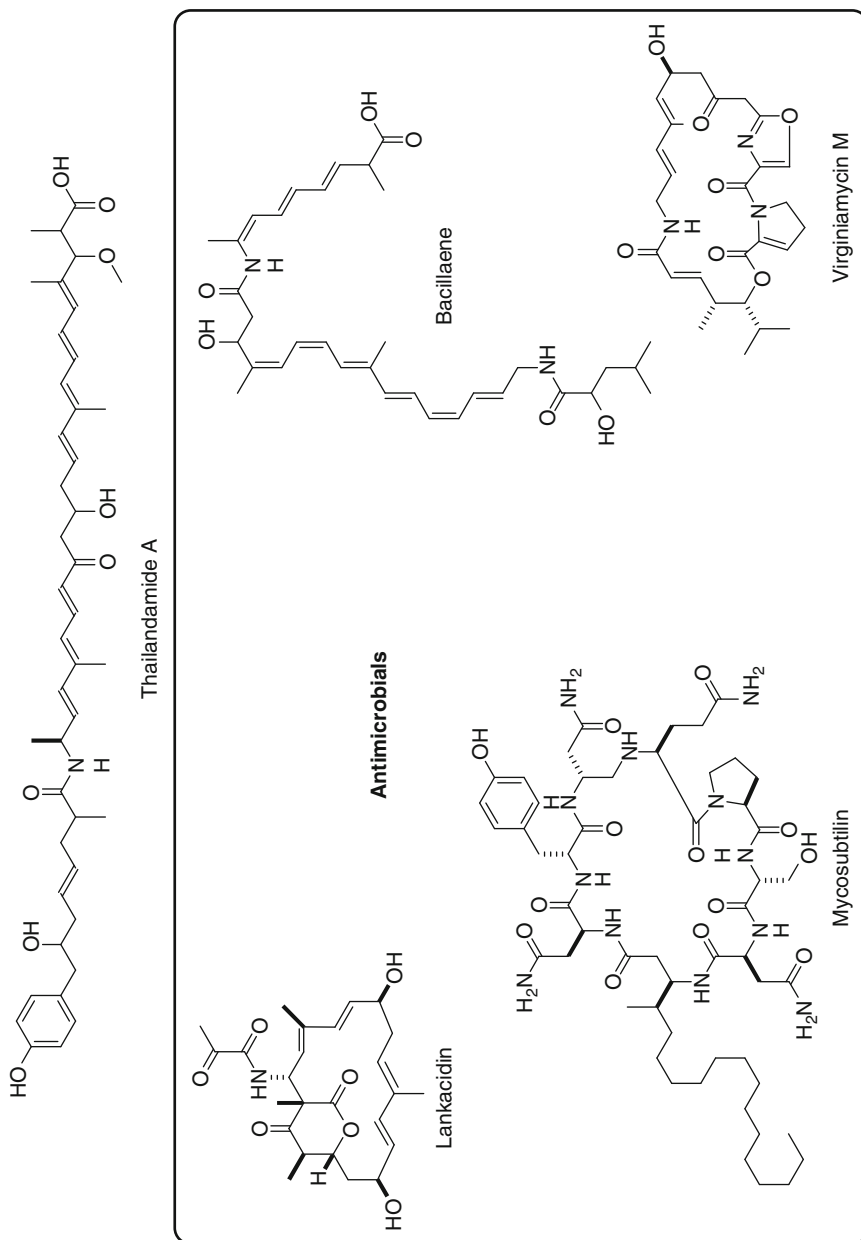


Fig. 18.6 (continued)

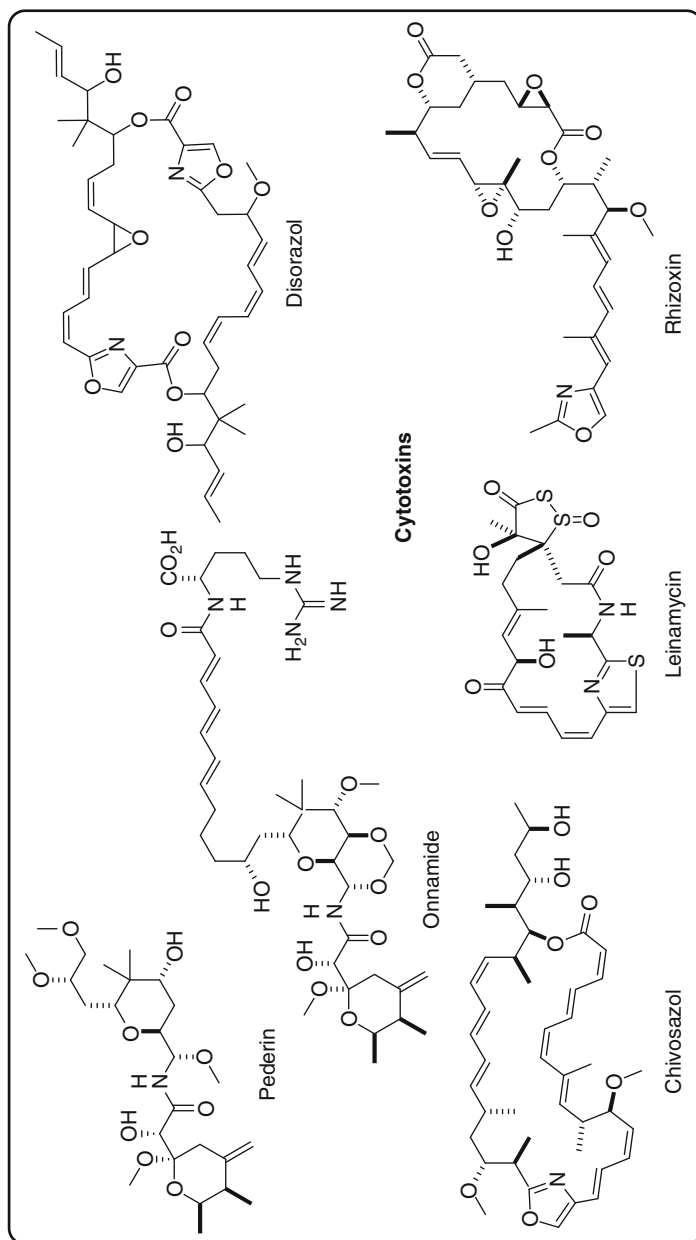


Fig. 18.6 *Trans* AT hybrid PKS/NRPS biosynthetic pathways grouped by bioactivity

studies that provide direct evidence for conversion of a specific natural product biosynthetic intermediate for its cognate enzyme offers key information to correlate pathways from unculturable marine microbial symbionts. Studies on the *trans* AT and β -branching pathways in the bryostatin biosynthetic pathway have offered unique insights into this important marine natural product with anticancer and neuroprotective activity [62, 67].

18.3.5 In Vitro Characterization of *Trans* AT Hybrid PKS/NRPS Pathways

Given the many unusual features of the *trans* AT hybrid PK/NRP biosynthetic pathways, the precise sequence of compound assembly and the exact role of specific domains cannot always be easily ascertained from either sequence analysis or in vivo biochemistry. A more direct approach toward understanding these issues is to perform detailed in vitro biochemical investigations employing recombinant enzymes. Using defined assay conditions, detailed enzymology studies can provide important details of these hybrid megasynthetases. Additionally, heterologous expression and purification of recombinant proteins enable the possibility of gaining key structural data and might eventually inform new avenues toward pathway reengineering in vitro. It is becoming increasingly apparent that rigorous in vitro examination of enzymes from a few select pathways has dramatically improved our understanding of the role of unusual domains and architecture in these pathways [63, 68–74].

18.3.6 Evolution, Biology, and Symbiosis of *Trans* AT Hybrid PKS/NRPS Systems

Elucidation of the biological roles of PKS, NRPS, and hybrid PK/NRP natural products that are produced by *trans* AT PKS/NRPS synthetases is a rapidly emerging field of research, particularly in relation to developing models of microbial symbiosis in natural product biosynthesis. Why do organisms expend so much energy and genome composition to generate these elaborate natural products? While the chemical ecology of some of these compounds has been explored, considerable work remains to understand the role these compounds serve for the producing organism [75]. Indeed, even the identity of the organism (host versus symbiont) that is responsible for natural product biosynthesis is an area of intense interest. Macroscopic eukaryotes including insects, plants, marine sponges, and tunicates have long been recognized as sources of diverse natural products. Yet time and time again, experimental evidence strongly suggests that associated microorganisms are responsible for many marine natural product biosyntheses, especially when similar compounds are isolated from taxonomically diverse producers. Cell separation experiments, as performed in the marine sponge *Theonella swinhoei*, have shown that the isolated fraction of bacteria colocalized with

secondary metabolite production [76]. The complexity of this problem becomes evident when it is recognized that up to 40% of the mass of a sponge may be composed of bacteria, fungi, and other microorganisms [77].

18.3.7 Onnamide/Pederin

18.3.7.1 Biological Activity and Structure of Trans AT Hybrid PK/NRP

Both onnamide and theopederin, a close analogue of pederin (Fig. 18.7), are nanomolar inhibitors of protein synthesis, leading to induction of ribotoxic stress response, p38 kinase activity, and apoptosis. These activities were discovered during a screen for activators of transforming growth factor β (TGF- β) expression [78]. It has been hypothesized that these compounds may directly bind to the eukaryotic ribosome, thus resulting in downstream activation of apoptotic pathways [78].

Onnamide and pederin each contain a similar carbon backbone with two tetrahydropyran rings linked through an amide bond. Furthermore, each features an exocyclic double bond. Differences between the two natural product compounds include the presence of an additional hydroxyl group in onnamide that results in formation of a third six-membered ring. Onnamide also contains a longer, conjugated side chain that terminates in an arginine residue. The structural similarity shared between onnamide and pederin was proposed as evidence for the existence of a related symbiont producer in natural product biosynthesis [79, 80] well before Piel obtained the gene clusters from the producing organisms [81, 82].

18.3.7.2 In Vivo Biochemistry of Trans AT Hybrid PK/NRP

The biosynthesis of pederin and onnamide will be discussed together due to the close chemical and biosynthetic similarities that are shared between the compounds and pathways [81–83]. The role of these pathways (Fig. 18.7) in settling the long-standing debate over the source of natural products in marine invertebrates (e.g., sponges, tunicates) is discussed below. Both pederin and onnamide are initiated from a PKS elongation module (OnnB/PedI) that begins with a GNAT-loading domain. A similar initiation mechanism is found in the curacin biosynthetic pathway [28]. The domain composition and arrangement is identical for each pathway over the first 12 domains, encompassing two PKS elongation modules. Interestingly, 2 unusual domains exist within these first 12 domains and have been annotated as crotonyl-CoA reductases. Divergence in biosynthesis of the two molecules occurs beyond this point. The onnamide biosynthetic machinery proceeds with a tandem triple ACP, whereas pederin biosynthesis continues with a tandem di-ACP. In addition, the final PKS module of OnnB contains only KS and ACP domains, whereas the final module in PedB features a KS domain, a domain of unknown function, a KR domain, and finally an ACP domain. The subsequent polypeptides, OnnI or PedF, share a high degree of similarity, with the arrangement of the first 12 domains being identical. Briefly, each polypeptide begins with a PKS elongation module, followed by an NRPS module, and

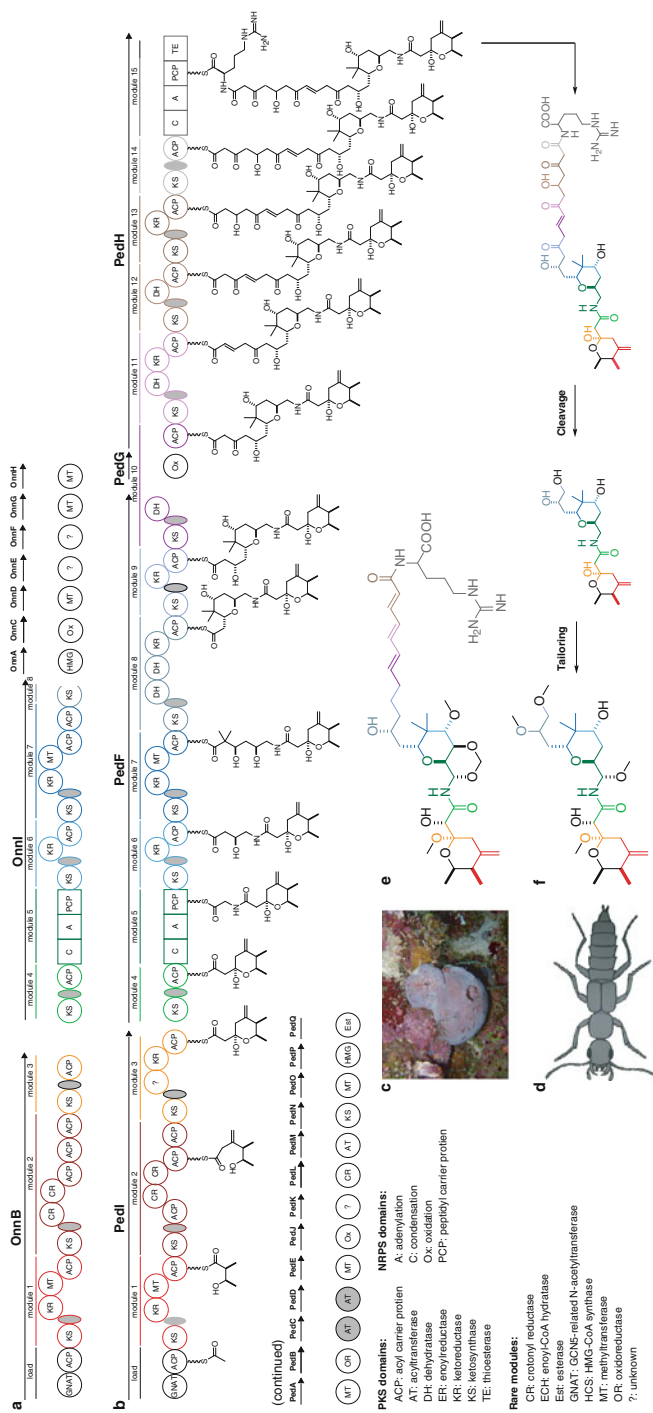


Fig. 18.7 Onnamide and pederin biosynthesis. The onnamide (**a**) and pederin (**b**) biosynthetic pathways are displayed with predicted intermediates. The onnamide (**c**) and pederin (**d**) symbiotic macroscopic host organisms are also displayed, as are the final products onnamide (**e**) and pederin (**f**)

a second PKS module. At this point in the biosynthetic pathways, divergence is observed. Here, OnnI terminates with tandem ACP domains, followed by a KS domain. It should be noted that the DNA sequence of onnamide biosynthetic pathway is presumably incomplete, and therefore OnnI does not likely represent the terminus of the metabolic system. This is because out of a 500,000-member clone library, only one cosmid containing the incomplete onnamide gene cluster was isolated [82]. In comparison, PedF continues with a single ACP domain that is followed by two additional PKS modules, the first of which contains a tandem DH didomain. At this point, two biosynthetic possibilities have been proposed. First, PedG catalyzed hydrolysis of the chain elongation intermediate from PedI and yields the pederin nascent intermediate (pretailored). Alternatively, chain extension continues through PedH, which results in a product having a very similar structure to onnamide. This “onnamide” type intermediate would then presumably be cleaved to give the beetle-derived product, pederin. The domain arrangement of PedH involves a presumed oxygenase, PedG, of the previous split module, PedF. PedH continues with four PKS elongation modules prior to the final arginine incorporating NRPS module that terminates with TE. Additional discrete proteins are also present in the pederin pathway. These include PedA/E/Q (methyltransferases), PedB (oxidoreductase), PedC/D/M (*trans* AT tridomain), PedJ (oxidase), PedK (unknown function), PedL (crotonyl-CoA reductase), PedN (KS), PedP (HMG-ACP synthase), and PedO (esterase). Several proteins with high sequence similarity are found in the onnamide pathway. These include OnnA (HMG-ACP synthase), OnnC (oxidase), OnnD/G/H (methyltransferases), and OnnE/F (unknown function) [81–83]. As a matter of caution, it is important to note that these pathway assignments are considered putative, as they have not been confirmed as the metabolite source through heterologous expression or through detailed biochemical analysis of corresponding purified proteins.

18.3.8 Evolution, Biology, and Symbiosis of *Trans* AT Hybrid PKS/NRPS Systems

One of the mysteries that have intrigued natural product chemists for years is how structurally similar natural products can be isolated from evolutionarily distinct hosts (e.g., marine sponges, myxobacteria). These discoveries have led to the hypothesis that microorganisms are the likely producers of many marine invertebrate-derived natural products. Support for this hypothesis was offered by Piel, who isolated, characterized, and comparatively analyzed the DNA encoding the biosynthetic pathways of pederin and onnamide from the rove beetle and a marine sponge, respectively. The isolation and subsequent screening of DNA from the gut bacteria of the pederin source (rove beetle) eventually lead to the identification of the pederin pathway that originated from an unculturable symbiont [81]. Subsequently, Piel hypothesized that a similar symbiotic relationship accounted for the existence of a homologous pathway for onnamide production in the marine sponge *Theonella swinhoei*. Screening of a *T. swinhoei* metagenomic DNA library led to

the identification of a biosynthetic pathway having a high similarity with that of pederin [82]. The relationship of pederin and onnamide represents a fascinating example in which similar natural product biosynthetic gene clusters are derived from unique, phylogenetically distinct strains from widely disparate macroorganisms. Extensive gene sequencing has identified that *Pseudomonas aeruginosa* is the beetle endosymbiont responsible for pederin production [84]. To date, the microbial symbiont of the sponge has yet to be determined, but the DNA appears to be of bacterial origin [83]. Further questions regarding evolution and divergence of the two pathways and host diversity remain to be fully explored.

Recent work to investigate the evolution of *trans* AT PKS systems, the main class of synthase isolated to date from marine microbial symbiotic organisms, may help frame the pertinent biological questions. Piel recently grouped known *trans* AT synthases and subjected them to multiple amino acid sequence alignments [66]. Interestingly, only the KS and MT domains showed conservation in all examined sequences. *Trans* AT KS specific clades formed in an intriguing manner. Domains did not cluster based on whether or not they were from the same gene cluster, as seen for *cis* ATs, but rather based on what final extension unit is generated. From this analysis, several insights are gained. First, it is possible to predict *trans* AT PKS product structure to a reasonable degree of accuracy, even in cases where pathways have reductive or β -branching domains acting in *trans*. Such a prediction was illustrated for thailandamide [66]. Secondly, and perhaps most importantly, Piel et al. revealed that *trans* AT systems have likely evolved through a very different mechanism compared to their *cis* AT PKS counterparts. In *trans* AT pathways, horizontal gene transfer and recombination appear to be the driving force, as opposed to recombination. This suggests that *trans* AT PKS pathways may be classified separately from their *cis* AT counterparts, much in the sense that PKS and NRPS pathways are to each other [66].

The rapidly growing number of complete genome sequences from free-living and symbiotic bacteria, as well as from environmental samples, is expected to lead to an increase in the number of characterized *trans* AT hybrid PKS/NRPS pathways [66]. Previous comparative studies made with significantly smaller amounts of sequence data began to show evidence of distinct clades forming between methylmalonyl-CoA *cis* ATs, malonyl-CoA *cis* ATs, and *trans* AT modular PKS domains [68]. Interestingly, it appears that *trans* AT PKS or PKS/NRPS systems may be underrepresented in current databases, as relatively larger numbers of *trans* AT PKS systems have been observed (relative to *cis* AT PKS systems) in random sequencing of bacterial strains [85].

18.4 Technologies

18.4.1 DNA Sequencing Strategies in Hybrid PK/NRP Systems

When searching for bioactive compounds in nature, or the genes that direct their biosynthesis, it is best to survey a relatively large pool of structural or genetic

diversity. However, given that 16 S rRNA gene sequence analysis suggests that less than 0.1% of bacterial species collected in a marine sample are amenable to traditional laboratory culturing techniques, alternative approaches become necessary [86]. One strategy involves the collection of whole environmental DNA (eDNA) and subsequent screening for biosynthetic gene clusters based on homology to known genes. The disadvantage of this approach is that it typically requires densely populated DNA libraries (e.g., pederin and onnamide). Even having access to large DNA libraries does not ensure successful identification of desired gene clusters, as was demonstrated in the recent search for the discodermolide biosynthetic pathway from the sponge *Discodermia dissoluta*. Screening of more than 150,000 cosmids produced over 4 GB of DNA sequence data but failed to identify the gene cluster [87]. Interestingly 90% of the DNA sequenced appeared to be bacterial in nature, thereby suggesting that the sponge does contain a diverse microbial community with high biosynthetic potential [87]. Because of this promise, investigators continue to pursue the development techniques to enable the efficient manipulation and screening of huge pools of DNA, such as clone pooling in semiliquid medium [88].

The rise of rapid and inexpensive whole genome DNA sequencing is also expected to have a profound impact on the ability to access data from environmental samples of microbial consortia (Fig. 18.8). Early experiments have demonstrated that there are seven diverse biosynthetic pathways in a single strain of *Salinispora tropica* [89]. Genome mining has also been applied in the search for rhizoxin pathway homologs in other source strains [90]. In the near future the ready access to inexpensive, high-throughput DNA sequencing will undoubtedly enable direct targeting of PKS and NRPS pathways from diverse metagenomic samples [91].

18.4.2 Mass Spectrometry in Hybrid PK/NRP Systems

High-performance mass spectrometry, particularly FT-ICR MS experiments [92], have been conducted to characterize a wide variety of enzyme-bound intermediates in PKS, NRPS, and hybrid PKS/NRPS pathways. Application of this technology has greatly enabled analysis of enzyme kinetics using radiolabel-free approaches by identifying and characterizing intermediates with a high degree of sensitivity and selectivity [92]. FT-ICR MS has also been applied toward the screening of new pathways. This work has relied on a phage display to express protein segments encoding thiolation domains, which are then identified in a high-throughput manner using loss of the phosphopantetheine prosthetic group as a specific signal [93]. New hybrid MS approaches, developed further by the Dorrestein laboratory, are also highly innovative. By using MALDI imaging to localize marine natural products to a specific location, micromanipulation can be employed to simplify the environmental sample prior to whole genome sequencing [94]. Finally, the combination of multiple analytical techniques, such as enzyme

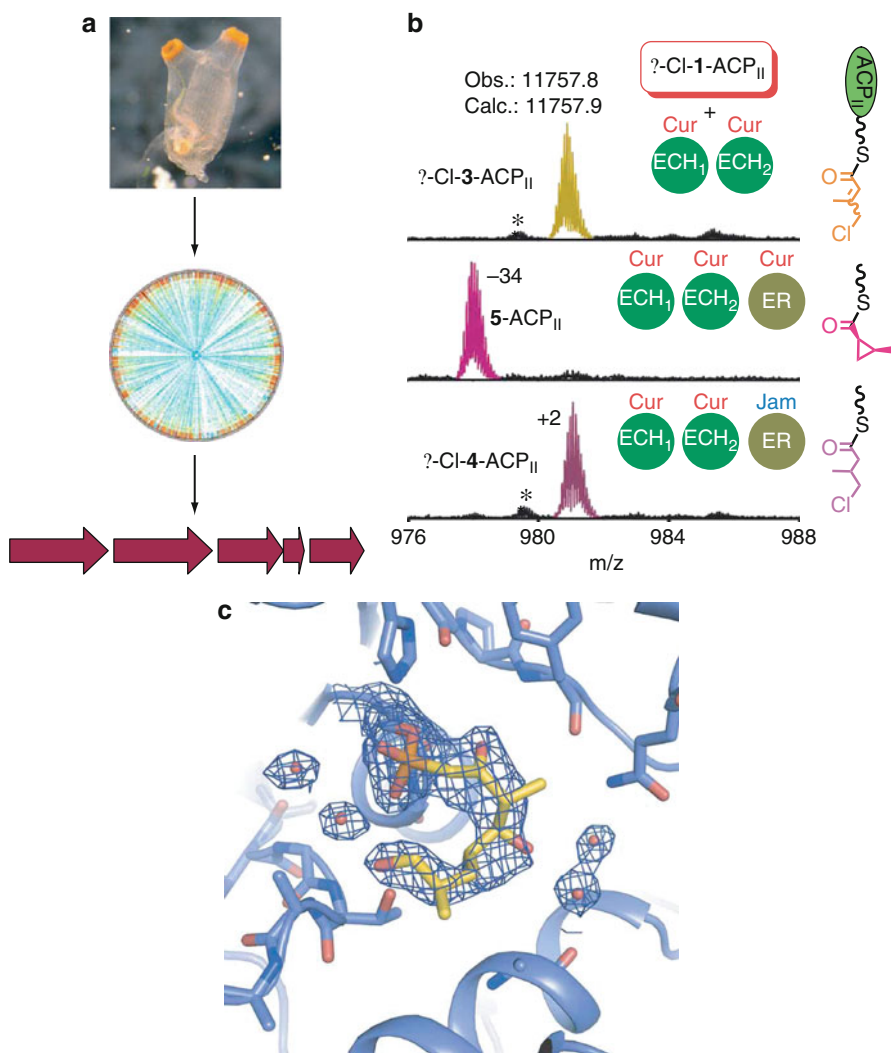


Fig. 18.8 Technology for improved analysis of natural product biosynthetic systems. (a) Metagenomic sequencing may be applied to symbiont–host systems to rapidly identify genes, which can then be probed *in silico* for biosynthetic genes. (b) Mass spectrometry allows for the direct interrogation of enzyme-bound intermediates in the curacin biosynthetic pathway. (c) Covalent probes and X-ray crystallography allow for active site specificity determining structures to be mapped in the pikromycin biosynthetic pathway

kinetics, FT-ICR mass spectrometry, and X-ray crystallography, enables the enzymology of diverse PKS/NRPS systems to be explored in remarkable detail, as was recently demonstrated in the curacin biosynthetic pathway β -branching cassette (Fig. 18.8) [28].

18.4.3 Structural Biology in PKS/NRPS Systems

X-ray crystallography and NMR-based structural analysis of biosynthetic enzymes can enhance our fundamental understanding of how these protein machines manufacture diverse natural products. The rate-limiting step for X-ray crystallography often resides in protein crystallization; however, high-throughput techniques to rapidly clone and express diverse gene constructs offer one viable strategy for overcoming this problem [95]. Fundamental questions, such as the nature of PKS/NRPS systems and whether they have a dimeric (PKS) or monomeric (NRPS) quaternary structure, can be addressed by structural analysis, as was demonstrated with recent crystallographic work in the type I iterative fatty acid synthase [96–101]. The most structurally well-characterized natural product biosynthetic system is the erythromycin (DEBS) modular PKS, which has been explored by X-ray crystallography through a series of excised catalytic domains and didomains [102]. One limiting factor in the complete structural determination of these megasynthases appears to be the overall flexibility of the ACP domains. Currently, structural information of ACPs has been derived by solution-phase NMR studies [103–105]. Emerging approaches for studying large protein complexes such as cryo-EM may also be integrated with high-resolution X-ray structural information as a step toward full understanding of these fascinating multicomponent biochemical machines.

18.5 Summary

By studying the coupled PKS and NRPS programming of PKS/NRPS pathways, a vast realm of biosynthetic space can be explored. Likewise, products of these pathways present a large pool of novel chemical entities that have been selected during evolution by providing an advantage to the producer/host. By leveraging these two pools of diversity, it is possible to access new tools to treat human health conditions within the sphere of cancer, immunomodulatory, infectious diseases, and other areas, as illustrated above. These clinically relevant marine-derived PK/NRP products represent a potent and expanding source of clinical leads. The coupling of this biosynthetic and chemical diversity is enabling us to take steps toward bypassing the traditional drawbacks of natural products research by providing facile access to metabolites through fermentation, and modification of existing products through pathway engineering.

Through further investigations of the unusual biosynthetic capabilities of the emerging class of noncanonical *trans* AT PKSs, we can hope to both expand our repertoire of capabilities while expanding our fundamental understanding of the flexibility of PK/NRP biosynthesis. Other developing topics such as the role of symbiosis in marine natural product biosynthesis seem to be uniquely located within these unusual *trans* AT systems. It is encouraging to look forward with the hope of applying modern techniques in molecular biology, biochemistry, and analytical chemistry to further dissect and manipulate the mixed PK/NRP natural products through rational design of their PKS/NRPS biosynthetic machinery.

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Abstract

Chemical halogenation often requires harsh reaction conditions and results in unwanted by-product formation. It is thus of great interest to investigate the biosynthesis of halogenated natural products and the biotechnological potential of halogenating enzymes. Most of the biogenic organohalogenes known today are marine-derived and often proposed to serve as antifeedant and antibacterial defense agents; however, knowledge on biological halogenation in marine organisms still is very limited. Today, mainly vanadate-depending haloperoxidases (Va-HPO) and nonheme Fe^{II}/α-ketoglutarate/O₂-dependent halogenases are described for secondary metabolite biosynthesis in marine

C. Wagner (✉) • G.M. König (✉)

Institute for Pharmaceutical Biology, University of Bonn, Nussallee 6, Bonn, Germany
e-mail: claudia.wagner@uni-bonn.de, g.koenig@uni-bonn.de

organisms. Beyond that, also enzymes utilizing *S*-adenosyl-L-methionine in halogen transfer are found in marine environments. This review aims to give a comprehensive overview on the different strategies used by nature to incorporate halogens into secondary metabolites.

19.1 Introduction

Approximately 4,500 compounds known to be produced by living organisms are organohalogens [1–4]. Structural classes range from simple phenolic or aliphatic compounds to complex polyketides and oligopeptides (Figs. 19.4, 19.6, 19.9, 19.10, 19.11, 19.12, 19.13). Biological activities are equally diverse, e.g., antibiotic and antitumor activity as known for chloramphenicol (Fig. 19.12), glycopeptide antibiotics, and cryptophycin (Fig. 19.9), or specific proteasome inhibition as found for salinosporamide A (Fig. 19.16). While from terrestrial organisms a variety of chlorinated metabolites are known, marine halogenated secondary metabolites are more commonly brominated. In general, fluorinated metabolites are extremely rare, mainly due to the high desolvation energy required to activate F^- in aqueous solution [5].

Overall, most of the biogenic organohalogens are marine-derived [1] and often proposed to serve as antifeedant and antibacterial defense agents. However, knowledge on biological halogenation in marine organisms still is very limited. Today, mainly vanadate-depending haloperoxidases (Va-HPO) and nonheme Fe^{II}/α -ketoglutarate/ O_2 -dependent halogenases are described for secondary metabolite biosynthesis in marine organisms. More recently, the unique *S*-adenosyl-L-methionine-requiring enzyme, Sall, has been identified to be involved in the salinosporamide A biosynthesis by the marine actinomycete *Salinispora tropica* [6]. Beyond that, to complete the picture, this review will also include the important group of $FADH_2$ -depending halogenases, even though such enzymes were not yet identified from marine organisms.

19.1.1 Classification of Halogenating Enzymes According to their Mechanism

Halogenating enzymes mainly can be grouped into two classes:

1. Less specific haloperoxidases (HPO), utilizing hydrogen peroxide and having heme or vanadate involved as cofactor.
2. Highly substrate-specific halogenases requiring dioxygen for enzymatic activity. In dioxygen-depending halogenases, either α -ketoglutarate, in nonheme Fe^{II}/α -ketoglutarate/ O_2 -dependent halogenases, or flavin, in $FADH_2$ -depending halogenases, is found to function as a cosubstrate.

Furthermore, methyltransferases are involved in the formation of the carbon-halogen bonds of CH_3Cl , CH_3Br , and CH_3I , and other enzymes requiring *S*-adenosyl-L-methionine as catalyst have been identified to be involved in fluorination and chlorination reactions [6, 7].

19.2 Haloperoxidases

Until the mid-1990s, the understanding of biological halogenation reactions was restricted to haloperoxidases (HPO). These enzymes generate hypohalous acid (HOX) or related halogenating intermediates, such as OX^- , X_3^- , and X^+ , by the reaction of a metal-bound hydroperoxy species with a halide ion (Fig. 19.1). In most cases, the halogenating species is then released from the enzyme to act on organic substrates that are susceptible to an attack by electrophiles. The enzymes are found to contain either heme or vanadate as cofactor in their active site [8–10]. In heme-containing HPOs, the formation of hypohalous acid is driven by a redox mechanism, whereas vanadate-containing HPOs do not change their oxidation state during the enzymatic cycle but rather function as Lewis acids. HPOs are further classified according to the halide ion which they are predominantly able to utilize for

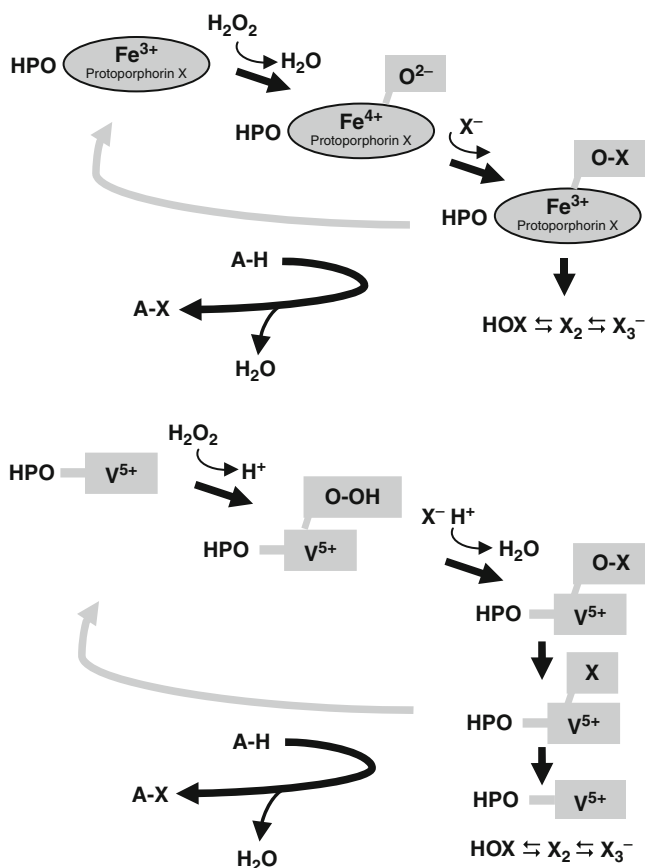


Fig. 19.1 Both heme- and vanadium-dependent HPOs are thought to generate bound hypohalite intermediates and hypohalous acid which react as X^+ equivalents with electron-rich substrates (X : halide, A : organic substrate)

halogenation [11]. Thus, the nomenclature is based on the most electronegative halide oxidized by the enzyme. Chloroperoxidases (CPOs) catalyze the oxidation of chloride, bromide, and iodide, while bromoperoxidases (BPOs) only catalyze the oxidation of bromide and iodide, and iodoperoxidases (IPOs) are specific for iodide oxidation [12]. However, hydrogen peroxide does not have the driving force to oxidize fluoride [8].

The first halogenating enzyme was described from the caldariomycin-producing fungus *Caldariomyces fumago* as a heme-containing HPO [13]. Hager and coworkers developed a spectrophotometric assay, using monochlorodimedone as a mimic of the natural precursor of caldariomycin, to monitor for HPO activity (Fig. 19.2). Based on this assay, several heme HPOs were subsequently discovered from diverse fungi, algae, and microorganisms [9, 10, 14]. The detected HPOs were shown to have a broad substrate specificity, accepting organic compounds, which are generally susceptible to electrophilic attack. Thus, regioselectivity was the same as that seen in chemical halogenations.

In addition to halogenating activity, ferric heme HPOs have been shown to share catalytic properties with at least three further classes of heme-containing oxidoreductases, namely, classical peroxidases, cytochrome P450 monooxygenases, and catalases [10]. Intensive studies on structural and functional aspects of the heme HPO have focused mainly on the initially described CPO from *C. fumago*. Under investigation was the chlorination activity of this enzyme, as well as its epoxidation and sulfoxidation activity in the absence of halide [10, 15–19]. A recent study on the chlorination mechanism confirmed that the final chlorine transfer to various substrates occurs outside the active site via a free diffusible species without any special mode of substrate recognition [20]. In contrast, epoxidation and sulfoxidation are performed regioselectively, providing *C. fumago* CPO as

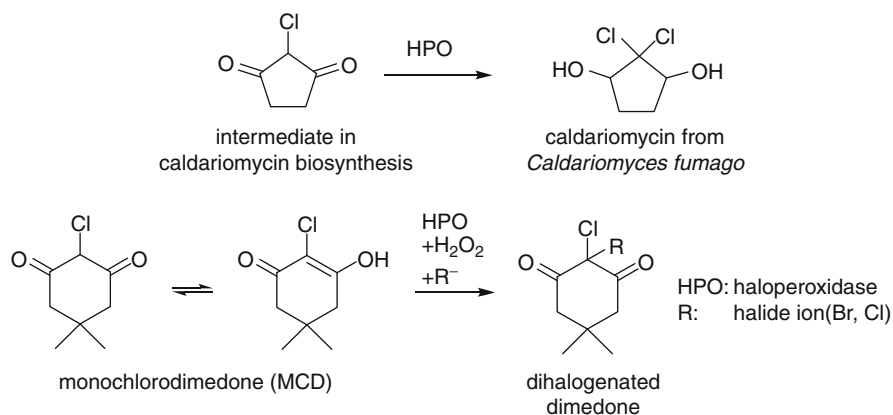


Fig. 19.2 2-Chloro-1,3-cyclopentanedione is a late intermediate in caldariomycin biosynthesis, the natural product from *Caldariomyces fumago*. Based on this reaction, the conversion of the synthetic analog monochlorodimedone is applied in HPO activity assays

a useful tool in synthetic applications. Further investigations were conducted towards the dehalogenation of trihalophenols and *p*-halophenols [21]. *C. fumago* CPO proved to be capable of catalyzing such degradation processes and was significantly more robust than other peroxidases. Thus, this CPO might be applicable in biodegradation of polychlorinated phenols and further noxious haloaromatic compounds, under reaction conditions often too harsh for other biocatalysts.

Vanadate ion-containing bromoperoxidases (Va-BPOs) have been isolated mainly from marine algae. This group of enzymes most likely seems to play a role in the formation of marine natural products, e.g., the halogenation and cyclization of terpenes [22]. Va-HPOs bind hydrogen peroxide and halides leading to a putative enzyme-bound or active site-trapped brominating moiety [23]. X-ray crystal structures of the Va-BPO from *Curvularia inaequalis* [24], *Ascophyllum nodosum* [25], and *Corallina officinalis* [26] displayed a channel leading to the vanadium binding site, which is proposed to influence substrate specificity [27]. Competitive kinetic studies, comparing the bromination of indole substrates by Va-HPO with enzyme-free preparations under aqueous conditions, showed that these reactions were not congruent, since Va-HPO preferably brominated indole derivatives even in the presence of other substrates, such as monochlorodimedone or phenol red [8, 28]. In the absence of a suitable substrate, however, HOBr is released from the enzyme and carries out unselective bromination as observed for aqueous bromine. The role of Va-BrPO in biosynthesis has been further established by the observation that the ratio of formed diastereomers was also found to differ between purely chemical and enzymatic reactions. Accordingly, asymmetric bromination and cyclization of the terpenoid precursor (*E*)-(+)-nerolidol could be demonstrated for Va-BPO, producing single diastereomers of the marine natural product β -snyderol as isolated from *Laurencia* sp. [27] (Fig. 19.3).

The first Va-BPO to be characterized was from the brown seaweed *Ascophyllum nodosum* [29]. However, with the isolation of a Va-BPO from the lichen *Xanthoria parietina*, it became obvious that this group of enzymes not only occurs in the marine environment but also can be found in terrestrial eukaryotic organisms [30]. Va-CPOs on the other hand have been mainly found in fungi even though, to date, halogenated natural products have not been identified from the corresponding strains [31]. The first indication of the potential involvement of a Va-CPO in the biosynthesis of a marine natural product has recently been discussed regarding the chlorination and cyclization of napyradiomycin (Fig. 19.12), a compound obtained from the marine sediment-derived *Streptomyces* sp. CNQ-525 [31, 32].

In contrast to the iron heme haloperoxidases, Va-HPOs do not catalyze the direct disproportionation of hydrogen peroxide and, therefore, have no catalase activity [33]. However, their structural similarity to acid phosphatases is noticeable, particularly in the domains providing the vanadate and phosphate binding site. Therefore, a common evolutionary origin is proposed as being likely [23].

Recent studies aim to characterize the active site in Va-HPO more precisely, whereby the residues involved in the selection and binding of the specific halide are the main focus [31]. Heterologous expression and mutagenesis studies of Va-BPO

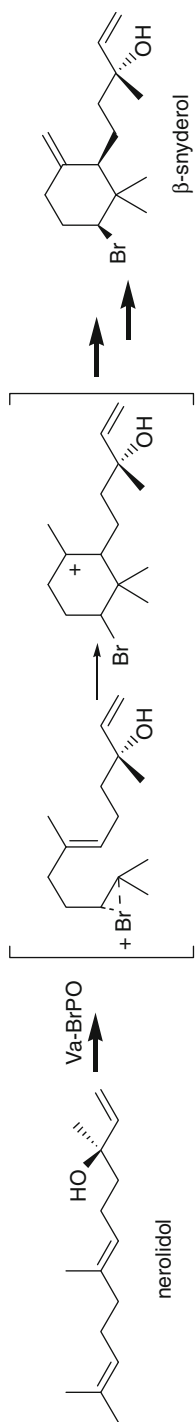


Fig. 19.3 Proposed mechanism of the stereospecific snyderol biosynthesis by Va-BrPO [27]

from *Curvularia inaequalis* and *Corallina officinalis* explore the potential of this type of enzymes in biotransformations [34, 35].

Hypohalous acid is a bactericidal agent, and many halogenated compounds have antimicrobial activity, illustrating the possible involvement of HPO systems in natural defense mechanisms. This might prevent biofouling by microorganisms on the surface of marine algae as well as act as an antifeeding system. Experiments with the marine alga *Laminaria digitata* demonstrated that natural HPO systems are also capable of mediating the deactivation of acylated homoserine lactones, which are important as cell-to-cell signaling molecules for biofilm formation [36]. This suggests that oxidized halogens may control biofouling not only via a bactericidal mechanism but also by possibly interfering with bacterial cell signaling systems. As described above, an involvement of HPOs in the biosynthesis of natural products has only been suggested in a very few cases [22, 27, 32]. The physiological function of CPOs in fungi is mainly proposed as being important for the degradation of plant cell walls. The hypohalous acid produced thus oxidizes lignocellulose and facilitates penetration of the fungal hyphen into a host [23]. Furthermore, Va-IPOs seem to play a role in iodine accumulation of brown algae as a main vector of the iodine biogeochemical cycle [37]. Species like *Laminaria digitata* are thereby able to take up an average content of 1% of their dry weight, representing approximately a 30,000-fold accumulation of iodine from seawater. Iodine efflux and the production of volatile halocarbons, then again, are proposed to be part of an early defense response to various biotic and abiotic stresses by these organisms. This assumption was strengthened, since the transcription of members of the Va-IPO gene family was demonstrated to be rapidly and highly induced as a defense response [38].

19.3 Nonheme Fe^{II}/α-Ketoglutarate/O₂-Dependent Halogenases

In the last years, evidence has accumulated that another class of halogenating enzymes, able to carry out chlorination of inactivated carbon centers, plays an important role in the biosynthesis of marine organohalogenes. Using α-ketoglutarate (α-KG) as cosubstrate, these halogenases are involved in the chlorination of terminal methyl groups of amino acids linked to peptidyl carrier proteins (Table 19.1).

Initial insight into their catalytic mechanism is derived from investigations on SyrB2, which chlorinates the γ-methyl group of L-threonine in syringomycin E (Fig. 19.4) biosynthesis in *Pseudomonas syringae* [39, 40]. Halogenation of L-threonine occurs only when bound to the peptidyl carrier protein SyrB1, while free L-threonine is not accepted as a substrate. Reactions performed with an excess of sodium bromide demonstrated that SyrB2 was also capable of incorporating bromine into the threonyl-S-protein [41], however, with a clear preference to chlorine over bromine. From crystallographic data [42], it was confirmed that Fe^{II} of the active site is complexed by two histidine residues. A halide ligand (chloride or bromide) together with α-KG and water coordinates the iron in the

Table 19.1 Fe^{II}/ α -ketoglutarate/O₂-dependent halogenases

Halogenases	Natural product <i>Organism</i>	Halogenated structural element	GenBank accession number [reference]
SyrB2	Syringomycin E <i>Pseudomonas syringae</i>	L-threonine ^a	U25130, AF047828 [40, 127, 128]
BarB1/BarB2	Barbamide <i>Lyngbya majuscula</i>	L-leucine ^b	AF516145 [48, 49, 129]
DysB1/DysB2	Dysidenin <i>Oscillatoria spongeliae</i> 35P1 ^c	N.S. ^d	AY628171 AY628172 [50]
CytC3	Armentomycin <i>Streptomyces</i> spp.	L-aminobutyrate ^e	n.d. ^f [55]
HctB	Hectochlorin <i>Lyngbya majuscula</i>	N.S. ^d	AY974560 [130]
CmaB ^g	Coronatine <i>Pseudomonas syringae</i>	L- <i>allo</i> -isoleucine	U14657 [57, 131]
KtzD ^h	Kutznerides <i>Kutzneria</i> sp. 744	N.S. ^d	EU074211 [132]
JamHal ⁱ	Jamaicamides <i>Lyngbya majuscula</i> JHB	N.S. ^d	AY522504 [51, 52]
CurHal ^j	Curacin A <i>Lyngbya majuscula</i> JHB	(s)-3-hydroxy-3- methylyglutaryl	AY652953 [52, 133]

^aOnly when bound to the peptidyl carrier protein SyrB1

^bThe triple chlorination is catalyzed by a tandem action of the two enzymes

^c*Oscillatoria spongeliae* 39P1: AY628173, AY628174 [50]; *Oscillatoria spongeliae* AY648943 [134]

^dNot specified

^eBound to the peptidyl carrier protein CytC2

^fNo sequence data available in GenBank

^gMediates the formation of the cyclopropane ring

^hHypothesized to be involved in the formation of the cyclopropane ring

ⁱEmbedded in the PKS module JamE

^jEmbedded in the PKS module CurA

resting Fe^{II} state (Fig. 19.5). Dioxygen attack results in decarboxylation of α -KG, and a highly reactive iron-oxo species (Fe^{IV} = O) is formed as a general key feature of catalysis by these α -oxoacid-dependent dioxygenases [43]. The Fe^{IV} = O abstracts a hydrogen radical from an aliphatic carbon center of the actual substrate, which, in turn, abstracts the halide from the coordination sphere. It has been shown that in vitro SyrB2 was rapidly deactivated during catalysis and no more than about seven turnovers of the enzyme were possible [43]. Further mechanistic studies, especially focusing on the preference of halogenation over hydroxylation during the catalytic cycle, are still ongoing, e.g., as recently published by de Visser and Latifi [44], Wong et al. [45], Matthews et al. [46, 47], and Kulik et al. [4].

For several marine natural products that are halogenated at an unactivated carbon center, analogous halogenating enzymes were suggested to be involved in their biosynthesis, e.g., barbamide, dysidenin, dysideathiazole, jamaicamides, and

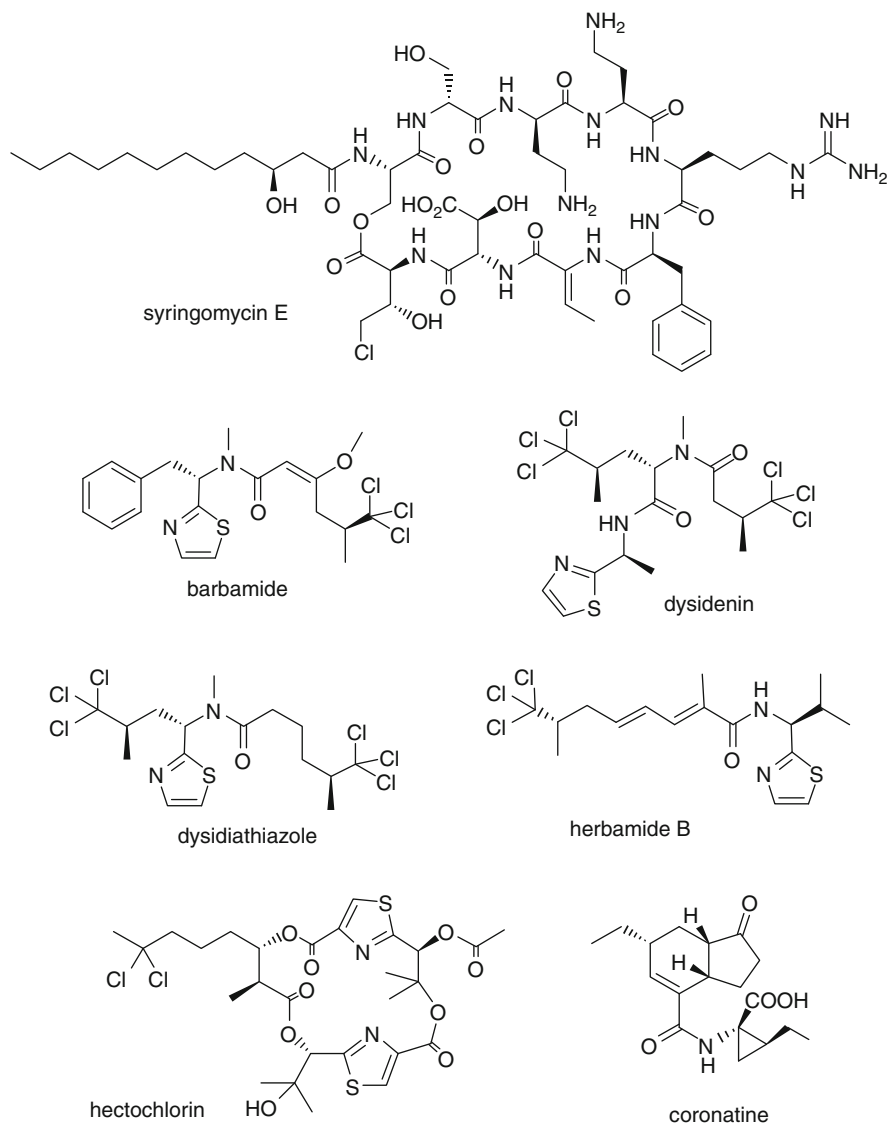


Fig. 19.4 (continued)

herbamide B (Fig. 19.4) [41, 48–54]. Indeed, in the barbamide gene cluster of *Lyngbya majuscula*, two genes, i.e., *barB1* and *barB2*, homologous to *syrB2* could be identified. The initial biosynthetic step is the chlorination of L-leucine to a trichloroleucine derivative, followed by a subsequent conversion to a unique trichloroisovaleryl starter unit in a mixed nonribosomal peptide (NRPS)/polyketide

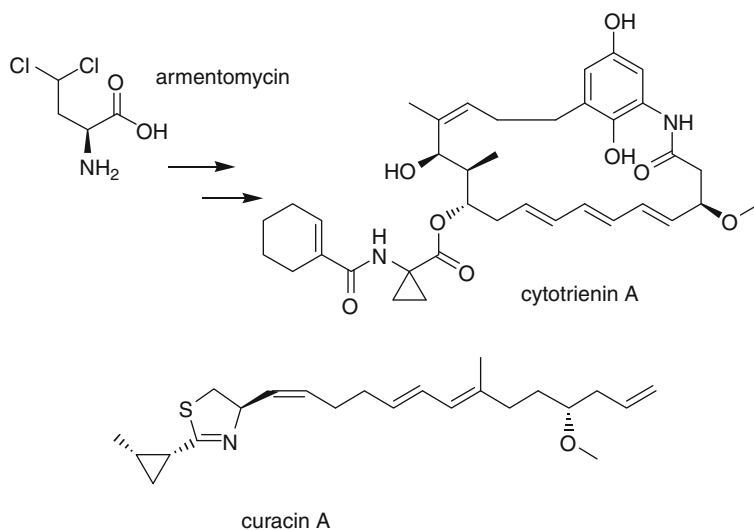


Fig. 19.4 Natural products to be halogenated by Fe^{II}/α-ketoglutarate/O₂-dependent halogenases. Cyclopropyl ring formation of coronatine is executed via a γ-chlorination of L-*allo*-isoleucine followed by intramolecular cyclization

(PKS) pathway [48, 49]. Regarding dysidenin production in dictyoceratid sponges, similar genes (*dysB1/dysB2*) were found and could be ascribed to the cyanobacterial symbiont *Oscillatoria spongelliae* [50].

A Fe^{II}/α-ketoglutarate/O₂-dependent halogenase homologous enzyme, CytC3, involved in the formation of the γ,γ-dichloroaminobutyrate armentomycin (Fig. 19.4) was identified from a soil *Streptomyces* sp. [55]. Interestingly, the γ,γ-dichloroaminobutyryl moiety is postulated to be further cyclized and to act as a precursor in cytotrienin A formation. CytC3 could be demonstrated to act on L-aminobutyrate bound to a peptidyl carrier protein, CytC2. Spectroscopic monitoring of the enzymatic reaction confirmed that the chlorination proceeds through an Fe^{IV} intermediate that cleaves the C–H bond of the amino acid substrate [56], as described above. By analogy, γ-chlorination of an L-*allo*-isoleucine by the Fe^{II}/α-ketoglutarate/O₂-dependent halogenase CmaB mediates the formation of the cyclopropane ring in coronatine (Fig. 19.4), which is produced by several *Pseudomonas syringae* strains [57]. The intermediate γ-chloroaminoacyl β-thioester is then converted to a γ-carbanion, which, in turn, is accessible to intramolecular cyclization [58]. Evidence for a very similar biosynthetic mechanism was observed for the marine secondary metabolite curacin A (Fig. 19.4). From the respective gene cluster of *Lyngbya majuscula*, it was deduced that the formation of the β-branched cyclopropane moiety is initiated by an analogous γ-chlorination step [52].

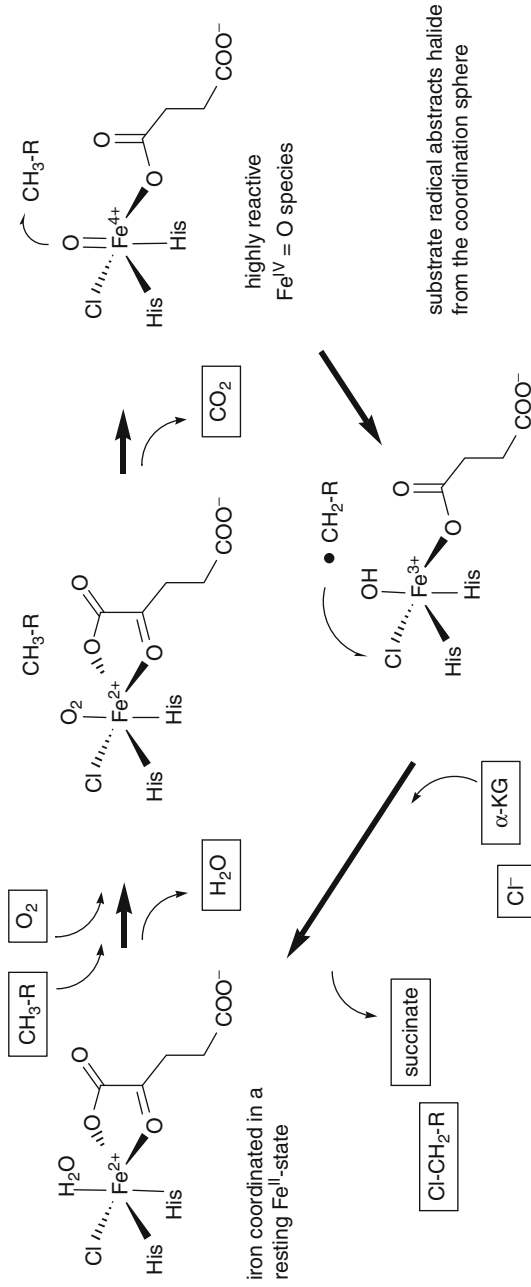


Fig. 19.5 Proposed mechanism of the catalytic cycle of Fe^{II}/α-ketoglutarate/O₂-dependent halogenases. R-CH₃ is the methyl group of the threonyl-S-protein substrate [2]

19.4 FADH₂-Dependent Halogenases

Even though not yet firmly linked to any biosynthetic pathway from organisms of the marine habitat, FADH₂-dependent halogenases form another very important class of halogenating enzymes and thus are included in this overview. This group of enzymes was first discovered when investigating pyrrolnitrin (Fig. 19.6) and chlorotetracycline (Fig. 19.9) biosynthesis [59, 60]. The four enzymes (PrnA, B, C, D) involved in pyrrolnitrin production have been identified from a 6.2-kb genomic DNA region of *Pseudomonas fluorescens* BL915 [59], and their function was proved by construction of deletion mutants for all four genes of the cluster [61]. PrnA (Table 19.2) and the PrnC (Table 19.4) were shown to act as highly substrate-specific halogenases, i.e., the tryptophan halogenase (PrnA) was not able to chlorinate the PrnC substrate monodechloramino-pyrrolnitrin and vice versa [62]. Both enzymes also perform the respective chlorination reaction highly regioselectively, and van Pée and coworkers demonstrated that PrnA is able to halogenate L-tryptophan in a site-specific manner to yield 7-chlorotryptophan [63]. Even though other indole derivatives were also accessible to halogenation by PrnA, they were chlorinated at different sites, i.e., at positions C-2 or C-3. Thus, for regioselectivity, the exact positioning of the specific biosynthetic intermediate at the active site of the halogenating enzyme seems to be of major importance and allows chlorination at a site of the molecule not accessible to chemical halogenation.

It was further shown that the enzymes, PrnA and PrnC ascribed to the two halogenating steps of pyrrolnitrin biosynthesis, require FADH₂ as cofactor [64, 65], which is produced from FAD and NADH by a flavin reductase. A direct contact between the halogenase and the flavin reductase is thereby not absolutely necessary since free diffusible FADH₂ can also be used. Even chemically reduced flavin, regenerated using organometallic complexes, can be utilized [66]. However, free FADH₂ is rapidly decomposed into FAD and H₂O₂ with molecular oxygen, which leads to a significant decrease in halogenase activity. Recent sequencing of the *Pseudomonas fluorescens* Pf-5 genome [67] has revealed that the complete gene clusters for pyrrolnitrin as well as pyoluteorin biosynthesis contain genes encoding for a flavin reductase. This gives rise to the assumption that a distinct flavin reductase specifically interacts with each halogenase to prevent loss of FADH₂ through autooxidation [68].

The mechanism for regioselective chlorination has been further characterized using a purified protein from a *P. fluorescens* BL915 PrnA overexpression system. Cocrystallization of the enzyme with tryptophan and FAD yielded yellow diamond-shaped crystals, indicating that FAD was bound to the protein [69]. From further investigations, it could be demonstrated that FAD and Cl⁻ are bound at the same site of the enzyme, while the tryptophan-binding module is located at a 10-Å distance [70]. FADH₂ reacts with O₂ and forms a peroxide-linked isoalloxazine ring, as generally known from flavin-dependent monooxygenases. Subsequently, HOCl is produced as chlorinating agent and channeled through an intraenzymatic tunnel to the substrate binding pocket. However, HOCl is not released from the enzyme to act in a freely diffusible form in solution. Dong et al.

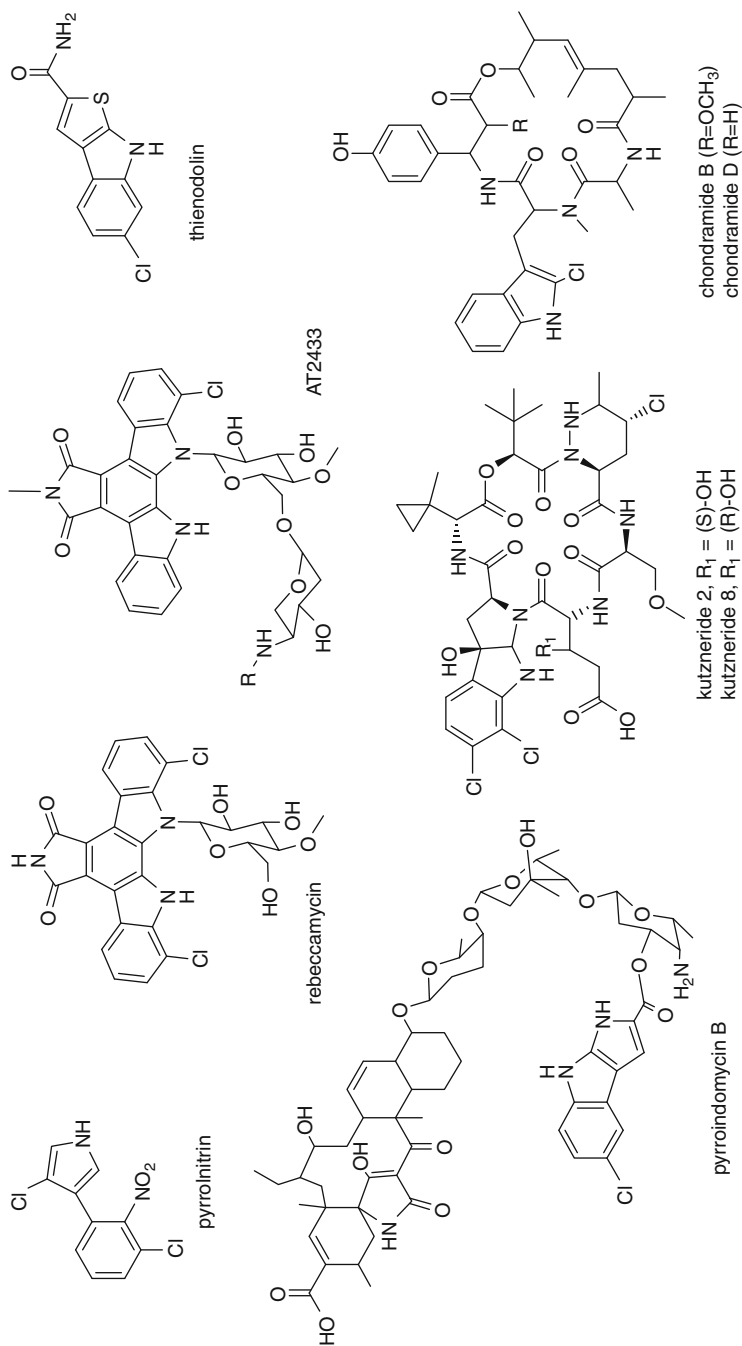


Fig. 19.6 Compounds with chlorinated indole moieties formed from tryptophan. In pyrrolnitrin, rebeccamycin, and AT2433 biosynthesis, a tryptophan-7-halogenase; in thienodolin biosynthesis, a tryptophan-6-halogenase; and in pyrroindomycin biosynthesis, a tryptophan-5-halogenase were identified to catalyze the initial biosynthetic step. In the kutznerides biosynthesis, a tryptophan-7-halogenase and a tryptophan-6-halogenase work in a tandem action to produce 6,7-dichloro-L-tryptophan. Only the tryptophan halogenation at position C-2 in chondramide B and D biosynthesis occurs during NRPS assembly

Table 19.2 FADH₂-dependent halogenases that halogenate tryptophan in the initial step of the respective natural product biosynthesis

Halogenases	Natural product <i>Organism</i>	Halogenated structural element	GenBank accession number [reference]
PmA	Pyrrrolnitrin <i>Pseudomonas fluorescens</i> BL915	Tryptophan at position C-7	PFU74493 [59]
RebH	Rebeccamycin <i>Lechevalieria aerocolonigenes</i> ATCC 39243	Tryptophan at position C-7	AJ414559 [72]
PyrH	Pyroindomycin B <i>Streptomyces rugosporus</i> LL-42D005	Tryptophan at position C-5	AY623051 [77]
Thal	Thienodolin <i>Streptomyces albogriseolus</i>	Tryptophan at position C-6	EF095207 [71]
KtzQ ^a	Kutznerides <i>Kutzneria</i> sp. 744	Tryptophan at position C-7	EU074211[132]
KtzR ^a	Kutznerides <i>Kutzneria</i> sp. 744	7-Cl-tryptophan at position C-6 ^b	EU074211[132]
AtmH	AT2433 <i>Actinomadura mellioura</i>	Tryptophan at position C-7	DQ297453 [135]

^aWorking in a tandem action, first KtzQ on unmodified tryptophan followed by KtzR on 7-Cl-L-tryptophan to form 6,7-dichlorotryptophan [136]

^bWith an approximate 120-fold preference over unsubstituted tryptophan [136]

postulated that chlorine may be hydrogen-bound to the Lys-79 residue located at the end of the tunnel. In this manner, chlorine would be activated by increased electrophilicity, allowing it to react with tryptophan. In addition, the importance of Glu-346 to stabilize and then deprotonate the substrate intermediate during this process was confirmed by site-directed mutagenesis experiments. The basis for regioselective halogenation is thus the controlled presentation of the substrate to the bound Cl-species via particular amino acid residues in the substrate binding site (Fig. 19.7) [71].

RebH (Table 19.2) is another tryptophan-7-halogenase which has been identified within the rebeccamycin (Fig. 19.6) biosynthetic gene cluster of *Lechevalieria aerocolonigenes* ATCC39243 [72, 73]. RebH was shown to catalyze the initial step of rebeccamycin biosynthesis converting L-tryptophan to 7-chlorotryptophan [74]. RebF catalyzes the NADH-dependent reduction of FAD to provide FADH₂ and thus acts together with RebH in a robust two-component reductase/halogenase system. From spectroscopically performed kinetic analysis of RebH, a detailed reaction scheme was proposed (Fig. 19.8) [75]. Initially, FADH₂ is transferred to a FAD(C4a)-oxygenated species, and from this FAD(C4a)-OOH intermediate (observed as an increase in absorbance at 390 nm), an OH⁺ equivalent reacts with a chlorine ion yielding HOCl and FAD(C4a)-OH. Finally, an increase in absorbance at 450 nm indicated the dehydration of FAD(C4a)-OH to fully oxidize FAD. The actual chlorination of tryptophan thus occurs independently after the oxidative

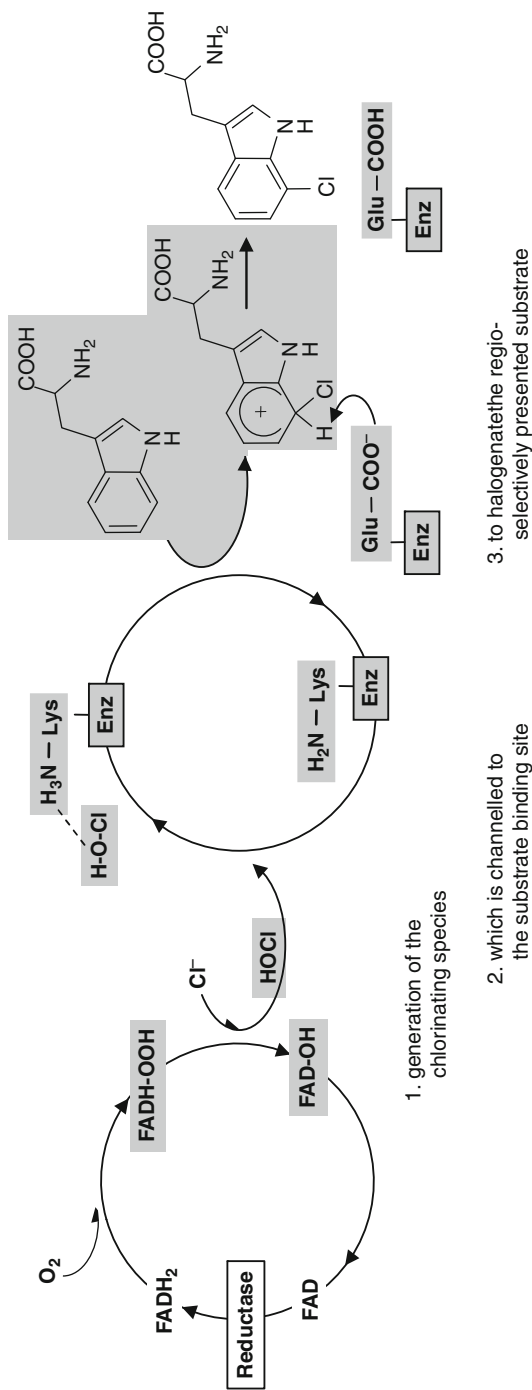


Fig. 19.7 Mechanism of the halogenation reaction of a FADH₂-dependent halogenase (gray-shaded are the processes that proceed within the halogenase enzyme)

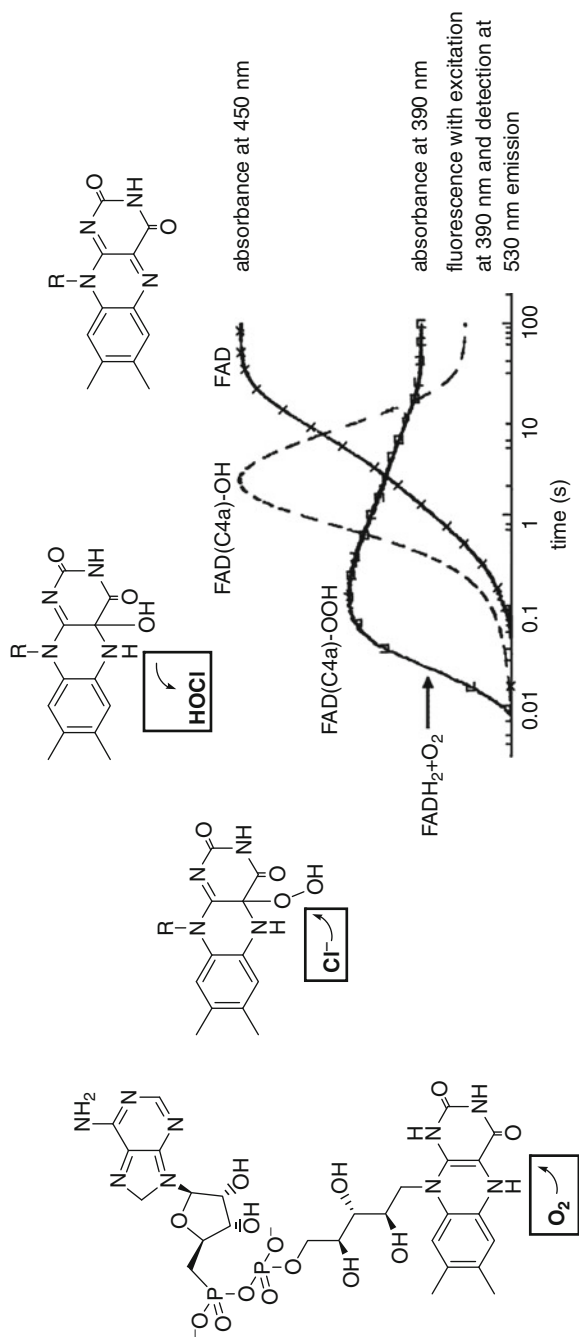


Fig. 19.8 Timing of flavin intermediates and product formation as spectroscopically monitored by Walsh and coworkers [75]

reaction of flavin is completed. Protein dynamics leading to conformational changes are assumed to shield the oxygenated FAD(C4a) intermediates from solvent, thereby preventing their rapid breakdown and providing a site for generating the chlorinating agent. Recently, it has been demonstrated that a stable long-living enzyme-bound chlorinating species ($t_{1/2}$ of 28 h at 25°C) is formed during the reaction of RebH with FADH₂, Cl⁻, and O₂, which remains on the active site even after removal of FAD until a substrate becomes available for reaction [76]. This chlorinating intermediate is proposed to be a covalently bound lysine chloramine (Lys79-εNH-Cl), located ideally to deliver a Cl⁺ equivalent for the electrophilic aromatic substitution of the tryptophan indole ring at C-7.

Further specific halogenases (Table 19.2) capable to chlorinate tryptophan at positions C-6 and C-5 were also found. A selective tryptophan-5-halogenase (PyrH) was shown to be involved in pyrroindomycin B (Fig. 19.6) biosynthesis of *Streptomyces rugosporus* LL-42D005 [77] as well as a tryptophan-6-halogenase (Thal) in the thienodolin (Fig. 19.6) production by *Streptomyces albogriseolus* [71], both ascribed to catalyze initial steps in the biosynthesis. From comparison of the crystal structure of the tryptophan-5-halogenase (PyrH) with that of the tryptophan-7-halogenases, significant differences in the tryptophan-binding module were observed. This, together with site-directed mutagenesis studies, further explained the regioselectively controlled chlorination of tryptophan, showing that the respective carbon atom to be halogenated is solely presented to the chlorine species, while other potential reactive sites are shielded [78].

In contrast to the above-mentioned halogenases, the tryptophan-2-halogenase, CmdE, which is associated with the formation of chondramides B and D (Fig. 19.6; Table 19.3) from the myxobacterium *Chondromyces crocatus* Cm c5, was demonstrated to be part of a biosynthetic assembly line [79]. Chondramides are of mixed NRPS/PKS origin, and, to date, CmdE is the only example of a tryptophan halogenase integrated in such a modular biosynthetic pathway. Consequently, it is not surprising that the highest homologies of CmdE can be found in halogenases like those involved in cryptophycin (CrpH), avilamycin A (AviH), and clorobiocin (Clo-Hal) biosynthesis (Table 19.3) rather than in the above-described typical tryptophan halogenases (Table 19.2), i.e., only 20% identity to PryH, while no significant similarity to the tryptophan-7-halogenases, PmA and RebH, was found [79].

In general, FADH₂-dependent halogenases can be grouped into those accepting free small molecules as described above and those that act on carrier-bound substrates. Further examples of halogenases involved in multienzymatic NRPS/PKS assembly lines are summarized in Tables 19.3 and 19.4, subdivided into those suggested to chlorinate phenolic moieties (Table 19.3, Fig. 19.9) as in complestatin [80] and glycopeptide antibiotic formation [81], e.g., vancomycin, and those that halogenate peptidyl carrier-bound pyrrole moieties (Table 19.4; Fig. 19.10), e.g., PltA in pyoluteorin biosynthesis [82]. In the latter case, proline is bound as a thioester to the carrier protein PltL and enzymatically desaturated to a pyrrolyl-S-PltL intermediate. This is then chlorinated regioselectively at position C-5 and subsequently at position C-4 of the heteroaromatic ring, as observed through temporal product formation. Both halogenations are catalyzed by the

Table 19.3 FADH₂-dependent halogenases that halogenate phenolic moieties as an integrated step in multienzymatic biosynthesis

Halogenases	Natural product <i>Organism</i>	Halogenated structural element	GenBank accession number [reference]
CmdE	Chondramides B/D <i>Chondromyces crocatus</i> Cm c5	Tryptophan at position C-2	AM179409 [79]
CTC-chl (=cts4)	Chlorotetracycline <i>Streptomyces aureofaciens</i> NRRL3203	4-Ketoanhydro-tetracycline ^a	D38214 [60, 122]
CrpH	Cryptophycin 1 <i>Nostoc</i> sp. ATCC 53789	Tyrosine	EF159954 [94]
ComH	Complestatin <i>Streptomyces lavendulae</i>	Hydroxyphenylglycine	AF386507 [80]
“Halogenase gene”	Vancomycin <i>Amycolatopsis orientalis</i>	N.S. ^b	AF486630 [137]
BhaA	Balhimycin <i>Amycolatopsis balhimycina</i> DMS5908	β-Hydroxy-tyrosine	Y16952 [81, 138]
Tcp21	Teicoplanin <i>Actinoplanes teichomyceticus</i> ATCC31131	Tyrosine and β-hydroxy-tyrosine	AJ605139 [139]
ORF10 (=dbv10)	A40926 <i>Nonomuraea</i> sp. ATCC39727	Dihydroxyphenylglycine and β-hydroxy-tyrosine	AJ561198 [140]
ApdC	Anabaenopeptilide 90B <i>Anabaena circinalis</i> 90	Tyrosine	AJ269505 [141]
McnD ^c	Cyanopeptolin-984 <i>Microcystis</i> sp. NIVA-CYA 172/5	Tyrosine	DQ075244 [142]
AerJ ^d	Aeruginosin peptides <i>Microcystis</i> sp. PCC 9812	3-(4-Hydroxyphenyl) lactic acid	AM773664 [143]
ChlB4	Chlorothricin <i>Streptomyces antibioticus</i> DSM 40725	6-Methylsalicylic acid	DQ116941 [144]
SgcC3	C-1027 <i>Streptomyces globisporus</i>	β-Tyrosine ^e	n.d. ^f [145]
CndH	Chondrochlora <i>Chondromyces crocatus</i> Cm c5	Tyrosine	AM988861 [88, 146]

^aIndicates that halogenation occurs while the elongating acyl chain is still tethered to carrier proteins during the PKS assembly line

^bNot specified

^cAlso identified from other *Microcystis* strains (AM773679, AM773678, AM773677, AM773676, AM773675, AM773674) [143]

^dAlso identified from other *Microcystis* strains (AM773663, AM773662, AM773661, AM773660, AM773659, AM773658, AM773657, AM773656, AM773655, AM773654 [143], PCC7806, NIES-98 [147])

^eIn vitro characterized to halogenate tyrosine tethered to a peptidyl carrier protein

^fNo sequence data available in GenBank

Table 19.4 FADH₂-dependent halogenases involved in the halogenation of pyrrole moieties

Halogenases	Natural product <i>Organism</i>	Halogenated structural element	GenBank accession number [reference]
PltA	Pyoluteorin	Proline ^a	AF081920 [82]
	<i>Pseudomonas fluorescens</i> Pf-5		
HrmQ	Hormaomycin	Pyrrole ^b	EU583477 [98]
	<i>Streptomyces griseoflavus</i> W-384		
PrnC	Pyrrolnitrin	Monodechloramino- pyrrolnitrin	PFU74493 [59]
	<i>Pseudomonas fluorescens</i> BL915		
HalB	Pentachloropseudilin	Pyrrole	AF450451 [148]
	<i>Actinoplanes</i> sp. ATCC33002		
Pyr29 ^c	Pyrrolomycin A, B, C, D	Proline	EF140901 [149]
	<i>Actinosporangium vitaminophilum</i> ATCC31673		

^aProline halogenation while bound to a peptidyl carrier protein

^bMost likely halogenation via a peptidyl carrier protein-bound proline
65% similarity to PltA

same enzyme, i.e., PltA. During this process, chlorination is specific for pyrrolyl-*S*-PltL, since prolyl-*S*-PltL or free pyrrole-2-carboxylate is not accepted as substrate for halogenation by PltA.

Even more halogenases involved in the chlorination of phenolic moieties, but not explicitly described to function as an integral part of enzymatic assembly lines, are shown in Table 19.5 (for structures, see Fig. 19.11).

Besides the FADH₂-dependent halogenases involved in halogenation of aromatic compounds, recognizing tryptophan/indole or phenol/pyrrole moieties, enzymes involved in the halogenation of aliphatic compounds are known (Table 19.6; Fig. 19.12). For example, for chloramphenicol biosynthesis in *Streptomyces venezuelae* ISP5230, the function of CmlS as a halogenating enzyme has been proved by gene disruption experiments, whereby corynecins were produced in place of chloramphenicol [83]. CmlS shows the highest homology to the FADH₂-dependent halogenase PltA (Table 19.4). It has been suggested that a substrate derived from glucose is halogenated and that dichloroacetyl-CoA is then attached to the amino group of the side chain of an enzyme-tethered *p*-aminophenylalanine [84]. For napyradiomycin (Fig. 19.12) from the marine sediment-derived *Streptomyces* sp. CNQ-525, not only Va-CPOs, as described above, are discussed to be involved in its biosynthesis but also a FADH₂-dependent halogenase, NapH2. The gene for the latter was found within the biosynthesis cluster. Thus, NapH2 is the first FADH₂-dependent halogenase described to be potentially involved in a halogenation reaction in a marine organism. Considering structural similarities between terrestrial and marine natural products, it may be conducted, however, that FADH₂-dependent halogenases very likely also contribute to the biosynthesis of many marine compounds (Fig. 19.13).

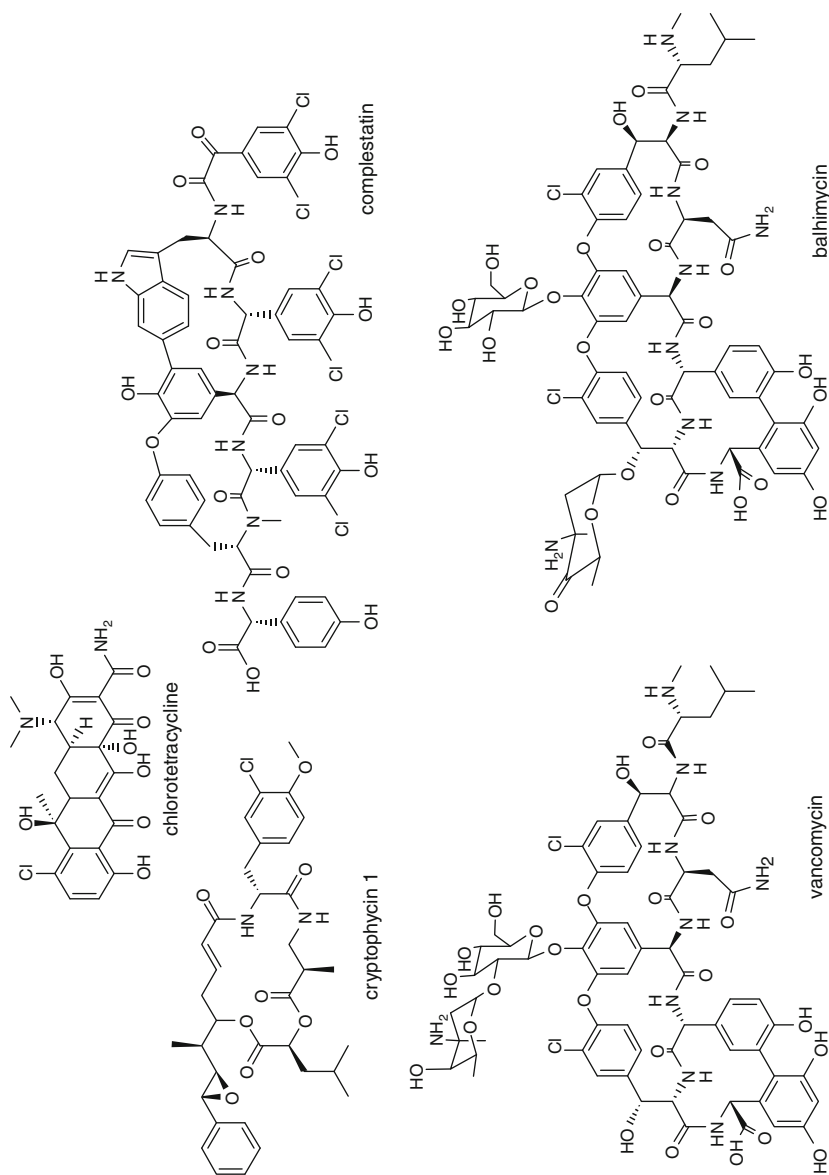


Fig. 19.9 (continued)

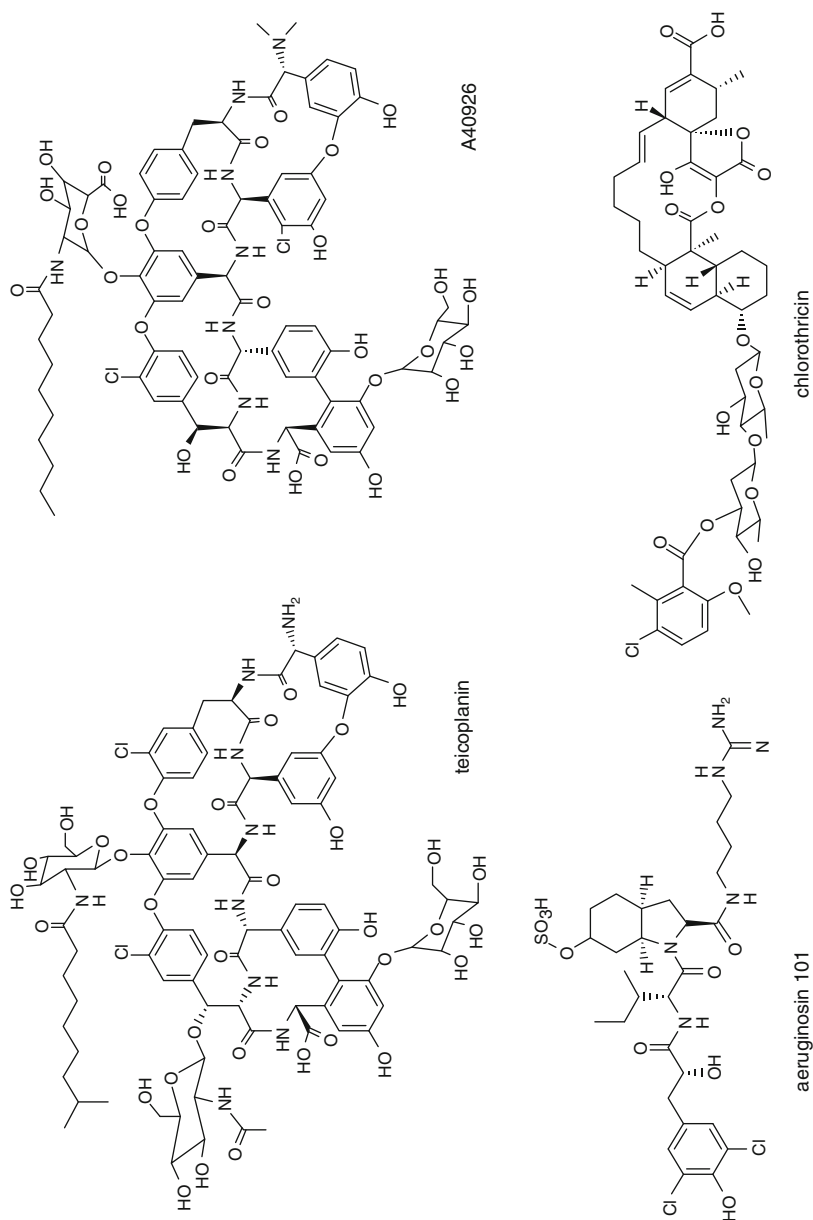


Fig. 19.9 (continued)

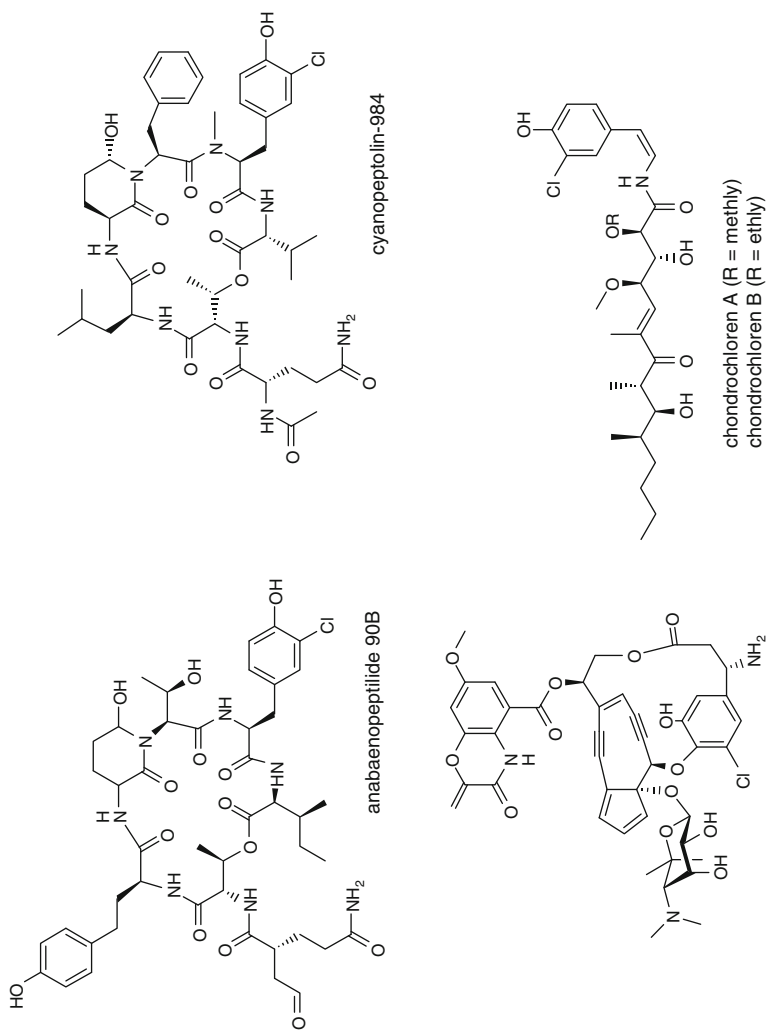


Fig. 19.9 Compounds with chlorinated phenolic structures where FADH₂-dependent halogenation most likely occurs within multienzymatic biosynthesis assembly lines (e.g., PKS/NRPS)

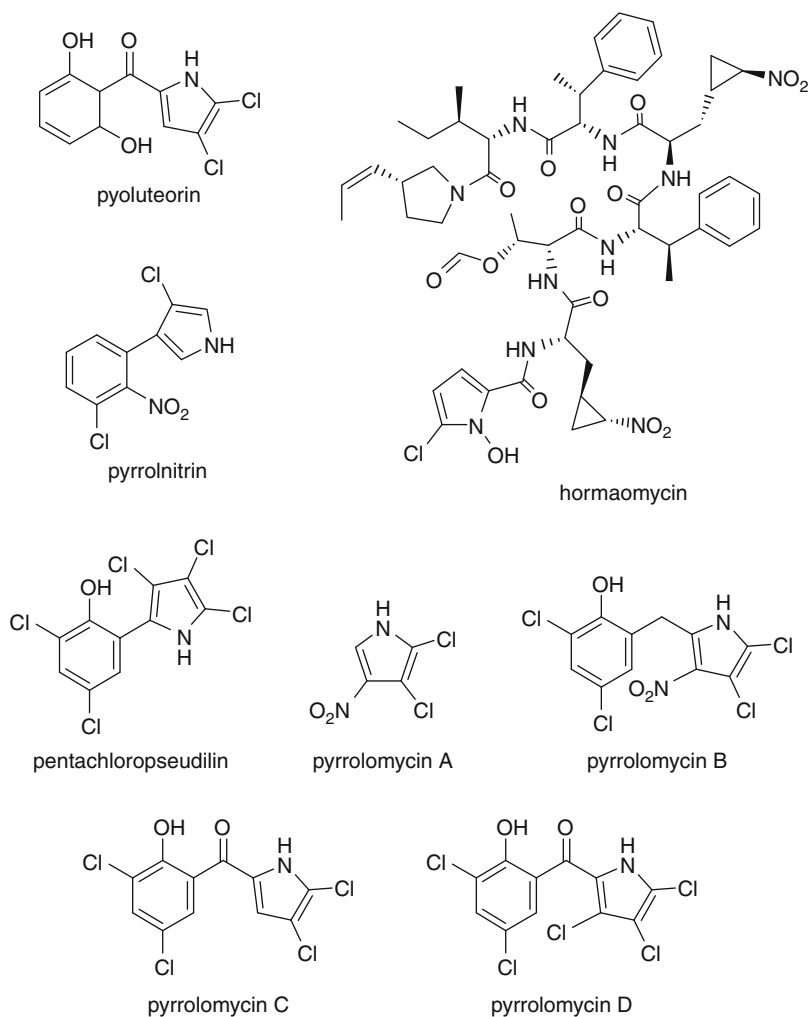


Fig. 19.10 Compounds with chlorinated pyrrole structural elements halogenated by FADH_2 -dependent halogenases

19.4.1 Sequence Specificities and Enzymatic Activity of FADH_2 -Dependent Halogenases

The *in vitro* enzymatic activity of halogenases has been investigated only in a very few cases until now, and the function of many biosynthetic genes as halogenases (Tables 19.2, 19.3, 19.4, 19.5, 19.6) was assigned only putatively. Nevertheless, halogenases are known to have an approximate size of 550 amino acids and thus to be encoded by a corresponding DNA consisting of 1,500–1,600 bp (Fig. 19.14).

Table 19.5 FADH₂-dependent halogenases involved in the halogenation of phenolic moieties

Halogenases	Natural product <i>Organism</i>	Halogenated structural element	GenBank accession number [reference]
Pyr16/17	Pyrrolomycin A, B, C, D <i>Actinosporangium vitaminophilum</i> ATCC31673	Phenol ^a	EF140901 [149]
Asm12	Ansamitocin P-3 <i>Actinosynnema pretiosum</i> ATCC31565	Proansamitocin ^b	AF453501 [150, 151]
n.d. ^c	Ochratoxin A <i>Penicillium nordicum</i>	Mellein intermediate ^d	n.d. ^c [152]
Clo-Hal	Clorobiocin <i>Streptomyces roseochromogenes</i>	Aminocoumarin	AF329398 [95, 153]
AviH	Avilamycin A <i>Streptomyces viridochromogenes</i> Tü57	Orsellinic acid ^e	AF333038 [154]
CalO ₃	Calicheamicin γ 1 <i>Micromonospora echinospora</i> spp. <i>calichensis</i>	Orsellinic acid	AF497482 [155]
SimD4	Simocyclinone D8 <i>Streptomyces antibioticus</i> Tü6040	Aminocoumarin	AF324838 [156]
RadH ^f	Radiciol <i>Chaetomium chiversii</i>	Phenol ^a	EU980390 [157]
ChlA	DIF-1 (differentiation-inducing factor 1) <i>Dictyostelium</i> strain Ax2	Phenol ^a	DDB_G0290825 ^g [158]

^aPhenol moiety polyketide derived

^bHalogenation of proansamitocin as first PKS-tailoring reaction

^cNo sequence data available in GenBank

^dPost-PKS

^eDichloro-isovermnic acid attached to the preformed heptasaccharide

^fAlso identified from *Pochonia chlamydosporia* (EU520419, termed Rdc2 [159])

^gAt dictyBase, <http://dictybase.org/>

The flavin binding site is located at the amino terminal end and includes a GxGxxG motive, which is extremely conserved within this enzyme group [85]. Another conserved region, i.e., WxWxIP, is found in the middle of the sequence [85]. The tryptophan residues of the latter motif are assumed to prevent the enzyme from catalyzing monooxygenase-type reactions by sterically hampering substrate binding next to the isoalloxazine ring of FADH₂ [71].

Further insight in the mechanism how FADH₂-dependent halogenases can halogenate such a wide range of substrates derived from the crystal structure of CmlS [86, 87], the halogenase involved in the chloramphenicol biosynthesis, in comparison to those characterized for tryptophan halogenases (e.g., PrnA) and CndH, a tyrosyl chlorinating halogenase acting during chondrochloren

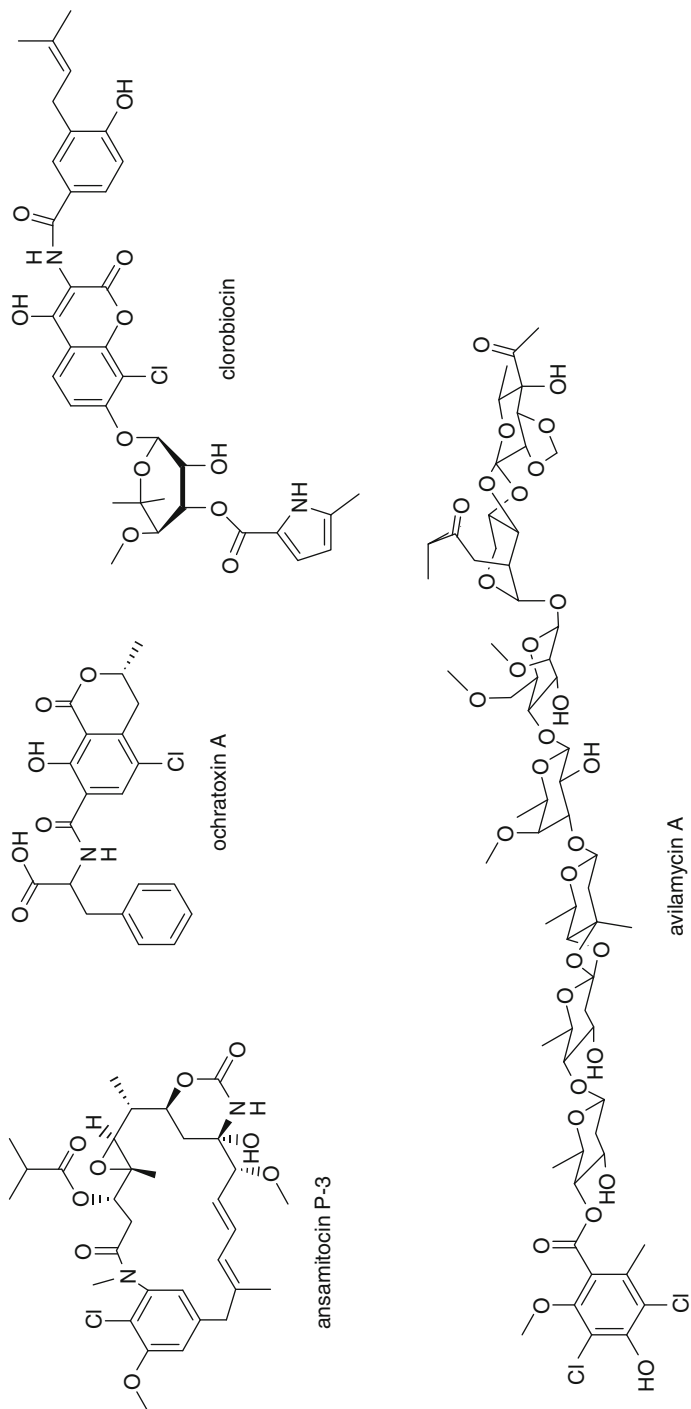


Fig. 19.11 (continued)

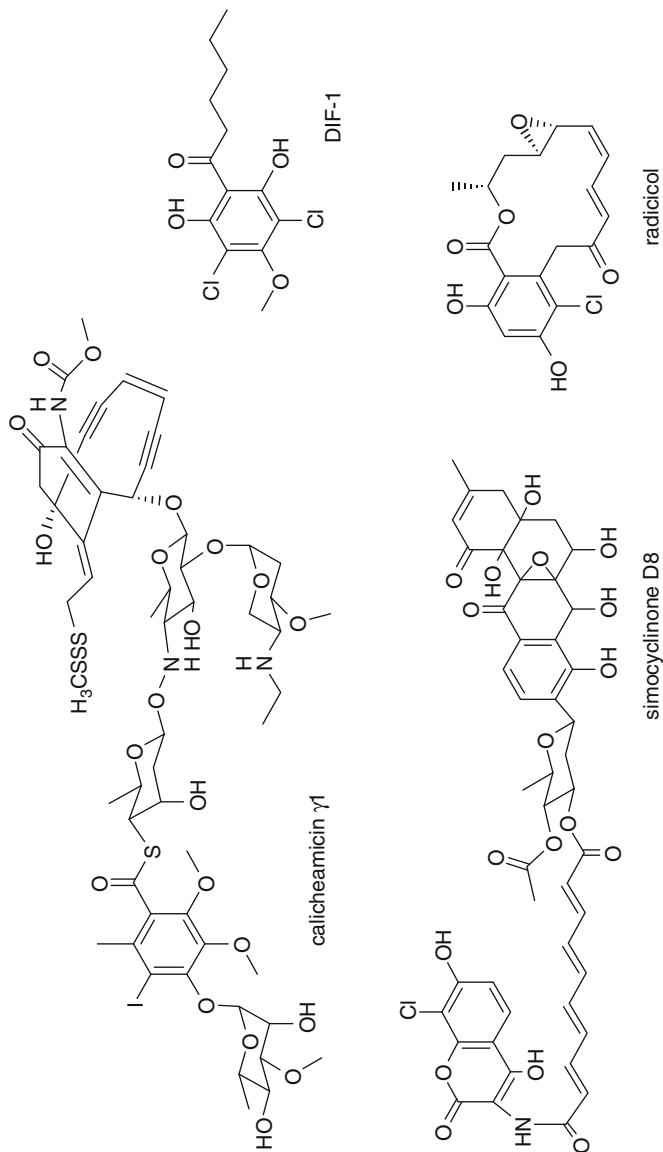
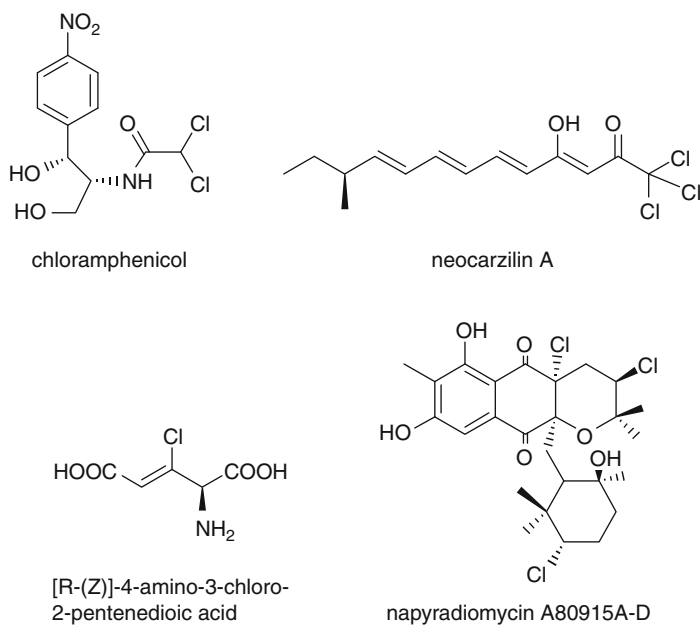


Fig. 19.11 Further compounds with halogenated aromatic substrates for which an involvement of FADH₂-dependent halogenases is discussed

Table 19.6 FADH₂-dependent halogenases discussed to be involved in the chlorination of aliphatic structural elements

Halogenases	Natural product <i>Organism</i>	Halogenated structural element	GenBank accession number [reference]
CmlS	Chloramphenicol <i>Streptomyces venezuelae</i> ISP5230	Aliphatic moiety ^a	AY026946 [83]
ORF3 ^b	Neocarzilin A <i>Streptomyces carinostaticus</i>	Aliphatic moiety	AB097904 [160]
n.d. ^c	(<i>R</i> -(<i>Z</i>))-4-amino-3-chloro-2-pentenedioic acid <i>Streptomyces viridogenes</i> ATCC39387	Aliphatic moiety ^d	DQ782376 [161]
NapH2	Napyradiomycin A80915A-D <i>Streptomyces</i> sp. CNQ-525	Aliphatic moiety ^e	EF397638 [32]

^aLikely in an enzyme-bound assembly line (similarity to PltA)^bSimilarity to HalB^cOnly partial gene sequence^dHalogenation postulated via a pyrrole intermediate^eAlso Va-CPOs (NapH1,3,4) identified within the gene cluster**Fig. 19.12** Compounds with chlorinated aliphatic moieties for which an involvement of FADH₂-dependent halogenases is discussed

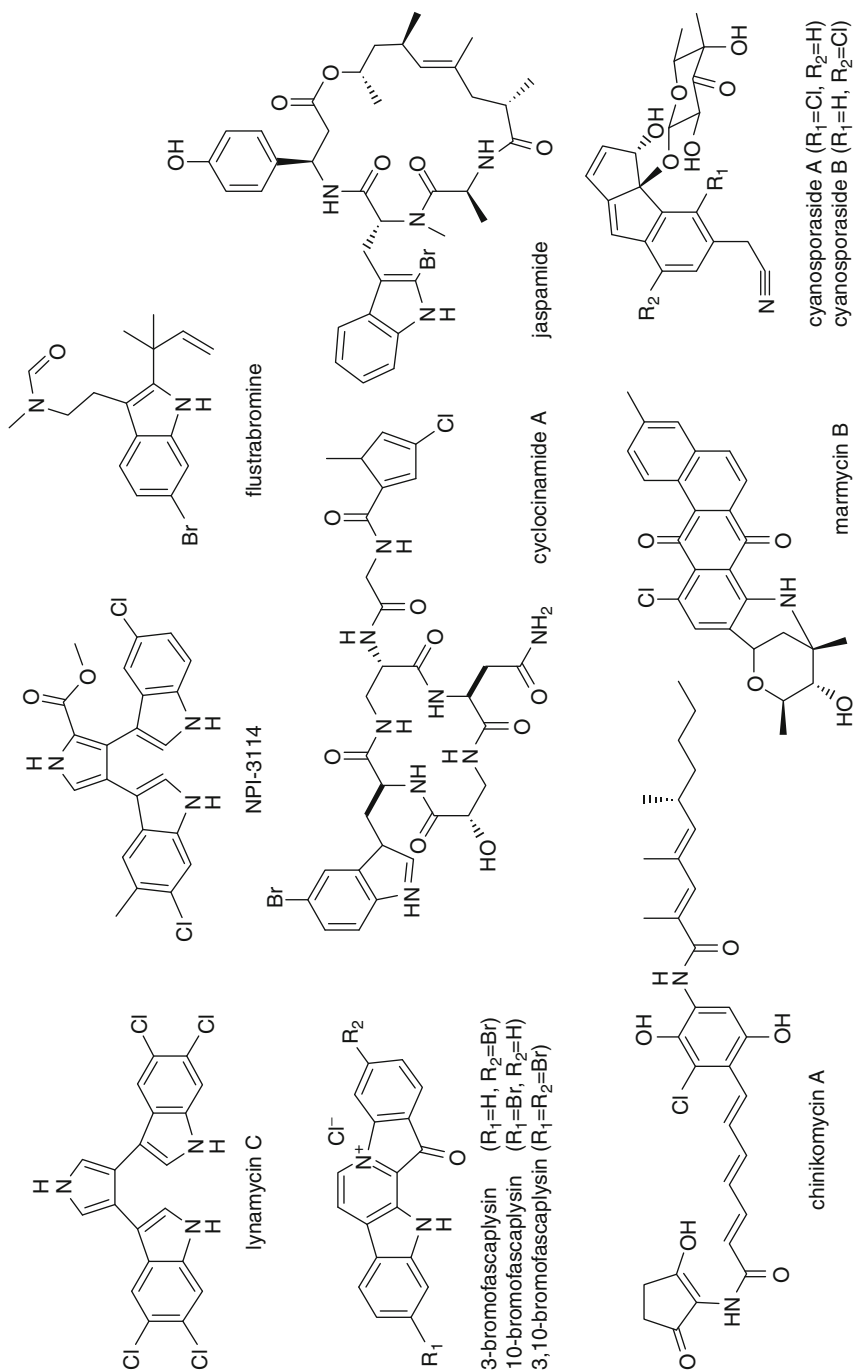


Fig. 19.13 (continued)

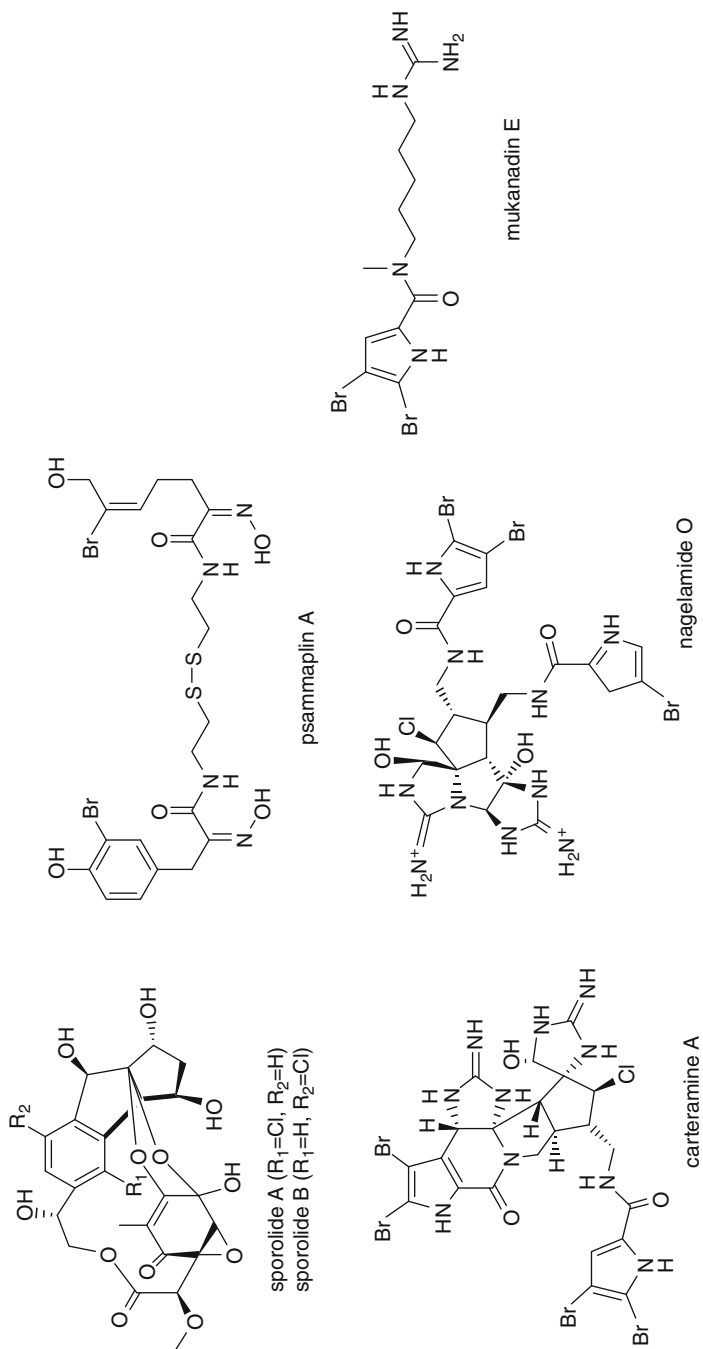


Fig. 19.13 Marine compounds potentially synthesized via corresponding $FADH_2$ -dependent halogenases, e.g., compounds with halogenated indole moieties as isolated from marine actinomycetes (dynamycins [162] and NPI 3114 [163]), algae (flustrabromine [164]), and sponges (bromofascapsylins [165], cyclocinamide A [166], as well as the chondramide analog jaspamide [167]). Secondary metabolites with halogenated phenol and pyrrole moieties are also known from various marine actinomycete (e.g., chinikomycins [168], sporolides [169], cyanosporasides [170], and marmycins B [171]) and sponges (psammaplins A [172], carteramine A [173], nagelamides [174], and mukonanadins [174])



Fig. 19.14 General amino acid (aa) sequence assembly of FADH₂-depending halogenases, showing the conserved motives in all FADH₂-depending halogenases

biosynthesis [88]. Based on characteristic features of these crystal structures, two variants of FADH₂-dependent halogenase have been distinguished [88]. Variant A enzymes (e.g., PrnA), acting on free small molecules, enclose their substrate completely in the active halogenation site. Thereby, the C-terminus of the enzymes seems to cover the active halogenation site and to somehow form a tunnel into which the substrate must enter. In variant B enzymes (CndH), the active center remains open, giving access to a sterically much larger carrier-bound substrate. From simple primary structure alignment, CmlS would rather be classified as a variant B halogenase; however, due to the occurrence of a bulky C-terminal lobe, it seems more likely that a free small molecule enters the active halogenation site (variant A enzyme). The structural diversity observed in the C-termini of FADH₂-dependent halogenases appears to reflect the overall diversity of substrates that are halogenated, potentially by sterically restricted access to the active halogenation site. Together with this, specific features within the active halogenating site contribute to the substrate selectivity and regioselectivity. In the case of CmlS, an overall hydrophobic pocket with three phenylalanine residues (F87, F304, F357) is present in the active halogenation site [87], in contrast to a glutamic acid accompanied by two histidine residues (E346, H101, H395) in PrnA, which are thought to ensure tryptophan halogenation. From the crystal structure of the tryptophan-5-halogenase PryH, it became obvious that as a result of amino acid insertion and deletions, compared to PrnA, the substrate binding pocket is substantially rearranged. As a result, tryptophan is bound differently, exposing the respective C atom for chlorination to the key lysine and glutamate residues, while the other sites of potential reactivity will be protected by the enzyme structure [78]. Amino acid sequence alignment of Thal (tryptophan-6-halogenases) and PrnA showed only few differences lining the active halogenation site, i.e., I56/I82/T348 in PrnA and V56/V86/S364 in Thal, which are potentially involved in the directed substrate presentation for regioselective halogenation [71].

Early studies investigating the incorporation of bromine instead of chlorine in chloramphenicol, chlorotetracycline, and pyrrolnitrin resulted in the formation of the corresponding bromo analogs, giving the first indication that the involved enzymes are not exclusively specific for chloride [89–91]. Thus, the ability of FADH₂-dependent halogenases to alternatively incorporate bromide instead of chloride has been subjected to further detailed investigations [92–94]. For PyrH (Table 19.2), it could be shown that in the presence of bromide, 5-bromotryptophan was obtained, although chlorination is favored. In any case, only the regioselective monohalogenation of tryptophan at the C-5 position occurred [77]. Similarly, Thal and RebH (Table 19.2) were demonstrated to catalyze monochlorination regioselectively, as well as monobromination of tryptophan in vitro resulting in

6- and 7-halotryptophan, respectively [71, 74]. Bromide ions were also able to compete with and replace chloride in the PltA (Table 19.4) reaction on pyrrolyl-*S*-PltL. However, the sterically larger bromide slowed down the halogenation reaction to 10–20% conversion in 1 h, as opposed to >90% when chloride was the only halide present [82].

19.4.2 Biotechnological Potential of FADH₂-Dependent Halogenases

The considerable progress made in understanding biological halogenation mediated through FADH₂-dependent halogenases gave rise to probing the biotechnological potential of these enzymes. The aim of such investigations was to allow halogenations at specific sites of substrates not accessible to direct chemical halogenation as well as to avoid the formation of unwanted by-products.

Combinatorial biosynthesis yielded new derivatives of the aminocoumarin antibiotics, novobiocin, clorobiocin, and coumermycin A1 (Fig. 19.15). Inactivation of the *clo-hal* gene in the clorobiocin biosynthetic gene cluster of *Streptomyces roseochromogenes* resulted in the formation of the hydrogen analog novclobiocin 101, and coexpression of the putative methyltransferase *novO* led to the production of novclobiocin 102, which is methylated at C-8 of the aminocoumarin ring [95]. More interestingly, coexpression of *clo-hal* in a *novO*⁻ mutant resulted in the chlorinated novobiocin derivative novclobiocin 114 [96]. An attempt to functionally replace *clo-hal* by the balhimycin halogenase (Table 19.3) *bhaA* both in the *clo-hal*⁻ and *novO*⁻ mutant, did not yield in the respective chlorinated aminocoumarin derivatives (clorobiocin or novclobiocin 114), thus underlining the different substrate specificity of Clo-Hal and BhaA [96]. However, introduction of *clo-hal* into the cluster of coumermycin A1 again resulted in the formation of the respective mono- and dichlorinated derivatives [97]. In a study investigating the halogenating potential of the hormaomycin halogenase HrmQ (Table 19.4) in combinatorial biosynthesis, coexpression experiments of *hrmQ* in a *cloN6*⁻ clorobiocin mutant strain were conducted [98]. The results confirmed that HrmQ specifically chlorinates pyrrole moieties at the C-5 position and thus yielded the new clorobiocin derivatives, novclobiocin 124 and 125.

As a result of their potential therapeutic applications as antitumor and neuroprotective agents [99, 100], great efforts have been made to generate derivatives of indolocarbazole alkaloids. Novel halogenated compounds were obtained by recombining genes found within the biosynthetic gene clusters of rebeccamycin and staurosporine with the halogenases RebH, PyrH, and Thal (Table 19.2). In this way, Salas and coworkers were able to generate “hybrid” indolocarbazoles by modifying the staurosporine aglycon using rebeccamycin chlorination, glycosylation, and sugar methylation activities. Besides nonhalogenated products, this approach yielded chloro- and dichloro-staurosporine derivatives [100]. The major bis-indole products obtained when coexpressing PyrH and Thal (Table 19.2) had a chloride substitution at positions C-5 and C-6 of the indole moiety, respectively.

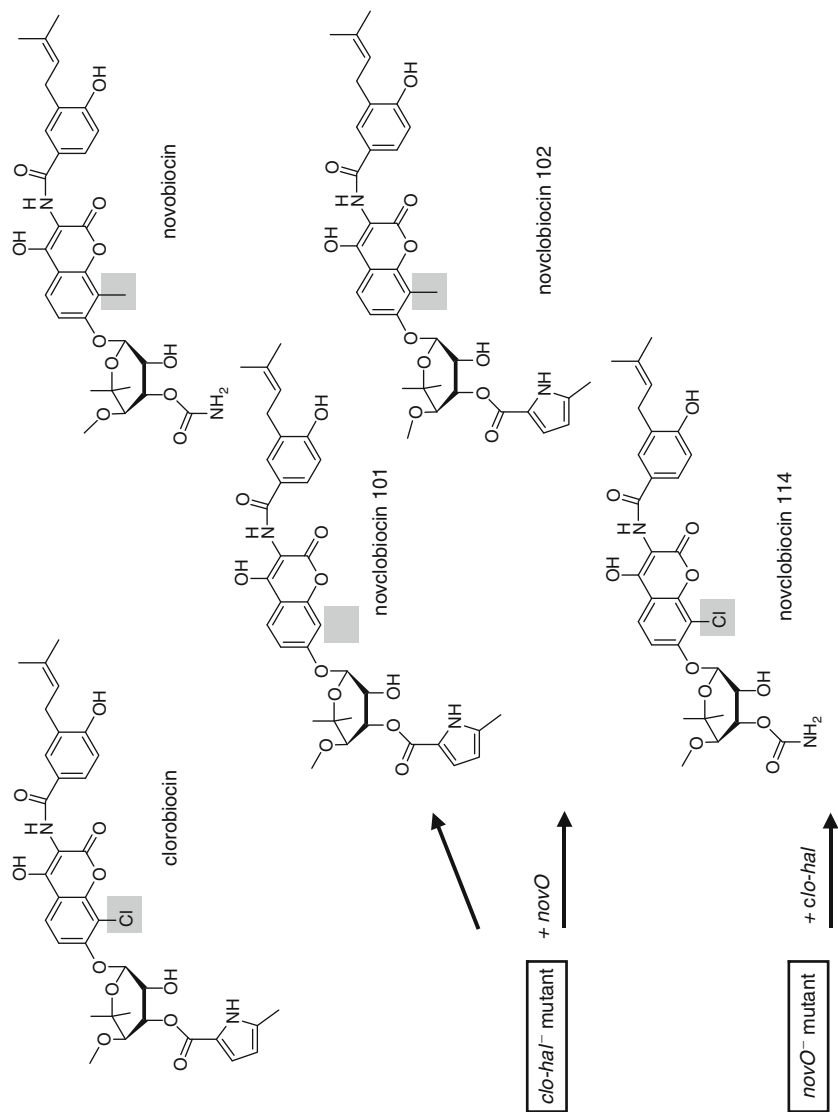
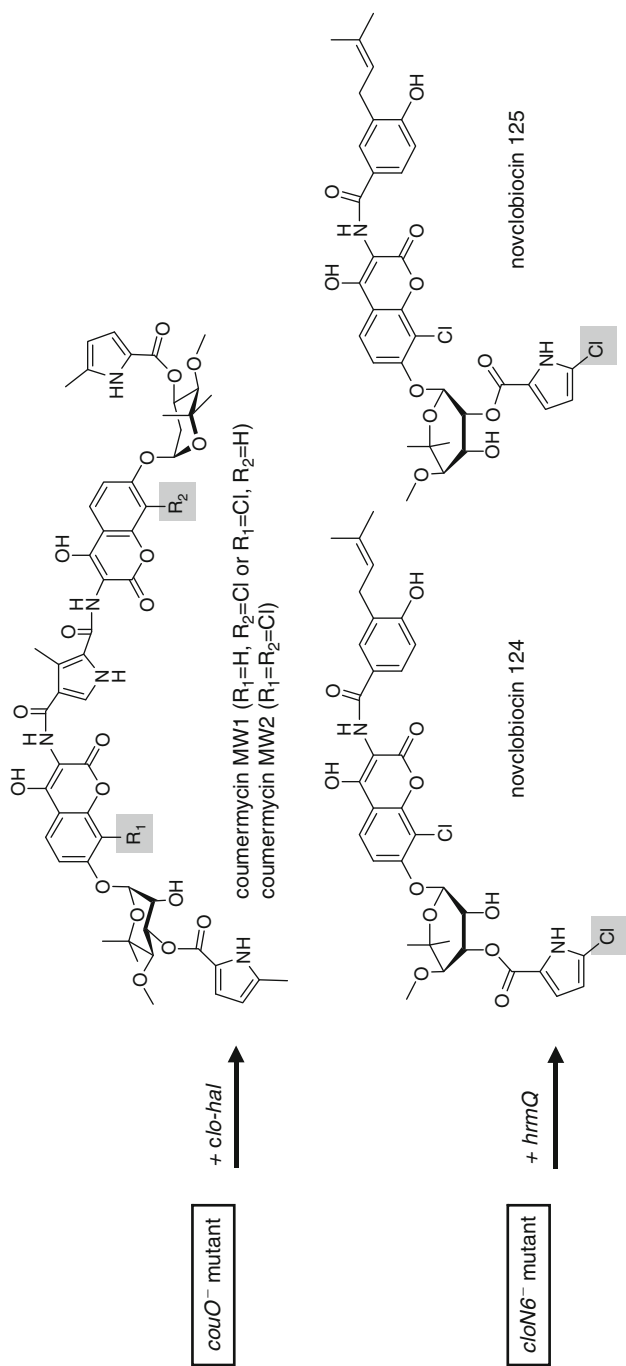


Fig. 19.15 (continued)

**Fig. 19.15** Novel aminocoumarin derivatives derived by combinatorial biosynthesis

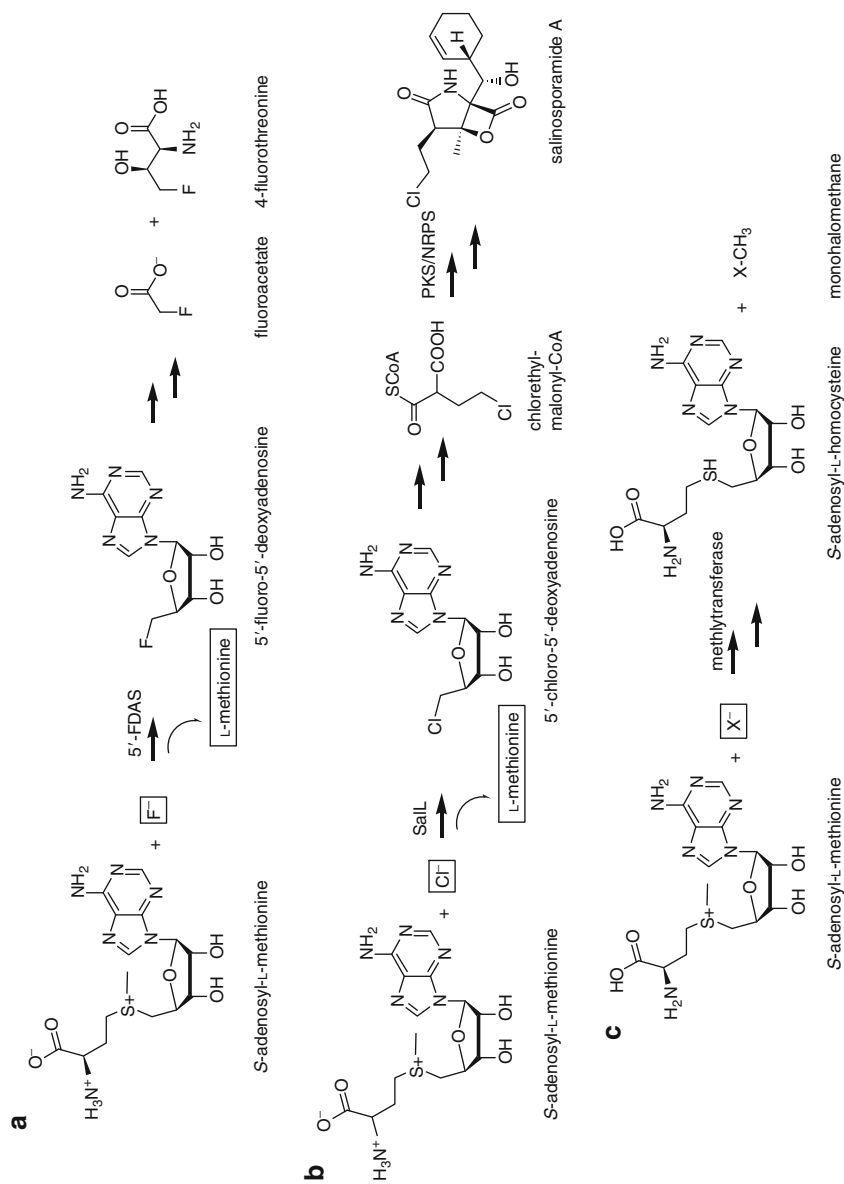


Fig. 19.16 (continued)

In another approach, Thal was investigated in a recombinant pyrrolnitrin producer strain [71]. Overexpression of *thal* yielded the new phenylpyrrole derivative, 3-(2'-amino-4'-chlorophenyl)pyrrole, but no pyrrolnitrin or aminopyrrolnitrin was detected. The authors concluded that the overproduction of Thal resulted in the chlorination of all the available tryptophan to 6-chlorotryptophan, which was then accepted by PrnB, the second enzyme in pyrrolnitrin biosynthesis catalyzing the subsequent ring rearrangement. However, the phenylpyrrole compound produced was not a substrate to PrnC for further halogenation reaction.

The use of tryptophan-5-halogenases (PyrH) (Table 19.2) in producing halogenated serotonin precursors has been the focus of further research [101]. The aim of these efforts was to obtain 5-bromotryptophan, which is regarded as a suitable intermediate for a subsequent nucleophilic hydroxylation to yield 5-hydroxytryptophan (oxitriptan). The latter is a component of many antidepressant drugs and, to date, commonly obtained by extraction of the seeds of the African plant *Griffonia simplicifolia*. The main limitation at this point is the low activity of the purified enzyme as well as the unsatisfactory production of the recombinant enzyme. Optimization of the reaction conditions, however, has already led to a nearly 20-fold improvement of the 5-bromotryptophan yield, and ongoing efforts aim to enhance the recombinant enzyme production [101]. The temperature sensitivity of the enzymes and the high NADH consumption to restore the cofactor FADH₂ for the halogenase reaction, however, hamper an economical application of these enzymes [102].

19.5 Halogenating Enzymes Utilizing S-Adenosyl-L-Methionine

Fluoride is the most nucleophilic halogen and does not allow any electrophilic or radical biological chemistry, as is known for Cl⁻, Br⁻, and I⁻. Even though, thermodynamically, the formation of carbon–fluoride bonds would be favorable, due to the extremely high desolvation energy required to activate F⁻ in aqueous solution, biological reactions with fluoride are rather rare [5]. Unique enzymes are needed to overcome this kinetic barrier, and, to date, the only one to be characterized is the 5'-fluoro-5'-deoxyadenosine synthetase (5'-FDAS). This enzyme was isolated from *Streptomyces cattleya* and utilizes S-adenosyl-L-methionine (SAM) as cosubstrate [7]. Fluoride is thereby thought to be placed in a hydrophobic pocket where desolvation is achieved as protein residues coordinate to water. In turn, a S_N2 substitution of methionine at SAM takes place [103]. In this way, 5'-fluoro-5'-deoxyadenosine is formed as an intermediate and subsequently converted to fluoroacetate and 4-fluorothreonine (Fig. 19.16a).



Fig. 19.16 SAM in biohalogenation processes. (a) Enzymatic conversion of inorganic fluoride to organic fluoride by 5'-fluoro-5'-deoxyadenosine synthetase. (b) The chlorinated moiety of salinosporamide A could be shown to derive from tetrose, and SalL was identified as a 5'-FDAS analog halogenating enzyme. The intermediate chloroethylmalonyl-CoA has been identified to act as an unusual starter unit for the subsequent PKS/NRPS biosynthesis part. (c) Methyltransferases mediate the transfer of a methyl group from SAM to a halide (X: halide ion)

For the biosynthesis of the potent proteasome inhibitor salinosporamide A (Fig. 19.16b) produced by the marine actinomycete *Salinispora tropica*, the deschloro analog, salinosporamide B, was initially presumed to be the direct precursor, and thus, the halogenation of the unactivated C-13 methyl group was suggested to be catalyzed by a nonheme iron halogenase. However, from feeding experiments, a different origin of the four-carbon moiety was demonstrated for these two molecules [104]. Thus, for salinosporamide B, a butyrate-derived ethylmalonyl-CoA was identified as a building block, whereas in salinosporamide A, an unprecedented PKS extender unit was shown to originate from a sugar precursor. The enzyme involved in the chlorination step (SalL) has been characterized as a 5'-FDAS similar enzyme, which converts SAM to 5'-chloro-5'-deoxyadenosine [6]. This sugar is subsequently converted to chloroethylmalonyl-CoA to further act as unique PKS extender unit [105]. The 5'-halo-5'-deoxyadenosine synthetase was shown to also be capable of utilizing bromide as well as iodide, but not fluoride.

Fluorine substitution is a prevalent strategy to enhance pharmacodynamic and pharmacokinetic properties of biologically active lead compounds; thus, the usefulness of the fluorinase 5'-FDAS to initiate C-F bonds in organohalogen synthesis has been further investigated. By genetic engineering, 5'-FDAS was successfully utilized in a *salL*-knockout mutant of *S. tropica* revealing fluorosalinosporamide [106]. Earlier studies, where this fluorometabolite was produced via chemical compensation of a *salL*-knockout mutant with synthetic 5'-fluoro-5'-deoxyadenosine, already showed that the proteasome inhibition activity of this salinosporamide derivative was slightly lower than that of the chlorinated natural product, however, also with reduced cytotoxicity [107]. This is thought to be due to a reversible binding of fluorosalinosporamide versus an irreversible binding of salinosporamide A. In further bioengineering approaches, the unique chloroethylmalonyl-CoA [105] and probably also analogous fluoroethylmalonyl-CoA [106] produced by salinosporamide A and respective genetically engineered biosynthetic systems may provide new opportunities in drug development. They may be used, e.g., as PKS extender units. Function of the fluorinase in isolated systems has already also been proven; thus, further application of this enzyme in *in vitro* biotransformation processes is conceivable [108].

SAM is also involved in the formation of monohalomethanes, albeit in a different way, namely, as methyl donor (Fig. 19.16c). At an early stage, Harper predicted that most likely other enzymes than haloperoxidases would be involved in the formation of halomethanes [109], and Wuosmaa and Hager were the first to detect and partially purify corresponding methyltransferases responsible for the methyl chloride production, e.g., from the red algae *Endocladia muricata* [110]. Several studies dealing with the emission of gaseous iodine and chlorine from the biosphere to the atmosphere resulted in the identification of respective enzymes in marine as well as terrestrial bacteria, macro- and microalgae, wood-rotting fungi, and terrestrial higher plants [111–113].

19.6 Concluding Remarks

In the last years, our understanding of biohalogenation processes has extended tremendously. Several groups of halogenating enzymes have been discovered and investigated on the biochemical and genetic level. Each group of these enzymes performs halogenation reactions on chemically distinct and different substructures, i.e., indole, phenol, pyrrole, and aliphatic moieties, using a specific reaction mechanism. The halogenation of marine natural products, however, is still not as well investigated as that of terrestrial metabolites.

A detailed insight to natural biological halogenation processes will not only further our understanding of natural biological halogenation processes but will also give rise to alternative methods for generating halogenated analogs of biologically active metabolites [10, 85, 114, 115]. By means of such enzymatic reactions, modified compounds may be generated with potentially improved biological properties [95, 116–118].

Investigations concerning the biotechnological potential of halogenating enzymes, however, are still in their infancy. Results obtained in the latter area so far prove that some halogenases can be expressed recombinantly and subsequently applied to directly halogenate suitable substrates, e.g., tryptophan halogenases [63, 71, 72, 100, 101]. Other halogenases only function in a multienzymatic biosynthetic environment, and combinatorial biosynthetic strategies need to be implemented to use their enzymatic capabilities.

For further details regarding biohalogenation beyond the scope of this book chapter, we recommend the comprehensive reviews based on the pioneering work of the research groups of van Pée and Walsh in the field of dioxygen-depending halogenases [64, 68, 85, 114, 118–123]. The recently published comparison of the halide-binding sites of different halogenating enzymes and their corresponding selectivities are discussed by Blasiak and Drennan [117]. Further insights concerning the mechanisms of enzymatic halogenation were described by Dolfing [124], Anderson and Chapman [2], and Murphy [115], as well as Naismith [5]. In addition, reviews focusing on haloperoxidases have recently been published by Hofrichter and Ullrich [10], Butler and Carter-Franklin [8], and Raugei and Carloni [125], as well as Bortolini and Conte [126] and Winter and Moore [31].

19.7 Study Questions

1. Name the different halogenating enzymes known for natural product biosynthesis.
2. What are the cofactors utilized within haloperoxidases?
3. Which is the actual halogenation agent of haloperoxidases?
4. How do chloroperoxidases, bromoperoxidases, and iodoperoxidases differ?
5. Where are iodoperoxidases mainly found?

6. What is the halogenation strategy within nonheme Fe^{II}/α-ketoglutarate/O₂-dependent halogenases?
7. Which are the structural elements halogenated by Fe^{II}/α-ketoglutarate/O₂-dependent halogenases?
8. Which is the actual halogenation agent within FADH₂ halogenases, and how is regioselective halogenation secured?
9. How are FADH₂ halogenases further classified?
10. What is the function of SAM within the respective halogenating enzymes?
11. Why are fluorinated metabolites so rare in nature?

19.7.1 Answer–Keywords

1. Haloperoxidases, halogenases, *S*-adenosyl-L-methionine-utilizing enzymes
2. Heme or vanadate as cofactors
3. Hypohalous acid (HOX. or related halogenating intermediates, such as OX⁻, X³⁻, and X⁺):
 - In heme HPO, the final chlorine transfer to various substrates occurs outside the active site via a free diffusible species without any special mode of substrate recognition.
 - Va-HPOs bind hydrogen peroxide and halides leading to a putative enzyme-bound or active site-trapped brominating moiety. In the absence of a suitable substrate, however, HOBr is released from the enzyme and carries out unselective bromination as observed for aqueous bromine.
4. Nomenclature is based on the most electronegative halide oxidized by the enzyme.
5. Va-IPOs seem to play a role in iodine accumulation of brown algae as a main vector of the iodine biogeochemical cycle.
6. A highly reactive iron-oxo species (Fe^{IV} = O) is formed within the catalytic cycle. This abstracts a hydrogen radical from an aliphatic carbon center of the actual substrate, which, in turn, abstracts the halide from the coordination sphere of the enzyme.
7. Fe^{II}/α-ketoglutarate/O₂-dependent halogenase are involved in the chlorination of terminal methyl groups of amino acids linked to peptidyl carrier proteins and, occasionally, in the formation of cyclopropane moieties.
8. Enzyme-trapped HOCl is produced as chlorinating agent and channeled through an intraenzymatic tunnel to the substrate binding pocket. Here this chlorinating intermediate is proposed to be a covalently bound lysine chloramine (Lys79-εNH-Cl). Regioselective halogenation is thereby secured by controlled presentation of the substrate to the bound Cl-species via particular amino acid residues in the substrate binding site.
9. Halogenases can be grouped into:
 - Those accepting free small molecules and those that act on carrier-bound substrates, e.g., involved in multienzymatic NRPS/PKS assembly lines

- Subdivided by the moieties to be chlorinated, i.e., aromatic compounds, recognizing tryptophan/indole or phenol/pyrrole moieties and enzymes involved in the halogenation of aliphatic compounds
10. Enzymes utilizing *S*-adenosyl-L-methionine (SAM) as cosubstrate:
 - Classically act in methyltransferases and, in this manner, are involved in the production of monohalomethanes.
 - Furthermore, in the unique enzyme 5'-FDA synthetase, substitution of methionine at SAM by fluoride takes place, and in turn, 5'-fluoro-5'-deoxyadenosine is formed as an intermediate (which is subsequently converted to fluoroacetate and 4-fluorothreonine). The chloro analog enzyme SaLL converts SAM to 5'-chloro-5'-deoxyadenosine, which is subsequently converted to chloroethylmalonyl-CoA to further act as unique PKS extender unit.
 11. Difficulties in the formation of fluorinated metabolites:
 - Extremely high desolvation energy required to activate F⁻ in aqueous solution makes biological reactions with fluoride rather rare.
 - Fluoride, as most nucleophilic halogens, does not allow any electrophilic or radical biological chemistry.
 - Unique enzymes are needed to overcome this kinetic barrier (e.g., hydrogen peroxide does not have the driving force to oxidize fluoride).

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Part 5

**Biomedical Potential of Marine
Natural Products**

Raymond J. Andersen, Dehai Li, Matt Nodwell, Michel Roberge, Wendy Strangman, and David E. Williams

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R.J. Andersen (✉) • D. Li • M. Nodwell • W. Strangman • D.E. Williams
Departments of Chemistry and Earth & Ocean Sciences, University of British Columbia,
Vancouver, BC, Canada
e-mail: raymond.andersen@ubc.ca, dehaili@chem.ubc.ca, mnodwell@chem.ubc.ca,
strangman@uncw.edu, davewill@chem.ubc.ca

M. Roberge
Department of Biochemistry & Molecular Biology, University of British Columbia, Vancouver,
BC, Canada
e-mail: michelr@interchange.ubc.ca

Abstract

This chapter illustrates the large number and variety of microtubule-targeting natural product chemotypes that have been discovered from marine organisms. Microtubules are the biological target of many marine natural products, and antimetabolic agents are potent toxins making them highly effective chemical defenses for algae and sessile or slow-moving invertebrates. Marine sponges account for roughly half of the new chemotypes, with the remainder coming from ascidians, soft corals, mollusks, macroalgae, blue-green algae, bacteria, and fungi.

20.1 Introduction

The widespread use of the antimetabolic plant natural products vincristine, vinblastine, paclitaxel, and synthetic analogs of these compounds to treat cancer has provided unparalleled validation of microtubules as a high-value molecular target for the development of new anticancer drugs [1–6]. Organisms living in the world's oceans have turned out to be an extremely rich source of potentially cytotoxic and structurally complex natural products that target microtubules. These antimetabolic marine natural products provide inspiration for the development of new chemical classes of anticancer drugs, and, as such, they have received considerable attention from both academic and industrial researchers who are interested in their bioactivity and chemistry. One major impediment to the development of any antimetabolic natural product into a useful drug is the sustainable production of an adequate supply of the natural product or an analog for clinical use. The intellectual and experimental challenge posed by the complex structures of antimetabolic marine natural products and the need for practical ways to produce them have engaged the synthetic organic chemistry community, resulting in the development of many elegant routes to these valuable targets. A number of antimetabolic marine natural products or synthetic analogs have cleared the multiple hurdles of the drug development pathway to reach phase I and phase II clinical trials, and there is the real hope that one or more of these will become clinically useful drugs alongside the Vinca alkaloids and the taxanes.

The primary goals of this chapter will be (1) to provide some basic background about the role of microtubules in the process of mitosis in order to illustrate how disrupting microtubule dynamics leads to inhibition of cell proliferation and cell death and (2) to present a comprehensive review of the known marine natural products that target microtubules. Natural product structures are grouped first according to their ability to inhibit or promote tubulin polymerization *in vitro* and second according to their putative biogenetic origins.

Another group of very interesting marine natural products, including the protein phosphatase inhibitors okadaic acid, the calyculins, and the spirastrellolides, arrest cells in mitosis at nM concentrations by inhibiting cell-signaling enzymes.

Antimitotic compounds in this category that do not target microtubules will not be reviewed in this chapter. A review of the extensive literature describing synthetic approaches to microtubule-targeting marine natural products is beyond the scope of this chapter, and only selected references will be provided.

20.2 Microtubules as an Anticancer Drug Target

20.2.1 The Biological Role of Microtubules in Mitosis

Microtubules are highly dynamic polymeric protein fibers that have important cellular roles in mitosis, transport, positioning of organelles, and determination of shape [1, 2]. The building blocks of microtubules are heterodimers of the homologous 50-kDa proteins α - and β -tubulin. These heterodimers polymerize in a head-to-tail fashion to form protofilaments, and alignment of 13 protofilaments in a parallel fashion creates the circular walls of a microtubule (Fig. 20.1). One end of the microtubule, the “+” end, has β -tubulin exposed, and the other “-” end has α -tubulin exposed. The α -tubulin unit in the heterodimer has a bound GTP nucleotide that can only be removed by protein denaturation. A second guanine nucleotide that can be either GDP or GTP is bound to an exchangeable site on the β -tubulin unit. Microtubule assembly requires occupancy of the exchangeable site on β -tubulin by GTP, which is hydrolyzed to GDP during polymerization. Once formed, the GDP remains bound to the polymer as long as the β -tubulin unit that it is associated with is still part of the microtubule. The presence of a small cap of tubulin with a GTP bound at the exchangeable site stabilizes the microtubule and inhibits depolymerization.

The length of the microtubules involved in equal partitioning of the duplicate chromosomes synthesized during S phase into daughter cells during mitosis is highly dynamic [7, 8]. Microtubules undergo two types of polymerization/depolymerization behaviors known as “dynamic instability” and “treadmilling.” In dynamic instability, microtubule plus and minus ends randomly and independently switch between phases of growth and shortening. The plus end changes length more rapidly and to a greater extent than the minus end. Dynamic instability is characterized by the rates of growth and shortening and the frequencies of “catastrophe” and “rescue.” Catastrophe is defined as a change in microtubule polymerization from growth or pause to shortening, and rescue is defined as a change from shortening to pause or growth. Pause is a period where no change in microtubule length is detectable by light microscopy. During treadmilling, the growth at the plus microtubule end is exactly balanced by shortening at the minus end, resulting in a net flow of individual tubulin units from the plus to minus ends without a change in overall length. Treadmilling is particularly important in mitotic spindles.

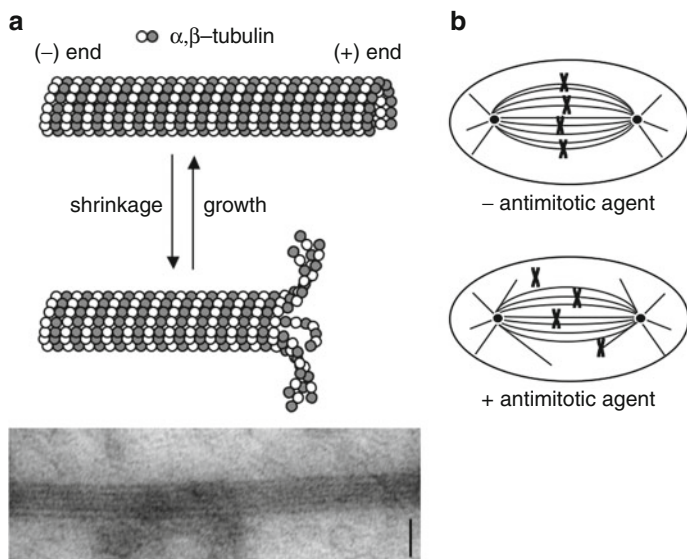


Fig. 20.1 Microtubules and the disruption of their mitotic function by antimetabolic agents. **(a)** Schematic representation of microtubules showing their growth and shrinkage cycle. The lower panel is an electron micrograph of a microtubule whose *in vitro* assembly from pure α - and β -tubulin was stimulated by ceratamine A (97). Scale bar, 30 nm. **(b)** Disruption of microtubule spindle dynamics leads to mitotic arrest. During a normal mitosis, the mitotic spindle aligns chromosomes at the metaphase plate before segregating them to the two daughter cells. Low concentrations of antimetabolic agents cause defects in microtubule dynamics that prevent the efficient capture and alignment of all chromosomes by spindle microtubules, leading to mitotic arrest

Disrupting microtubule dynamics during mitosis is the main effect of anticancer drugs that target microtubules [1, 2]. When cells enter mitosis, the interphase microtubule network disassembles and is replaced by a highly dynamic population of spindle microtubules. During prometaphase, a bipolar mitotic spindle forms. Microtubules radiating from microtubule-organizing centers (MTOC) make extensive growth and shortening excursions probing the cytoplasm until they become attached to chromosomes at their kinetochores. Once microtubules from one MTOC have become attached to a kinetochore, the growth and shortening of microtubules from a second MTOC has to be dynamic enough to allow them to become attached to the kinetochore of the sister chromatid, thereby creating a complete bipolar spindle. During metaphase, the attached chromosomes become aligned along the equatorial region of the spindle, and they are kept in alignment by tension caused by dynamic instability and treadmilling of the kinetochore microtubules (Fig. 20.2). During anaphase, the chromosomes are pulled apart and toward

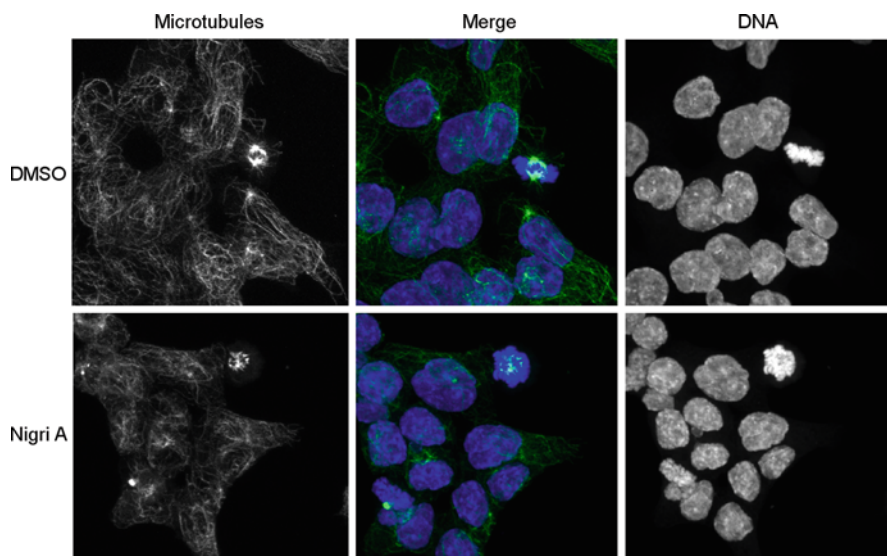


Fig. 20.2 Induction of mitotic arrest by the dimethyl ester of nigriganoside A (**101**). Microtubules were visualized by immunostaining (*left panels*) and chromosomes with the DNA dye Hoechst 33342 (*right panels*). The central panels show merged pictures with microtubules in green and chromosomes in blue. A normal metaphase cell with a bipolar mitotic spindle and aligned chromosomes is shown in control cells (*upper panels*). A cell arrested at mitosis with an abnormal spindle and misaligned chromosomes is seen in the dimethyl ester of nigriganoside A (**101**)-treated sample (*lower panel*)

the spindle poles by depolymerizing microtubules. In telophase, the cell begins to constrict to form two daughter cells, each having one complement of the chromosomes. A series of mitotic checkpoints monitor the progress of spindle formation and chromosome separation during mitosis, and if there are flaws in any of the steps, the cell cycle will be arrested in mitosis, leading to inhibition of cell proliferation and cell death.

Microtubule-targeting natural products are usually described as microtubule “stabilizers/polymerizers” or “destabilizers/depolymerizers” based on their ability to promote or inhibit the polymerization of pure tubulin *in vitro* [1, 2, 6] (Fig. 20.3). However, this classification is misleading because the effects on *in vitro* tubulin polymerization leading to changes in microtubule mass are usually observed only at micromolar concentrations, while the effects of the compounds on cell death are frequently observed at nanomolar concentrations. Evidence now indicates that it is the ability of microtubule-targeting drugs to modulate essential microtubule dynamics at low concentrations without necessarily altering microtubule mass that leads to mitotic arrest and cell death. Cancer cells are thought to be more

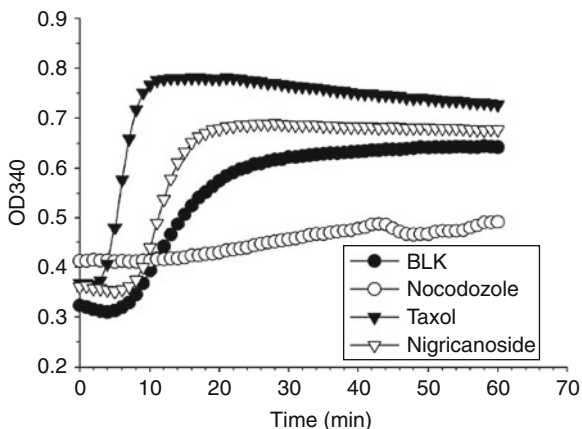


Fig. 20.3 In vitro microtubule polymerization assay. Tubulin spontaneously polymerizes into microtubules when incubated with GTP at 32°C. Microtubule formation may be monitored by turbidimetry at 340 nm. The graph shows that the microtubule depolymerizing agent nocodazole prevents microtubule formation while the microtubule-polymerizing agents taxol and the dimethyl ester of nigricanoside A (**101**) enhance the rate of microtubule assembly

susceptible to microtubule-targeting drugs than normal cells in part because they divide more rapidly, and therefore, they more frequently pass through mitosis where they are vulnerable to disruption of microtubule dynamics. Recent studies have shown that some microtubule-targeting agents are extremely effective at collapsing tumor vasculature in mouse models, leading to death of tumor cells due to lack of oxygen and nutrients [9, 10]. The antivasculture effects are often observed at concentrations well below the cytotoxic concentrations of the drugs, raising the possibility of effective metronomic drug treatment regimes aimed at tumor vasculature with reduced cytotoxic side effects.

20.2.2 Drug Binding Sites on Tubulin

Most known microtubule-targeting antimitotic drugs bind to one of four well-described sites on tubulin, although several of the marine natural products presented below have revealed new binding sites [1, 6]. The first of the known sites is the taxane binding site, and it only has a high affinity for drugs when tubulin has polymerized into microtubules. Compounds that bind at the taxane site, such as paclitaxel, cause hyperassembly of microtubules with increased stability in the in vitro polymerization assay (Fig. 20.3). Cells arrested in mitosis with these microtubule “stabilizing” drugs show an increase in microtubule density, and their microtubules are much shorter than normal and aggregated into bundles.

Compounds that bind to the other three sites all inhibit tubulin polymerization into microtubules *in vitro*, and compound-arrested cells show a thinning or complete disappearance of microtubules along with subtle defects in spindle function. The first group of “destabilizing” antimetabolic agents alkylate the thiol group of Cys-239 in tubulin, and some of these inhibit the ability of tubulin to bind colchicine. A second group of “destabilizing” compounds competitively inhibit colchicine binding to tubulin. The third group of destabilizers bind to a region of tubulin known as the “Vinca domain” because of their ability to interfere with the binding of vincristine and vinblastine to tubulin. Some of these compounds are competitive inhibitors of Vinca alkaloid binding, and others are noncompetitive inhibitors.

20.2.3 Approaches to Discovering Antimetabolic Marine Natural Products

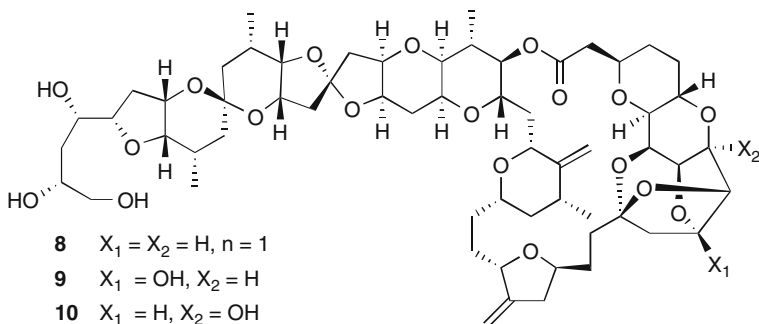
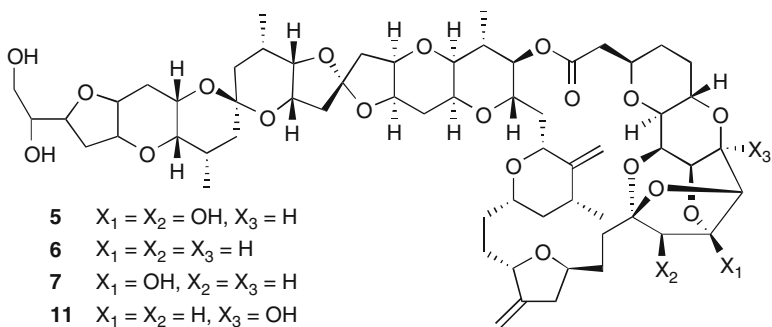
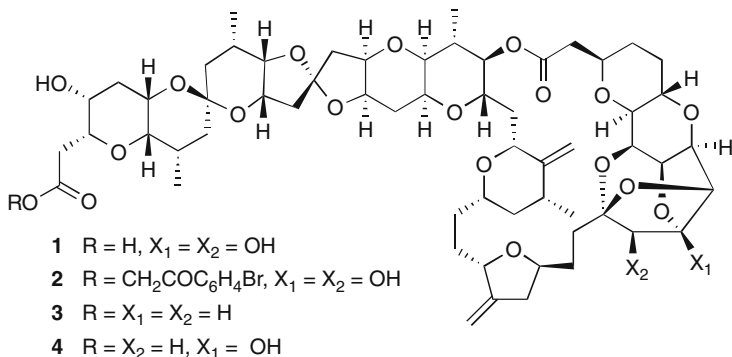
The majority of microtubule-targeting natural products, including the Vinca alkaloids and paclitaxel, were initially discovered because they were potentially cytotoxic, and it was only much later, when their mechanism of action was investigated in detail, that they were found to arrest cells in mitosis and modulate tubulin polymerization *in vitro*. Horwitz’s seminal discovery that paclitaxel stabilizes microtubules and the subsequent success of paclitaxel in the clinic stimulated a vigorous worldwide search for additional natural product chemotypes possessing this important biological activity [11]. As part of this search, several new assays that can directly detect antimetabolic agents in crude extracts have been used to aid the discovery of microtubule-targeting marine natural products.

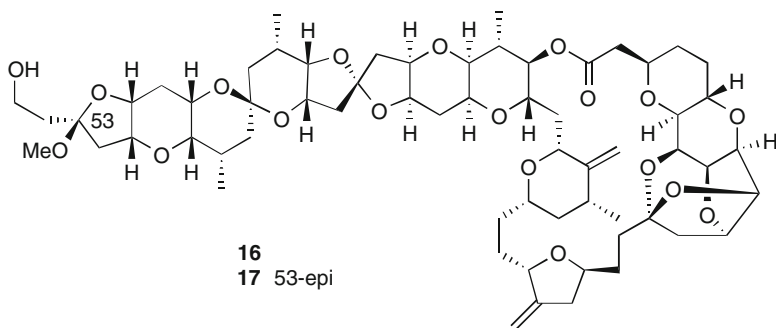
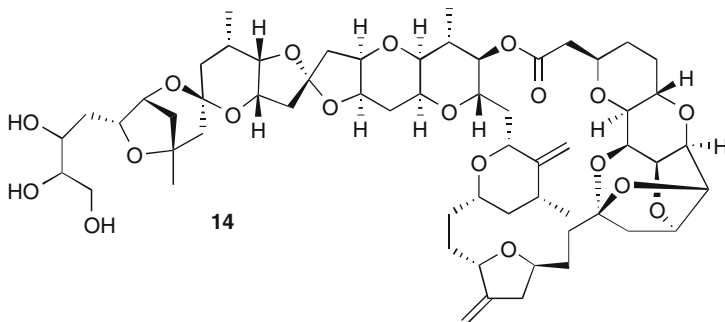
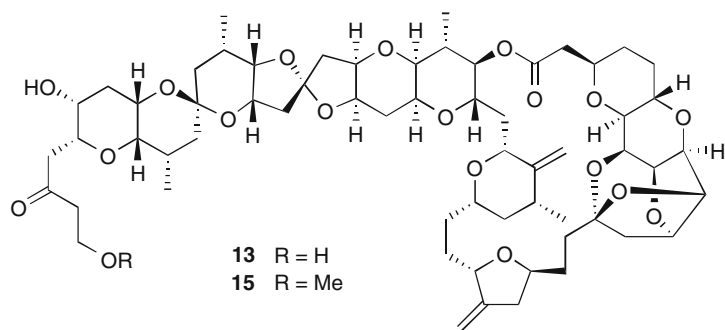
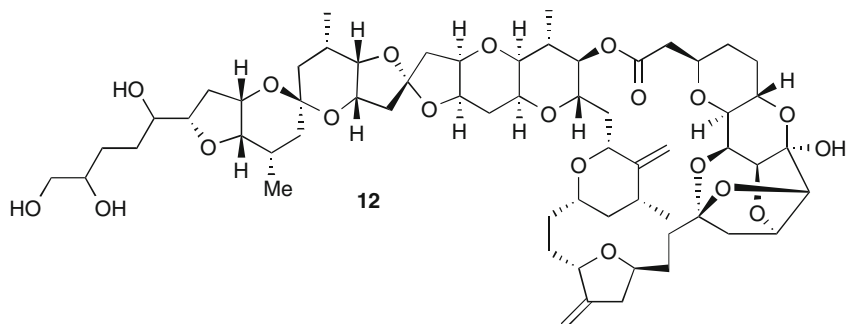
Roberge developed a robust and sensitive cell-based assay for antimetabolic agents that uses the monoclonal antibody TG3 to detect a phosphoepitope on the nuclear protein nucleolin that is only present in mitosis [12]. Microscopic examination of tubulin in cells that have been arrested by a hit in the assay can often reveal if the active components are microtubule-depolymerizing or microtubule-stabilizing agents. In this way, the assay can be used as an effective direct screen for microtubule-stabilizing natural products. Barrows developed a cell-based assay that takes advantage of the ability of dibutyl-cAMP to rapidly induce a spherical morphology in rat glioma cells [13]. The morphological change is due to tubulin polymerization, and therefore, microtubule “destabilizing” antimetabolic natural products will inhibit the rounding up. Spherical cells can be selectively aspirated from 96-well plates leaving behind unresponsive cells resulting from treatment with a tubulin-depolymerizing agent, that are quantified by treatment with MTT and spectrophotometric detection of the formazan product. Namikoshi and coworkers have used a modification of the *in vitro* tubulin polymerization assay [14] and the deformation of mycelia germinated from conidia of the rice plant pathogenic fungus *Pyricularia oryzae* [15] to screen marine extracts for antimetabolic agents.

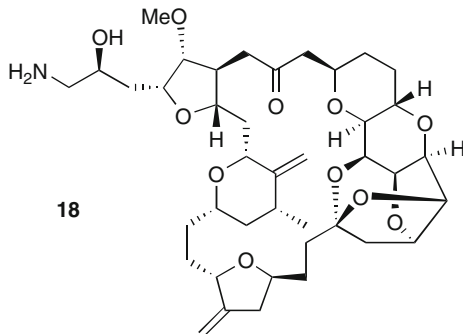
20.3 Microtubule-Depolymerizing Agents

20.3.1 Polyketides

20.3.1.1 Halichondrins and Halistatins







Uemura's group reported the isolation of the polyether macrolide norhalichondrin A (**1**) from the Japanese sponge *Halichondria okadai* Kadota in 1985 [16]. The structure of **1**, including the absolute configuration, was elucidated by single crystal X-ray diffraction analysis of the *p*-bromophenacyl ester derivative (**2**). The same sponge subsequently yielded norhalichondrins B (**3**) and C (**4**); homohalichondrins A (**5**), B (**6**), and C (**7**); and halichondrins B (**8**) and C (**9**) [17]. In 1993, Pettit and coworkers reported the isolation of halistatin 1 (**10**), an isomer of halichondrin C, from the sponge *Phakellia carteri* collected in the Republic of Comoros [18]. They later described the structure of halistatin 2 (**11**) [19], obtained from *Axinella* cf. *carteri* also collected in the Comoros, and halistatin 3 (**12**) obtained from a *Phakellia* sp. collected in the Federated State of Micronesia [20]. Blunt, Munro, and coworkers reported the isolation of isohomohalichondrin B (**13**) [21], neonorhalichondrin B (**14**), 55-methoxyisohomohalichondrin B (**15**), 53-methoxyneoisohomohalichondrin B (**16**), and 53-epi-53-methoxyneoisohomohalichondrin B (**17**) from specimens of the sponge *Lissodendoryx* sp. obtained by dredging in deep water (>100 m) off the Kaikoura Peninsula in New Zealand [22]. They also reported an analog neohomohalichondrin B that has the same constitution as halistatin 3 (**12**), but since no direct comparison was made between the two compounds and neither Pettit or Munro and Blunt assigned the configuration of the side chain chiral centers, it is not possible to say if the compounds are identical or not.

Halichondrin B (**8**) was reported by Uemura to be a potent in vitro cytotoxin (IC₅₀ vs. B-16 melanoma = 0.093 ng/mL), and it also showed impressive %T/C values (157–244) in vivo against the same cell line [17]. Hamel et al. evaluated halichondrin B (**8**) and homohalichondrin B (**6**) in the NCI 60 cell line panel and used the COMPARE analysis to show that it was an antimitotic agent [23]. Halichondrin B was found to inhibit the polymerization of purified tubulin in vitro (IC₅₀ 7.2 μM) and noncompetitively inhibit vinblastine binding. The promising anticancer activity of halichondrin B and the limited supply stimulated

its total synthesis by Kishi and coworkers [24]. As part of the synthetic efforts, scientists at Eisai Research Institute made more than 180 analogs, and they found that eribulin (E7389) (**18**), containing only the macrolide fragment of halichondrin B, was just as active as the natural product in vitro and in vivo [25–27].

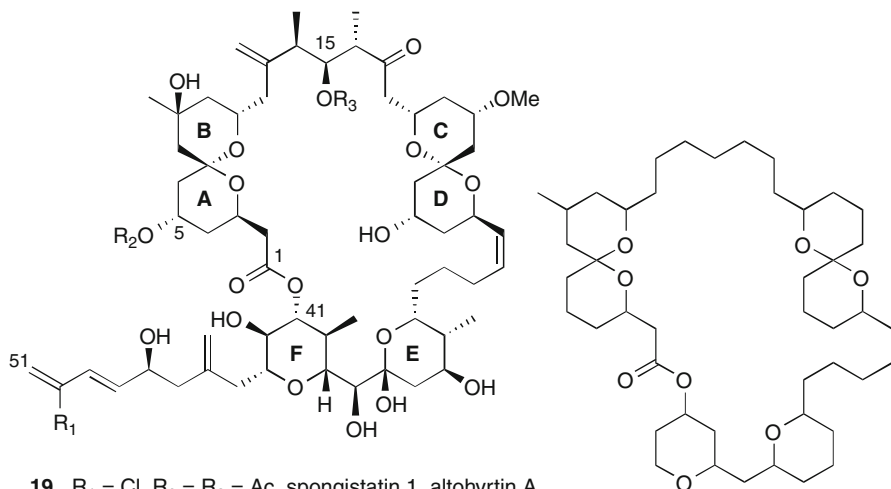
More detailed studies showed that unlike other antimetabolic drugs such as vinblastine and paclitaxel that suppress both shortening and growth phases of microtubule dynamic instability, eribulin (**18**) did not affect shortening events nor the catastrophe or rescue frequencies, but it did significantly reduce the rate and extent of microtubule growth [28]. It also generated tubulin aggregates that are different from those created by other antimetabolic drugs [29]. These results showed that eribulin (**18**) has a novel mechanism of action involving modulation of microtubule dynamics. Eribulin (**18**) has entered a series of phase I and phase II anticancer clinical trials [30, 31].

20.3.1.2 Spongistatins/Altohyrtins/Cinachyrolide

In 1993, the Pettit, Fusetani, and Kitigawa groups independently reported the isolation of members of a family of potentially cytotoxic macrolides from extracts of marine sponges. Spongistatin 1 (**19**) was isolated by Pettit's group from a *Spongia* sp. collected in the Republic of the Maldives in the Indian Ocean [32]. Approximately 14 mg of spongistatin 1 was obtained from 400-kg wet weight of the sponge ($3 \times 10^{-7}\%$ yield), and the paucity of material limited the initial structure elucidation to a determination of the molecule's constitution. Evaluation of spongistatin 1 (**19**) in the NCI 60 cell line panel showed potent broad-spectrum activity (GI_{50} s of 0.25–0.35 nM), and analysis of the pattern of cellular selectivity revealed that it was a microtubule-interactive antimetabolic agent. Pettit proposed the name "spongipyran" for the macrocyclic skeleton (**20**) of spongistatin 1.

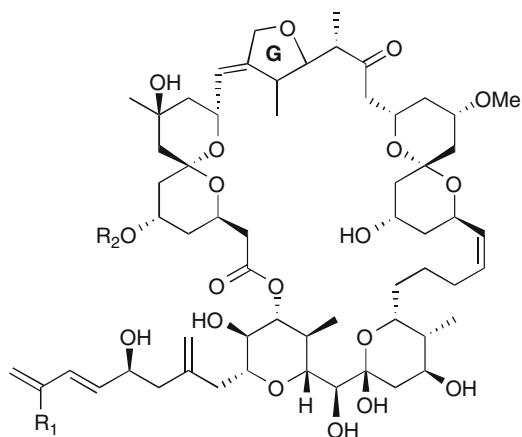
Fusetani et al. reported the isolation of cinachyrolide A (**21**), which differs from spongistatin 1 (**19**) only by the absence of an acetate ester at C-15, from extracts of a sponge in the genus *Cinachyra* collected off Hachijojima Island 300 km south of Tokyo [33]. They determined the relative configurations of each of the A/B, C/D, and E/F pairs of tetrahydropyran rings and their attached substituents by analysis of NOESY and scalar coupling constant data, but they were not able to relate the relative configurations of the pairs to each other (i.e., A/B to C/D or E/F). Fusetani reported that cinachyrolide A was cytotoxic in vitro against murine leukemia cells with an IC_{50} of <0.6 ng/mL.

Kitigawa and coworkers reported the isolation of altohyrtin A from extracts of the sponge *Hyrtios altum* collected in Okinawa [34]. They determined the constitution of the molecule and the relative configurations of each of the spiroketal and tetrahydropyran ring systems by analysis of NMR data. Altohyrtin A has the same constitution as that reported for spongistatin 1 (**19**). Kitigawa's group subsequently reported isolating altohyrtins B (**22**) and C (**23**) and 5-desacetyl altohyrtin A (**24**) from *H. altum* [35], and Pettit's group reported the isolation of spongistatins 2 (**23**) and 3 (**24**) from the *Spongia* sp. [36].



- 19** $R_1 = \text{Cl}$, $R_2 = R_3 = \text{Ac}$ spongistatin 1, altohyrtin A
21 $R_1 = \text{Cl}$, $R_2 = \text{Ac}$, $R_3 = \text{H}$ cinachyrolide A, spongistatin 4
22 $R_1 = \text{Br}$, $R_2 = R_3 = \text{Ac}$ altohyrtin B
23 $R_1 = \text{H}$, $R_2 = R_3 = \text{Ac}$ altohyrtin C, spongistatin 2
24 $R_1 = \text{Cl}$, $R_2 = \text{H}$, $R_3 = \text{Ac}$ 5-desacetylaltohyrtin A, spongistatin 3
26 $R_1 = \text{H}$, $R_2 = \text{Ac}$, $R_3 = \text{H}$ spongistatin 6

20



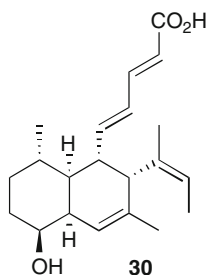
- 25** $R_1 = \text{Cl}$, $R_2 = \text{H}$ spongistatin 5
27 $R_1 = \text{H}$, $R_2 = \text{H}$ spongistatin 7
28 $R_1 = \text{H}$, $R_2 = \text{Ac}$ spongistatin 8
29 $R_1 = \text{Cl}$, $R_2 = \text{Ac}$ spongistatin 9

Kitigawa's group determined the complete absolute configuration of the altohyrtins (**19**, **22**, **23**, **24**) using a combination of the modified Mosher ester NMR approach and exciton chirality CD methodology [37, 38]. They also proposed

that the absolute configurations of the spongistatins and cinachyrolide A were identical to the altohyrtrins, as shown in **19**, **22**, **23**, and **24**. Proof that altohyrtrin A was identical to spongistatin 1 and altohyrtrin C was identical to spongistatin 2, and that they had the absolute configurations shown in **19** and **23**, was provided by Kishi's total synthesis of **19** [39] and Evans' total synthesis of **23** [40]. Pettit et al. subsequently reported the isolation of spongistatin 4 (**21**), which is identical to cinachyrolide A, and spongistatins 5 (**25**), 6 (**26**), 7 (**27**), 8 (**28**), and 9 (**29**) from the sponge *Spirastrella spinispirulifera* collected along the Southeast Coast of Africa [41–43].

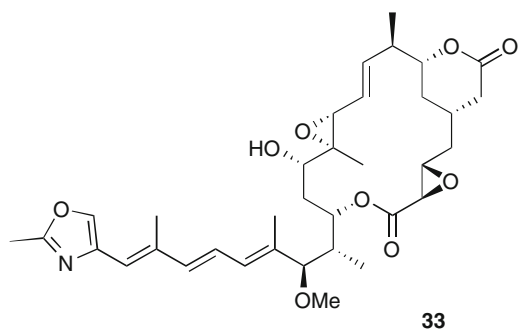
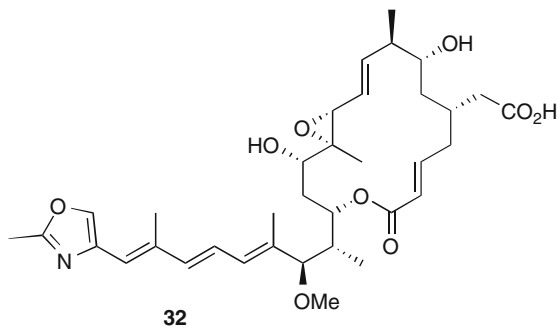
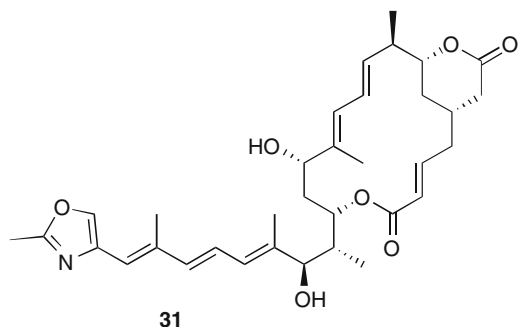
The spongistatins/altohyrtrins/cinachyrolides contain a number of notable structural features including the two spiroketal systems (A/B and C/D rings) and the two tetrahydropyran rings (E and F) embedded in a 42-membered macrocycle and the vinyl chloride functionality in the side chain. Further studies of the interaction of spongistatin 1 with tubulin showed that it is a noncompetitive inhibitor of vinblastine and dolastatin 10 binding, leading to the proposal that the spongistatins bind to a site on β -tubulin that is close to but distinct from those where the Vinca alkaloids and peptide antimetabolic agents bind [44]. A lack of material has hindered the animal testing and preclinical evaluation/development of this family of compounds. One report, described as a personal communication, indicates that curative responses with no associated toxicities have been observed in human melanoma and ovarian carcinoma xenografts at doses of 25 $\mu\text{g}/\text{kg}$ of spongistatin 1 (**19**) [45]. Recent synthetic efforts have been focused on generating practical routes aimed at making grams of the spongistatins, which should facilitate further biological evaluation of this family of potent antimetabolic agents [46].

20.3.1.3 Phomopsidin



Namikoshi et al. isolated the polyketide phomopsidin (**30**) from cultures of the fungus *Phomopsis* (strain TUF 95 F47) obtained from a fallen mangrove branch collected on the bottom of a coral reef in Pohnpei [47, 48]. The antimetabolic activity of the culture extract was detected using a screening method that looks for deformations of mycelia germinated from conidia of the fungus *Pyricularia oryzae* [15]. Phomopsidin (**30**) inhibited the polymerization of purified bovine tubulin in vitro with an IC_{50} of 5.7 μM . Stable-isotope feeding studies have shown that phomopsidin is a linear nonaketide with the branching methyl groups coming from SAM.

20.3.1.4 Rhizoxin Analogs

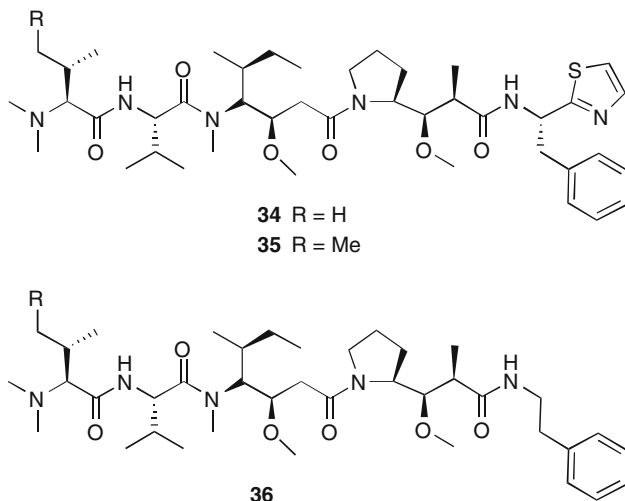


Roberge et al. isolated the known rhizoxin analog WF-1360 C (**31**) and the new seco acid **32** from laboratory cultures of a marine bacterial isolate MK7020, identified as a *Pseudomonas* sp., collected off the coast of British Columbia [12]. Compounds **31** and **32** were active in Roberge's cell-based assay for antimittotic agents (**31**: IC₅₀ 52 nM, **32**: IC₅₀ 8 nM), and it is assumed that they inhibit tubulin polymerization in a manner similar to rhizoxin (**33**) [49]. The discovery that bacteria produced rhizoxins was unexpected since rhizoxin and related analogs had previously only been isolated from the rice seedling blight fungus *Rhizopus chinensis* and other unidentified fungal species in the same genus [50]. Subsequently, it was discovered that *Rhizopus* sp. had an associated bacterial

endosymbiont in the genus *Burkholderia* that was actually responsible for producing the rhizoxins isolated from *Rhizopus* cultures [51]. Bacteria in the genera *Burkholderia* and *Pseudomonas* are closely related taxonomically. Rhizoxin (33) has been evaluated in phase II clinical trials [52].

20.3.2 Peptides and Mixed Polyketide/Peptide

20.3.2.1 Dolastatins, Symplostatin, and Belamide

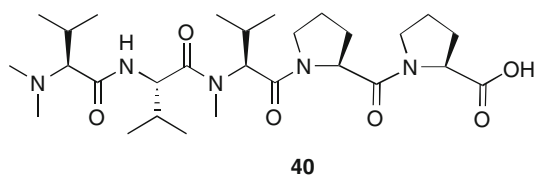
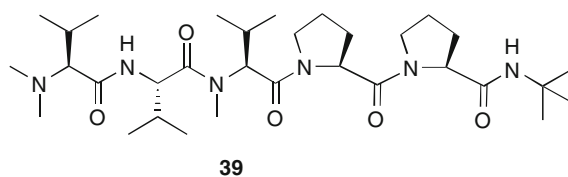
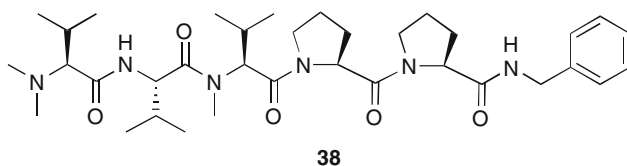
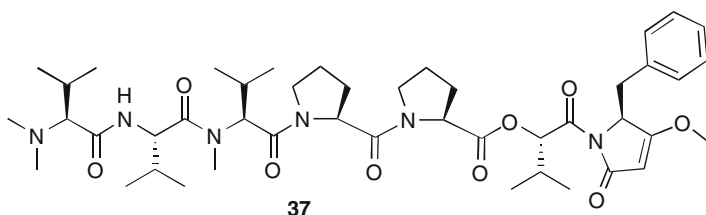


In 1987, Pettit's group reported the constitution of the potently cytotoxic linear peptide dolastatin 10 (34) isolated from extracts of the Indian Ocean sea hare *Dolabella auricularia* (in vitro ED_{50} = 0.046 ng/mL vs. P388 murine leukemia) [53]. Dolastatin 10 (34) was present in the sea hare extracts in extremely small quantities (ca. \approx 1 mg in 100 kg), making the assay-guided isolation and structure elucidation exceptionally challenging. The report of its structure was the culmination of a 15-year sustained effort. Pettit's group subsequently reported the total synthesis of dolastatin 10 (34), which established its complete absolute configuration [54]. The four nonprotein amino acids dolavaline (Dov), dolaisoleucine (Dil), dolaproline (Dap), and dolaphenine (Doe) were first encountered in dolastatin 10. Two of these amino acids, dolaisoleucine and dolaproline, appear to be derived from isoleucine and proline residues that have been homologated with acetate units, a hallmark of cyanobacterial metabolism. Consistent with this biogenetic observation, dolastatin 10 (34) and the closely related analog symplostatin 1 (35) have both been isolated from field samples of cyanobacteria in the genus *Symploca* collected in Palau and Guam [55].

Hamel and coworkers have shown that dolastatin 10 (34) inhibits tubulin polymerization and the associated GTP hydrolysis in vitro (IC_{50} 1.2 μ M),

noncompetitively inhibits the binding of vinblastine to tubulin, interferes with nucleotide exchange, induces an intra- β -tubulin crosslink between Cys-12 and either Cys-201 or Cys-211, and induces the formation of nonmicrotubule polymers of tubulin plus microtubule-associated proteins (MAP) in the presence of GTP [56, 57]. Dolastatin 10 showed potent *in vivo* activity in a variety of mouse models of cancer [38], and it has been evaluated in several phase I and phase II anticancer clinical trials [58–61].

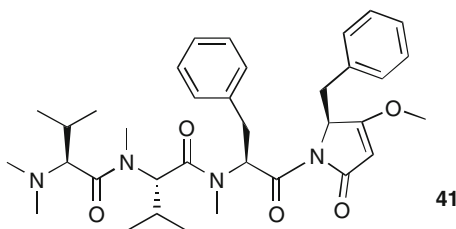
Miyazaki and coworkers synthesized a series of dolastatin 10 analogs and found that TZT-1027 (Soblidotin) (**36**) missing the thiazole ring also showed excellent antitumor activity in mouse models [62, 63]. Further studies on TZT-1027 revealed a selective antivasular effect on tumor vessels [64], and it was proposed that TZT-1027 kills tumors in mouse models by exerting a combination of indirect antivasular effects and direct cytotoxic effects [65]. TZT-1027 has been evaluated in both phase I and phase II clinical trials [66–68].



In 1989, Pettit's group reported the isolation of the cytostatic depsipeptide dolastatin 15 (**37**) from extracts of the same Indian Ocean sea hare *Dolabella*

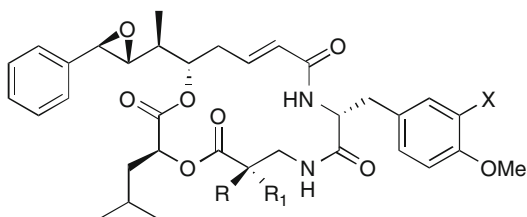
auricularia that was the source of dolastatin 10 (**34**) [69]. Dolastatin 15 (**37**) was also a trace component in the extract (6.2 mg from 1,600-kg wet weight of mollusc), and it too showed potent inhibition of the growth of the murine leukemia P388 cell line in vitro (ED_{50} 2.4 ng/mL). Pettit et al. established the absolute configuration of dolastatin 15 (**37**) via total synthesis [70]. The structure of dolastatin 15 (**37**) is similar to dolastatin 10 (**34**) in the dolavaline-valine sequence at the *N*-terminus and in the aromatic character of the *C*-terminus. After extensive investigations of the effects of dolastatin 15 (**37**) on P388 cells, Bai et al. concluded that the toxicity of the depsipeptide resulted from interference with mitosis [71]. However, they found that the interaction of dolastatin 15 (**37**) with purified tubulin was very weak and the most convincing evidence that it was an inhibitor of tubulin polymerization was the disappearance of microtubules in cells treated with relatively high concentrations of the drug. Further studies using Hummel-Dreyer chromatography provided evidence for weak binding of dolastatin 15 to the Vinca domain of tubulin [72].

A number of synthetic analogs of dolastatin 15 (**37**) have been tested for biological activity. These include cemadotin (LU103793) (**38**) [73] and tasidotin (ILX651) (**39**) [74]. Jordan et al. found that cemadotin strongly suppressed dynamic instability of microtubules [75]. It reduced the rate and extent of growth and shortening, increased the frequency of rescue, and increased the amount of time spent in a paused state. Cemadotin did not inhibit vinblastine binding to tubulin, so it was concluded that the cytotoxicity of cemadotin was caused by suppression of spindle microtubule dynamics as a result of binding at a novel site on tubulin. Tasidotin (**39**) was also shown to modulate spindle microtubule dynamics in a fashion similar to cemadotin, (**38**) and it was found that it is a prodrug for the much more potent *C*-terminus carboxylic acid metabolite **40** [76]. Cemadotin (**38**) [77, 78] and tasidotin (**39**) [79] have both been evaluated in clinical trials.

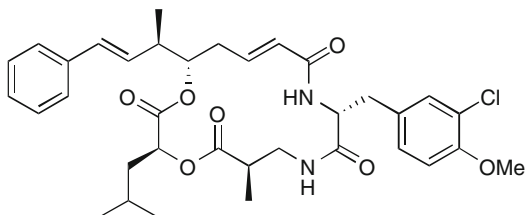


Belamide A (**41**), a truncated structural analog of the dolastatins, was reported by Gerwick and coworkers in 2006 [80]. This highly methylated linear tetrapeptide was isolated from the marine cyanobacterium *Symploca* sp., and it contains the *N*-terminal *N,N*-dimethylvaline and *C*-terminal benzyl methoxy pyrrolinone moieties characteristic of the dolastatins. Belamide A (**41**) has been shown to have moderate cytotoxicity (IC_{50} of 0.74 μ M against HCT-116 cells), and it disrupts microtubules at 20 μ M.

20.3.2.2 Cryptophycins and Arenastatin



- 42** R = R₁ = H, X = H
43 R = Me, R₁ = H, X = Cl
44 R = Me, R₁ = H, X = H
47 R = R₁ = Me, X = Cl



- 45** R = Me, X = Cl
46 R = Me, X = H

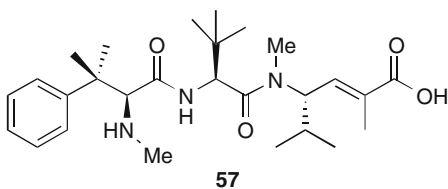
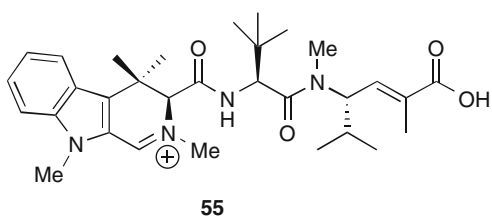
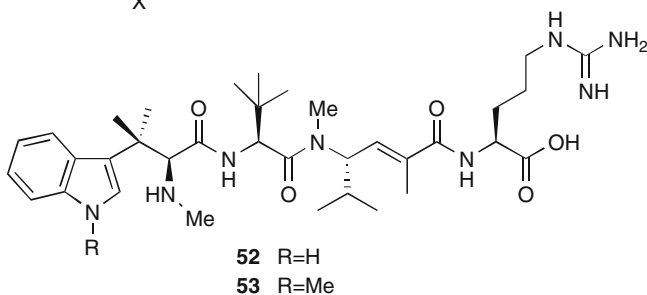
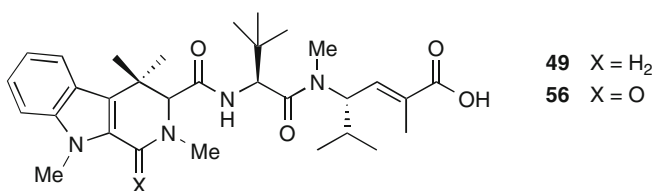
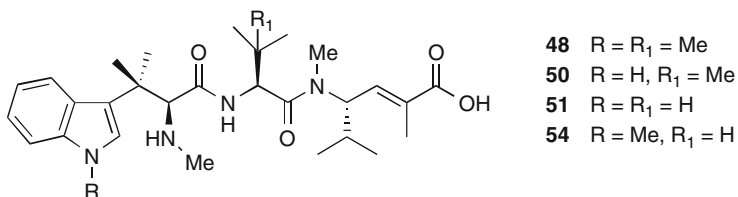
Kitagawa and coworkers reported in 1994 the isolation of the cyclic depsipeptide arenastatin A (**42**) from specimens of the sponge *Dysidea arenaria* collected in Okinawa [81]. Arenastatin A was cytotoxic to KB cells in vitro with an IC₅₀ of 5 pg/mL. The absolute configuration of arenastatin A (**42**) was determined by Kitagawa's group using NMR analysis and the chiral synthesis of a methanolysis degradation product [82]. Also in 1994, Moore's group reported the isolation of cryptophycins A (**43**) to D (**46**) from laboratory cultures of the freshwater cyanobacterium *Nostoc* sp. (GVS 224) [83]. Crude extracts from the *Nostoc* cultures had attracted Moore's attention because they showed significant tumor-selective cytotoxicity in the Corbett assay.

Total synthesis confirmed the assigned structures of **43** to **46** and led to a revision in the assignment of the configuration of the α -amino acid residues to D [84]. Both the Kitagawa and Moore groups noted that scientists at Merck had previously isolated an antifungal depsipeptide they named cryptophycin from extracts of a cultured *Nostoc* sp. [85]. The Merck group had not determined any of the relative or absolute configurations for their compound, which turned out to be identical to Moore's cryptophycin A (**43**). Moore's group went on to isolate a large number of additional cryptophycins from *Nostoc* sp. cultures, including cryptophycin 24 that turned out to be identical to Kitagawa's arenastatin (**42**) [86, 87]. The isolation of arenastatin (**42**) from a cyanobacterium culture confirmed the speculation that the material isolated from the Okinawan sponge *D. arenaria* was in fact a microbial natural product.

Cryptophycin A (**43**) inhibits tubulin polymerization in vitro, disassembles preformed microtubules, inhibits nucleotide exchange, causes tubulin to aggregate into small ring-shaped oligomers, and noncompetitively inhibits the binding of vinblastine but not colchicine to tubulin by binding to the Vinca domain [88, 89]. Cryptophycin A is 100 to 1,000 times more potent than vinblastine or paclitaxel as an antiproliferative agent. It is a powerful disrupter of microtubule dynamics, with

its major effects being to decrease the shortening rate and length of depolymerization during a shortening event and enhancing the number of rescue events [90]. It also inhibits the growth rate and length grown but less effectively than the shortening rate. Cryptophycin-52 (**47**), a synthetic analog of cryptophycin A (**43**), has been evaluated in phase I clinical trials [91, 92].

20.3.2.3 Hemiasterlins, Criamides, and Milnamides



Hemiasterlin (**48**) was first isolated by Kashman's group in 1994 from the sponge *Hemiasterella minor* (Kirkpatrick) collected in Sodwana Bay, South Africa [93]. At virtually the same time, Crews and coworkers reported the isolation of milnamide A (**49**) from the sponge *Auletta cf. constricta* collected in Milne Bay, Papua New Guinea [94]. Hemiasterlin (**48**) is a tripeptide comprised of the rare amino acid *tert*-leucine and the two novel amino acids 4-amino-2,5-dimethylhex-2-enoic acid and *N,N'*, β,β -tetramethyltryptophan. Milnamide A (**49**) has a β -carboline, formally derived from *N,N'*, β,β -tetramethyltryptophan via a Pictet-Spengler condensation with formaldehyde, in place of the *N,N'*, β,β -tetramethyltryptophan residue in hemiasterlin (**48**). The 4-amino-2,5-dimethylhex-2-enoic acid residue in **48** and **49** appears to have a biogenetic origin involving *N*-methylvaline and propionic acid building blocks. There were no relative or absolute configurations assigned to the amino acids in hemiasterlin (**48**) or milnamide A (**49**) in the original reports of their structures.

Andersen's group reported the isolation of hemiasterlin (**48**), hemiasterlins A (**50**) and B (**51**), and criamides A (**52**) and B (**53**) from the sponge *Cymbastela* sp. collected on reefs off of Madang, Papua New Guinea [95]. All three amino acids in hemiasterlin and the arginine residue in the criamides were shown to have the *L* configuration by a combination of Marfey's analysis on the natural product and single crystal X-ray diffraction analysis of hemiasterlin methyl ester [96]. Andersen et al. reported the first total synthesis of hemiasterlin (**48**), and they showed that the synthetic material had bioactivity identical to the natural samples [97].

Boyd and coworkers reported finding hemiasterlins in two sponges also collected in Papua New Guinea. An *Auletta* sp. yielded the known compounds hemiasterlin (**48**) and hemiasterlin A (**50**), along with the new tripeptide hemiasterlin C (**54**) [98]. Two *Siphonochalina* spp. were also found to contain the same hemiasterlin tripeptides **48**, **50**, and **54**. Ireland's group reported isolating hemiasterlin (**48**), milnamide A (**49**), and the new compound milnamide D (**55**) from specimens of *Cymbastela* sp. collected in Milne Bay, Papua New Guinea [99], and Crews' reinvestigation of *Auletta* sp. yielded milnamide C (**56**) [100]. An enantioselective total synthesis of milnamide A (**49**) and the observation that it undergoes facile autoxidation to milnamide D (**55**) confirmed that the absolute configurations of the milnamides were the same as the hemiasterlins and suggested that milnamide D (**55**) may have a nonbiogenic origin [101].

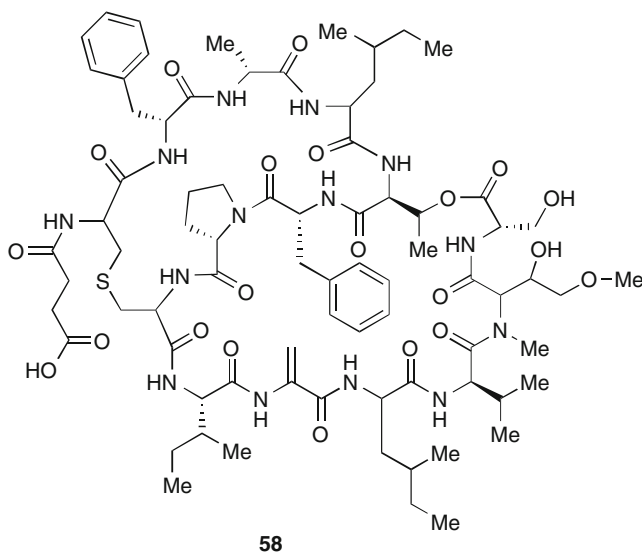
Kashman reported that hemiasterlin (**48**) showed *in vitro* cytotoxicity against murine leukemia P388 cells at a concentration of ≈ 19 nM [93]. Andersen and coworkers reported an IC_{50} of 87 pM versus P388 for hemiasterlin (**48**), over two orders of magnitude lower than Kashman's value [95], and potent activity was also observed against a small panel of human cancer cell lines. The milnamides are also cytotoxic but much less potent than the hemiasterlins [94, 98]. Roberge and coworkers examined the effects of hemiasterlins on cell cycle progression in human mammary carcinoma MCF-7 cells and found that hemiasterlins block cells in mitosis at the same concentrations that showed cytotoxicity [102]. Microscopic examination showed that hemiasterlins arrested cells at a metaphase-like

stage with effects on the morphology of the mitotic spindle that were similar to those caused by tubulin-targeting agents such as vinblastine. High concentrations of hemiasterlin caused complete microtubule depolymerization, and at low concentrations, cells displayed bipolar spindles with long astral microtubules or multiple asters. Chromosomes failed to align at metaphase and were unable to proceed through later stages of mitosis because of activation of the spindle checkpoint. Roberge concluded that hemiasterlins exert their cytotoxic effects by inhibiting spindle microtubule dynamics at mitosis.

Detailed studies of the interactions of hemiasterlin (**48**) with tubulin showed that it inhibited tubulin polymerization *in vitro* ($IC_{50} = 1 \mu M$), noncompetitively inhibits the binding of vinblastine, competitively inhibits the binding of dolastatin 10, inhibits nucleotide exchange on β -tubulin, and induces the formation of tubulin aggregates with a ring-like structure [103, 104]. Overall, these effects resembled, but were not identical to, those of dolastatin and cryptophycin A, which bind to the same site on tubulin.

Neiman et al. synthesized a small library of hemiasterlin analogs, including the phenylalanine analog HTI-286 (**57**) that has been evaluated in phase I and phase II clinical trials [105–108]. The tubulin-binding properties of HTI-286 [109] have been probed with STD-NMR [110], photoaffinity probes [111], and synthesis of numerous analogs [112, 113]. HTI-286 has also been shown to have promising activity in mouse models of prostate and bladder cancer [114, 115].

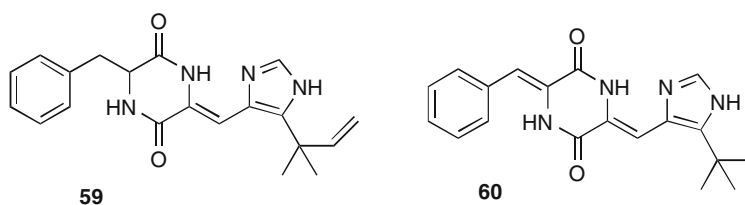
20.3.2.4 Vitilevuamide



In 1999, Ireland and coworkers reported the isolation of vitilevuamide (**58**) from the ascidian *Didemnum cuculiferum* collected in the Beqa lagoon in Fiji [116, 117].

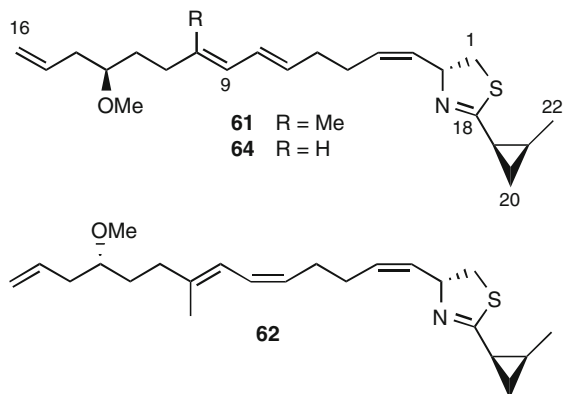
Vitilevuamide was also isolated from another acidian *Polysyncranton lithostrotum*, indicating that it may be produced by microbial symbionts. The structure of this bicyclic 13-membered peptide was determined by NMR and mass spectral analysis and shown to contain the unusual amino acids lanthionine, a monosulfide analog of cystine, and *N*-methyl methoxinine. In vitro studies showed that vitilevuamide (**58**) was an inhibitor of tubulin polymerization at 2 μM , noncompetitively inhibited vinblastine binding, stabilized colchicine binding, and only affected dolastatin 10 binding at high concentrations, indicating that it likely has a unique binding site. Further in vivo studies determined that vitilevuamide (**58**) had an ILS of 70% at 30 $\mu\text{g}/\text{kg}$ against P388 murine leukemia.

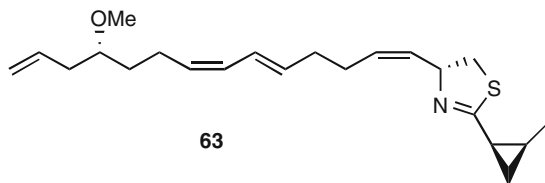
20.3.2.5 Halimide



In 2000, Fenical and coworkers reported the discovery of halimide (**59**) in a patent [118, 119]. The *S*-isomer of this prenylated cyclic dipeptide was isolated from an unidentified fungal strain collected from the surface of an alga in the genus *Halimeda*. Halimide is a tubulin-depolymerizing agent that binds to the colchicine-binding site on tubulin [119]. It showed no cross-resistance to multidrug-resistant cancer cell lines expressing a P-glycoprotein drug efflux pump and caused tumor regression in an in vivo model of Taxol-resistant breast cancer. SAR studies at Nereus Pharmaceuticals have resulted in the discovery of an analog (NPI-2358: Plinabulin) **60** that is currently in phase II clinical trials [119].

20.3.2.6 Curacins

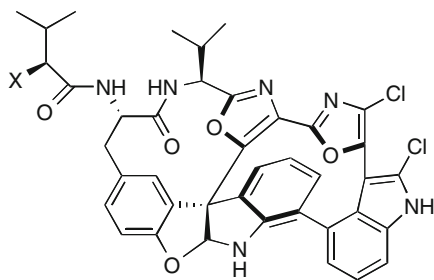




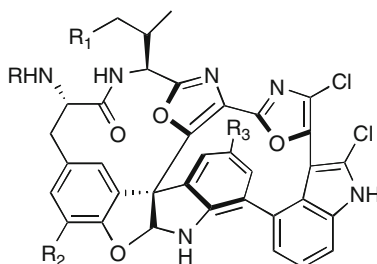
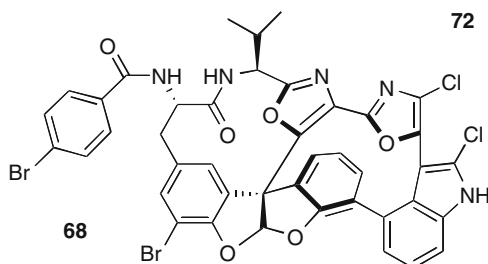
Curacin A (**61**) was isolated by Gerwick's group in 1994 from extracts of a field sample of the blue-green alga *Lyngbya majuscula* collected in Curaçao that showed potent brine shrimp toxicity and antiproliferative activity [120]. Further examination of the initial Curaçao collection of *L. majuscula* subsequently led to the isolation of the minor analogs curacins B (**62**) and C (**63**) [121], while a Virgin Islands collection yielded curacin D (**64**) [122]. The absolute configuration of curacin A (**61**) was established by comparison of degradation products obtained from the natural product with the same compounds prepared enantiospecifically via synthesis [123] and was confirmed by White's asymmetric total synthesis [124]. Stable-isotope feeding studies showed that the atoms in curacin A (**61**) come from one cysteine (S, N, and C-1 to C-3), ten acetate units (C-4 to C-16 and C-18 to C-22), and two units of S-adenosylmethionine (C-17 and OMe) [125]. Analysis of the biosynthetic genes showed that the metabolic pathway is comprised of a nonribosomal peptide synthase (NRPS) and multiple polyketide synthases (PKSs). Further studies of the curacin A (**61**) biosynthetic pathway have revealed that cryptic chlorination and sulfonation steps are involved in the formation of the cyclopropyl ring and the terminal alkene functionalities, respectively [126, 127].

Evaluation of curacin A (**61**) in the NCI cell line panel and analysis of its differential cytotoxicity pattern using the COMPARE algorithm provided the first indication that the compound was a tubulin-binding agent [120]. Curacin A inhibited the polymerization of purified tubulin in vitro with an IC_{50} of 0.7 μ M, and it was found to strongly inhibit the binding of colchicine but not vinblastine to tubulin. More detailed studies showed that curacin A was a competitive inhibitor of colchicine binding and that its binding rate to tubulin is rapid and its dissociation rate from tubulin is extremely slow due to its extremely large association constant [128, 129]. It is a potent in vitro cytotoxin that inhibits the growth of cancer cells at low nM concentrations. Curacin A has conjugated diene and a thiazoline substructure that makes it sensitive to acid, base, and air oxidation, and it is extremely lipophilic. These instability and unfavorable solubility properties have prevented the preclinical evaluation and development of the natural product. Nevertheless, the promising biological activity of the curacins coupled with their novel structures have stimulated extensive synthetic efforts toward making analogs that might have more promising drug-like properties [130].

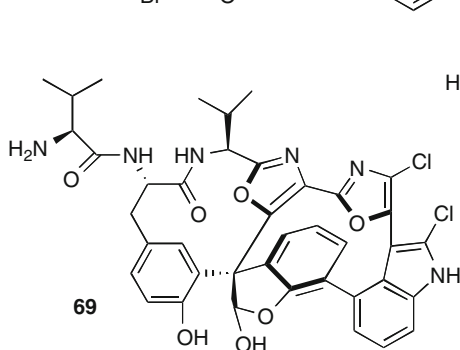
20.3.2.7 Diazonamides



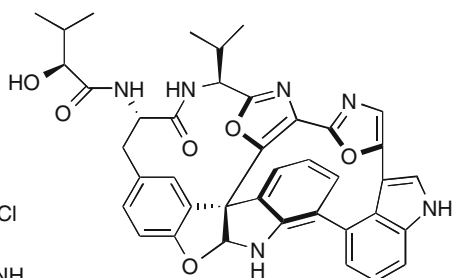
65 X = OH

70 X = NH₂66 R = R₁ = R₃ = H, R₂ = Br67 R₁ = R₃ = H, R₂ = Br, R = *p*-bromobenzoyl71 R₁ = CH₃, R = R₂ = H, R₃ = Cl72 R₁ = CH₃, R = R₂ = R₃ = H

68



69



73

The potentially cytotoxic cyclic peptides diazonamides A (**65**) and B (**66**) (diazonamide A: IC₅₀ < 15 ng/mL vs. HCT-116 human colon carcinoma cell line) were isolated in 1991 by Fenical, Clardy, and coworkers from extracts of the colonial ascidian *Diazona chinensis* collected on the ceiling of a small cave along the coast of Siquijor Island in the Philippines [131]. The *p*-bromobenzoyl derivative of diazonamide B was initially assigned as structure **68** via analysis of single-crystal X-ray diffraction and mass spectrometry data. Working from structure **68** for diazonamide B and the NMR data for the closely related metabolite diazonamide A led to the assignment of structure **69** to diazonamide A. It was assumed that a hemiketal in natural diazonamide B, that was assigned to the same position in structure **69** proposed for diazonamide A, had been converted to the

ketal observed in the X-ray analysis of *p*-bromobenzoyl derivative of diazonamide B during preparation of the *p*-bromobenzoyl ester.

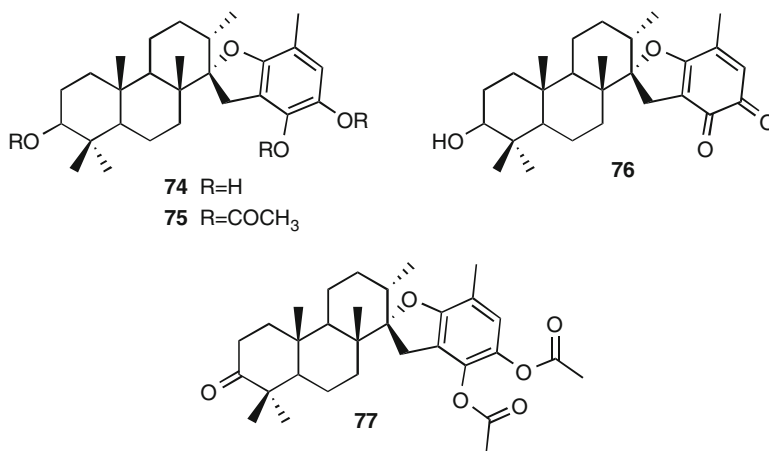
The extremely novel chemical structures of the diazonamides and their potent cytotoxic activity immediately captured the imagination of the synthetic chemistry community. Harran and coworkers completed a total synthesis of the structures **68** and **69** proposed for the *p*-bromobenzoyl derivative of diazonamide B and diazonamide A, respectively, and showed that neither of them corresponded to the natural materials [132]. They proposed the alternate structures **65** for diazonamide A and **67** for the *p*-bromobenzoyl derivative of diazonamide B [133], and these were confirmed by Nicolaou's total synthesis of the revised structure of diazonamide A [134].

A subsequent investigation of a *Diazonia* sp. collected in Indonesia yielded the additional diazonamides C (**70**), D (**71**), and E (**72**), which all displayed modest cytotoxicity [135].

Hamel and coworkers reported that diazonamide A (**65**) is a potent inhibitor of *in vitro* tubulin polymerization, strongly inhibits tubulin-dependent GTP hydrolysis, has little effect on nucleotide exchange from tubulin, shows no inhibition of the binding of radiolabeled vinblastine or dolastatin 10 to tubulin, and does not induce formation of stable tubulin aggregates [136]. This combination of properties suggested a unique mode of binding to tubulin. However, subsequent preclinical assessment of the diazonamide analog AB-5 (**73**) found that it does not bind directly to tubulin but instead induces mitotic arrest by interacting with a specifically proteolyzed form of ornithine δ -amino transferase involved in spindle formation [137]. AB-5 showed very promising *in vivo* activity against human tumor xenografts in mice with an absence of overt toxicity.

20.3.3 Meroterpenoids

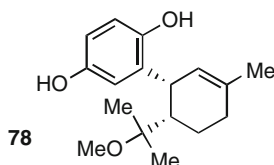
20.3.3.1 Stypodiolis



In 1979, Fenical, Clardy, and coworkers reported the discovery of stypotriol (**74**), stypotriacetate (**75**), and stypoldione (**76**) from the marine brown algae

Styopodium zonale and reported their toxic and anti-fish feeding activities [138]. Further biological investigations by Jacobs, Wilson, and coworkers in the 1980s revealed that these compounds showed micromolar microtubule-disruptive activities, inhibited cytokinesis, and arrested cells in the G2 stage of development [139, 140]. In 1998, Maccioni et al. reported the isolation of 14-keto-stypodiol diacetate (77) from the algae *Styopodium flabelliforme* collected off the coast of Easter Island, which they determined to have similar activity against microtubules [141].

20.3.3.2 Methoxyconidiol

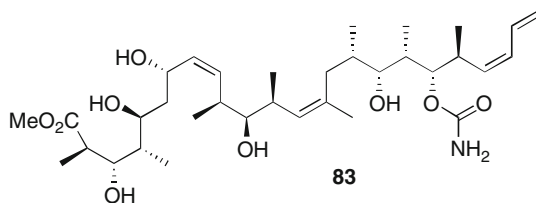
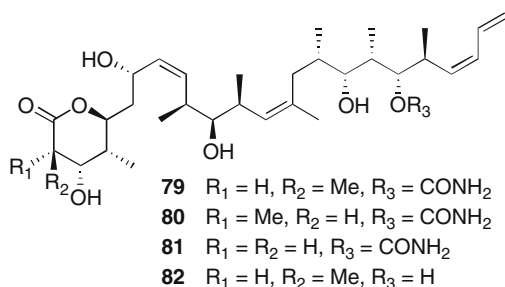


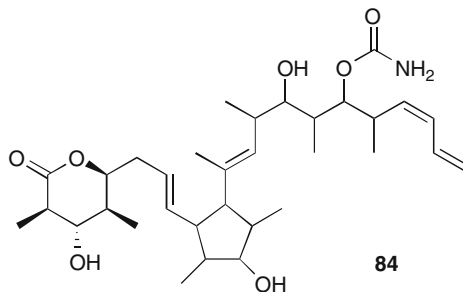
Methoxyconidiol (**78**) was isolated by Banaigs and coworkers in 2005 from the ascidian *Aplidium aff. densum* collected off the coast of Masirah Island, Oman [142]. Initial biological investigations showed that it was moderately active against microbial proliferation and inactive at millimolar concentrations against mammalian tumor cell lines. Further investigation in sea urchin embryos revealed that methoxyconidiol arrests cells in M phase, completely blocks cytokinesis, and disrupts the establishment of the mitotic spindle at 10 μM while having no effect on DNA replication [143].

20.4 Microtubule-Stabilizing Agents

20.4.1 Polyketides

20.4.1.1 Discodermolides



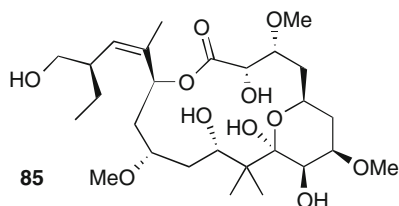


The polyketide lactone discodermolide (**79**) was isolated in 1990 by Gunasekera et al. from extracts of the sponge *Discodermia dissoluta* collected at Lucay on Grand Bahama Island [144]. X-ray diffraction analysis of a crystal of **79** confirmed the constitution assigned from the NMR data and established the relative configuration. Schreiber's group synthesized both (+) and (–) optical antipodes of **79**, which showed that the natural product was the (+) enantiomer [145, 146]. A dozen years after their first report, Gunasekera et al. reported the isolation of 2-*epi*-discodermolide (**80**), 2-*des*-methyldiscodermolide (**81**), 19-*des*-aminocarbonyldiscodermolide (**82**), 5-hydroxymethyldiscodermolate (**83**), and 9(13)-cyclodiscodermolide (**84**) from samples of sponges in the genus *Discodermia* collected in waters around the Bahamian archipelago [147].

Gunasekera et al. reported that discodermolide inhibited the *in vitro* proliferation of P388 murine leukemia cells with an IC_{50} of 0.5 $\mu\text{g/mL}$, inhibited the growth of *Candida albicans*, and suppressed the two-way mixed-lymphocyte response of both murine splenocytes and human peripheral blood lymphocytes at 0.5 and 5 $\mu\text{g/mL}$, respectively, with greater than 85% viability of the splenocyte cells [148]. ter Harr et al. showed that discodermolide was an antimetabolic agent that stabilizes microtubules in cells and in biochemical systems more potently than taxol and binds competitively to the taxoid site on β -tubulin [149, 150]. Kowalski et al. showed that discodermolide was not a substrate for the P-glycoprotein efflux pump and was potently cytotoxic toward paclitaxel-resistant cancer cell lines [151]. At the time of its discovery, discodermolide (**79**) joined taxol and the epothilones as only the third class of compounds, and the first marine natural product, known to stabilize microtubules. The analogs **80** to **83** showed *in vitro* cytotoxicity comparable to discodermolide, but the analog **84** having an additional ring was almost completely inactive [147].

The novel structure of discodermolide (**79**) combined with its ability to stabilize microtubules and inhibit the growth of paclitaxel-resistant cancer cell lines made it an extremely attractive candidate for clinical development. As with all drug candidates isolated from marine invertebrates, a limiting factor in the clinical evaluation of discodermolide was the availability of material. A landmark 36-step synthesis carried out by scientists at Novartis in collaboration with Paterson's group at Cambridge University generated 60 g of (+)-discodermolide, which enabled early phase clinical trials [150, 151]. Unfortunately, the trials had to be stopped when indications of toxicity surfaced [152, 153].

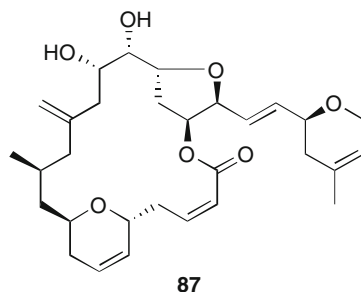
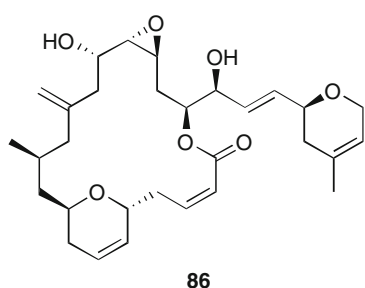
20.4.1.2 Peloruside A

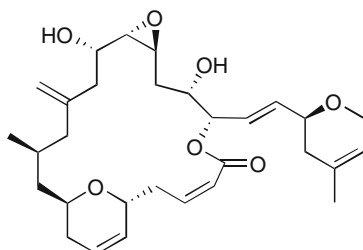


Peloruside A (**85**), a cytotoxic 16-membered macrolide, was isolated by Northcote's group in 2000 from extracts of the sponge *Mycale hentscheli* collected in Pelorus Sound on the north coast of the South Island, New Zealand [154]. The same sponge extract also yielded the previously known cytotoxins mycalamide A and pateamine. Detailed analysis of the NMR data obtained for peloruside A (**85**) led to the elucidation of the molecule's constitution and complete relative configuration. The absolute configuration was established by De Brabander's report of the total synthesis of (–)-peloruside A, which turned out to be the enantiomer of the natural product **85** [155].

Northcote et al. reported that peloruside A (**85**) was cytotoxic to murine leukemia P388 cells at 10 ng/mL [154]. A more detailed investigation showed that peloruside A (**85**) caused cancer cells to arrest in the G₂-M phase of the cell cycle and, like paclitaxel, induced tubulin to form long straight microtubules at 37°C [156]. The microtubules formed in the presence of peloruside A were stable at 0°C and in the presence of 5 mM CaCl₂. Subsequent studies found that peloruside A is not a good substrate for the P-glycoprotein efflux pump, was active against drug-resistant cell lines with point mutations in the paclitaxel binding site on β-tubulin, and was not able to displace the fluorescent paclitaxel derivative Flutax-2 from tubulin [157]. These data suggested that peloruside A (**85**) binds at a site that is different from the paclitaxel binding site. Positive synergistic effects on tubulin polymerization and *in vitro* cytotoxicity have been observed with peloruside A (**85**) and other microtubule-stabilizing agents that bind to the taxoid site [158, 159]. Aquaculture [160] and total synthesis [161] approaches are both being explored as avenues for the large-scale production of peloruside A (**85**) needed to support further preclinical evaluation of this interesting anticancer drug candidate.

20.4.1.3 Laulimalides (Fijianolides)



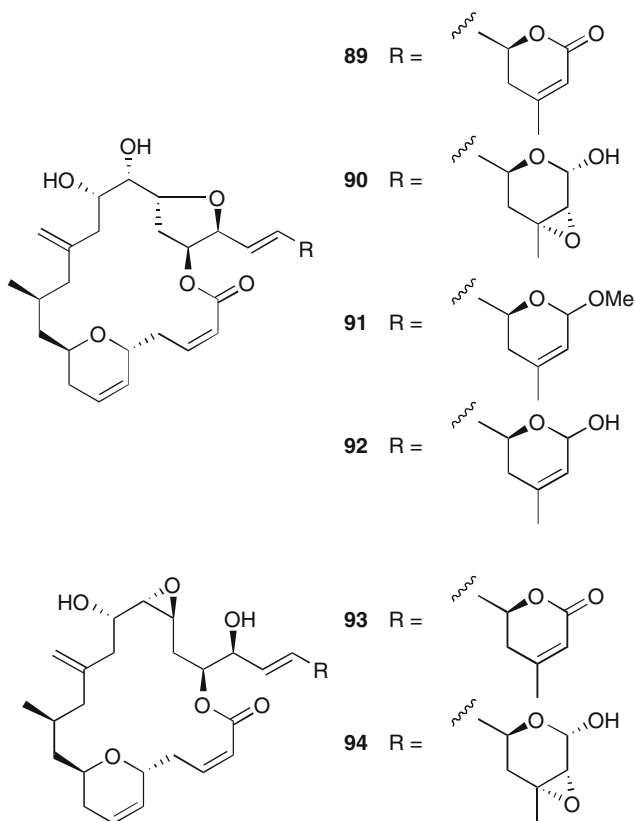


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Crews' group at UCSC [162] and the Scheuer, Moore, and Paul groups jointly at Hawaii and Guam [163] reported the structures of the cytotoxic polyketide macrolides laulimalide (fijianolide B) (**86**) and isolaulimalide (fijianolide A) (**87**) in back-to-back papers published in 1988. The simultaneous reports from the two groups resulted in two initial sets of names for **86** and **87**, but most subsequent references to these macrolides have used the laulimalide designation, perhaps due to the slightly earlier submission date of the manuscript originating from the Hawaiian/Guam groups. Crews' group isolated **86** and **87** from specimens of the sponge *Spongia mycofijiensis*, and a nudibranch *Chromodoris lochi* found attached to the sponge, collected in Vanuatu. The Scheuer, Moore, and Paul groups isolated **86** and **87** from the Indonesian sponge *Hyatella* sp. and specimens of the nudibranch *C. lochi* grazing on the sponge. It was subsequently proposed that Crews' specimen of *S. mycofijiensis* should be reclassified as *Cacospongia mycofijiensis* [164]. Scheuer, Moore, and Paul named the compounds laulimalides after the Hawaiian term "laulima" used to describe "people working together" since the three groups cooperated in their discovery. The initial reports of **86** and **87** described constitutions and relative configurations for the laulimalides that were based on analysis of NMR data. A re-isolation of laulimalide (**86**) from the sponge *Fasciospongia rimosa* collected in Okinawa generated crystals that confirmed the structural features assigned from NMR data and facilitated an assignment of the absolute configuration via single-crystal X-ray diffraction analysis [165]. The same sponge yielded neolaulimalide (**88**) [166].

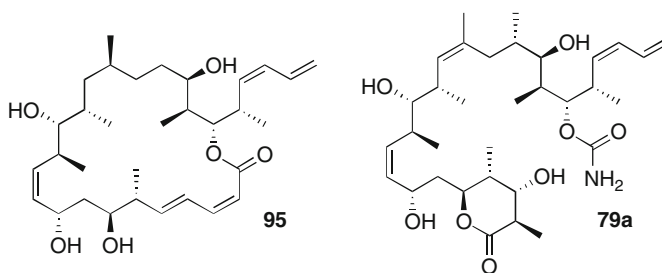
Crews reported modest cytotoxicities (IC_{50} s of 0.5–11 $\mu\text{g/mL}$) for **86** and **87** versus HT-29 human colon tumor cells and P388 murine leukemia [162], while the Hawaiian/Guam groups reported more potent cytotoxic activity (IC_{50} 15 ng/mL) for laulimalide (**86**) and isolaulimalide (**87**) ($IC_{50} > 200$ ng/mL) against the KB cell line [163]. Interest in the laulimalides intensified after Mooberry, Davidson, and coworkers reported that **86** and **87** were microtubule-stabilizing agents that stimulated tubulin polymerization in vitro more effectively than paclitaxel and were poor substrates for the P-glycoprotein efflux pump [167]. Further investigations showed that laulimalide binds to a site on the tubulin polymer that is distinct from the taxoid site [168]. Consistent with this finding, microtubules formed in the presence of both laulimalide and paclitaxel contained near-equimolar quantities, relative to tubulin, of both drugs, and laulimalide and paclitaxel synergistically enhanced tubulin

polymerization *in vitro* [169]. It has been suggested that laulimalide (**86**) and peloruside (**85**) bind to the same or overlapping site(s) on microtubules [158].



A reinvestigation of *C. mycofijiensis* by Crews' group resulted in the isolation of sufficient quantities of laulimalide (**86**) for preliminary *in vivo* evaluation and also identified six new analogs named fijanolides D (**89**) to I (**94**) [170]. Laulimalide (**86**) was shown by Crews and coworkers to significantly inhibit the growth of HCT-116 tumor xenografts in SCID mice. There have been several total syntheses of laulimalide (**86**) aimed at providing material for further biological evaluation [171, 172]. Notable among these efforts was the synthesis of gram quantities of laulimalide (**86**) by scientists at Eisai Research Institute [173]. In contrast with Crews' report, the Eisai group found that synthetic laulimalide (**86**) exhibited only minimal tumor growth inhibition *in vivo* that was accompanied by severe toxicity and mortality, leading them to the conclusion that the unfavorable efficacy to toxicity ratio *in vivo* made it a poor candidate for clinical development.

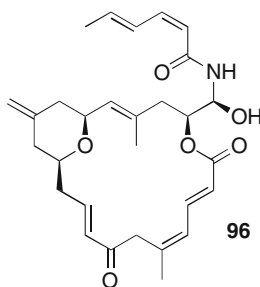
20.4.1.4 Dictyostatin-1



In 1994, Pettit and coworkers reported the isolation of the cytotoxic polyketide macrolide dictyostatin-1 (**95**) from extracts of an Indian Ocean marine sponge identified as a *Spongia* sp. (order: Dictyoceratida) that was collected in the Maldives [174]. The initial structure elucidation was based on analysis of the NMR data obtained from a very small sample (≈ 1.4 mg), and it only provided the constitution of the molecule and the configurations of the disubstituted alkenes. Even though no IC_{50} s were reported, dictyostatin-1 was described as being cytotoxic toward murine leukemia P388 cells in vitro. Almost a decade later, Wright's group isolated dictyostatin-1 from extracts of a sponge identified as a *Corallistidae* sp. that was collected by submersible at a depth of 442 m off the north coast of Jamaica in the Caribbean [175]. Paterson and Wright's groups determined the relative configuration of dictyostatin-1 (**95**) using J-based configurational analysis and molecular modeling [176]. The absolute configuration was established by Paterson's total synthesis of (–)-dictyostatin-1 [177].

Wright and coworkers found that dictyostatin-1 (**95**) induced the polymerization of tubulin in vitro to form microtubules that were stable at low temperatures and that it was highly potent as an in vitro cytotoxin against paclitaxel-resistant cancer cell lines expressing the P-glycoprotein efflux pump [175]. Further studies by Day and coworkers showed that dictyostatin-1 (**95**) strongly inhibited the binding of discodermolide (**79**) to microtubules and that both compounds had equivalent activity as inhibitors of the binding of radiolabeled epothilone B and paclitaxel to microtubules [178]. They concluded that the macrocyclic template of dictyostatin-1 (**95**) was likely a model for the bioactive conformation of discodermolide binding (**79a** above) to the taxoid site, as proposed by Paterson et al. [176].

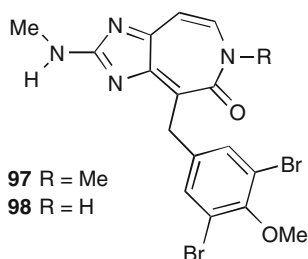
20.4.1.5 Zampanolide



Tanaka and Higa isolated the cytotoxic macrolide (–)-zampanolide (**96**) from extracts of the sponge *Fasciospongia rimosa* collected at Cape Zampa, Okinawa in 1996 [179]. Specimens of the same sponge collected at Shimoji Island, Okinawa, had previously yielded laulimalide (**86**) and neolaulimalide (**88**) [166]. The absolute configuration of (–)-zampanolide (**96**) was established by Smith et al.'s total synthesis of the enantiomer (+)-zampanolide [180]. Northcote, Miller, and coworkers re-isolated zampanolide (**96**) from a Tongan collection of *C. mycofijiensis* and showed that it is a microtubule-stabilizing agent with potent in vitro cytotoxicity ($IC_{50} \approx 7$ nM) against paclitaxel-resistant human ovarian cancer cells A2780 overexpressing the P-glycoprotein efflux pump [181].

20.4.2 Alkaloids

20.4.2.1 Ceratamines

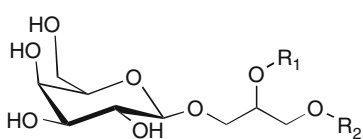


In 2003, the Roberge and Andersen groups reported the isolation of the novel heterocyclic alkaloids ceratamines A (**97**) and B (**98**) from extracts of the marine sponge *Pseudoceratina* sp. collected in Papua New Guinea that showed promising activity in Roberge's cell-based assay for antimetabolic agents [12, 182]. At the time of discovery, the imidazo[4,5-*d*]azepine core heterocycle in the ceratamines had no precedent at any oxidation state among known natural products. Nodwell's synthesis of desbromoceratamine analogs provided confirmation of the natural product structure and illustrated the importance of the bromine atoms for full biological activity [183, 184]. Coleman and coworkers reported the first synthetic route to ceratamines A (**97**) and B (**98**) that has the potential to produce sufficient quantities of the natural products for preclinical evaluation [185].

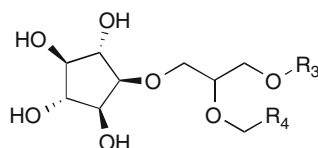
Roberge et al. showed that the ceratamines are microtubule-stabilizing agents that either do not bind to the paclitaxel site or bind with an affinity that is too low to displace radiolabeled paclitaxel from microtubules. The ceratamines generated an unusual mitotic arrest phenotype involving formation of pillar-like structures of tubulin that extended vertically from the basal surface of the cell-cycle-arrested cells [186].

20.4.3 Glycolipids

20.4.3.1



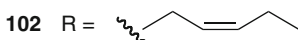
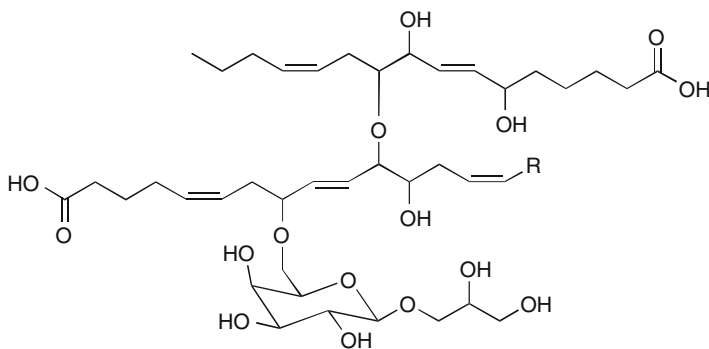
99 $R_1 = \text{fatty acyl}, R_2 = \text{fatty acyl}$



100 $R_3 = \text{fatty acyl}, R_4 = \text{alkyl}$

Namikoshi and coworkers reported in 2002 that mixtures of glycolipids of general structures **99** and **100** isolated from the Okinawan sponge *Pseudoceratina* sp. showed stimulation of microtubule assembly from purified tubulin in vitro at rather high concentrations [14]. There was no indication that glycolipids **99** or **100** were cytotoxic or could arrest cells at mitosis.

20.4.3.2 Nigricanosides



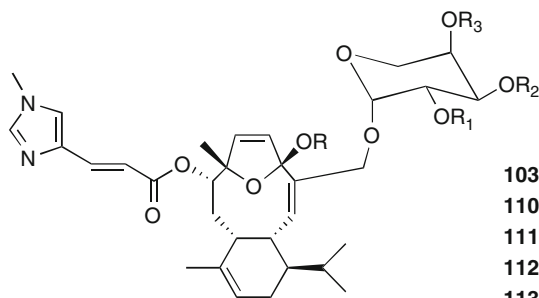
In 2007, the Andersen and Roberge groups reported the bioassay-guided isolation of the potentially cytotoxic glycolipids nigricanosides A (**101**) and B (**102**) from extracts of the green alga *Avrainvillea nigricans* collected in Dominica [187]. Crude extracts of *A. nigricans* attracted attention because they showed strong activity in Roberge's cell-based assay for antimitotic agents. However, the nigricanosides were present in the extract in trace quantities ($\approx 2 \times 10^{-6}\%$ wet wt.), and only repeated collections of the alga over an 8-year period produced sufficient material for structure elucidation. The methyl ester of nigricanoside A was found to stimulate the polymerization of pure tubulin in vitro at 10 μM ,

arrest human breast cancer MCF-7 cells in mitosis with an IC_{50} of 3 nM, and inhibit the proliferation of both MCF-7 and HCT-116 cancer cells with IC_{50} s of ≈ 3 nM.

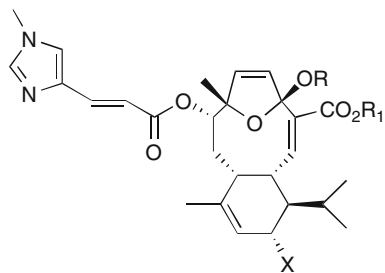
Although the nigricanosides contain the same structural components as the monogalactosyldiacylglycerols that are major membrane lipids in higher plants and blue-green algae, the oxidation of the fatty acids to oxylipins and the ether linkages connecting the oxylipins to each other and to the galactose residue in the nigricanosides are without precedent, making them the first examples of a new class of ether-linked glycolipids. The lack of information about the relative or absolute configurations of the stereogenic centers in the nigricanosides is a major impediment to the preparation of material for biological evaluation via total synthesis. MacMillan and coworkers have reported initial progress toward resolving the configurational details of the nigricanosides [188].

20.4.4 Terpenoid Glycosides

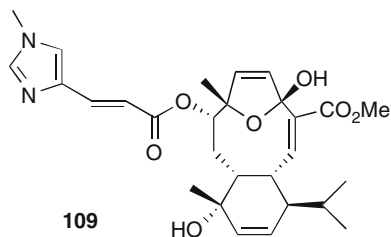
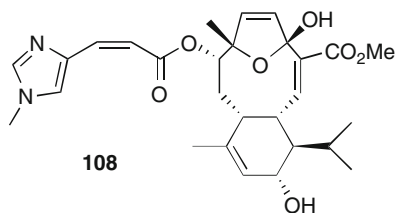
20.4.4.1 Eleuthosides/Sarcodictyins

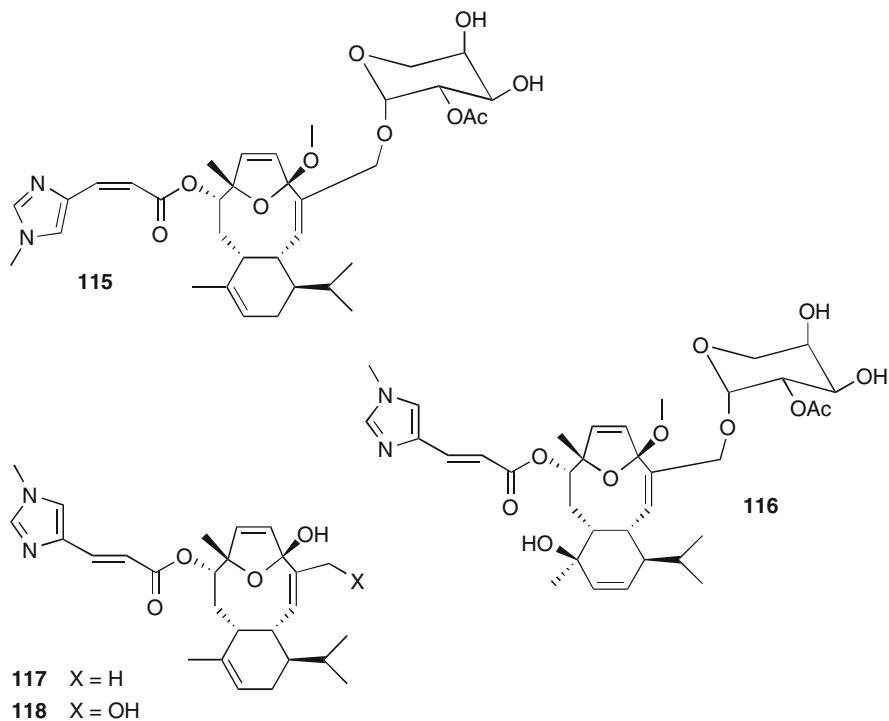


- 103** R = Me, $R_1 = \text{Ac}$, $R_2 = R_3 = \text{H}$
110 R = H, $R_1 = R_2 = \text{Ac}$, $R_3 = \text{H}$
111 R = H, $R_1 = R_3 = \text{Ac}$, $R_2 = \text{H}$
112 R = $R_2 = R_3 = \text{H}$, $R_1 = \text{Ac}$
113 R = Me, $R_1 = R_2 = R_3 = \text{H}$
114 R = Me, $R = R_2 = R_3 = \text{H}$, $R_2 = \text{Ac}$



- 104** R = X = H, $R_1 = \text{Me}$
105 R = X = H, $R_1 = \text{Et}$
106 R = H, X = OH, $R_1 = \text{Me}$
107 R = H, X = OAc, $R_1 = \text{Me}$





In 1997, Fenical's group reported the isolation of the potentially cytotoxic diterpene glycoside eleutherobin (**103**) ($IC_{50}s \approx 10\text{--}15$ nM against a panel of tumor tissue cell lines) from extracts of a rare soft coral identified as an *Eleutherobia* sp. that they had collected near Bennett's Shoal in Western Australia [189]. The same paper revealed that eleutherobin stabilized microtubules and was a competitive inhibitor of paclitaxel binding. Eleutherobin is related to the sarcodictyins A (**104**) to F (**109**) isolated by Pietra's group in 1987 [190] and 1988 [191] from the Mediterranean soft coral *Sarcodictyon roseum*, and to the eleuthosides A (**110**) and B (**111**) isolated by Kashman's group from the South African soft coral *Eleutherobia aurea* in 1996 [192].

The Andersen and Roberge groups reported in 2000 that they had discovered eleutherobin (**103**) in extracts of the abundant Caribbean octocoral *Erythropodium caribaeorum* using Roberge's cell-based antimetabolic assay as a screening tool [193]. Extracts of *E. caribaeorum* showed strong mitotic arrest in the assay, and microscopic examination of cells arrested in mitosis revealed evidence of tubulin bundling similar to the effects caused by paclitaxel. In addition to eleutherobin, the *E. caribaeorum* extract also yielded the new analogs **112** to **118**, which all showed antimetabolic activity in the cell-based assay [193, 194]. Cultured specimens of *E. caribaeorum*, several generations removed from the wild stock, continue to produce eleutherobin in roughly the same amounts as found in wild specimens, suggesting that mariculture could be a sustainable source of

the compound for drug use [195]. As part of the investigation of *E. caribaeorum*, it was shown that eleutherobin itself is an isolation artifact formed by reaction of the actual natural product desmethyleleutherobin (**112**) with methanol during the extraction and purification steps [194]. The fortuitous formation of a crystal of eleutherobin in an NMR sample dissolved in DMSO-*d*₆ led to the determination of its solid state and solution conformations via analysis of X-ray diffraction and solution NOE data [196].

Chemical transformations of natural eleutherobin revealed that the $\Delta^{2',3'}$ olefin in the *N*-methylurocanic ester moiety is essential for antimitotic activity [197]. Nicolaou's group reported the first total syntheses of sarcodictyin A (**104**) [198], eleutherobin (**103**) [199], and analogs for SAR [200], and Danishefsky's group reported the second total synthesis of eleutherobin a year later [201]. Ojima and Danishefsky incorporated the eleuthosides into one of the first proposals for a common pharmacophore for microtubule-stabilizing natural products [202].

Fenical, Fairchild, and coworkers [203] as well as Hamel's group at NIH [204] reported detailed evaluations of the cytotoxicity and tubulin interactions of eleutherobin (**103**) and sarcodictyins A (**104**) and B (**105**). These studies confirmed that eleutherobin is a potent in vitro cytotoxin against cancer cell lines, is a microtubule-stabilizing agent capable of inducing tubulin polymerization to form microtubules that are resistant to cold or Ca-ion-induced depolymerization, may be a substrate for the P-glycoprotein efflux pump, and binds to the taxoid site on tubulin.

20.5 Summary

This chapter illustrates the large number and variety of microtubule-targeting natural product chemotypes that have been discovered from marine organisms. Marine sponges account for roughly half of the new chemotypes, with the remainder coming from ascidians, soft corals, mollusks, macroalgae, blue-green algae, bacteria, and fungi. The histories of laulimalide, dictyostatin-1, and zampanolide show that there is frequently a significant period of time, often a decade or more, between the discovery of potent new cytotoxins and the recognition that they target microtubules. Therefore, it is likely that more microtubule-targeting agents remain to be identified among already known marine natural product cytotoxins.

It seems reasonable to ask why microtubules should be one of the favored biological targets of marine natural products. The answer may simply be that antimitotic agents are potent toxins making them highly effective chemical defenses for algae and sessile or slow-moving invertebrates. The amino acid sequence of tubulin is highly conserved in eukaryotes [205], enabling antimitotic agents to show broad-spectrum activity against varied eukaryotic organisms, a desirable trait for a chemical deterrent.

Some challenges for the simple view that antimitotic marine natural products are defensive agents include the fact that many of the compounds show significant

geographic variation in occurrence and are present in the source organisms in extremely low concentrations, perhaps too low to be effective deterrents, and the increasing circumstantial evidence suggesting that many natural products isolated from marine invertebrates are produced by symbiotic or dietary prokaryotes. It is possible that prokaryotes associated with invertebrates make antimetabolic agents specifically for their own benefit, perhaps to help establish or maintain their populations when they are free living or within the host, and that the compounds offer no particular advantage to the invertebrate source organisms.

Alternatively, establishing a complex symbiotic relationship for chemical deterrent production may offer some advantages to invertebrates. Bacterial cells do not use microtubules for chromosome segregation. Instead, they rely on a mechanism involving attachment of their duplicated chromosome to the plasma membrane. With the apparent exception of a single phylum (verrucomicrobia), bacteria do not have tubulin genes or microtubules [206]. The absence of the tubulin target in bacteria makes it easier for them to produce antimetabolic agents that specifically affect eukaryotes without affecting the producing prokaryote.

Unfortunately, although a great deal is known about the effects of antimetabolic marine natural products on cancer cells, almost nothing is known about their toxic or feeding deterrent effects on potential predators or competitors of the source organisms, or whether or not the source organisms are resistant to the antimetabolic agents extracted from their tissues. Future work on antimetabolic marine natural products would ideally extend beyond their medicinal potential to also address the important issues of what are the actual producing organisms, microbes, or invertebrates, and what are the ecological roles, if any, of these potent cytotoxins.

The wide acceptance of microtubules as a highly validated anticancer drug target has meant that almost all of the marine natural products that target microtubules have attracted significant interest as drug leads. This interest has resulted in the development of synthetic methodology suitable for the gram scale production of several of the antimetabolic natural products or simpler pharmacophore analogs required to support their preclinical development and ultimately clinical trials. To date, 11 microtubule-targeting marine natural products or synthetic analogs have been evaluated in phase I/phase II clinical trials. With the exception of discodermolide, all of the compounds that have been taken into clinical trials are depolymerizing agents. The evaluation of microtubule-stabilizing marine natural products has generally lagged behind, and most of these have not even been evaluated in animal models yet due to the limited supply of compound that has been available. None of the antimetabolic marine natural product clinical trial candidates have progressed beyond phase II trials, and many have been pulled from further trials due to toxicity or lack of sufficient efficacy. Therefore, even though widespread scientific interest in this class of marine natural products as drug leads remains, there are still no new drugs inspired by these lead compounds on the short-term horizon. This may change as more drug candidates based on microtubule-stabilizing marine natural products progress to clinical trials in the coming years.

20.6 Study Questions

1. Given that there are many extremely potent microtubule-targeting antimitotic natural product drug leads already known and in clinical development, is there any compelling need to identify new microtubule-targeting natural product chemotypes for anticancer drug development, or have we already gone as far as we can in terms of modulating microtubule dynamics with small molecules? Explain your answer in detail.
2. What attributes would one look for in new antimitotic drug candidates that would distinguish them from paclitaxel, the Vinca alkaloids, and the other marine natural products described in this review? How would you screen crude extracts and pure compounds for these properties?
3. Identify an unexplored environmental niche and group of source organisms that might be a rich source of new antimitotic marine natural products. Briefly rationalize your choice and explain how you would explore this niche for new natural product chemistry.
4. Which of the antimitotic marine natural products described in this review that have been isolated from extracts of marine macroorganisms such as algae, sponges, soft corals, or ascidians might actually be produced by associated microorganisms? Provide a rationale for each compound that you have identified as having a putative microbial source. Suggest some experiments that could be used to test the possibility of a microbial origin for the compounds.
5. Propose a biogenesis for spongistatin 1 (**19**).
6. Propose a biogenesis for diazonamide (**65**).
7. Propose a biogenesis for ceratamine A (**97**).
8. Propose biochemical mechanisms for (1) the addition of the oxygen atoms to the fatty acid chains, (2) the formation of the ether linkage between the two fatty acid chains, and (3) the formation of the ether linkage between the fatty acid and the galactose residues in nigricanoside A (**101**).

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Abstract

Protozoa are the causative agents of human diseases which affect more than one billion people and cause more than one million deaths per year, with a particular incidence in developing countries. The major contribution to these dramatic numbers is given by malaria, followed by leishmaniasis and trypanosomiasis (African trypanosomiasis and Chagas' disease).

E. Fattorusso (✉) • O. Tagliatela-Scafati (✉)
Dipartimento di Chimica delle Sostanze Naturali, Università di Napoli Federico II,
Via Montesano 49, Naples, Italy
e-mail: fattoru@unina.it, scatagli@unina.it

In this chapter we have provided an overview of the most significant contributions given by marine natural product chemistry to the field of antiprotozoan drug research. We have selected more than 70 marine secondary metabolites belonging to different chemical classes, which are active (commonly only *in vitro* data are available) against one or more protozoan strains. When available, details on structure–activity relationship studies and investigation of the mechanisms of action have been provided.

21.1 Introduction

Protozoa is a large family (including over 30,000 different genera) of microorganisms classified as unicellular eukaryotes. Protozoa were previously grouped in the kingdom of Protista, together with the plant-like algae and fungus-like slime molds, and frequently protozoa are referred to be the link between plants and animals. Protozoa usually range from 10 to 50 micron, but they can grow up to 1 mm and can be easily identified using a microscope. Protozoa have traditionally been divided on the basis of their means of locomotion into flagellates, amoeboids, sporozoans, and ciliates.

Protozoa exist throughout aqueous environments and soil, and they prey upon unicellular or filamentous algae, bacteria, and microfungi, and, therefore, they are believed to play a vital role in controlling bacterial populations and biomasses. All protozoa digest their food in stomach-like compartments called vacuoles. As components of the micro- and meiofauna, protozoa are an important food source for microinvertebrates. Thus, the ecological role of protozoa in the transfer of bacterial and algal production to successive trophic levels is important. Some protozoa have life stages alternating between proliferative stages (e.g., trophozoites) and dormant cysts. As cysts, protozoa can survive harsh conditions, such as exposure to extreme temperatures and harmful chemicals, or long periods without access to nutrients. The cyst form enables parasitic species to survive outside of the host, and allows their transmission from one host to another. When protozoa are in the form of trophozoites, they actively feed and grow.

Single-celled protozoal parasites are the causative agents of diseases which affect more than one billion people per year with a particular incidence in tropical countries. The major contribution to these dramatic numbers is given by malaria, caused by protozoans belonging to the genus *Plasmodium*, with *P. falciparum* being responsible for most severe forms of the disease and most fatal cases. The improvement of hygienic conditions, the massive use of insecticides, and the discovery of different drugs played a great role in the nearly complete extinction of malaria in developed countries. Unfortunately, malaria is still a common cause of death (approximately one million per year) in the tropical countries of Africa, Asia, and America, and most of the victims are children under the age of five: every 30 s a child dies of malaria [1]. The increase in the number of fatal cases registered in recent years is principally due to the spread of mosquitoes (vectors of *Plasmodium*

into humans) resistant to common insecticides and, more importantly, the emergence of multidrug-resistant strains of *Plasmodium*. The latter problem makes many of the available drugs useless, leaving some efficacy only to the artemisinin-based therapies.

The mortality of the remaining protozoal diseases is much less marked (nearly 100,000 deaths per year), but their morbidity is also extremely high, severely affecting the quality of life of the infected people. African trypanosomiasis (sleeping sickness) is caused by *Trypanosoma brucei* species, which invade the central nervous system, leading to behavioral changes, coma, and, if untreated, death [2]. Chagas' disease is caused by *T. cruzi* and transmitted by a blood-sucking insect (triatome), which bites the victim and contaminates the wound with infected feces. The disease, which is also known as South American trypanosomiasis, is one of the major health problems in Latin America. Leishmaniasis is caused by over twenty species of intracellular parasites belonging to the genus *Leishmania*, which are transmitted to humans by sand flies. This disease can give different clinical symptoms including cutaneous, mucosal, and visceral forms [3]. Both the cutaneous and mucosal forms can cause severe deformities to patients, including ulcerative skin lesions and the destruction of mucous membranes, in some cases leading to permanent disfigurement. The visceral form of the disease, caused principally by *L. donovani*, *L. infantum*, and *L. chagasi*, represents the greatest threat to human health, with symptoms ranging from fever and weight loss to hepatosplenomegaly, leading to death in untreated cases [4].

Other protozoa, causing less-dramatic human diseases, are *Toxoplasma gondii*, *Giardia lamblia*, and *Entamoeba histolytica*. *Toxoplasma gondii* infects most genera of warm-blooded animals, including humans, but the primary hosts are cats (more precisely, the felid family). Contact with raw meat or with feces of infected cats is the more significant source of human infections in many countries. During the first few weeks, the infection typically causes a mild flu-like illness with muscle ache, but, in healthy adults, there is no other following symptom. However, people with a weakened immune system, such as those infected with advanced HIV disease, those who have recently received an organ transplant, or those who are pregnant, may become seriously ill, and it can occasionally be fatal. The parasite can cause encephalitis and can affect the heart, liver, and eyes.

Giardia lamblia is a flagellated protozoan parasite that colonizes and reproduces in the small intestine, causing giardiasis, an affection which does not spread via the bloodstream and remains confined to the lumen of the small intestine. *Giardia* infection can occur through ingestion of dormant cysts in contaminated water, food, or by the fecal–oral route. Symptoms of infection include diarrhea, steatorrhea, epigastric pain, nausea, diminished interest in food, and vomiting, and the infection can be particularly severe and prolonged in patients who are immunocompromised, or who have decreased gastric acid secretion. Finally, *Entamoeba histolytica* is an anaerobic parasitic protozoan whose infection can lead to amoebic dysentery or amoebic liver abscess. Symptoms can include fulminating dysentery, bloody diarrhea, weight loss, abdominal pain, and amoeboma. The amoeba can

actually “bore” into the intestinal wall, causing lesions and intestinal symptoms, and it may reach the blood stream. From there, it can reach different vital organs of the human body, usually the liver, but sometimes the lungs, brain, spleen, etc. A common outcome of this invasion of tissues is a liver abscess, which can be fatal if untreated.

The chemotherapeutic options to control and treat these protozoal infections are dramatically limited to few classes of sometimes old drugs which, in many cases, are associated with severe toxicity and variable efficacy. In some cases (as for giardiasis and leishmaniasis), antibiotics are very effective, but in many cases, the costs of treatments are unaffordable (e.g., amphotericin B for treatment of leishmaniasis). These considerations, together with the emerging resistance against many drug classes, make discovery and development of new, safe, and effective antiprotozoan agents a pressing need.

In this chapter we will describe the contribution given by marine chemistry to the field of antiprotozoan drug research. Marine organisms constitute a universally recognized source of potentially bioactive molecules which have been enzymatically engineered and biologically validated. In particular, marine invertebrates are producers of a number of potent antibiotic agents and intense research efforts have been devoted in recent years to the discovery of potential antiprotozoan lead compounds. Following the lines of the most pressing needs and of the most significant research efforts, we have decided to focus our attention on three protozoan pathologies, namely, malaria, leishmaniasis, and trypanosomiasis. We will provide a picture of the most significant leads found in marine organisms against these diseases, describing them in separate paragraphs, although some of these leads are active against two or more different diseases. A number of periodic reviews of the literature can be consulted to gain updated information about the activity of marine compounds against protozoa [5]. Moreover, some detailed reviews focused on the most promising classes of marine antimalarial lead compounds [6] are present in the literature.

21.2 Malaria

21.2.1 Clinical Symptoms and Social Impact

Malaria is an infectious disease caused by *Plasmodium falciparum* and by several other protozoans belonging to the genus *Plasmodium*. The protozoan comes in contact with humans through the vector contribution of female *Anopheles* mosquitoes. Within 30 min after injection into the blood stream, the parasite (in the sporozoites form) infects hepatocytes, multiplying asexually and asymptotically for a period of 6–15 days. When the protozoans reach the merozoite stage, they are released from the liver and invade the erythrocytes, starting to feed on the hemoglobin. After proliferation, the rupture of the erythrocyte membrane and the consequent liberation of other merozoites that invade other erythrocytes cause

the massive infection and the symptoms. A small portion of merozoites develops into the sexual stage of gametocytes, a form that is able to restart the life cycle of the malaria parasite when a mosquito takes a blood meal from an infected person [7].

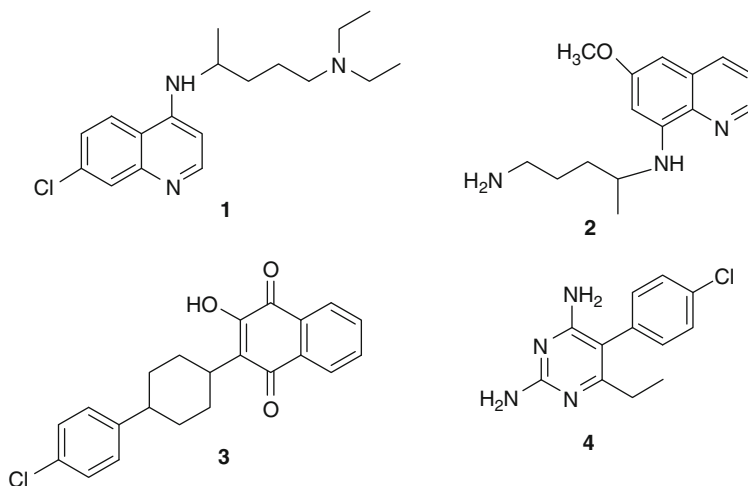
The clinical symptoms of malaria infections are almost exclusively attributable to parasites in the erythrocytic stage. The rupture of infected erythrocytes is associated with the release into the blood stream of cell debris responsible for the characteristic fever spike patterns by the induction of interleukin-1 and tumor necrosis factor. In the lethal cases, a specific protein produced by the protozoan is embedded into the cell membrane of the infected erythrocyte, and, as a consequence of this modification, the erythrocyte sticks to the walls of capillaries causing obstruction of vessels. When this mechanism operates at the level of brain vessels, the loss of consciousness is the first symptom, but if this form of cerebral malaria is not treated immediately, it is soon followed by death.

It is now widely accepted that the optimal strategy to combat against malaria infections should necessarily be multilateral and combine different approaches based both on prevention (mosquito nets, insect repellents, vaccines, prophylaxis) and treatment of infections (drugs). Both the number of different strains causing the pathology and their tendency to genetic mutations posed great obstacles to the development of the vaccine strategy. At the moment, RTS,S is heading phase III trials, and it appears to be the most promising malaria vaccine candidate [8]. This vaccine candidate is a recombinant protein that fuses a part of the *P. falciparum* sporozoite protein with the hepatitis B surface antigen molecule. Combined with a proprietary GSK adjuvant system, RTS,S induces the production of antibodies as well as of white blood cells that are believed to diminish the capacity of the malaria parasite to infect, survive, and develop in the human liver. In addition to inducing partial protection against malaria, the RTS,S vaccine candidate stimulates a protective immune response to hepatitis B, a common infection in developing countries.

The drug treatment of malaria infections holds an important place in the history of medicinal chemistry and of natural product chemistry. Indeed, the first specific treatment for malaria dates back to the seventeenth century when the bark of cinchona trees was used to face infections of malaria that was endemic not only in Africa and Asia but also in several parts of Europe and North America. Later, malaria was the first disease to be treated with an active principle isolated from a natural source, quinine, isolated from the cinchona bark in 1820, and, later again, the first human disease to be treated with a synthetic drug (methylene blue in 1891).

In the course of twentieth century, especially during World War II, a series of effective synthetic antimalarial drugs have been developed. Unfortunately, the available chemical weapons to treat malaria cases are largely based on these old molecules, as 4-aminoquinolines (e.g., chloroquine, **1**), 8-aminoquinolines (e.g., primaquine, **2**), naphthoquinones (e.g., atovaquone, **3**), or dihydrofolate reductase inhibitors (e.g., pyrimethamine, **4**). These molecules largely contributed to the

nearly complete eradication of malaria in developed countries; currently, their association with artemisinin analogues represents the most advanced malaria treatment.



Although the above remedies can give some good results, the therapeutic choices are evidently too limited. Indeed, in our days malaria still continues to be an extremely important threat to the health and economic prosperity of the human race, constituting a major cause of morbidity and mortality in tropical countries of Asia, Africa, and South America. The reality is probably worse than that commonly conceived: about 40% of the world population lives in countries where the disease is endemic; a recent analysis estimates between 700,000 and 2.0 million deaths each year from malaria (over 75% of them are African children) and between 400 and 900 million acute febrile episodes per year in African children under the age of 5 living in malaria-endemic regions where there is limited or inadequate access to formal healthcare [9]. In the eastern and southern African regions, an estimated 30% of all recorded deaths during pregnancy are attributed to malaria infection. Part of the reason for the failure to control malaria in these areas is the emergence and spread of resistance to first-line antimalarial drugs, cross-resistance between the members of the limited number of drug families available, and in some areas, multidrug resistance [10]. It has been estimated that in the last 30 years only four to five new drugs have been registered against malaria. This picture dramatically illustrates the unquestionable evidence that efforts of pharmaceutical companies are obviously not proportional to the number of deaths for a pathology but principally to the potential market of the developed drugs. Not surprisingly, funds invested in the malaria research by academic and nonprofit agencies (e.g., EU, MMV, and Gates foundation) overcome those invested by pharmaceutical companies.

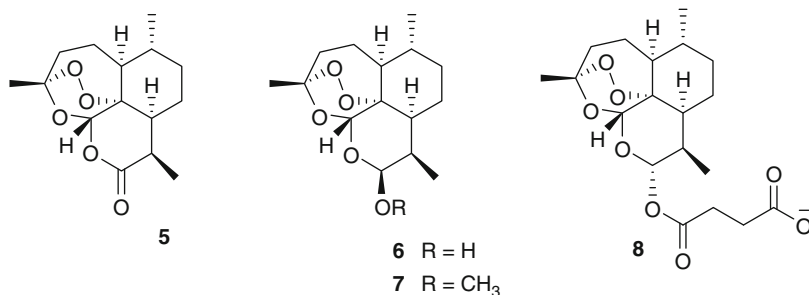
On the other hand, the sequencing of the entire genome of both the malarial parasite and its insect vector disclosed a number of potential pharmaceutical targets

to prevent and/or treat the disease [11]. Therefore, the pharmacological therapy will likely remain also in the near future an important strategy in the fight against malaria. However, it is now recognized that the next significant advancement in the field of antimalarial drugs will not be obtained through the discovery of a single potent compound but through the introduction of an innovative drug to be used in a combined therapy, preferably composed by molecules acting at different stages of the malaria parasite life cycle. For example, studies conducted with the rodent model *P. chabaudi* revealed that the stress conditions imposed by drug treatment determine an increase in the gametocyte production, and gametocytes have been shown to have a much longer lifespan than the asexual stages. These observations are important from a public health point of view, as they imply that the use of an antimalarial drug, although beneficial at the individual level, might be detrimental for the community, leading to an increase of malaria transmission, or, at least, guaranteeing the transmission of the parasites. The rationale for designing antimalarial combinations acting also on gametocytes and on sporogonic stages developing in the vector derives from these considerations.

In the following paragraphs, we will highlight the contribution of marine chemistry to the field of antimalarial research, with particular emphasis on recent discoveries. Marine antimalarials are divided into four different classes basing on their chemical structures: (1) endoperoxides, (2) isonitrile-containing derivatives, (3) alkaloids, and (4) quinones and other compounds.

21.2.2 Endoperoxides

The development of antimalarial endoperoxide-containing drugs started with the discovery of the potent activity exhibited by artemisinin (5), a low-nanomolar antimalarial active also against chloroquine-resistant strains of *Plasmodium* [12] and acting in the early form of the malarial blood stages. Artemisinin is a cadinane sesquiterpene lactone embedding a 1,2,4-trioxane moiety, isolated from leaves of the sweet wormwood, *Artemisia annua* (Compositae). In spite of the presence of adjacent peracetal, acetal, and lactone functionalities, artemisinin is a stable and easily crystallizable compound.



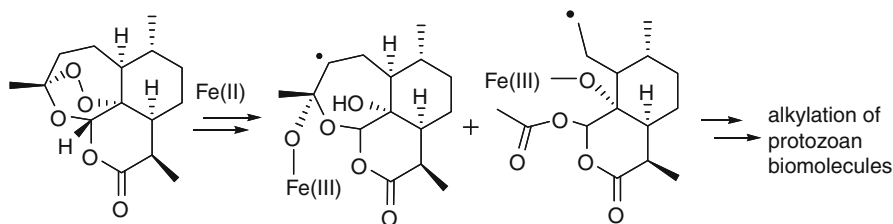


Fig. 21.1 The C-centered radical species postulated for the antimalarial activity of artemisinin

A number of semisynthetic artemisinin derivatives have been prepared, as dihydroartemisinin (**6**), the oil-soluble artemether (**7**), and the water-soluble artesunate (**8**). Although a total synthesis of artemisinin has also been reported [13], it is not a sustainable supply of this drug.

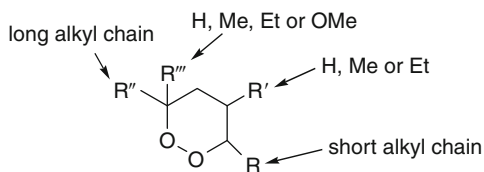
The endoperoxide linkage is essential for the antimalarial activity of artemisinin and of its derivatives, as proved by the inactivity of deoxyartemisinin, an artemisinin derivative lacking the endoperoxide bridge. The most widely accepted hypothesis on the mechanism of action of artemisinins postulates that the endoperoxide bond of these molecules, interacting with the iron(II) center of the heme unit, released in the food vacuole during the digestion of hemoglobin, gives rise to oxygen-centered radicals. As a result of an intramolecular rearrangement, these reactive species are converted into free C-centered radicals, toxic to the parasite through alkylation of macromolecular targets (Fig. 21.1). Most likely, artemisinin activity is not mediated by interaction with a single enzyme, also in the light of the scarce tendency of this compound (and its analogues) to develop resistance. It has been proposed that the Fe(II)-containing species interacting with the endoperoxide bond is not heme [14]; however, this hypothesis does not change the general lines of the delineated mechanism of action.

Endoperoxide-containing compounds of marine origin constitute a rather large group of secondary metabolites, some of which exhibit a quite potent *in vitro* antimalarial activity. In some cases, a number of semisynthetic or totally synthetic derivatives have been prepared. Unfortunately, only few of the isolated endoperoxide marine metabolites have been tested for their antimalarial activity, and, therefore, data available could have been even more rich and informative.

Commonly, these molecules possess a simple six-membered 1,2-dioxxygenated ring (1,2-dioxane) bearing two or three alkyl/aryl groups of different length and complexity (Fig. 21.2). A small number of molecules show some variations on this general structure: (1) 1,2-dioxolanes, (2) molecules showing a double bond between the two nonoxygenated carbons of the ring, and (3) molecules showing an additional ring fused to the dioxane ring.

An important feature of these compounds is the nature of the substituent R''' . Indeed, molecules linking H, methyl, and ethyl groups at that position are simple 1,2-dioxanes, while molecules linking a methoxy group are peroxyketal

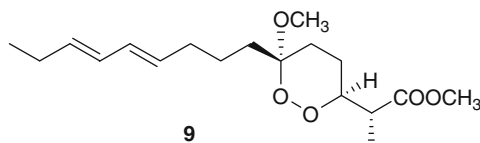
Fig. 21.2 General structure of dioxane antimalarials of marine origin



derivatives. In this chapter, marine endoperoxides have been divided in two categories according to this structural feature.

21.2.2.1 Peroxyketal Endoperoxides

The parent compounds in the class of 3-alkoxy-1,2-dioxane (peroxyketals) derivatives are peroxyplakoric acids and their methyl esters (e.g., peroxyplakoric acid B3 **9**), isolated from *Plakortis* sp. [15].



These marine derivatives showed a potent *in vitro* activity ($IC_{50} = 50$ ng/mL against *P. falciparum*) with a good selective toxicity index (about 200). The simple structures of these compounds made possible the total syntheses of the natural molecules and of several analogues [16]. A number of evidence pointed to the critical importance of the “long” alkyl side chain for the antimalarial activity within this class. For example, a synthetic analogue showing a methyl group in place of the nonadienyl group was almost completely devoid of activity, while a pentyl group proved to be well compatible with the antimalarial activity, retaining the *in vitro* potency of the natural analogues. When these compounds were examined *in vivo* against *P. berghei* infection, they showed little antimalarial potency because of the relative instability in mouse serum. This undesired finding was demonstrated to be due to the hydrolysis of the ester function to the much less active carboxylic acid derivative. In order to enhance the stability in physiological media, a number of semisynthetic analogues were prepared; the monoethyl amide analogues proved to be stable to hydrolysis in the serum and showed a good *in vivo* activity [17].

The reaction of peroxyplakoric ester analogues with Fe(II) species was explored to mimic the interaction with heme and gain further information on the structural requirements for the biological activity [18]. Analysis of the products obtained upon this reaction suggested the formulation of the mechanism of action illustrated in Fig. 21.3. Similarly to artemisinin, the peroxyketal derivative is believed to interact with the Fe(II) center of the heme residue with consequent homolytic cleavage of the O–O bond. In this case, the O-centered radical should be almost exclusively located at the oxygen attached to the methoxy-linking carbon. This

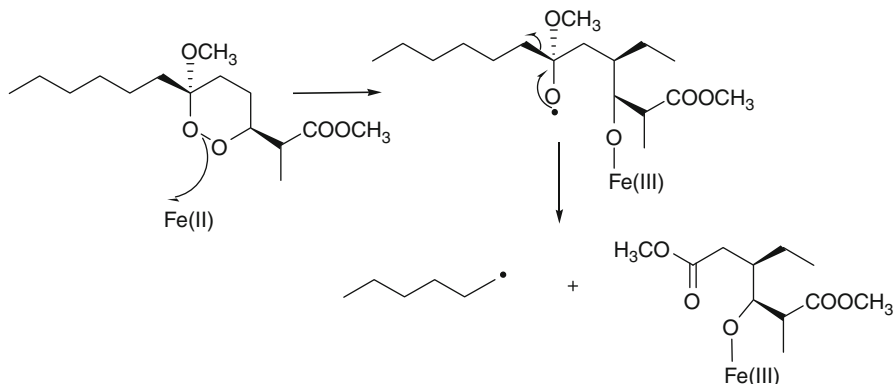
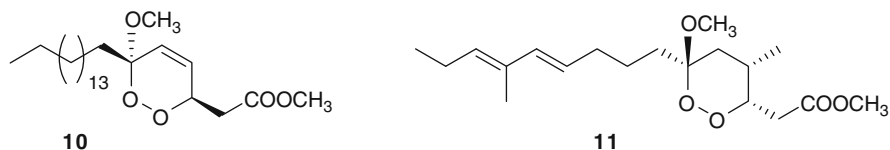


Fig. 21.3 The postulated mechanism of action of peroxyplakoric derivatives

radical would evolve through a regiospecific carbon–carbon cleavage producing a neutral methyl ester species and a very reactive primary carbon radical which should be the toxic species responsible for the death of the parasite. Although this model has the merit of providing a rationale for the observed importance of the alkyl side chain, it should also be noted that some synthetic compounds, potentially producing reactive carbon radicals, failed to show a significant activity.

The low antimalarial activity observed for chondrillin (**10**) [19], a marine endoperoxide strictly related to peroxyplakoric derivatives, indicated that the presence of a double bond within the 3-methoxy-1,2-dioxane skeleton is detrimental for the activity. However, a negative pharmacokinetic role played by the long C₁₆ saturated alkyl chain cannot be excluded.

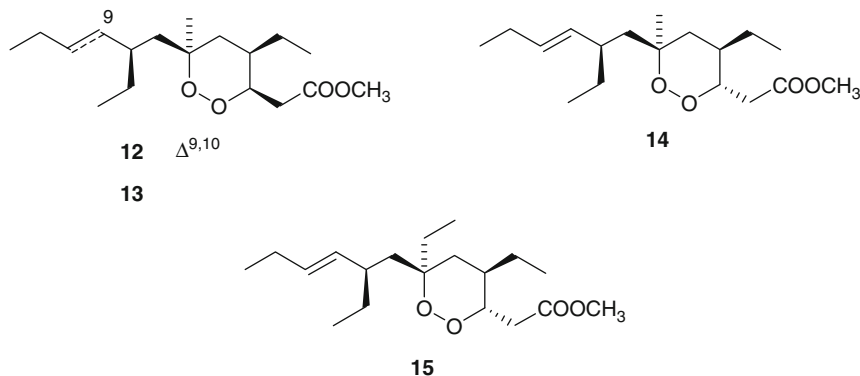


An Indonesian specimen of *Plakortis* sp. afforded some endoperoxide peroxyketals, named manadoperoxides (e.g., manadoperoxide B **11**) [20], whose structures are strictly reminiscent of those of peroxyplakoric derivatives (see **9**). They differ almost exclusively for the position of a methyl group, which is moved from the short alkyl chain to the dioxane ring. This corresponds to a difference in the last two steps of the hypothesized polyketide biogenesis: for peroxyplakoric derivatives the last two units are, most likely, acetate–propionate, while in the case of manadoperoxides, the sequence of the last two incorporated units should be reversed, i.e., propionate–acetate. Surprisingly, this minor structural change caused a dramatic decrease in the antimalarial activity (IC₅₀ of **11** = 3.70 μM).

A computational study revealed that, in the populated conformations for manadoperoxides, the endoperoxide linkage is either not accessible to heme iron or it cannot evolve to produce a toxic C-centered radical. This result evidences that also minor structural changes can have a deep impact on the antimalarial activity, when they affect the conformational behavior of the molecule, and, consequently, its ability to interact with heme and produce the toxic C-centered radical, responsible for the final activity.

21.2.2.2 Nonperoxyketal Endoperoxides

The parent compound of this class of marine antimalarials is plakortin (**12**), a simple 1,2-dioxane metabolite with a likely butyrate-based polyketide biosynthetic origin. This molecule was isolated more than 30 years ago from *Plakortis halichondrioides*, as a mild antibacterial agent [21], but it was later reisolated in remarkable amounts from the Caribbean sponge *Plakortis simplex*, and the absolute configuration at the four stereogenic carbons of plakortin was determined [22]. A number of related endoperoxide derivatives were isolated from the same source. These include dihydroplakortin (**13**) [22], 3-epiplakortin (**14**) [23], and plakortide Q (**15**) [23].



These compounds exhibited a quite good antimalarial activity, and, similarly to artemisinin, they were more potent on the W2 strain ($IC_{50} \approx 0.3 \mu M$) and devoid of cytotoxicity [24]. To further investigate the structure–activity relationships in the plakortin series, a number of semisynthetic derivatives were prepared [25]. Among them, the plakortin diol, obtained upon reduction with Zn/AcOH of the endoperoxide bond, proved to be completely inactive, thus providing an unambiguous evidence of the crucial role of the endoperoxide bond for the antimalarial activity. A multidisciplinary investigation, based on molecular dynamics/mechanics, ab initio calculations, and chemical reactions, provided interesting insights into the mechanism of the antimalarial action of plakortin derivatives [26]. These molecules, after interaction of the endoperoxide bond with Fe(II), should

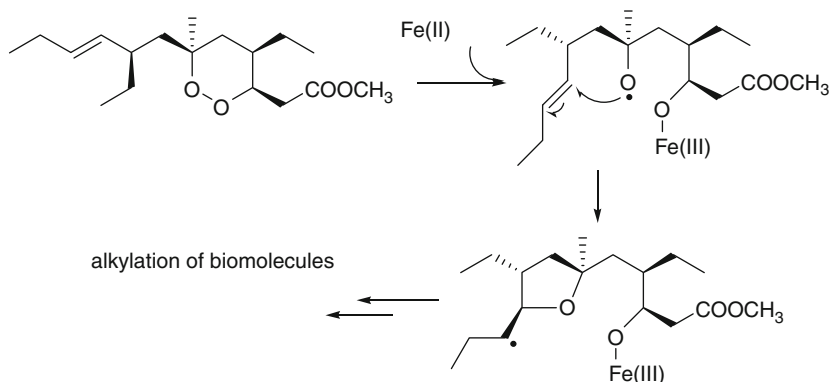
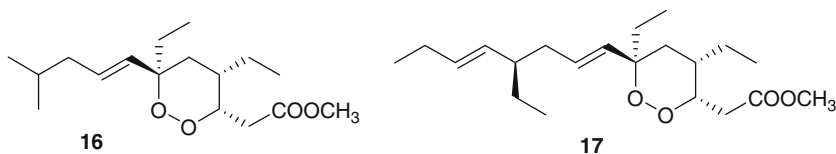


Fig. 21.4 The mechanism proposed for the antimalarial action of plakortin

give rise to the formation of an oxygen radical, followed by rearrangement to give a carbon radical centered on the "western" alkyl side chain, the toxic intermediates responsible for subsequent reactions leading to plasmodium death (Fig. 21.4). It is interesting to notice that in this case the cleavage mechanism, postulated for peroxyplakoric derivatives (see before), should not operate, being completely substituted by a rearrangement evolution of the oxygen radical.

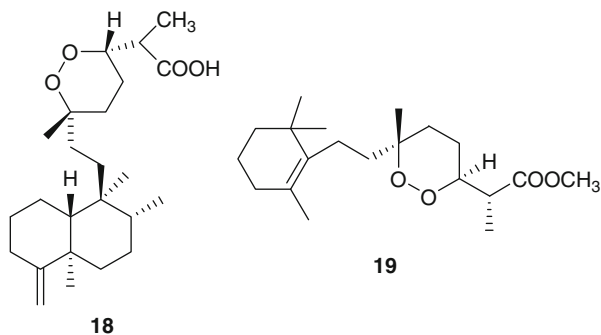
Following this mechanism, the very low *in vitro* antimalarial activity ($IC_{50} > 8 \mu\text{g/mL}$) of plakortides L (**16**) [27] and O (**17**) [28], in spite of their similarity with the plakortin scaffold, could be explained. Indeed, the side-chain double bond, directly attached at the dioxane ring, likely prevents the evolution of the oxygen radical to a side-chain carbon radical.



Strong evidence has been gathered about the plakortin production by the microbial population hosted by the sponge *Plakortis simplex* [29]. In the future, an approach based on identification, cloning, and expression of the gene cluster(s) for plakortin or related compounds, from the metagenome of the sponge, could allow the production of these molecules by low-cost bacterial fermentation, thus fulfilling one of the essential requirements for antimalarial drugs of the next generation.

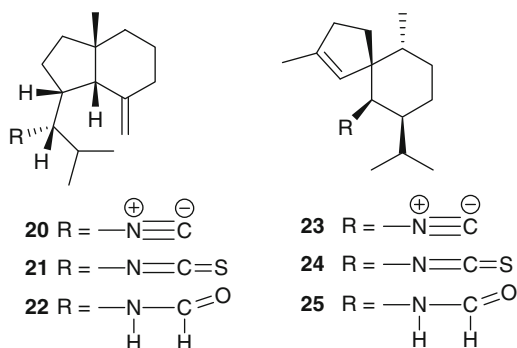
Compared to polyketide-based compounds, very few marine endoperoxide-containing terpenoids have been tested for their antimalarial activity, and none

of them showed an antimalarial activity comparable to that of molecules belonging to the plakortin family. Sigmosceptrellin A (**18**), a norsesiterpene derivative of spongal origin, showed a discrete activity against *P. falciparum* ($IC_{50} \approx 450$ ng/mL) [30], and, interestingly, its epimer, named sigmosceptrellin B, was four times less active [31]. Methyl-3-epinuapapuanate (**19**) is a norditerpene derivative isolated from the New Caledonian sponge *Diacarnus levii*, showing a moderate activity against chloroquine-resistant strains of *P. falciparum* [32].

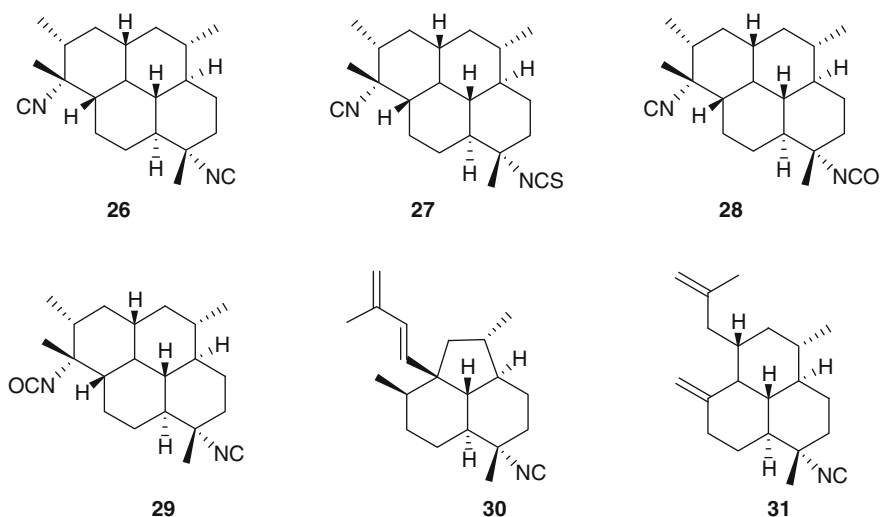


21.2.3 Isonitrile-Containing Compounds

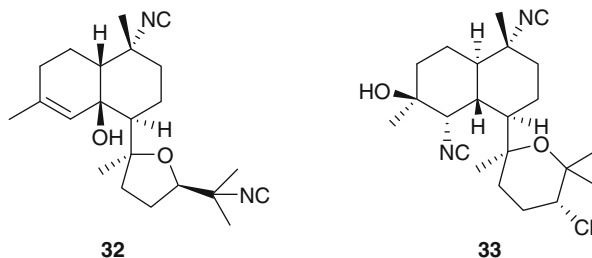
Isonitrile-containing terpenoids are typically marine secondary metabolites. The first isolated compound of this class is axisonitrile-1 (**20**), isolated in 1973 from the marine sponge *Axinella cannabina*, where it co-occurred with the strictly related axisothiocyanate-1 (**21**) [33]. The same source successively proved to contain a number of related metabolites, as axamide-1 (**22**), [34] axisonitrile-3 (**23**), axisothiocyanate-3 (**24**), and axamide-3 (**25**) [35].



More recently, axisonitrile-3 (**23**) has been reisolated from the sponge *Acanthella klethra* and found to possess a potent antimalarial activity both on chloroquine-sensitive (D6, 142 ng/mL) and chloroquine-resistant (W2, 17 ng/mL) *P. falciparum* strains [36]. The closely related axisothiocyanate-3 (**24**) was inactive, suggesting a crucial role for the isonitrile functional group. Following these remarkable findings, a number of isonitrile-containing secondary metabolites have been isolated from different marine sources, particularly marine sponges of the Axinellidae and Halicondridae families. The chemical analysis of *Cymbastela hooperi* (Axinellidae) afforded a series of diterpenes based on amphilectane, isocycloamphilectane, and neoamphilectane skeletons and bearing isonitrile, isothiocyante, and the rare isocyanate functionalities [37]. These molecules displayed a significant (low nM range) and selective in vitro antimalarial activity, and the co-occurrence of several strictly related analogues suggested some structure–activity relationships. Comparison among the activities exhibited by the closely related isocycloamphilectanes **26** (IC_{50} = about 4 ng/mL), **27** (IC_{50} = about 40 ng/mL), and **28** (IC_{50} = about 60 ng/mL) illustrated the relative potency of isonitrile, isothiocyante, and isocyanate groups, supporting the previous observation that the bioactivity is particularly associated to the presence of the isonitrile group. However, the location of functional groups also plays a role, as suggested by the comparison between the activities of compounds **28** and **29** (IC_{50} = about 3 ng/mL), where the positions of isocyanate and isonitrile groups are interchanged. Moreover, the activity of the neoamphilectane derivative **30** (IC_{50} on D6 = 90 ng/mL; on W2 = 30 ng/mL) is considerably higher than that of compound **31**, indicating that the carbon skeleton can modulate the antiplasmodial activity of isonitrile derivatives [38].



Kalihinols, further isonitrile-containing antimalarial derivatives, have been isolated from the Japanese sponge *Acanthella* sp. (e.g., **32–33**) [39]. These molecules, belonging to the class of the kalihinane diterpenoids, showed a potent antiplasmodial activity in the very low nanogram range [e.g., kalihinol A (**33**), $IC_{50} = 0.4$ ng/mL].



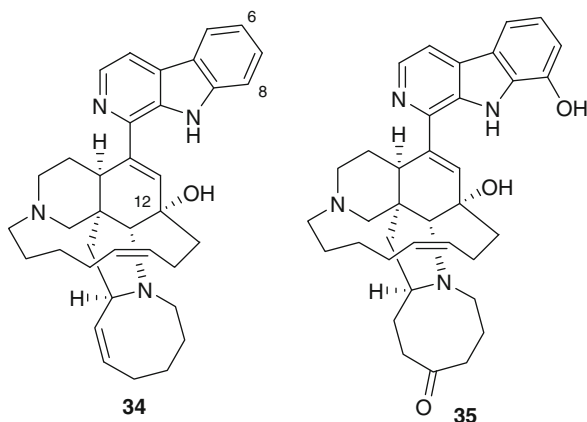
Isonitrile antimalarials have been proposed to interact with free heme by forming a coordination complex with the iron center, thus inhibiting the transformation of heme into β -hematin and then hemozoin, a polymer produced by *Plasmodium* in order to neutralize the toxic (detergent-like) free heme produced in the food vacuole. In addition, isonitriles were shown to prevent both the peroxidative and glutathione-mediated destruction of heme under conditions that mimic the environment within the malaria parasite [40]. The pharmacophore must possess an overall lipophilic rigid molecular core comprising at least a tricyclic framework carrying an isonitrile group and establishing further hydrophobic interactions above the ring plane.

21.2.4 Alkaloids and Peptides

This heterogeneous group of compounds includes some marine antimalarials with very different carbon frameworks, but with the common feature of the presence of one (or more) nitrogen atoms. In many cases, the biosynthetic origin of these compounds is not known as well as the mechanism of their antimalarial action.

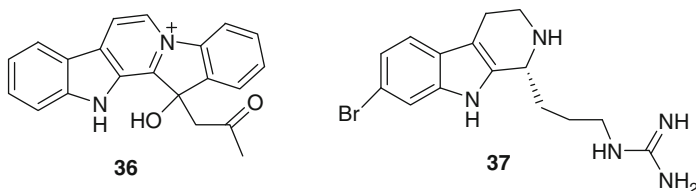
The most important members of this class are manzamines, very complex polycyclic (seven to eight rings or more) alkaloids characterized by an intricate heterocyclic system attached to a β -carboline moiety, first reported from an Okinawan sponge belonging to the genus *Haliclona* [41]. Since the first report of manzamine A (**34**), at least 60 additional manzamine-type alkaloids have been reported from taxonomically unrelated sponges belonging to different genera (e.g., *Xestospongia*, *Ircinia*, and *Amphimedon*) and different orders. These findings strengthen the hypothesis that manzamines are not true sponge metabolites but, more likely, they have a symbiotic origin. Accordingly, microbial community

analyses for one of the most common manzamine-producing sponges resulted in the identification of *Micronospora* as the bacterial strain producing manzamines [42]. A recent paper hypothesized a common biosynthetic route for cyclostelletamines, halicyclamines, and manzamines, thus highlighting the existence of “nature diversity-oriented syntheses” [43].



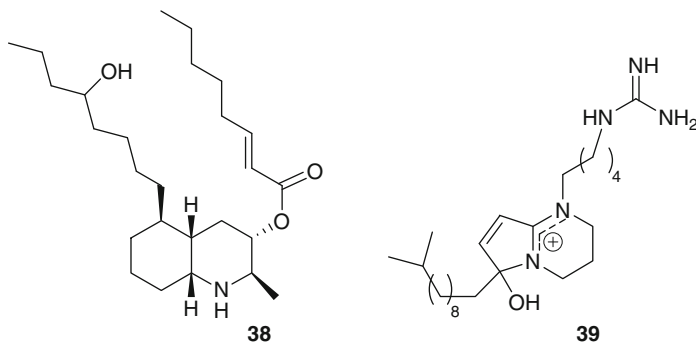
Hamann et al. disclosed the antimalarial potential of manzamine A and of its 8-hydroxy derivative [44]. These molecules were found to potently inhibit the growth of *Plasmodium falciparum* both in vitro ($IC_{50} \approx 5.0$ ng/mL) and in vivo. Unfortunately, the therapeutic index of these molecules is somewhat narrow (gastrointestinal distress), and further studies are needed to improve this value. Interestingly, a closely related derivative of manzamine A, manzamine F (**35**), was completely devoid of activity ($IC_{50} > 1,000$ ng/mL), thus evidencing the key role of the eight-membered ring. Similarly, the attachment of the hydroxyl group at position 6, in place of position 8, has a deleterious impact on the antimalarial activity, as indicated by the lower potency of 6-hydroxy-manzamine A [45]. The crucial role of a free hydroxy group at position 12 has also been highlighted by a recent study reporting that acetylation of this group significantly reduced the antimalarial activity [46].

Manzamines have also been reported to be antibacterial and antituberculosis agents and to exhibit activity against AIDS opportunistic pathogens as the protozoan *Toxoplasma gondii* [47] (see “Introduction” for a brief description of this parasite). More recently, manzamine A and derivatives have been shown to possess inhibitory activity against glycogen synthase kinase-3 (GSK-3) with potential application in Alzheimer’s disease [48].



The β -carboline group is also present in the structures of homofascaplysin A (**36**), isolated from the sponge *Hyrtios erecta* [49], and of bromotripargyne (**37**) from *Ancorina* sp. [50]. These alkaloids showed good activity against chloroquine-resistant *P. falciparum* strains, but in the first case a marked toxicity toward human cells was detected.

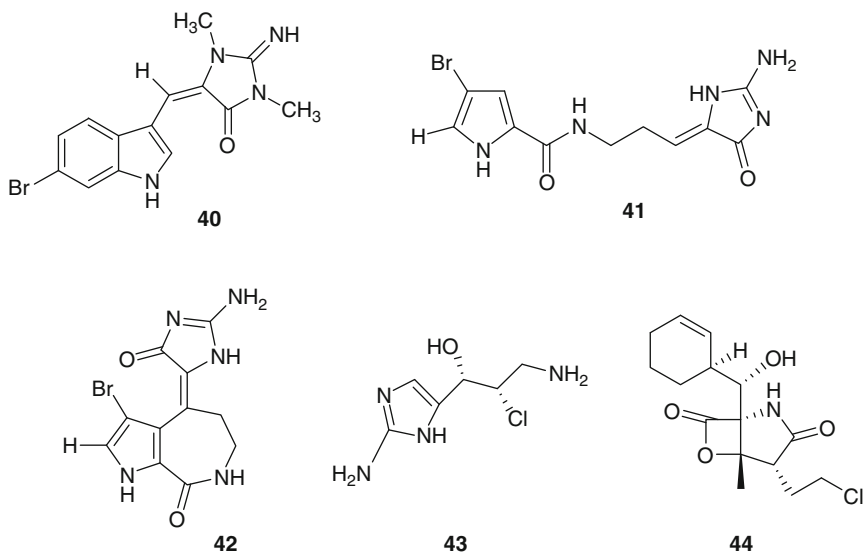
Lepadins are decahydroquinoline derivatives bearing a linear eight-carbon chain obtained from two tunicates of Australian origin, *Clavelina lepadiformis* [51] and *Didemnum* sp. [52]. Lepadin E (**38**) exhibited a significant antimalarial activity ($IC_{50} = 400$ ng/mL), while its analogues lacking the *2E*-octenoic acid ester functionality were completely inactive. Authors have proposed that this conformationally mobile side chain could serve to stabilize nonbonding interactions with heme, or with any other “receptor” molecule. Phloeodictynes (e.g., **39**) are marine antimalarials, and similarly to lepadins they show a bicyclic nitrogen-containing ring system bearing a long alkyl chain. They have been isolated from sponges belonging to the genus *Oceanapia* [53, 54] as good antimalarial agents ($IC_{50} = 300$ ng/mL) against the chloroquine-resistant FGB1 strain of *P. falciparum*.



6-Bromoaplysinopsin (**40**) is a simple indole derivative first isolated in 1985 [55] and later reobtained from the sponge *Smenospongia aurea* [56], active against the D6 clone of *P. falciparum*. A recent study, aimed at evaluating the antiprotozoan potential of bromopyrrole alkaloids [57], identified dispacamide B (**41**) and spongiacidin B (**42**) as good antimalarial agents. Interestingly, both these compounds, similarly to bromoaplysinopsin, show the presence of an aminoimidazolone (alkylidene glycoyamidine) ring. Interestingly, a very simple 2-aminoimidazole derivative, girolline (**43**), extracted from *Cymbastela cantharella* [58], showed antiplasmodial activity in the IC_{50} range of 77.0–215.0 nM and was active in vivo at a dose of 1.0 mg/kg/day. The aminoimidazole moiety was necessary for the antimalarial activity since the synthetic analogues of two series, 5-deazathiogirolline and 4-deazathiogirolline, without the aminoimidazole moiety, were devoid of any activity.

Salinosporamide A (**44**), a γ -lactam alkaloid isolated from a marine bacterium of the new genus *Salinispora* [59], has been found to be a parasite proteasome inhibitor and to possess a significant antimalarial activity in vitro

($IC_{50} = 11.4$ nM) [60]. Salinosporamide was determined to act in the erythrocytic stage and maintained its potent activity in a malaria mouse model with inhibition of the parasite growth in treated mice at extremely low doses (130 μ g/kg).

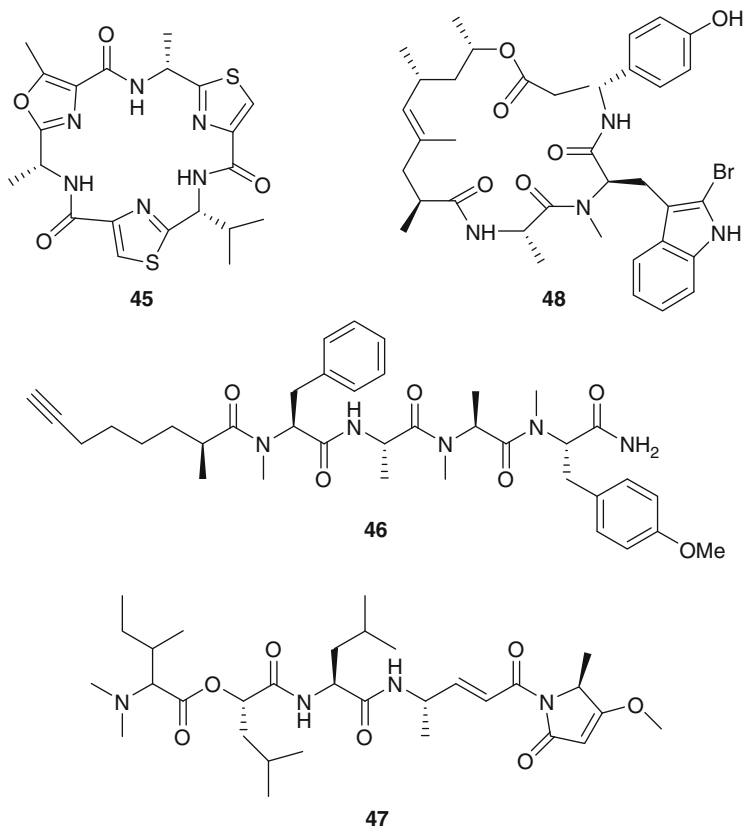


Two modified cyclic hexapeptides, venturamides (e.g., venturamide A, **45**), isolated from the marine cyanobacterium *Oscillatoria* sp., exhibited a moderate activity against *P. falciparum* ($IC_{50} \approx 6\text{--}7$ μ M) [61], with a good selectivity. A similar antimalarial profile was also exhibited by dragomabin (**46**), a linear alkynoic lipopeptide isolated from a Panamanian strain of the marine cyanobacterium *Lyngbya majuscula* [62]. Gallinamide A (**47**), isolated from *Schizothrix* species, containing an *N,N*-dimethyl isoleucine terminus, exhibited moderate in vitro antimalarial activity [63]. Jasplakinolide (**48**), a cyclic peptide isolated from the marine sponge *Jaspis* sp., markedly decreased parasitemia of *P. falciparum* by virtue of an apical protrusion that appears to interfere with the erythrocyte invasion by the merozoites and whose mechanism of formation is possibly related to an increase in F-actin content of the treated merozoites [64].

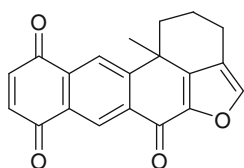
21.2.5 Quinones and Other Antimalarial Compounds

In the frame of a search for *Plasmodium* protein kinase inhibitors, the previously known xestoquinone (**49**) [65] proved to be a selective active inhibitor of Pfnek-1, a never-in-mitosis/*Aspergillus* (NIMA)-related protein kinase of *P. falciparum* [66]. However, the in vitro antiplasmodial activity of xestoquinone was moderate ($IC_{50} \approx 3$ μ M). A series of quinone derivatives, named alisiaquinones (e.g., **50**) structurally related to xestoquinone, have been isolated from an unidentified New Caledonian sponge [67].

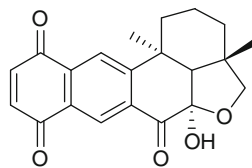
Not surprisingly they showed activity against Pfnek-1 and a micromolar antiplasmodial activity similar to those exhibited by xestoquinone. However, quite interestingly, alisiaquinone C (**51**), bearing an additional heterocycle formed by a taurine substituent, exhibited a submicromolar activity ($IC_{50} \approx 0.1 \mu M$) on *P. falciparum*. This higher activity of alisiaquinone C resulted to be unrelated to inhibition of Pfnek-1, but it was due to a significant inhibition of the plasmodial enzyme farnesyl transferase.



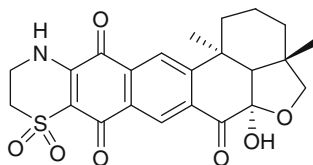
The polyether **52**, obtained from the marine *Streptomyces* sp. H668, exhibited a significant in vitro antimalarial activity ($IC_{50} \approx 150 \text{ ng/mL}$), with a good selectivity [68]. Similarly, to other polyethers of terrestrial origin, probably, this compound acts as ionophore on protozoan-infected cell membrane. Pycnidione (**52**), isolated from the marine fungus *Phoma* sp. [69], exhibited significant antiplasmodial activity against three strains of *P. falciparum* ($IC_{50} = 0.15\text{--}0.4 \mu M$). The structural similarities between pycnidione and the known antimalarial agent atovaquone, (Malarone[®]), widely used in the malaria prophylaxis, appear of particular interest.



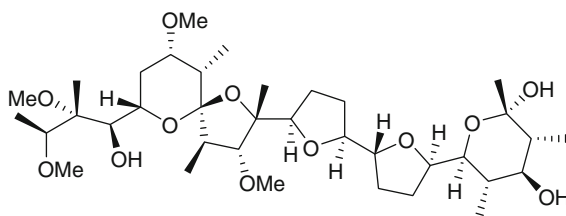
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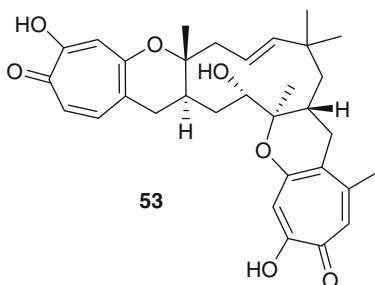
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21.3 Leishmania

21.3.1 Clinical Symptoms and Social Impact

Leishmaniasis is an animal and human infection caused by over 20 different protozoan parasites belonging to the genus *Leishmania* (e.g., *L. donovani*, *L. infantum*, *L. chagasi*). It is transmitted by the bite of *Lutzomyia* and *Phlebotomus* sand flies (subfamily Phlebotominae). The sand flies inject the infective stage, metacyclic promastigotes, during blood meals. These are phagocytized by

macrophages and transform into amastigotes which are able to affect different tissues and cause the differing clinical manifestation, depending in part on which *Leishmania* species is involved and partly also on the immunological status of the infected individual. Some forms of the disease are transmissible to humans only from animals (zoonosis), but some other can be diffused between humans.

The most important types of human leishmaniasis are cutaneous leishmaniasis (characterized by skin sores, sometimes called Jericho button) and visceral leishmaniasis (also known as kala-azar), a severe and potentially fatal form in which the parasites have migrated to the vital organs with frequent damages to the spleen and liver [3]. The cutaneous leishmaniasis commences with a sore at the bite site but can progress in diffuse cutaneous leishmaniasis (with widespread skin lesions which resemble leprosy) and mucocutaneous leishmaniasis (extending to tissues of nose and mouth and can cause permanent disfigurement).

Leishmaniasis is diffused in tropical and subtropical countries with particular incidence in the Indian subcontinent, in Northeastern African (as Sudan), or Central and South American (as Brazil) countries. It affects as many as 12 million people worldwide, with 1.5–2 million new cases each year. The visceral form of leishmaniasis has an estimated incidence of 0.5 million new cases and about 50,000 deaths each year, and it appears that the incidence of fatal forms of human leishmaniasis is increasing. The World Health Organization has designated leishmaniasis as a category 1 disease, signifying that it is an emerging and uncontrolled global health problem.

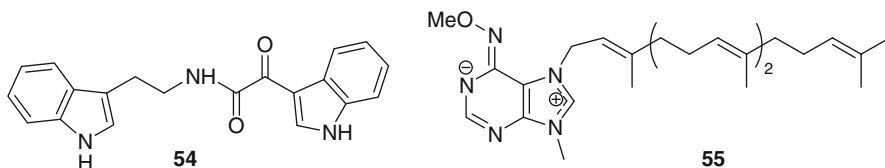
The treatment of leishmaniasis is made particularly difficult by the intramacrophagic location of the infectious form. Victims of this illness present an immune deficiency and are not able to eliminate the parasites through a natural mechanism of defense. Moreover, malnutrition is associated with certain cases of leishmaniasis. Parallel infection with diseases such as malaria and pneumonia increases the fatality of the illness if it is not diagnosed and treated in time. The problem of leishmaniasis has been worsened by the evolution of AIDS due to parallel infections in AIDS patients, as well as by the development of drug resistance by parasites. The traditional treatment for leishmaniasis is based on drugs containing antimony (pentavalent antimonials), e.g., meglumine antimoniate (Glucantime) and sodium stibogluconate (Pentostam). These are very old drugs and their introduction dates back to the 1940s. The resistance developed by parasites against these drugs [70] and the possibility of severe renal and cardiac side effects at the recommended doses strongly encourage the search of effective alternatives. Two potent antibiotics (amphotericin and paromomycin) and miltefosine are becoming frequently used to treat leishmaniasis, although their cost can be sometimes unaffordable for people with least socioeconomic ability. Miltefosine is a phosphocholine analogue originally developed as anticancer agent which is an effective drug for visceral and cutaneous leishmaniasis [71]; it appears to be well tolerated and has also the advantage of the oral formulation, but it is already facing instances of resistance in some areas. Interestingly, HIV protease inhibitors (nelfinavir and ritonavir) have been found to be active against *Leishmania* species and are currently investigated as possible therapeutic options for leishmaniasis [72]. Furthermore, the genomic sequencing of *Leishmania* is a stimulating result which could provide sources for vaccine candidates and potential targets for drug therapies.

The number of marine metabolites active against *Leishmania* parasites is significantly lower compared to those exhibiting antimalarial activity, but this is likely a consequence of the lower number of compounds tested. Some marine compounds exhibited both antimalarial and antileishmanial activities: those included in the following paragraphs have been tested exclusively against *Leishmania*, or, alternatively, their antileishmanial activity is more significant compared to the antimalarial one. For example, manzamines (see Sect. 21.2.4) showed also discrete antileishmanial activity; however, their antimalarial activity is surely more significant being comparable to that of the reference compound artemisinin. Noticeably, in very few cases, the mechanism of the antileishmanial action has been investigated.

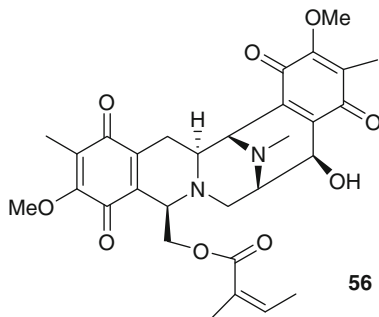
21.3.2 Alkaloids and Peptides

Dihydrocoscinamide (**54**), a synthetic analogue of the coscinamide indole alkaloids, obtained from the sponge *Coscinoderma* sp., exhibited a nearly complete inhibition against promastigotes and amastigotes of *Leishmania donovani* at 10 $\mu\text{g/mL}$ [73]. A series of synthetic analogues of **54** were also prepared, but only the compound showing methylation at both indole nitrogens proved to be equally active.

Agelasines are purino-terpene alkaloids isolated from sponges of the genus *Agelas* showing different pharmacological activities, including antibacterial, anti-fungal, and antifouling activities. Some synthetic analogues of agelasines have been prepared, and one of them (**55**) was found to potently inhibit the growth of *L. infantum* ($\text{IC}_{50} = 0.09 \mu\text{g/mL}$) with a good selectivity index [74].

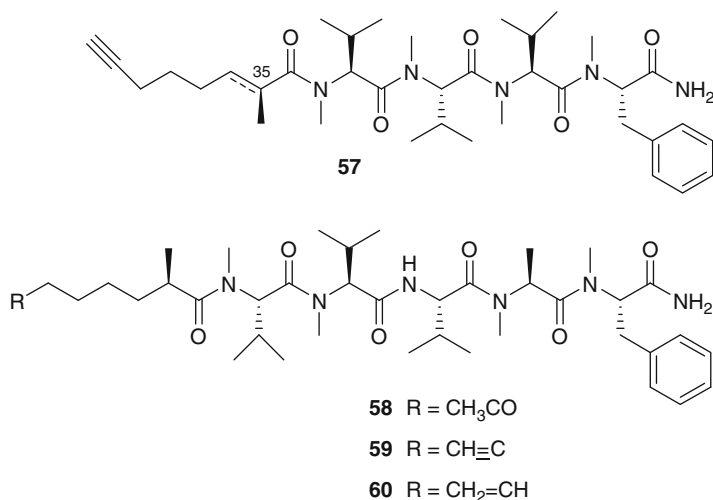


Renieramycin A (**56**) is a complex quinone-containing alkaloid isolated from the sponge *Neopetrosia* sp. which showed a dose-dependent inhibition of the growth of *Leishmania amoensis* with an IC_{50} of 0.2 $\mu\text{g/mL}$ [75]. Some quinone derivatives also proved to be active against malaria protozoans (see Sect. 21.2.5).



An emerging class of marine antileishmanial compounds is given by modified linear lipopeptides isolated from cyanobacteria. *Lyngbya majuscula* afforded the extensively *N*-methylated dragonamide E and its 35(36)-dihydroderivative dragonamide A (**57**), which exhibited antileishmanial activity in the 5- μ M range [76]. Interestingly, dragonamide B, showing an *N*-methylleucine in place of the carboxy terminal *N*-methylphenylalanine, was devoid of antileishmanial activity.

Screening of *Lyngbya majuscula* from the Caribbean coast of Panama led to the identification of two related antileishmanial lipopeptides, almiramides B–C (**59–60**), and their nonactive analogue, almiramide A (**58**) [77]. These molecules show an additional Ala residue, a different pattern of *N*-methylation, and an opposite configuration of the α -carbon of the lipophilic side chain. Their antileishmanial potency was slightly better ($IC_{50} = 2.4$ and 1.9 μ M, respectively) compared to dragonamides. The lack of antileishmanial activity for almiramide A (**58**) indicates the pivotal role played by the unsaturated terminus on the lipophilic side chain. In the same study, screening of a synthetic library of almiramide analogues with various modifications at the C- or N-terminus afforded several compounds with similar antileishmanial activity but improved selectivity.

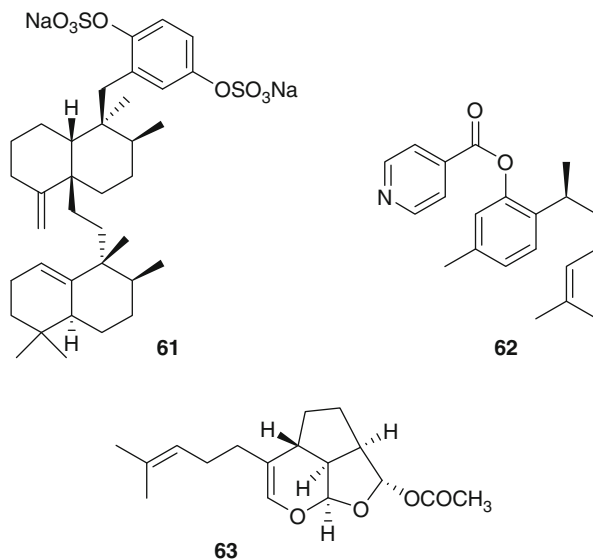


21.3.3 Terpenoids

A number of marine terpenoids have shown a discrete activity against *Leishmania* parasites. The disulfated meroterpenoid isoakaterpin (**61**) from the Brazilian marine sponge *Callyspongia* sp. was shown to inhibit *Leishmania* sp. adenosine phosphoribosyl transferase (APRT) with an $IC_{50} = 1.05$ μ M [78]. APRT is a specific parasite enzyme which is a component of the purine salvage pathway. In principle, the inhibitory activity of isoakaterpin should be highly selective since,

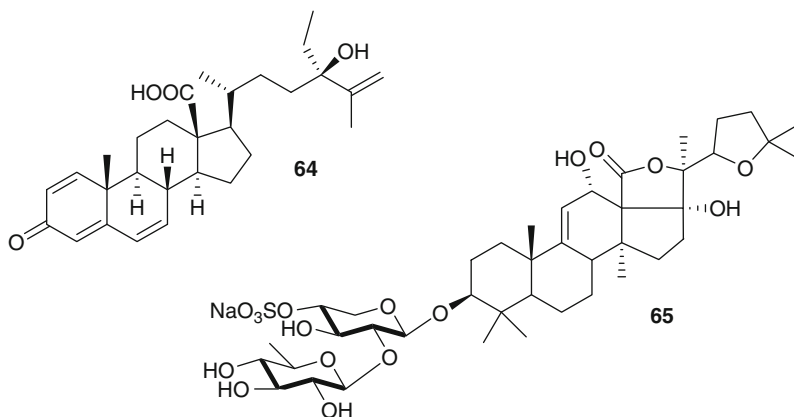
while parasites lack the de novo pathway, mammals have de novo and salvage purine synthesis pathways. Isoakaterpin is the first marine natural product to show inhibition of APRT; however, since its chemical structure is relatively similar to that of other marine meroterpenoids, further investigations of this class of compounds would be particularly interesting.

The phenol moiety is also present in the structure of the marine sesquiterpene (+)-curcuphenol isolated from sponges of the genera *Didiscus* and *Myrmekioderma* showing a moderate activity against *Leishmania* spp. ($IC_{50} = 11 \mu M$). A number of semisynthetic derivatives of (+)-curcuphenol showing esterification of the phenol group have been prepared and evaluated against protozoan parasites [79]. In particular, compound **62** showed a dramatic increase of the antileishmanial activity compared to the parent compound ($IC_{50} = 0.6 \mu M$). The basicity of the pyridine ring is likely to be important in this activity increase since analogues showing a phenyl or an indole in place of the pyridine proved to be less active.



Another sesquiterpene, euplotin C (**63**), isolated from the marine ciliate protist *Euplotes crassus*, showed a moderate activity ($IC_{50} = 4.6 \mu M$) against two *Leishmania* species [80]. The highly oxidized steroids norselic acids A–E (e.g., norselic acid A, **64**), isolated from the Antarctic sponge *Crella* sp., showed antileishmanial activity in the 2- μM range [81]. These compounds are reminiscent of the dimeric sterols crellastatins, and they could be conceived as their monomeric units. Interestingly, these monomers lack the potent cytotoxicity exhibited by the corresponding dimers.

The coral reef sea cucumber *Actinopyga lecanora* afforded the previously reported tetraglycosylated triterpene holoturin A and the diglycosylated holoturin B (**65**), which share the same aglycone moiety. Holoturin B displayed a good in vitro and moderate in vivo antileishmanial activity [82].

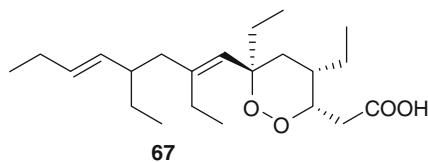
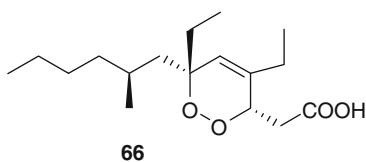


21.3.4 Endoperoxides

Endoperoxide polyketides from *Plakortis* sponges constitute a prominent class of marine antimalarials (see Sect. 21.2.2), but some of them have also been shown to exhibit a good antileishmanial activity, once again indicating the potential of this class of compounds for the treatment of parasitic diseases.

The Palauan sponge *Plakortis* aff. *angulospiculatus* afforded the two endoperoxide polyketide acids **66** and **67** which showed inhibition of growth of *Leishmania mexicana* with LD₅₀ = 0.29 μg/mL and 1.00 μg/mL, respectively [83]. The enantiomer of **67** was later isolated from a Korean specimen of *Plakortis* sp. [84] and found to exhibit exactly the same activity of **67**. This enantiomer was then coupled at the C1 position of ircinol A, and the ircinol-cyclic peroxide ester exhibited an increased antileishmanial activity with IC₅₀ = 0.7 μg/mL [85]. Furthermore, plakortide P, a diastereoisomer of **67**, showed leishmanicidal activity with IC₅₀ = 1.9 μg/mL [86]. In the same study, the mode of action of plakortide P was investigated, and it was evidenced that it eliminated efficiently intracellular amastigotes by other than NO upregulation, probably involved in the specific leishmanicidal activity. It is interesting to notice that all these results on the antileishmanial potential of marine endoperoxide have been obtained practically

with molecules sharing the single carbon framework of **67**. Likely, a thorough investigation of the antileishmanial potential of the many endoperoxides isolated to date would give interesting outcomes.



21.4 Trypanosoma

21.4.1 Clinical Symptoms and Social Impact

Trypanosoma infections in humans show different clinical symptoms according to the specific protozoan involved in the human infection. African trypanosomiasis (sleeping sickness) is caused by *Trypanosoma brucei gambiense* (representing more than 90% of reported cases) and *T. brucei rhodesiense* (found in Eastern and Southern Africa, it accounts for less than 10% of reported cases) [87]. These parasites are transmitted to humans by tsetse fly (*Glossina* genus) bites which have acquired their infection from human beings or from animals harboring the human pathogenic parasites. At first the trypanosomes multiply in subcutaneous tissues, blood, and lymph. Then, the parasites cross the blood-brain barrier and infect the central nervous system. The process can take years with *T. b. gambiense*. When the parasites invade the central nervous system, they lead to behavioral changes, coma, and ultimately, if untreated, death. Disturbance of the sleep cycle, which gives the disease its name, is an important feature of this second stage of the disease. Tsetse flies are found throughout sub-Saharan Africa in vegetation by rivers and lakes, in gallery forests, and in vast stretches of wooded savannah, and, thus, sleeping sickness threatens millions of people in 36 countries with an estimated number of cases between 50,000 and 70,000 per year. The rural populations living in regions where transmission occurs and which depend on agriculture, fishing, animal husbandry, or hunting are the most exposed to the bite of the tsetse fly and therefore to the disease.

Treatment of African trypanosomiasis is based on molecules which were introduced at the beginning of the twentieth century. For the treatment of the first stage, pentamidine and suramin are the preferred treatments, while to treat the second, cerebral stage, the arsenic derivative melarsoprol is practically the only therapeutic option [88]. Melarsoprol has many disadvantages: it can induce a reactive encephalopathy (encephalopathic syndrome) which can be fatal (3–10%); moreover, an increase of resistance to the drug has been observed in central Africa. In recent

years, only one compound, DB2897 (a synthetic analogue of pentamidine), received serious clinical evaluation against African trypanosomiasis, but further development was discontinued in 2008.

Chagas' disease (South American trypanosomiasis) is caused by *T. cruzi* with the vector contribution of a blood-sucking insect (triatome), which bites the victim and contaminates the wound with infected feces. Disease may also be spread through blood transfusion and organ transplantation, ingestion of food contaminated with parasites, and from a mother to her fetus.

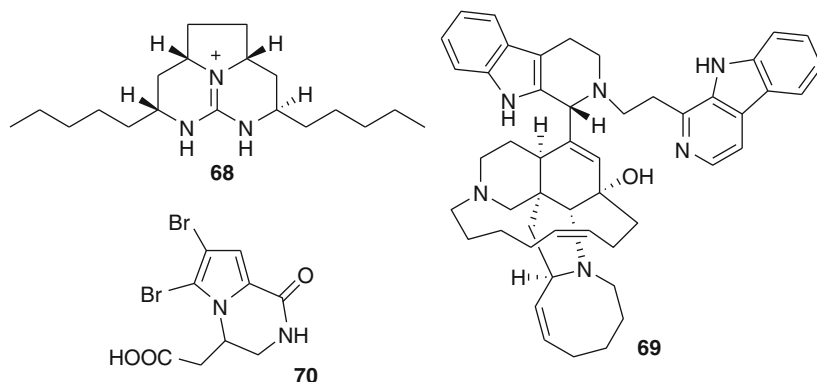
The symptoms of Chagas' disease vary over the course of an infection. In the early, acute stage, symptoms are mild, being restricted to local swelling at the site of infection. After 4–8 weeks, untreated individuals with still active infections enter the chronic phase of Chagas' disease. This is asymptomatic for 60–80% of chronically infected individuals, but 20–40% of them will develop life-threatening heart and digestive system disorders, including cardiomyopathy, which causes heart rhythm abnormalities and may result in sudden death. About one third of patients go on to develop digestive system damage, resulting in dilation of the digestive tract (megacolon and megaesophagus), accompanied by severe weight loss. It is estimated that as many as 8–11 million people in Mexico, Central America, and South America have Chagas' disease, some of whom do not know they are infected. There is no vaccine against Chagas' disease, and the currently available drug treatments are benznidazole (a 2-nitroimidazole) and nifurtimox (now no longer manufactured), which can cause side effects in many patients including skin disorders, brain toxicity, and digestive system irritation. Also in this case, the recent sequencing of *T. cruzi* genome promises to reveal new possible drug targets [89].

21.4.2 Marine Antitrypanosomal Agents

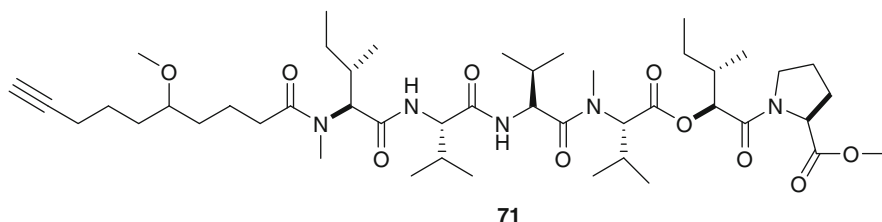
The number of marine natural products tested against trypanosomiasis is very limited, and less than ten molecules have shown encouraging results. These molecules, all grouped in this paragraph, belong to the classes of alkaloids, terpenes, and endoperoxide derivatives, thus closely paralleling the above-cited classes of antileishmanial compounds.

Merobatzelladine A (**68**) and its close analogue merobatzelladine B, tricyclic guanidine alkaloids with hexahydro-5,6,6a-triazaacenaphthalene ring system, isolated from the sponge *Monanchora* sp., inhibited *T. brucei* with $IC_{50} = 0.24 \mu\text{g/mL}$. The same molecules also exhibited a good antimalarial activity and antimicrobial activity against *Vibrio anguillarum* [90]. A new member of the manzamine family, zamamidine C (**69**), possessing a second β -carboline ring via an ethylene unit at N-2 of manzamine D, obtained from the sponge *Amphimedon* sp. [91], showed activity against *T. brucei* with an $IC_{50} = 0.24 \mu\text{g/mL}$, accompanied by antimalarial activity in the same concentration range. A recent investigation of the antiprotozoal activity of bromopyrrole alkaloids from Agelasida and Axinellida sponges [57] selected longamide B (**70**) as a promising agent against *T. brucei*

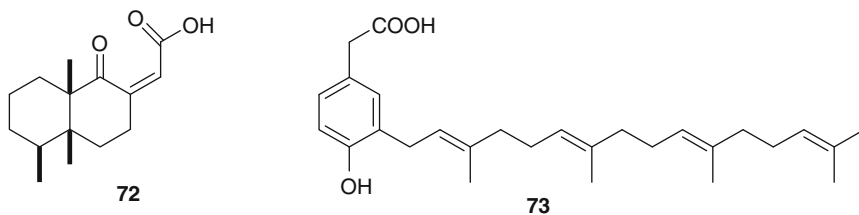
rhodesiense with $IC_{50} = 1.53 \mu\text{g/mL}$ and a selectivity index of 10. Since the related longamide A, showing a hydroxyl group in place of the $-\text{CH}_2\text{COOH}$, is inactive, this latter moiety should play a critical role for the bioactivity.



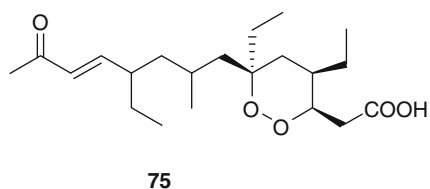
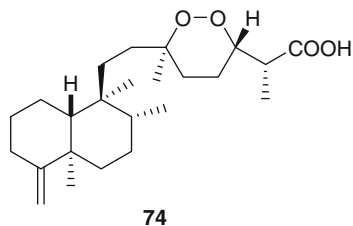
Viridamide A (**71**) is a lipopeptide from the cyanobacterium *Oscillatoria nigroviridis* which showed antitrypanosomal (against *T. cruzi*) activity with $IC_{50} = 1.1 \mu\text{g/mL}$ [92]. Viridamide A also exhibited significant activity against *Leishmania mexicana*.



A simple antitrypanosomal sesquiterpene, aignopsanoic acid A (**72**), has been recently obtained from the sponge *Cacospongia mycofijiensis* [93]. The activity of this compound against *T. brucei* was moderate ($IC_{50} = 6.0 \mu\text{g/mL}$), but, interestingly, the natural analogue showing isomerization of the carbon-carbon double bond geometry (*E* in place of *Z*) was about five times less active. The simple meroterpenoid **73** was found to be very active against *T. brucei rhodesiense* with $IC_{50} = 0.60 \mu\text{g/mL}$ [94].



Marine endoperoxy-containing derivatives proved to be active also against *Trypanosoma*, although a few studies have been carried out in this field. (–)-Sigmoidseptrellin B (**74**), isolated together with new and known peroxyterpenes from the marine sponge *Diacarnus bismarckensis*, showed a very good activity ($IC_{50} = 0.20 \mu\text{g/mL}$) against *T. brucei* [95], and it constitutes an excellent starting point for SAR modifications. Sigmoidseptrellin B had been evaluated also against *P. falciparum* but it showed only a moderate activity (see Sect. 21.2.2.2), lower than the antimalarial activity exhibited by its diastereomer sigmoidseptrellin A. Fractionation of the crude extract obtained from the Australian marine sponge *Plakortis* sp. led to the isolation of the polyketide endoperoxide **75**, which showed an IC_{50} value of 49 nM against *Trypanosoma brucei brucei* [96], qualifying it as one of the most potent marine natural product against African trypanosomiasis. A related compound with modified side chain showing a carboxylic acid group in place of the conjugated ketone group exhibited a 20-fold reduction of activity. The structural similarity between compound **75** and compound **67**, active against *Leishmania* (see Sect. 21.3.4), is remarkable.



21.5 Concluding Remarks

Infectious diseases caused by protozoan parasites, including malaria, African trypanosomiasis, Chagas' disease, and leishmaniasis, are major public health threats in developing countries where, according to the figures of World Health Organization, they affect about one billion people and cause more than one million deaths per year. These pathologies are often called "tropical diseases" or "neglected diseases" to express the relatively scarce attention that pharma industry devote to the development of effective therapies to prevent and treat them. It has been estimated that only 16 of the nearly 1,400 new drugs marketed between 1975 and 1999 were developed for the treatment of neglected diseases [97].

In recent years the drug discovery programs launched by academia and public agencies have resulted in the identification of some lead compounds to hopefully develop effective alternatives to the old drugs used, whose efficacy is diminishing due to the multidrug resistance developed by parasites and to severe side effects, sometimes completely preventing their utilization.

The aim of this chapter was to provide an overview of the most significant contributions given by marine research in the field of antiprotozoal lead compounds. Although this chapter cannot be considered exhaustive, we have listed

which we believe are the most interesting compounds against tropical diseases. Other marine compounds showing a high degree of cell toxicity or a too low level of activity have not been considered. Thus, the chapter includes about 70 marine secondary metabolites belonging to different chemical classes. It is noteworthy that some alkaloids, linear peptides, and endoperoxides appear to possess a broad-spectrum antiprotozoan activity. Manzamines, isonitriles as kalihinols, salinosporamide, plakortin (for the antimalarial activity), almiramides, isoakaterpin (for the antileishmanial activity), merobatzelladine, sigmosceptrellin B, and the endoperoxide polyketide **75** (for the antitrypanosomal activity) are, in our opinion, the most promising molecules emerging from this survey. Unfortunately, with the exception of manzamines, in none of these cases, the investigation has significantly surpassed the initial stage of assessment of *in vitro* (in very few cases, *in vivo*) activity. It should be admitted that, especially in the cases of antileishmanial and antitrypanosomal agents, the evaluation of marine natural products as antiprotozoan agents is still in its infancy. It is significant that practically all the antitrypanosomal agents cited in [Sect. 21.4.2](#) have been discovered in the last 2 years. Detailed structure–activity relationship studies, investigation of the mechanisms of action, optimization of the chemical structures for pharmacokinetics and pharmacodynamics, and complete evaluation of the toxicity profiles are greatly expected in the near future for marine antiprotozoans. Then, the big issue of the low-cost production of the selected molecule(s) will be open.

21.6 Study Questions

1. The *Target Product Profile* (TPP), published by Medicine for Malaria Venture (MMV), is a list of requirements that a new molecule should satisfy in order to be evaluated as clinical candidate for antimalarial therapy. Among these requirements, oral activity and a cost treatment that should be not more than 1\$ for simple malaria and 5\$ for cerebral malaria are of particular relevance. Should an antimalarial agent from the sea ever follow these indications? What is the role that antimalarials from the sea could play? Explain your answers in detail.
2. Propose a list of realistic requirements for a marine compound exhibiting antimalarial activity.
3. Propose a biosynthetic pathway for the polyketide plakortin (see [Sect. 21.2.2.2](#)). The key step is the formation of the endoperoxide linkage. Some alternative possibilities can be proposed for this step.
4. (a) The isonitrile group, very uncommon in natural products, is present in a series of terpenes with potent antimalarial activity. Propose a biosynthetic origin for this group. (b) The isonitrile group resembles the structure of carbon monoxide, a known ligand of heme Fe(II). Could this observation be important for the mechanism of action of antimalarial isonitriles?
5. Discovering untapped natural sources of novel antiprotozoal compounds remains a major challenge. Discuss how combinatorial chemistry and genomics can complete and/or guide this investigation on marine organisms.

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Mechanism-based Screening for Cancer Therapeutics with Examples from the Discovery of Marine Natural Product-based HIF-1 Inhibitors

22

Dale G. Nagle and Yu-Dong Zhou

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Abstract

Recent advances in cancer genetics combined with an increasing number of new methods in molecular and cell biology provide exciting new antitumor drug targets and a wide array of means to design bioassay systems for the discovery of novel cancer chemotherapeutics. Marine natural products continue to play a vital role in molecular-targeted antitumor drug discovery. Although most recognize the critical and expanding role mechanism-based antitumor bioassays play in modern anticancer drug discovery, few natural products chemists have specific training in bioassay technology. Critical bioassay development factors are outlined and introduced at a level intended to provide a basic understanding to

D.G. Nagle (✉) • Y.-D. Zhou

Department of Pharmacognosy, School of Pharmacy, The University of Mississippi, Oxford, MS, USA

e-mail: dnagle@olemiss.edu, ydzhou@olemiss.edu

a general audience. These include molecular target identification, antitumor target validation, selection of assayable biochemical processes, data acquisition methods, experimental controls, bioassay validation and statistical methods, experimental artifacts, active compound identification, and the dereplication of nuisance compounds. Marine natural products have been identified that inhibit the activation of the anticancer drug target hypoxia-inducible factor-1 (HIF-1). Bioassay systems and recent results from marine HIF-1 inhibitor discovery programs are used to illustrate important factors that must be considered when using molecular-targeted antitumor bioassay methods.

22.1 Introduction

Marine natural products research is a dynamic and constantly changing field that has evolved and adapted new technologies with cutting-edge molecular and cell biology. Modern high-field multidimensional nuclear magnetic resonance (NMR) methods facilitate the rapid structure elucidation of minute quantities of pharmacologically active natural products. Advances in microbial sourcing have yielded exciting new biological diversity. This is especially true in the field of marine natural products, where marine bacteria and fungi have begun to eclipse sponges and other invertebrates as important sources of novel chemistry (see ► [Chap. 3](#)) [1–5].

The activation of oncogenes and/or the inactivation of tumor suppressor genes plays an important role in the etiology and progression of cancer, an assemblage of diseases that result from accumulated mutations. Our knowledge of cancer genetics has expanded rapidly during the past few decades. Since the initial discovery of oncogenes, the field of cancer biology has grown to include the elucidation of the molecular mechanisms that underlie tumorigenesis, tumor growth, progression, metastasis, tumor cell death, and treatment resistance. As a result, mechanism-based drug discovery efforts have prospered and molecular-targeted agents (i.e., trastuzumab) are in clinical use. By integrating critical technological advancements with a growing number of important molecular mechanism-based antitumor targets, marine natural products research currently plays a vital role in anticancer drug discovery [6, 7]. In addition, newly developed strategies aim to alter the genetic regulation of secondary metabolite biosynthesis. Taken together, these advances show great promise to increase the structural diversity of natural products for drug discovery.

While the face of natural products chemistry has dramatically changed, the therapeutic potential of compounds identified in anticancer marine natural product programs remains inexorably tied to the quality of the bioassay methods used to direct the discovery efforts. In this respect, there is a fundamental need for cutting-edge molecular and biomedical research to support nearly all aspects of contemporary antitumor drug discovery. Most natural products chemists recognize the importance of excellent bioassays to support their research efforts. Yet, few chemists are specifically trained to critically evaluate the cell biology that supports the

potential significance of anticancer targets or the molecular biology involved in the design of molecular-targeted antitumor bioassay methods. To ensure the quality of these efforts, the most successful programs usually depend on strong collaborative research efforts with molecular and tumor cell biologists, pharmacologists, and experts in the design of high-throughput bioassay systems.

Important factors that must be considered when using modern molecular-targeted antitumor bioassay methods comprise a relatively short list of drug target-associated, bioassay method-dependent, and test sample source-specific factors. These may include, but are not limited to, the following list of points that require careful consideration: (a) identification of a molecular target; (b) validation of the antitumor target; (c) selection of a measurable biochemical, chemical, or biological process for the assay; (d) methods used to acquire or measure the data; (e) use of experimental controls; (f) bioassay validation and the application of appropriate statistical methods; (g) possible experimental artifacts; (h) active compound identification; and (i) nuisance compounds and methods for chemical dereplication. It may not be feasible to expect all natural products chemists to become experts in bioassay systems. Nonetheless, a general appreciation for these important assay components is critical to the success of every molecular-targeted antitumor drug discovery process.

The transcription factor hypoxia-inducible factor-1 (HIF-1) has emerged as an important target for anticancer drug discovery [8–12]. Hypoxic conditions (decreased oxygen tension) that are present within actively growing tumor masses activate HIF-1. The heterodimeric protein complex known collectively as HIF-1 then regulates the transcriptional response to tumor hypoxia [13]. Numerous natural products have been identified that regulate HIF-1 activation and suppress tumor-related HIF-1 target genes [14–16]. Because of its current distinction in the drug discovery process, HIF-1 has been selected as a representative example to demonstrate the importance of the previously outlined points that must be considered in the design and implementation of molecular-targeted bioassays used in the discovery of antitumor natural products. Screening efforts have shown the marine invertebrate and algal extracts in the U.S. National Cancer Institute's Open Repository to be a valuable source of new regulators of HIF-1 signaling [14]. Compounds isolated from marine organisms appear to either inhibit or promote HIF-1 activation. In addition to its coverage of basic concepts in molecular-targeted antitumor drug discovery, this chapter highlights the emerging role of marine natural products as potential regulators of HIF-mediated hypoxic signaling.

22.2 Bioassay Target Selection

Perhaps, nowhere in natural product-based drug discovery is bioassay target selection more important than in the field of molecular-targeted antitumor drug discovery. Traditional antitumor drug discovery has relied heavily on tumor cell viability assays for the identification of new natural product-based anticancer compounds [17–19]. Assay target selection consisted mainly of a choice in tumor cell lines and/or in the design of specific assays to discriminate between agents that

produce either a cytostatic or cytotoxic effect. In these cases, the bioassay target can be considered the tumor class, which is equated to the tumor cell line tissue source. Although this strategy may currently be considered less fashionable, it continues to produce some of the most promising anticancer marine natural products (salinosporamide [20, 21] and Yondelis/ET-743/trabectedin [22, 23]). Marine natural products researchers have taken advantage of modern high-throughput bioassays to identify new compounds that function through an assorted array of antitumor molecular targets [14].

The definition of an antitumor molecular target is somewhat subjective. One investigator may consider an enzyme/enzymatic activity, protein-protein interaction, or protein-DNA interaction as the molecular target. Superficially, enzymes such as receptor protein kinases, cyclin-dependent kinases, checkpoint kinases, topoisomerases, DNA polymerases, and other proteins that mediate important reactions can be thought of in this way. In this case, an antitumor molecular target is something as conceptually straightforward as a specific protein or protein-mediated biochemical reaction. However, another drug discovery group may consider the disruption of a genetically controlled process as the molecular target, even though many individual steps may be involved in regulating the control of the overall process. In this case, the molecular target is viewed more as a complex set of biochemical and genetic events that may involve many proteins or other macromolecules. Under this broader definition, antitumor molecular targets include such occurrences as apoptosis-related cellular signaling, mammalian target of rapamycin (mTOR)-regulated protein expression, proteasome-mediated protein degradation, heat shock protein-dependent protein stability, etc. This broader view also includes the targeting of specific genes and the transcriptional or translational events involved in protein-mediated processes. According to this broader definition, drug discovery groups may employ assays that specifically examine the effects of small molecules on the multistep processes that regulate the expression or function of genes that are considered to be important in tumorigenesis, tumor progression, or metastasis. In this light, oncogenic gene transcription and the proteins involved in regulating tumor-associated gene transcription have emerged as major targets for anticancer drug discovery programs that focus on the regulation of specific tumor-specific gene function [24].

The distinctions between various molecular target definitions quickly blur when one considers the interactions between the systems involved in each class of antitumor molecular target. Enzymes may be considered biochemical targets, but enzymes can regulate the synthesis of proteins that control gene expression. Similarly, oncogenes may code for the production of enzymes or other proteins that play an important role in biochemical processes that enhance the growth and spread of tumors. Oncogenes may also code for transcription factors that regulate the expression of other genes involved in tumorigenesis. In such cases, each specific step in the process of DNA replication, transcription, translation, and protein function may represent a potentially druggable step within a single molecular target.

Hypoxia is one of the signature features of the tumor microenvironment. The rapid growth of tumor cells outstrips the capacity of tumor blood vessels to supply oxygen. Newly formed tumor blood vessels often fail to mature, and the tumor blood flow is sluggish and irregular [25]. The combination of increased oxygen demand and insufficient oxygen delivery yields hypoxic regions that are commonly found in solid tumors. Clinical studies indicate that the extent of tumor hypoxia correlates with advanced disease stages and poor prognosis. Unlike normal cells from the same tissue, tumor cells are often chronically hypoxic [26]. Since hypoxia can activate both survival and death programs, it serves as a form of physiological pressure that selects for the oncogenically transformed cells with diminished apoptotic potential [27]. The tumor cells that have adapted to a hypoxic environment are more aggressive [25, 26, 28]. Because of hypoxia-associated resistance to radiation treatment and chemotherapy, hypoxic tumor cells are considered an important contributor to malignant progression and disease relapse [25, 26]. Approaches such as breathing carbogen (95% O₂, 5% CO₂) have been employed to overcome tumor hypoxia by increasing tumor oxygenation. Most of the initial drug discovery efforts target the direct effects of hypoxia – lack of cellular oxygen – by either discovering chemical sensitizers that improve the outcome of radiation or developing hypoxic cytotoxins that selectively kill hypoxic cells [25, 26]. No hypoxic cytotoxin is currently approved, and there is only one bioreductive drug (tirapazamine) in clinical trials [29]. Although mixed results have been reported from clinical trials with tirapazamine, it is undeniable that drugs that target tumor hypoxia have significant therapeutic potential as part of a combination therapy [30]. Clearly, tumor hypoxia represents an important unmet therapeutic need, and molecular-targeted drug discovery efforts should be directed at this target.

Hypoxia-inducible factor-1 is an important molecular target for anticancer drug discovery that targets tumor hypoxia. First discovered as the transcriptional activator that binds to the promoter of human erythropoietin (*EPO*) gene and activates transcription under hypoxic conditions [31], HIF-1 was later shown to regulate the expression of genes that promote cellular adaptation and survival under hypoxic conditions [32, 33]. For example, Semenza and coworkers [32, 33] have generally classified the HIF-1 target genes that enhance the survival of hypoxic tumor cells into the following major functional groups: (1) those that increase oxygen delivery by promoting erythropoiesis [erythropoietin (EPO), transferrin, etc.], angiogenesis [vascular endothelial growth factor (VEGF), etc.], and vasodilatation (heme oxygenase, nitric oxide synthase II, etc.); (2) those that decrease oxygen consumption by switching to anaerobic metabolism (glucose transporter 1, glycolytic enzymes that include hexokinase 1, hexokinase 2, aldolase A, enolase 1, lactate dehydrogenase A, etc.); and (3) those that promote autocrine growth/survival (insulin-like growth factor II, etc.). Recent studies indicate that HIF-1 also regulates the expression of genes that are involved in processes ranging from tumor cell immortalization, genetic instability, dedifferentiation, invasion, metastasis, to treatment resistance [32–34]. These observations suggest that HIF-1 plays an important role in the etiology and malignant progression of cancers.

22.3 Molecular Target Validation

Molecular target validation is the process of establishing that a potential molecular target is essential for a disease process and that inhibition (or dysregulation) of that specific target can produce a potential therapeutic benefit. Screening efforts that use poorly validated antitumor molecular targets can be extremely expensive and time consuming in identifying active compounds that may fail to produce a significant antitumor effect in living cells. Demonstrating that a drug or other representative inhibitor of the molecular target produces the desired therapeutic outcome in patients may be the ultimate form of target validation. For example, the validation of antitumor targets such as tubulin/microtubules or topoisomerases may be considered solidly validated as druggable molecular targets by the therapeutic efficacy of the microtubule-targeted anticancer drugs vincristine and paclitaxel and by the topoisomerase inhibitors topotecan and etoposide, respectively. However, most innovative molecular-targeted marine natural product discovery programs aim to identify potential new agents that function through nontraditional mechanisms, rather than simply seek to isolate compounds that act in the same manner as clinically approved drugs. Under these conditions, molecular target validation can be considered the construction of an evidence-based case to support the essential nature and causative role of the target to a specific disease. Evidence to validate the target can come from clinical studies, but is most often derived from a combination of *in vitro* and preclinical animal-based experimental results.

Drugs often fail in clinical studies because they either do not produce the desired therapeutic effect or because they exhibit severe side effects, or toxicities, that render them unsafe for patient use [35]. Both reasons for the clinical failure of new drugs have been attributed to a lack of thorough target validation [35]. Therefore, it is essential to design a strategy for target validation that not only evaluates the therapeutic relevance of the target but that will also examine the specificity of the molecular target for the biochemical or physiological processes that contribute to the disease process. This is crucial in order to discriminate between disease-specific activity and off-target-related effects. While many *in vitro* cell-based methods (e.g., DNA-microarray or proteomic-based systems) are widely used in target validation, the most convincing data usually come from those models that more closely represent the disease condition in humans [36]. Various forms of gene/target knockout models are used to examine the physiological relationship between a specific gene, or gene product protein, and a particular disease phenotype. Traditional gene knockout methods (e.g., homologous recombination-based methods) and alternative gene knockdown or silencing methods (e.g., RNA interference) have proven invaluable as *in vivo* means to validate the critical role of a selected molecular target for a specific disease process [37]. Data from animal-based models that include physiological, genomic, or proteomic results from *in vivo* models are generally considered important for reliable target validation [35].

As a model for a validated antitumor drug target, multiple lines of evidence support the critical involvement of HIF-1 in the growth, progression, and metastatic spread of various forms of cancer [8–12]. In line with the laboratory findings, clinical studies indicate that overexpression of the oxygen-regulated HIF-1 α protein correlates with advanced disease stages, treatment resistance, and poor prognosis among patients with tumors derived from tissues that range from brain to breast [25, 26]. In general, the availability and activity of the oxygen-regulated HIF-1 α subunit determines the activity of HIF-1, a heterodimer of the bHLH-PAS (basic helix-loop-helix–PER-ARNT-SIMM) proteins HIF-1 α and HIF-1 β /ARNT (aryl hydrocarbon receptor nuclear translocator). Under normoxic conditions, HIF-1 α protein is degraded rapidly (protein half-life <5 min) while HIF-1 β protein is constitutively expressed. In many of the clinical specimens examined, the expression of HIF-1 α protein is directly linked to the extent of tumor hypoxia. The decrease in oxygen tension inhibits the hydroxylases that tag HIF-1 α protein for degradation and inactivation. The stabilized HIF-1 α protein then translocates into the nucleus, heterodimerizes with HIF-1 β protein, binds to the hypoxia response elements (HREs), and activates transcription of HIF-1 target genes (Fig. 22.1). In other cases such as renal clear cell carcinoma, HIF-1 α protein is expressed at high levels even under well-oxygenated conditions [38]. One of the molecular mechanisms for hypoxia-independent induction of HIF-1 α protein is the loss of function of the tumor suppressor von Hippel-Lindau gene (VHL). The VHL gene product pVHL mediates the degradation of HIF-1 α protein by proteasome. In the presence of oxygen and iron, HIF-1 α proteins are modified posttranslationally by prolyl hydroxylases [39–41]. The prolyl hydroxylated HIF-1 α proteins are then recognized by pVHL, polyubiquitinated by the pVHL-associated E3 ubiquitin ligase complex, and degraded by the proteasome. Inactivation of pVHL due to loss of function prevents the degradation of HIF-1 α protein. As a result, HIF-1 is activated under normoxic conditions and the HIF-1 regulated pathways such as angiogenic processes are highly active. In addition to the loss of function of VHL, other tumor-specific mechanisms that induce HIF-1 α protein and activate HIF-1 in a hypoxia-independent manner include the activation of oncogenes such as ras (rat sarcoma viral oncogene homolog), src (avian sarcoma viral oncogene), myc (avian myelocytomatosis viral oncogene homolog), and the loss of tumor suppressor genes such as PTEN (phosphatase and tensin homolog) [42, 43].

Results from numerous animal-based studies further support the notion that HIF-1 is an important molecular target for anticancer drug discovery [44, 45]. In general, overexpression of a gene product in tumor cells does not necessarily support the role of that particular gene as a molecular target for cancer therapeutics. It is anticipated that the inhibition of a true molecular target will suppress tumor progression, while the activation of a molecular target will promote tumor progression in animal-based models. Most of the animal-based studies that substantiate HIF-1 as a target for molecular-based therapeutics focus on the HIF-1A gene.

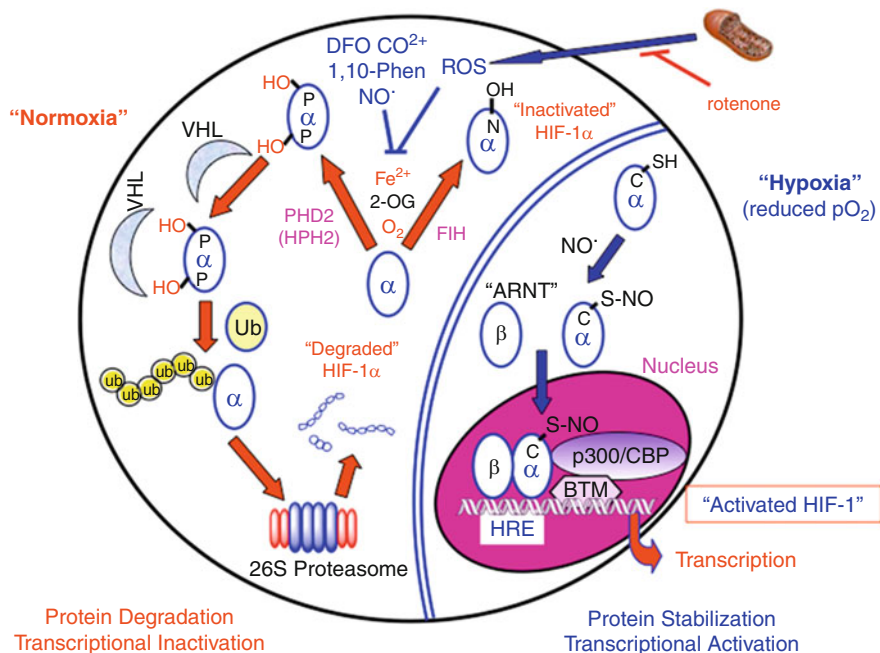


Fig. 22.1 Hypoxic regulation of hypoxia-inducible factor-1 (HIF-1). The transcription factor HIF-1 is a heterodimer composed of an HIF-1 α subunit that is regulated by cellular oxygen levels and an HIF-1 β subunit (also known as ARNT) that is constitutively expressed. Under normoxic conditions, HIF-1 α protein is hydroxylated at specific proline residues by Fe²⁺/2-oxoglutarate/O₂-dependent prolyl hydroxylase enzymes (e.g., PHD2). This prolyl-hydroxylation “tags” HIF-1 α protein for von Hippel-Lindau tumor suppressor protein (pVHL)-E3 ubiquitin ligase-mediated polyubiquitination. The “ubiquitin-tagged” HIF-1 α protein is then rapidly degraded by the 26S proteasome. Hydroxylation of an asparagine residue in the C-terminal transcriptional activation domain (CTD) contributes another level of oxygen-dependent regulation by inactivating HIF-1 α protein. Like PHD2, this asparaginyl hydroxylase [“factor inhibiting HIF” (FIH)] is also an Fe²⁺/2-oxoglutarate/O₂-dependent hydroxylase that modifies the asparagine residue in the CTD region of HIF-1 α protein. Once hydroxylated, the interaction between HIF-1 and the coactivator CBP/p300 is disrupted and transcriptional activation is blocked. Besides hypoxic conditions, HIF-1 α protein can be stabilized by addition of iron chelators, transition metals, nitric oxide radical (NO⁻), or inhibitors of PHDs [e.g., dimethylxaloylglycine (DMOG)]. Such inducing conditions inactivate the prolyl hydroxylases that tag HIF-1 α protein for ubiquitination and proteasomal degradation, and suppress the asparaginyl hydroxylase that normally inactivates the transcriptional activity of HIF-1. In addition, binding between HIF-1 and CBP/p300 can be enhanced by direct nitrosylation of a sulfhydryl moiety in HIF-1 α . When the level of O₂ decreases to a level below a certain threshold, reactive oxygen species (ROS) generated by hypoxic mitochondria inhibit PHD2 and FIH by oxidizing the Fe²⁺ in their catalytic sites. Natural products that inhibit the mitochondrial electron transport chain (e.g., rotenone) block HIF-1 activation by suppressing the hypoxia-induced increase in ROS production by mitochondria. This promotes the PHD2-mediated degradation and FIH-facilitated inactivation of the HIF-1 α subunit (Figure and caption reproduced with the permission of D.G. Nagle [© 2010] at the University of Mississippi)

22.4 Selection of Measurable Biochemical Processes Suitable for Bioassay Development

Since HIF-1 is a transcription factor, a cell-based reporter assay should be selected as the method to monitor the activity of HIF-1. Upon induction and activation, HIF-1 binds to the HRE present in the promoter region and activates transcription of the reporter gene [45, 46]. In general, the reporter gene may encode an enzyme such as luciferase, whose activity can be easily measured in a high-throughput format. The activity of the reporter (e.g., luciferase) correlates with the expression of the reporter gene that serves as an indicator of HIF-1 activity. It is anticipated that compounds/extracts that activate HIF-1 will increase the activity of the reporter, while HIF-1 inhibitory compounds/extracts will decrease the reporter activity. The advantage of such a cell-based reporter assay is that it will detect a wide range of chemicals with dissimilar mechanisms of action. The challenge is that it may take considerable effort to resolve the mechanism(s) of action once the active compounds are identified. In the event that the active compound(s) has been well characterized, the compound may serve as a molecular probe to further investigate the crosstalk between signaling pathways.

In contrast, assays that monitor one specific step within a signaling pathway will facilitate the discovery of active leads with a defined mechanism of action. For example, an assay measuring the activity of a particular kinase can be used to identify inhibitors of that particular kinase. Among the approaches used to discover HIF-1 inhibitors, one is to identify compounds that can disrupt the interaction between HIF-1 and the coactivator CBP/p300 [(cAMP-response element-binding protein)-binding protein/E1A-binding protein, 300 kD] [47]. In general, the activity of HIF-1 is determined by the availability and activity of the oxygen-regulated HIF-1 α subunit (Fig. 22.1). In the presence of oxygen and iron(II), the HIF-1 α subunits are hydroxylated by prolyl hydroxylases, and this posttranslational modification triggers pVHL-mediated proteasome degradation of HIF-1 α proteins [39–41]. Upon a reduction in cellular oxygen levels or in the presence of iron chelators, the hydroxylation reaction is inhibited and the stabilized HIF-1 α proteins translocate into the nucleus, heterodimerize with HIF-1 β subunits, and activate gene transcription. The interaction between HIF-1 and CBP/p300 enhances the formation of the transcriptional initiation complex and increases the transcription of target genes. Oxygen-dependent asparaginyl hydroxylation of HIF-1 α protein (Asn803) by factor inhibiting HIF (FIH) abrogates the interaction between HIF-1 and CBP/p300. To discover disruptors of HIF-1 α /p300 interaction, Kung and colleagues employed a time-resolved fluorescence high-throughput screening assay to detect the binding between a 41-amino-acid HIF-1 α -derived polypeptide representing the minimal p300/CBP binding domain and a glutathione-S-transferase (GST) fusion protein that contains the 122-amino-acid minimal HIF-1 α -binding domain from p300 (GST-CH1) [47]. The biotinylated HIF-1 α -derived polypeptide was immobilized onto streptavidin-coated plates. The interactions between the HIF-1 α polypeptide and the GST-CH1 fusion protein were examined using time-resolved fluorescence to monitor a europium-conjugated anti-GST

antibody probe. A library of >600,000 natural products and synthetic compounds was evaluated, and the dithiodiketopiperazine metabolite chetomin was identified as a submicromolar inhibitor of HIF-1 α /p300 interaction. The advantage of such a biochemical process-based assay is that it can be used to discover active compounds that selectively target a specific predetermined mechanism. However, some of the active compounds identified in this type of *in vitro* assays may not be further pursued if they fail to demonstrate efficacy in cell-based systems. In the case of chetomin, it exhibited anticancer efficacy *in vivo*. Since the CH1 domain is also required for CBP/p300 to serve as a coactivator to other transcriptional activators, the relative “nonspecificity” and subsequent toxicity prevented the further development of chetomin as a chemotherapeutic drug.

Small-molecule HIF-1 inhibitors have also been identified using other approaches such as an ELISA (enzyme-linked immunosorbent assay)-based assay that detects the interaction between the HIF-1 α and HIF-1 β PAS A domains [48]. As previously discussed, biochemical process-based *in vitro* assays may facilitate the discovery of HIF inhibitors that target one specific mechanism or process. For enzyme-based assays, the recombinant protein should retain the native and active conformation. Active compounds identified from the screening effort may have a higher possibility of being active in cell-based assays, if they can penetrate the host cells. In the case of *in vitro* assays that monitor protein interactions, the proteins used are often only polypeptides or otherwise truncated proteins that contain the domain(s) of interest. These “protein” reagents may not retain the native conformation that is required for proper binding. As such, a large percentage of the actives from the primary screening efforts with such biochemical assays may fall out of the “hit list” when evaluated in cell-based systems. In addition, further studies are still required to discern the specificity and the bioavailability of active compounds before the agent can be advanced to animal-based studies.

22.5 Techniques Used to Acquire or Measure the Bioassay Data

Following rapid advances in molecular techniques, most of the assay-related reagents are available from commercial sources. For screening purposes, it is important to select the method(s) that is suitable for a high-throughput format as well as cost effective. In the case of discovering small-molecule HIF-1 inhibitors, we have chosen a cell-based luciferase assay as the format for primary screening [49]. In this cell-based assay, the activity of HIF-1 correlates with the enzymatic activity of the luciferase reporter. The luciferase assay itself is straightforward, and the reagents are readily available from commercial sources. In addition, other accessories such as cell culture plates and plate readers are available in both 96- and 384-well format for the purpose of screening. Cell-based reporter assays require cellular uptake of the reporter constructs by either transient or stable transfection. The transient transfection method is relatively fast, but the cells need to be transfected every time the assay is performed. The stable transfection approach is relatively time consuming in regard to the initial effort to establish

a genetically modified cell line that has incorporated the reporter construct into its genome. However, once a stable cell line is established, the cells can be directly assayed without transfection.

Upon selecting a transient transfection approach for our HIF-1 inhibitor discovery efforts, the initial studies were directed at identifying the optimal model system for the cell-based reporter assay. A panel of human breast tumor cell lines that represent different disease stages and malignant progression were selected as *in vitro* models (early stage estrogen dependent: T47D and MCF-7; highly metastatic estrogen independent: MDA-MB-231). First, the conditions for transient transfection were optimized in each cell line using a control construct (pGL3-control, Promega) that expresses luciferase under the control of a constitutively active promoter. Second, a cell-based reporter assay for HIF-1 activity was performed in each cell line. The objective was to identify the cell line with the highest level of HIF activation. In order to improve screening efficiency, a robust assay with a high level of induction was sought to provide a low rate of background noise-associated false-positive experimental artifacts. The cells were transiently transfected with the pHRE3-TK-luc reporter to monitor HIF-1 activity and exposed to inducing conditions that activate HIF-1. The conditions that activate HIF-1 range from hypoxia (decreased oxygen tension), iron chelators, transition metals (Co^{2+} , Ni^{2+} , etc.), to oncogenic mutations (activation of oncogenes and/or inactivation of tumor suppressor genes). In solid tumors, hypoxia is a common pathophysiological condition and the extent of tumor hypoxia correlates with advanced disease stages and poor prognosis. Since HIF-1 is a key regulator of hypoxia-regulated gene expression that promotes tumor cell adaptation to hypoxia and overall treatment resistance, compounds that inhibit hypoxic activation of HIF-1 represent potential drug leads that selectively target tumor hypoxia. The focus of our discovery project was the identification of small molecules that inhibit HIF-1 activation by hypoxia. Among the cell lines examined (Fig. 22.2), T47D breast tumor cells exhibited the highest level of HIF-1 induction upon hypoxic exposure (1% O_2 /5% CO_2 /94% N_2 , 16 h). This T47D cell-based HIF-1 reporter assay produced the greatest signal to noise (background) ratio. The effectiveness of the cell-based reporter assay for detecting HIF-1 inhibitors was examined with a known HIF-1 inhibitor, MEK1 (meiosis-specific serine/threonine protein kinase) inhibitor PD98059. In MCF-7, MDA-MB-231, and T47D cells, PD98059 inhibited HIF-1 activation by hypoxia with comparable potencies (Fig. 22.3). Further cell viability studies in T47D cells excluded the possibility of false positives due to cytotoxicity.

22.6 Design and Use of Proper Experimental Controls

In an ideal situation, all molecular-targeted screening efforts should be conducted in a statistically significant way ($N \geq 3$) to achieve accuracy and reliability. However, it is time consuming and not feasible for many small academic laboratories with limited resources to examine tens of thousands of samples in triplicate. To meet this challenge, one approach is to include some element of replication and

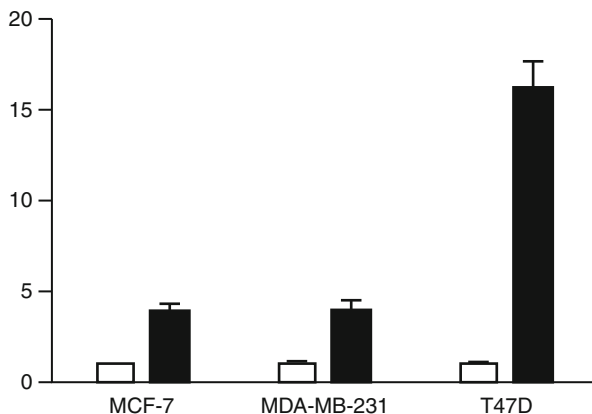


Fig. 22.2 Cell line-dependent hypoxic activation of HIF-1 determined in a cell-based reporter assay. Three human breast tumor cell lines (MCF-7, MDA-MB-231, and T47D) were transiently transfected with a pHRE-TK-Luc construct and exposed to hypoxic conditions (1% O₂/5% CO₂/94% N₂, 16 h). Control cells were incubated under normoxic conditions (95% air/5% CO₂, 16 h). The cells were lysed, and luciferase activity was determined and presented as relative luciferase activity to the control. Data shown are averages from one representative experiment performed in triplicate, and the error bars indicate one standard deviation

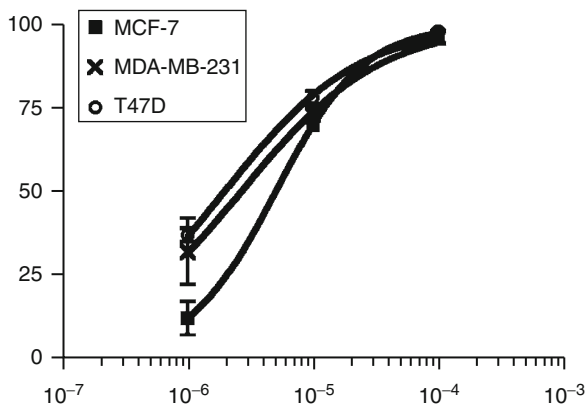
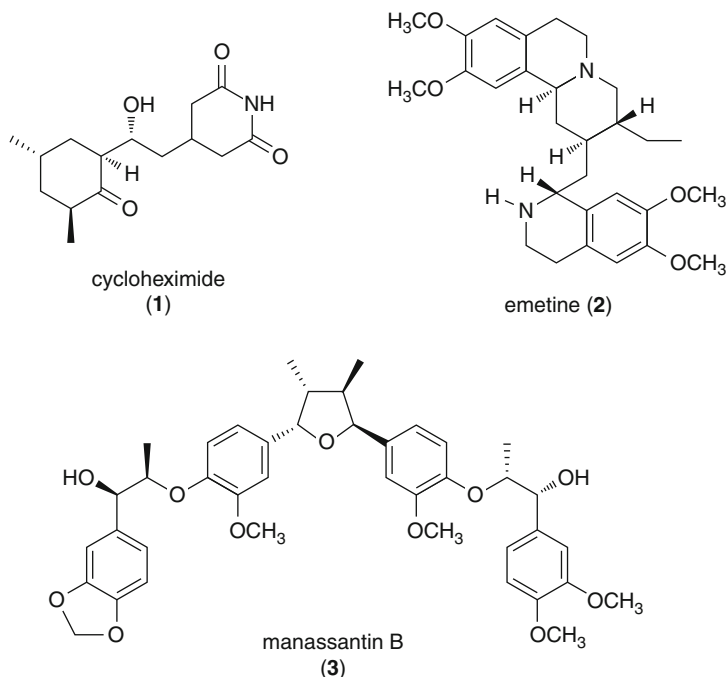


Fig. 22.3 PD98059 inhibits hypoxic activation of HIF-1 in a concentration-dependent manner. Human breast tumor cells (MCF-7, MDA-MB-231, and T47D) were transiently transfected with a pHRE-TK-Luc construct and exposed to hypoxic conditions (1% O₂/5% CO₂/94% N₂, 16 h) in the presence of PD98059 at the final concentrations of 1, 10, and 100 μM. The cells were lysed, and luciferase activity was determined and presented as percent inhibition of the solvent-treated control. Data shown are averages from one representative experiment performed in triplicate, and the error bars indicate one standard deviation

proper experimental controls to ensure the effectiveness of the bioassays. If an assay is deemed effective, then we can assume that the results obtained with the samples will have a higher probability of accuracy. In the T47D cell-based reporter assay for HIF-1 activity, the ratio of luciferase activity under hypoxic conditions

versus that under normoxic conditions serves as an indicator for the extent of HIF-1 activation. The inhibition of HIF-1 activity observed in the presence of an HIF-1 inhibitor (e.g., cycloheximide) (**1**) indicates the effectiveness of the assay for detecting HIF-1 inhibitors [50]. Other HIF-1 inhibitors have also been used as positive controls in HIF-1 bioassays. These positive controls include the nonselective alkaloid-based protein synthesis inhibitor emetine (**2**) [51–53] and *Saururus cernuus* dineolignan HIF-1 inhibitor manassantin B (**3**) [54].



Upon identification of the proper controls, another factor that impacts the screening outcome is the final concentration of the test sample. When the sample concentration is too high, nonspecific and/or less potent inhibitors will appear as positives in the assay, and this will lead to an unmanageably high hit rate. As shown in Fig. 22.4a, approximately 78% of the extracts on a 96-well sample plate inhibited HIF-1 activation by >50% when tested at the concentration of 50 $\mu\text{g}/\text{mL}$. In contrast, the hit rate in the primary assay was reduced to 2% when the same samples were examined at 5 $\mu\text{g}/\text{mL}$ (Fig. 22.4b).

22.7 Bioassay Validation and the Application of Appropriate Statistical Methods

The results of molecular-targeted antitumor assays can only be considered reliable if the experiments are properly controlled, the bioassay methods have been

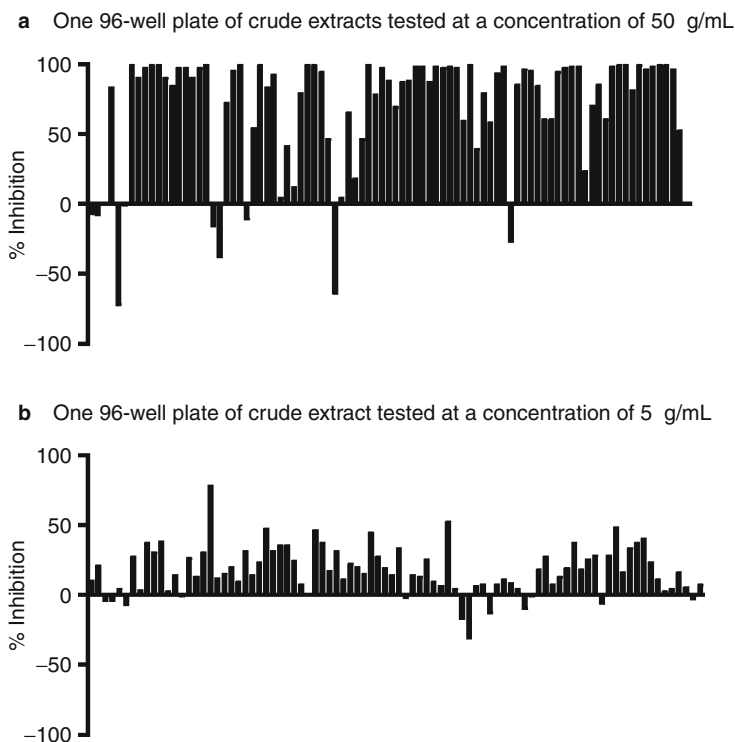


Fig. 22.4 Results for hypoxia-induced HIF-1 inhibitory effects observed for a representative 96-well plate of extracts evaluated at two different final concentrations. T47D human breast tumor cells were transiently transfected with a pHRE-TK-Luc construct and exposed to hypoxic conditions (1% O_2 /5% CO_2 /94% N_2 , 16 h) in the presence and absence of natural product-rich extracts. The cells were lysed, and luciferase activity was determined and presented as percent inhibition relative to a nontreated hypoxic control. **(a)** Approximately 78% of the extracts on a 96-well sample plate of chemically diverse plant extracts inhibited HIF-1 activation by $>50\%$ when tested at the concentration of 50 $\mu\text{g/mL}$. **(b)** When the identical 96-well plate of extracts was evaluated at a final concentration of 5 $\mu\text{g/mL}$, the corresponding hit rate in the primary assay was reduced to only 2%

rigorously validated, and the results are analyzed using suitable statistical methods for the particular bioassay design. Despite the fact that these criteria are necessary for the publication of manuscripts that specifically describe new bioassay methods, such standards are seldom given sufficient attention in publications that describe the biological activities associated with either marine or terrestrial natural products. It is relatively common to see publications that combine the isolation and structure elucidation, total synthesis, and other aspects of medicinal chemistry with biological testing results. All too often these reports focus on the natural products chemistry but fall short in respect to their standards for the bioassay acquisition methods and statistical data analysis. Experimental results are commonly reported

without including the data for positive or negative experimental controls, IC_{50} values are frequently reported without any indication of experimental replication, and structure-activity relationship studies are sometimes supported by tables of results that do not specify the magnitude of the observed experimental error or if the differences in bioactivity between structurally related compounds have statistical significance.

It is beyond the scope of this chapter to describe the statistical methods by which various molecular-targeted bioassays must be evaluated. However, recent articles, reviews, and texts provide a detailed perspective of statistical methods used to analyze and evaluate bioassay data [55–59].

In order to ensure the reliability of bioassays used to screen extracts, active chromatographic fractions, and purified natural products from marine organisms, these assays must be validated with respect to an array of assay parameters (robustness, linearity, accuracy, precision, sensitivity, and specificity). For our screening purposes, we define these bioassay validation terms in a similar manner to the “Guidelines for Industry” text on Validation of Analytical Procedures of the International Conference on Harmonisation (ICH) [60–62]:

- Assay “robustness” is a measure of an assay’s tendency to be susceptible to minor background variation in responses and is reflected by the magnitude of response (or signal) relative to background variation (or noise). Robust bioassays are generally more sensitive and require fewer replicates to observe statistical significance.
- Assay “linearity” is the ability of the assay to obtain test results that are uniformly proportional (within a specific range) to either the molecular/biochemical process evaluated or, in the case of analytical procedures, directly proportional to the concentration of sample.
- Assay “accuracy” is a measure of how close the results of the assay are relative to accepted reference or control values.
- Assay “precision” is the variation between multiple replicates and is generally expressed in terms of standard deviation, coefficient of variation, etc. Bioassay precision is a measure of experiment to experiment repeatability (intra-assay precision within a given laboratory), intermediate variation (between various equipment, personnel, etc.), and assay reproducibility between different laboratories. The sensitivity is a measure of the minimum detection limits of a bioassay method.
- Assay “specificity” is determined by the ability of the assay method to specifically respond to the desired molecular or biochemical process, relative to the bioassay’s susceptibility to false positives due to off-target effects produced by test substances.

Shen and colleagues took an siRNA (small interfering RNA)-based loss-of-function screening approach to identify potential druggable targets that control the HIF-1 pathway [63]. A non-small-cell lung carcinoma H1299 cell-derived stable HIF-1 reporter cell line (H1299_HRE) was established. Expression of this luciferase reporter was under the control of the HRE from the enolase promoter and hypoxic exposure increased luciferase activity by three- to fivefold. For assay

validation, H1299_HRE cells were transfected with an HIF-1A siRNA as a positive control and a scramble siRNA as a negative control. The transfected cells were exposed to hypoxic conditions and the luciferase activities determined. The assay used in this initial screening had Z-factor values that were greater than 0.5. This indicated that the H1299_HRE-based reporter assay was suitable for high-throughput screening. The Z-factor is a simple statistical parameter used to assess assay quality, defined as $Z\text{-factor} = 1 - [3 \times (\sigma_p + \sigma_n)] / |\mu_p - \mu_n|$ [64]. The four parameters are the means (μ) and the standard deviations (σ) of the controls [positive (p) and negative (n)]. An ideal assay will yield a Z-factor of 1, an excellent assay Z-factor between 0.5 and 1.0, a marginal assay Z-factor between 0 and 0.5, and a highly variable assay will produce a Z-factor less than 0.

Based on the Z-factor analysis, the H1299_HRE-based reporter assay was considered suitable for high-throughput screening (HTS) and was used to examine an siRNA library against approximately 4,000 druggable targets. However, confirmation studies revealed that the hits identified in the primary assay were caused by siRNA-mediated off-target gene silencing that nonspecifically inhibited HIF-1. The H1299_HRE cells were used to establish a 384-well-based reporter assay for HIF-1 activity. A library of 691,200 small molecules was examined in this assay (Z-factor 0.18), and this chemical genomics approach led to the identification of alkyliminophenylacetate compounds as potent HIF-1 inhibitors. The low Z-factor indicates that this latter HTS assay would have only marginal reliability.

22.8 Bioassay Method-Specific Experimental Artifacts

Every assay format has method-specific advantages and disadvantages. For the purpose of HTS screening, most bioassays employ colorimetric, fluorescent, or luminescent methods to measure the outcomes. In the case of marine organism extracts, many substances in the crude extracts can potentially interfere with fluorescence- or luminescence-based methods due to autofluorescence or quenching of the fluorescent and/or luminescent signals. To reduce the rate of false positives associated with method-related experimental artifacts, the active samples should be first evaluated in a secondary screening system that acts as a control for substances that particularly interfere with the selected bioassay method. For example, active extracts that inhibit HIF-1 activation in our previously described T47D cell-based reporter assay are then examined in T47D cells that are transfected with a control construct (pGL3-control) [49, 65]. The pGL3-control construct contains a simian virus 40 (SV40) promoter and enhancer sequences that strongly express a modified firefly luciferase reporter gene (luc+) in many mammalian cell lines. A false positive that inhibits the luciferase reaction and/or expression will also suppress luciferase activity in the tumor cells that have been transfected with the control construct. Similarly, active samples identified using a fluorescence-based method can be evaluated in a separate fluorescence-based assay for an unrelated target. In general, false positives associated with

a specific method will inhibit all similar assays that examine unrelated targets using the same assay method. In this respect, it is critical to establish a screening protocol that incorporates procedures that remove method-related experimental artifacts.

22.9 Identification of Active Marine Natural Products

Just as demonstrating clinical efficacy results is the most definitive form of target validation, the identification of therapeutically effective compounds that regulate the selected molecular target can be considered strong practical proof of bioassay validation. The subject of molecular-targeted anticancer marine natural product discovery has been reviewed with respect to antitumor compounds that were specifically identified through the use of molecular-targeted bioassays [6].

To date, only a relatively small number of marine natural products have been found to inhibit HIF-1 activation in various tumor cell lines (reviewed in 14). The University of Mississippi HIF discovery program identified most of these marine-derived HIF-1 inhibitors [66]. Over 10,560 lipid extracts of marine invertebrates and algae crude extracts have been evaluated in the primary T47D human breast tumor cell-based reporter assay for the ability to inhibit hypoxia-induced HIF-1 activation [49]. As previously described, the extracts were examined in the T47D cell-based reporter assay (5 $\mu\text{g}/\text{mL}$ = 5 ppm) and the threshold for actives was set at $\geq 70\%$ inhibition. Actives from the primary screen were subjected to a panel of additional bioassays designed to aid in the confirmation, prioritization, deselection, and dereplication process (Fig. 22.5).

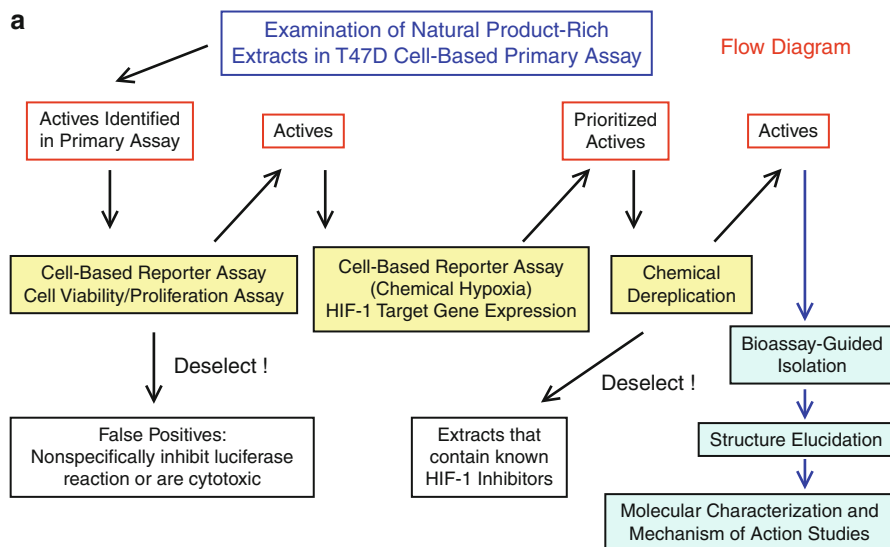


Fig. 22.5 (continued)

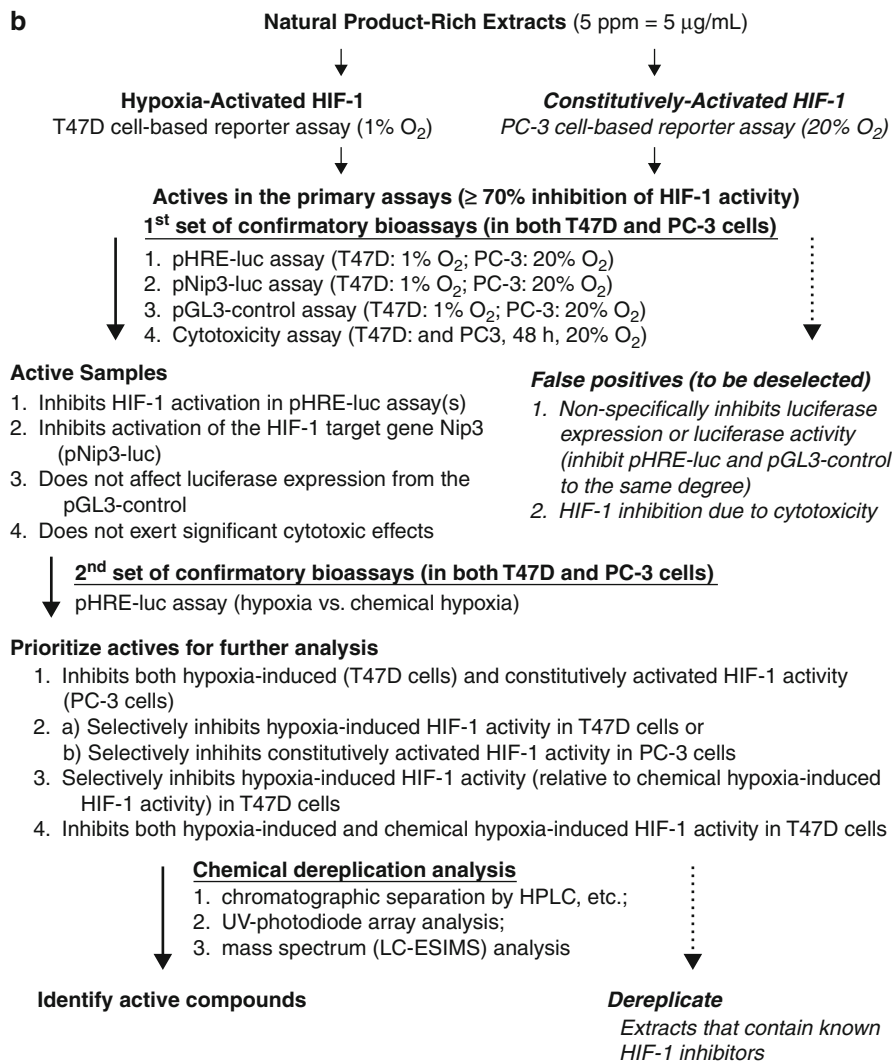


Fig. 22.5 Flow diagrams depicting representative bioassays used in HIF-1 inhibitor confirmation, prioritization, deselection, and dereplication process. (a) General flow diagram outlining HIF-1 bioassay evaluation system; (b) specific experimental protocols used to confirm, prioritize, deselect, and dereplicate extracts, fractions, and purified compounds detected in primary HIF-1 luciferase reporter assay system

Since the number of samples in the NCI Open Repository of marine invertebrate and algae extracts [67] was relatively large (10,560 lipid extracts), screening results from this large group of samples were analyzed and summarized in the following synopsis. A total of 109 active extracts (1% hit rate) were identified in the primary screen (Fig. 22.6a). Over one-half of the active samples were lipid extracts of marine sponges (57 out of 109). Although, a broad range of organisms were shown to have HIF-1 inhibitory activity (sea hares, algae, echinoderms, bryozoans, nudibranchs, and cnidarians). Active extracts were subjected to additional bioassays that include the following: (1) a pNip3-luc reporter assay for detecting substances that inhibit HIF-1 activation [68]; (2) a pGL3-control (Promega) reporter assay to deselect false positives that inhibit luciferase expression/activity [49, 65]; (3) a cell proliferation/viability assay to exclude cytotoxic extracts; and (4) a pHRE-TK-Luc reporter assay to confirm the initial results and discern the specificity toward the inhibition of low-oxygen (1% O₂) hypoxia-induced HIF-1 activation relative to the ability of chemical hypoxia [1,10-phenanthroline (10 μM)] to induce HIF-1 activation. Between 80% and 90% of the active extracts were confirmed upon retesting. Less than one-half of the samples suppressed tumor cell proliferation/viability by more than 50%. Over 50% of the active extracts showed selectivity for inhibiting hypoxia-induced HIF-1 activation over chemical hypoxia-induced HIF-1 activation. From the original 109 extracts that were active in the primary T47D cell-based reporter assay, 40 extracts (0.38% of the 10,560 extracts examined) withstood confirmatory secondary testing and were prioritized for further study (Fig. 22.6b). Samples from the NCI Open Repository are available on a first-come-first-serve basis, and the availability of many extracts is extremely limited. Supply-based prioritization suggested that only 33 extracts (out of the original 109 active extracts) were available from the NCI-Developmental Therapeutics Program (NCI-DTP) in sufficient quantity (typically 2–4 g) to guarantee any probability of successful bioassay-guided isolation and structure elucidation efforts, to ensure that the quantities of active pure compounds isolated would be adequate for *in vitro* mechanistic studies, and/or to evaluate for efficacy *in vivo*. Based on results from the biological confirmatory studies and the quantity of samples available, about one-third of the samples were assigned as “high-priority” for isolation efforts.

This synopsis exemplified several of the advantages of sourcing the NCI Open Repository – the large number of samples available for HTS assays, low-cost access to chemical diversity, logistical ease relative to investigator-initiated collection efforts and intellectual property negotiations, and the ability to identify new pharmacological activities even for “known” natural products. Efforts to source NCI samples are also associated with a number of disadvantages. These include limited sample availability due to previous use by other investigators and a lack of samples from microbial sources. Despite these possible disadvantages, a variety

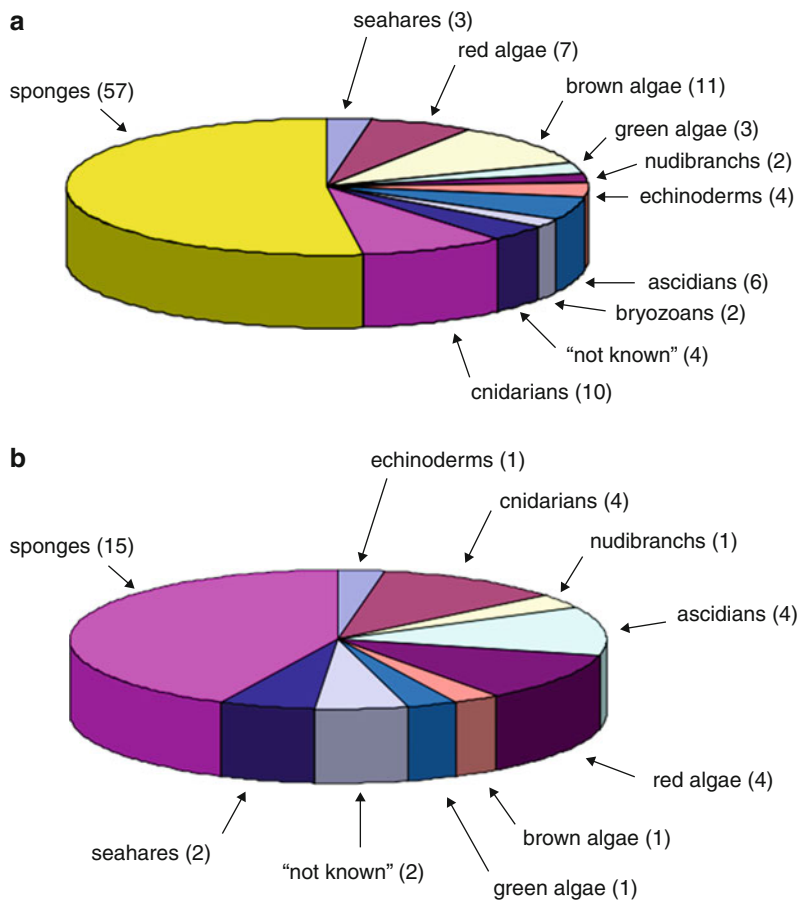


Fig. 22.6 Charts illustrating numbers and distribution of marine organism extracts found to inhibit HIF-1 activation in a cell-based reporter assay. Lipid extracts (10,560) from the NCI Open Repository of marine invertebrate and algae extracts were examined for the ability to inhibit hypoxia-induced HIF-1 activation in a T47D breast tumor cell line-based luciferase reporter assay. **(a)** Primary screening revealed 109 extracts strongly inhibited HIF-1 activation in the primary assay (a $\geq 70\%$ decrease in pTK-HRE3-Luc). **(b)** Only 40 extracts remained following secondary evaluation in assays designed to confirm and prioritize the samples that were shown to be active in the primary reporter assay. Extracts from a variety of marine organisms were found to contain substances that potentially inhibited hypoxic-induced HIF-1 activation (Figures and caption reproduced with the permission of D.G. Nagle [© 2010] at the University of Mississippi)

Table 22.1 Examples of marine natural products that inhibit HIF-1 activation

Compound name (no.)	Source	IC ₅₀ (μM) ^a	References
Laurenditerpenol (4)	<i>Laurencia intricata</i>	0.4	[70]
7-Hydroxyneolamellarin (5)	<i>Dendrilla nigra</i>	1.9	[53]
Furospogonide (6)	<i>Lendenfeldia</i> sp.	2.9	[72]
Sodwanone V (7)	<i>Axinella</i> sp.	15	[73]
9,9'-Oxybis-neocomantherin (8)	<i>Comantheria rotula</i>	0.8	[65]
Neocomantherin (9)	<i>C. rotula</i>	1.9	[65]
Comantherin (10)	<i>C. rotula</i>	2.7	[65]
5,8-Dihydroxy-6-methoxy-2-propyl-4 <i>H</i> -benzo[<i>g</i>]chromen-4-one (11)	<i>C. rotula</i>	0.6	[65]
8- <i>O</i> -Methylneocomantherin (12)	<i>C. rotula</i>	2.0	[65]
TMC-256A1 (13)	<i>C. rotula</i>	0.9	[65]
Comaparvin (14)	<i>C. rotula</i>	3.0	[65]
Mycalenitrile-6 (15)	<i>Mycale</i> sp.	7.8	[74]
Mycalenitrile-7 (16)	<i>Mycale</i> sp.	8.6	[74]
Caulerpin (17)	<i>Caulerpa</i> spp.	10	[75]
Strongylophorine 2 (18)	<i>Petrosia strongylata</i>	8 ^b	[76]
Strongylophorine 3 (19)	<i>P. strongylata</i>	13 ^b	[76]
Strongylophorine 8 (20)	<i>P. strongylata</i>	6 ^b	[76]
Latrunculin A (21)	<i>Negombata magnifica</i>	6.7	[52]

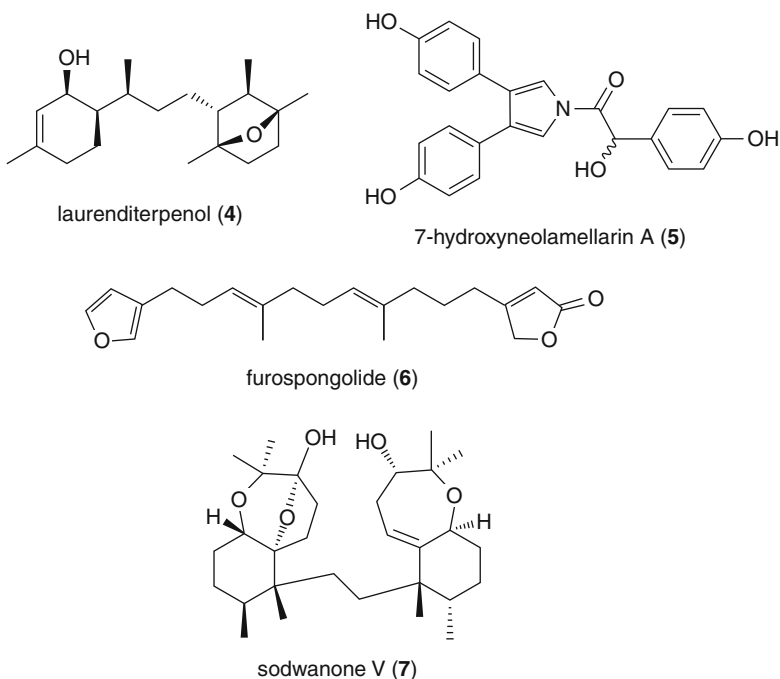
^a IC₅₀ values for hypoxia (1% O₂)-induced HIF-1 activation in a T47D cell-based reporter assay, unless otherwise noted

^b EC₅₀ values for hypoxia (1% O₂)-induced HIF-1 activation in a U251 cell-based reporter assay

of novel HIF-1 inhibitors were discovered from the available samples, and some of these were described in two recent reviews on natural product-derived inhibitors of HIF-1 (Table 22.1) [14, 69].

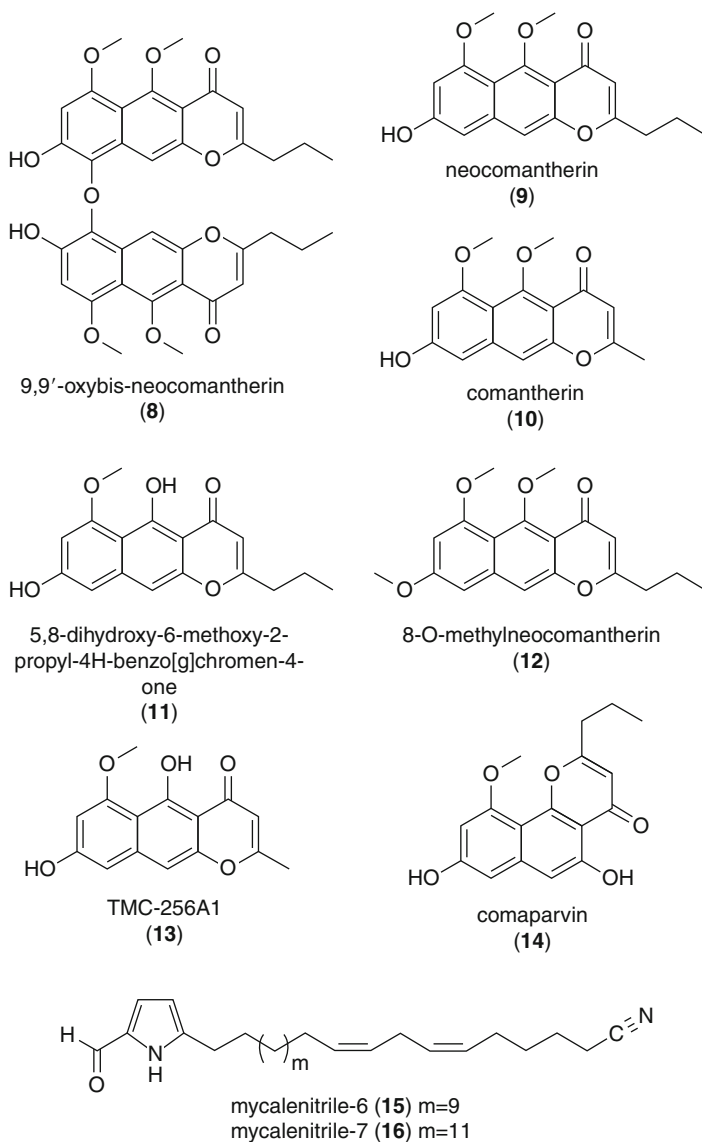
Once the active compounds were isolated, a combination of spectroscopic and spectrometric methods including multidimensional NMR spectroscopy and high-resolution mass spectrometry (HRMS) were employed to elucidate the structures of active compounds. This unique HIF-1 inhibitor discovery effort that combined the chemical diversity offered by natural products with effective and reliable bioassays has resulted in the identification of some of the most potent HIF-1 inhibitors known [16]. The first marine natural product found to inhibit hypoxia-induced HIF-1 activation in tumor cells was from the lipid extract of a Jamaican collection of the red alga *Laurencia intricata* Lamouroux (Rhodomelaceae). Laurenditerpenol (**4**), a novel bicyclic diterpene, was found to be the active constituent of the alga. Compound **4** inhibited hypoxia (1% O₂)-induced HIF-1 activation in T47D cells at submicromolar concentrations (Table 22.1) [70]. The absolute configuration of **4**

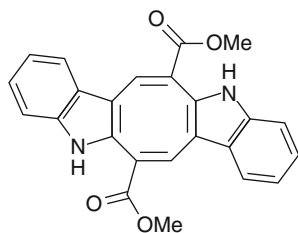
has recently been defined by total synthesis [71]. Total synthesis may also afford sufficient quantities of **4** and various related isomers for further biological evaluation and a study of structure-activity relationships (SARs).



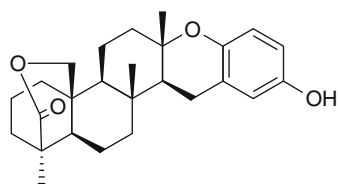
The NCI Open Repository of marine invertebrate and algae extracts has proven to be a valuable source of small-molecule inhibitors of HIF-1 activation. These marine natural product-based HIF-1 inhibitors include the sponge metabolites 7-hydroxyneolamellarin (**5**) [53], furospongolide (**6**) [72], and a series of sodwanone and yardenone triterpenoids [i.e., sodwanone V (**7**)] [73]. Similarly, benzo[*g*]chromen-4-one and benzo[*h*]chromen-4-one pigments (**8–14**) from a tropical marine crinoid (Comasteridae) were also found to inhibit hypoxia-induced activation of HIF-1 [65]. However, these benzochromenones were not further pursued because their ability to inhibit HIF-1 activation did not translate into a significant effect on the HIF-1 target genes examined (i.e., secreted VEGF) and, for all practical purposes, these crinoid pigments are now considered possible nuisance compounds. Recently, bioassay-guided fractionation of an active extract of a *Mycale* sp. sponge yielded 18 new and 8 previously reported lipophilic 2,5-disubstituted pyrroles, collectively known as mycalenitriles and mycalazals [e.g., mycalenitrile-6 (**15**) and mycalenitrile-7 (**16**)] [74]. The red pigment caulerpin (**17**) was first isolated from green algae of the genus *Caulerpa* [75].

Caulerpin (**17**) inhibited hypoxia-induced and 1,10-phenanthroline-induced HIF-1 activation [51]. The angiogenic factor VEGF is regulated by HIF-1. Caulerpin (10 μM) suppressed hypoxic induction of secreted VEGF protein and the ability of hypoxic T47D cell-conditioned media to promote tumor angiogenesis in vitro.

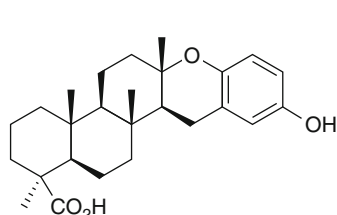




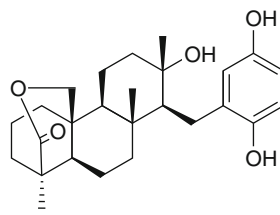
caulerpin (17)



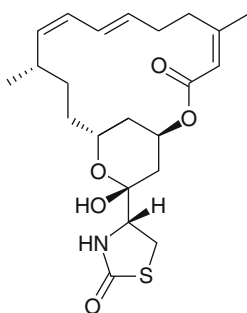
strongylophorine 2 (18)



strongylophorine 3 (19)



strongylophorine 8 (20)



latrunculin A (21)

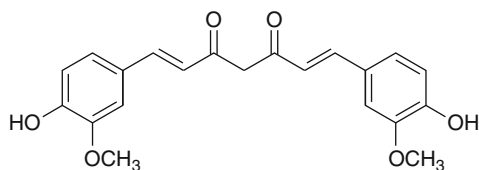
In addition to sourcing from the NCI Open Repository, several laboratories have reported the isolation and identification of HIF-1 inhibitors from their field collections of marine organism extracts. Ireland and coworkers recently found that an extract from a Papua New Guinea collection of the sponge *Petrosia (Strongylophora) strongylata* significantly inhibited HIF-1 activation at 1 $\mu\text{g/mL}$ [76]. Through a process of bioassay-guided isolation, three previously reported strongylophorine meroditerpenoids were identified to be responsible for the

observed HIF-1 inhibition. Strongylophorines 2 (**18**), 3 (**19**), and 8 (**20**) inhibited hypoxia-induced HIF-1 activation in a genetically engineered U251 human glioma cell-based luciferase reporter assay [76]. The Red Sea sponge macrolide latrunculin A (**21**) disrupts actin polymerization and inhibits microfilament formation by reversibly binding to actin monomers [77–79]. This sponge-derived actin inhibitor has recently been shown to inhibit hypoxia-induced HIF-1 activation in T47D cells [52]. Not only are these marine natural products inhibitors of HIF-1 activation in tumor cells, but many appear to function through mechanisms that have not yet been recognized to regulate HIF-1 activity. A summary of the marine-derived HIF-1 inhibitors discovered in this program is provided in [Table 22.1](#).

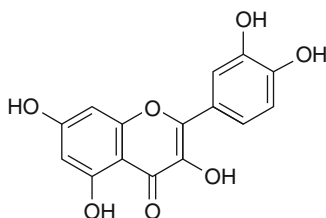
22.10 Dereplication of Nuisance Compounds

The concept of “nuisance” compounds is highly subjective and depends on the focus of the individual antitumor discovery group. In high-throughput screening, nonselective compounds that exert a variety of effects on various assay systems are typically considered nuisance compounds. Similarly, if the research program is solely interested in the discovery of novel chemical entities with a particular pharmacological activity, the researchers may consider all previously identified known compounds that show activity in other systems to be nuisance compounds. Each particular type of bioassay method is associated with assay-specific nuisance compounds. Chemically reactive compounds, including certain phenolic compounds, may nonselectively bind to proteins and inhibit enzyme-based assays [80, 81]. Pigments and other colored natural products can interfere with colorimetric assays. It is widely known that fluorescence-based assays may be susceptible to interference by fluorescent natural products [e.g., curcumin (**22**)] or compounds such as the flavonoid quercetin (**23**) that acts to quench the fluorescence [82]. Poorly controlled fluorescence-based bioassays have been used to support the premise that these natural products regulate a plethora of diverse molecular targets. Although less appreciated, pigmented and fluorescent natural products may also interfere with luciferase reporter gene assays that rely on fluorescent reagent formulations to enhance their light readouts. Cytotoxic natural products may be considered nuisance compounds when observed in cell-based bioassays that screen for inhibitors of a tumor cell selective molecular target. Similarly, compounds that do not penetrate cell membranes may be regarded as nuisance compounds in solution-based enzyme/protein-based *in vitro* assays. In such cases, whether or

not certain compounds are regarded as nuisance compounds depends on the particular objectives of the screening program.



curcumin (**22**)



quercetin (**23**)

Just as in other forms of natural product screening, molecular-targeted drug discovery programs that aim to identify marine natural product-derived anticancer agents must avoid the unnecessary replication of previously identified inhibitors (or activators) of the selected molecular target and common substances that exert nonselective effects on biological systems. One of the most powerful and inexpensive means to reduce the replication of chemical isolation and structure elucidation efforts in marine natural products is the use of chemotaxonomic literature related to the particular marine organism. Databases of marine natural products literature are readily accessible to most molecular-targeted drug discovery groups. These include general chemical (Chemical Abstracts Service (American Chemical Society)-SciFinder/SciFinder Scholar [83]) and biological (U.S. National Library of Medicine/National Institutes of Health-MEDLINE database accessible through PubMed [84]) databases. Highly specialized marine natural product databases (Marinlit [85]) that include searchable NMR and other spectroscopic data are also available and can greatly enhance chemical dereplication efforts. These databases can be used to identify known compounds and to distinguish previously reported redundant biological activities that may be associated with a particular marine natural product. Dereplication with chemotaxonomic data from chemical and biological literature databases is most efficient when examining well-characterized species of marine invertebrates and algae, but may be only of limited utility in screening programs that focus on poorly characterized new species of cultured marine microbes. One potential limitation of the use of chemotaxonomic literature for chemical dereplication efforts is that many species of marine organisms are

poorly characterized chemically as well as taxonomically [2, 86]. Since most marine natural products chemists are not in the habit of regularly reporting known compounds when they are found to occur in new species, estimates of the potential chemical diversity of many readily collectible species may be significantly underestimated. Chemical and biological dereplication for many of these species is often achievable by analysis of the chemotaxonomic and pharmacological literature related to other members of the same genera or taxonomic family. While practical limitations exist, the importance of chemical and biological databases in reducing the need for unnecessary marine natural product isolation and structure elucidation efforts cannot be overstated.

The subject of natural product dereplication has been the subject of recent reviews [87]. Compound dereplication strategies also commonly include various libraries of compound data sets that are used with a “hyphenated” technique that combines a purification method with a spectroscopic or spectrometric detection system. Sarker and Nahar have recently reviewed the field of hyphenated separation and spectroscopic/spectrometric techniques with respect to various classes of natural products [88]. Typical examples may include traditional methods such as high-performance liquid chromatography (HPLC) coupled with ultraviolet (UV) photodiode detection. Dereplication efforts have more recently come to rely on methods that combine liquid chromatography (LC) and mass spectrometry (MS) or nuclear magnetic resonance (NMR) spectroscopy. Tandem LC-MS and LC-MS-MS methods are among the most sensitive means to derePLICATE known compounds. While inherently less sensitive, coupled LC-NMR methods have the advantage that they can be simultaneously used for dereplication and the structure elucidation of new natural products. Hyphenated techniques and their use in the dereplication of natural products are further described in recent reviews [87].

The expenditure of unnecessary efforts due to the occurrence of natural products that act by relatively general means to produce numerous nonspecific effects in bioassay systems must also be reduced. The previously described methods of compound dereplication can be used to identify known compounds that exert nonselective effects on assay systems. Alternatively, experimental procedures with appropriate controls can be designed directly into the assay systems to dramatically cut the number of bioassay “hits” that result from active compounds with no selectivity for the molecular target. This strategy can readily deselect nuisance compounds without requiring any sample purification, chemical analysis, or other dereplication procedure. Examples of this type of bioassay design-based nuisance compound dereplication include the use of alternative isoforms of a particular enzyme in a parallel screening platform [89] and the concurrent measurement of cell viability with cell-based bioassays for a molecular target that should not produce a cytotoxic effect on certain cell types.

The need to derePLICATE known marine natural product HIF-1 inhibitors has only recently emerged as several groups have begun to identify marine invertebrate and

algae compounds that inhibit HIF-1 activation (reviewed in 14). The marine natural product-based HIF-1 inhibitors described in Table 22.1 include algal metabolites, crinoid benzochromenone pigments, latrunculin actin inhibitors, terpenes, and various lipids from marine sponges. In addition, various HIF-1 discovery groups have examined terrestrial natural products [15, 16] and synthetic pure compound libraries [63] and have reported that compounds that regulate certain central cellular biochemical processes may also suppress HIF-1 activation. Both academic and industrial HIF-1 screening efforts have found that mitochondrial electron transport chain (ETC) inhibitors suppress HIF-1 activation by hypoxia [63, 70], presumably by interfering with mitochondrial reactive oxygen species (ROS)-mediated signaling and destabilizing HIF-1 α protein under hypoxic conditions. The emerging role of mitochondrial reactive oxygen species (ROS) on the regulation of HIF-mediated hypoxic signaling is highlighted by a recent review by Hamanaka and Chandel [90]. New classes of unique ETC inhibitors have been identified that may prove to be pharmacological leads or valuable probes of HIF-1 signaling and mitochondrial function. However, at some point, these terrestrial and marine mitochondrial ETC inhibitors may be deemed biochemically active nuisance compounds, for the purpose of HIF-1 inhibitor drug discovery. Similarly, the expression of HIF-1 α protein and subsequent activation of HIF-1 can be strongly suppressed by pharmacologically active compounds that inhibit eukaryotic protein translation [15, 50, 91, 92]. While translation inhibitors have been found to inhibit HIF-1 signaling in tumor cells, the off-target effects associated with the generalized inhibition of protein synthesis may limit the therapeutic potential of these compounds and render such agents to be essentially nuisance compounds, at least for the purpose of bioassay dereplication.

22.11 Concluding Remarks

The field of antitumor marine natural products research has evolved over the years to incorporate an emphasis on molecular-targeted drug discovery. These changes have dramatically increased the appreciation among most natural products chemists for molecular and cell biology in natural product-based drug discovery. This shift in focus has also spurred a similar need for a general understanding of the factors that must be considered when using modern molecular-targeted antitumor bioassays. Researchers working in natural products must be acutely aware of the nature and validity of their selected molecular target, consider what particular methods their assays will use to measure the target processes, make sure appropriate controls are used, appreciate how the data will be analyzed, understand how the assay method will be validated, and establish suitable means for chemical dereplication. The scientific validity and clinical potential of any newly discovered antitumor natural product are only as solid as the reliability of the biological data that support its potential activity. This is true not only for the researchers involved in mechanism-based drug discovery; it is also true for those involved in the peer

review process. If manuscripts and grant proposals that involve molecular-targeted natural products research are not held to acceptable standards, the value of this discipline to the broader drug discovery community will be diminished. Therefore, an appreciation for all of these factors is essential for modern molecular-targeted antitumor drug discovery. Through mechanism-based drug discovery efforts, marine natural products have been identified that potently inhibit the hypoxia-induced activation of HIF-1 in tumor cells. As an important antitumor molecular target, the bioassay systems used in the identification of new HIF-1 inhibitors provide compelling examples to illustrate the various components of molecular-targeted bioassay design and analysis that are essential for the discovery of antitumor marine natural products.

22.12 Study Questions

1. Why is it important for natural products chemists (even those that do not perform their own bioassays) to have an understanding of the biological principles involved in bioassays and the important considerations used to evaluate assay quality?
2. Why are thoroughly validated and established molecular targets often less-exciting targets for novel drug discovery than newer, less fully validated, targets?
3. Why is the mere overexpression of a particular gene (or protein) in a disease condition insufficient to validate the gene (or protein) as a disease-specific molecular target?
4. What are the potential consequences of poor or inadequate molecular target validation in the drug discovery and development process?
5. What features of the transcription factor hypoxia-inducible factor-1 (HIF-1) make it a suitable representative molecular target to illustrate each of the principles involved in quality bioassay design and analysis?
6. What is the difference between bioassay validation and target validation?
7. Why is it critical for bioassay method validation to include both positive and negative control compounds?
8. Why is the definition of a bioassay “nuisance” compound in any particular bioassay considered to be subjective?
9. Why is compound dereplication so vital to a successful high-throughput screening assay-based drug discovery effort?
10. Chemical and biological literature databases are among the most economical sources of compound information regarding the production of specific natural products by any given species of organism. What are the practical limitations of literature databases in regard to the marine natural product dereplication efforts?

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Y. Nakao (✉)

School of Advanced Sciences and Technologies, Waseda University, 3-4-1, Okubo, Shinjuku-ku, Tokyo, Japan

N. Fusetani

Fisheries and Oceans Hakodate, Graduate School of Fisheries Sciences, Hokkaido University, 3-1-1, Minato-cho, Hakodate, Japan

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Abstract

Marine invertebrates are the rich source of small molecules with unique chemical skeletons and potent bioactivities; however, the major biological activities tested for marine natural products have been mainly limited to the traditional phenotype-oriented bioactivities such as cytotoxicity or anti-microbial activities. Enzyme inhibition is the target-oriented bioactivity and small molecule inhibitors are quite useful for controlling biological processes and understanding complicated biological phenomena. Recently, it has been recognized that the natural products are superior source of small molecule probes useful for the chemical biology. Especially, marine-derived enzyme inhibitors still remain to be fully investigated in spite of their high potentials as a source of unique compounds. In this chapter, selected enzyme inhibitors from marine invertebrates are described.

23.1 Introduction

Enzymes are vital to living organisms, maintaining the homeostasis of their lives by mediating/regulating numerous biochemical events, including metabolism, catabolism, cellular signal transduction, cell cycles, and development. Dysfunction, overexpression, or hyperactivation of the enzymes are often associated with human diseases as evidenced from the molecular-based analysis of diseases. Umezawa's pioneering work on enzyme inhibitors resulted in the discovery of

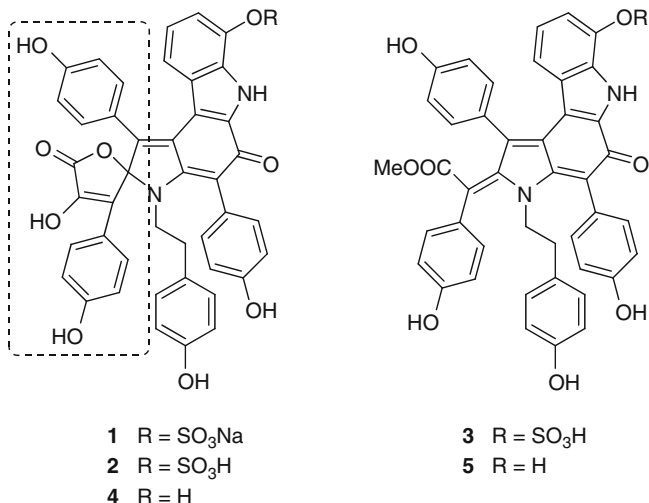
numbers of valuable compounds from terrestrial microorganisms [1]. Thereafter, search for small molecular enzyme inhibitors has been actively conducted in both academia and pharmaceutical industries, and a considerable number of enzyme inhibitors have been developed as drugs, including blockbusters such as statins. However, only recently, the majority of the marine natural products chemists started systematic programs for discovering enzyme inhibitors; the first systematic investigation was done by our group for H,K-ATPase inhibitors [2]. Although a large proportion of enzyme inhibitors reported from marine organisms were known compounds found to inhibit enzymes in the reevaluation of activities, these known compounds with new activities are important for the related research areas such as chemical biology. It may be predicted that the trends of marine natural products chemistry will move from finding merely “*new structures*” to finding “*new activities*” of known compounds. Recent reevaluation of natural products as a superior source of small molecule probes useful for studying biological phenomena is encouraging natural products chemists to investigate compounds with new activities.

In this chapter, we will describe the structures and activities of selected enzyme inhibitors isolated from marine invertebrates. Some inhibitors are not from marine invertebrates, but they are related to structures from microorganisms. Synthetic enzyme inhibitors based on the marine natural products are also described. Most of them were designed based on the crystal structures of enzyme–inhibitor complexes and gave a detailed insight into the modes of action. However, we excluded most of bromotyrosines, polyacetylenes, and highly sulfated steroids which are often termed “nuisance compounds,” because they show a variety of biological activities including inhibition of enzymes. Inhibitors are listed according to the classification of target enzymes (EC number).

23.2 Oxidoreductases (EC 1.-.-)

23.2.1 Aldose Reductase (EC 1.1.1.21)

Aldose reductase catalyzes the reduction of glucose to sorbitol with concomitant conversion of NADPH to NADP⁺. The highly activated enzyme under hyperglycemic environment results in unusual accumulation of sorbitol in the eye lens or peripheral nerves that lead to retinopathy, cataract, neuropathy, nephropathy, or cardio-vascular diseases. Three polycyclic *bis*-indoles (**1–3**) from a marine sponge *Dictyodendrilla* sp. strongly inhibited bovine lens aldose reductase with IC₅₀ values of 49, 125, and 112 nM, respectively. Interestingly, the sulfate group in **1** and **2** did not influence the activity (**4**: IC₅₀ 102 nM), while the sulfate group in **3** potentiated the activity (**5**: IC₅₀ 567 nM) [3].

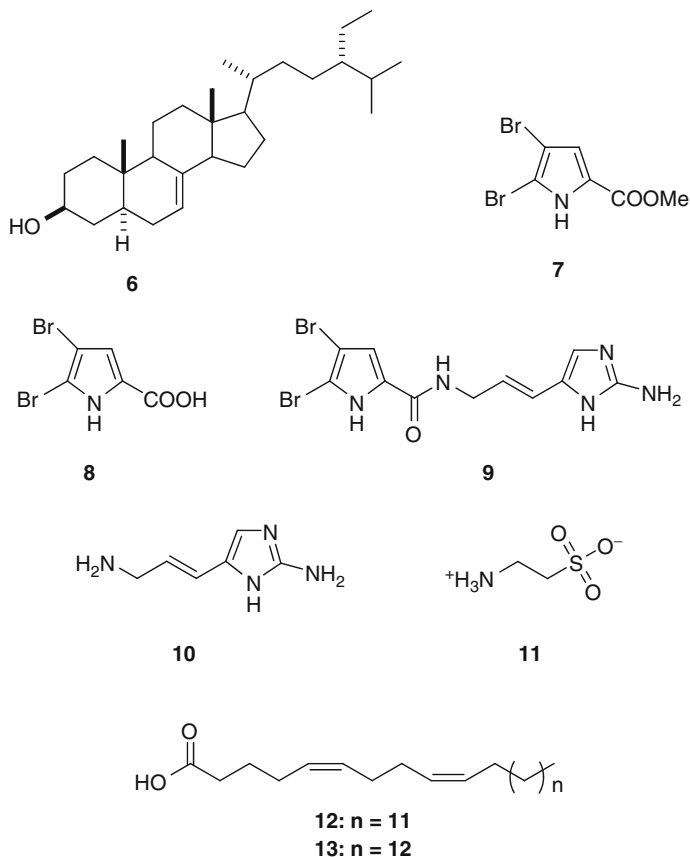


23.2.2 Enoyl-ACP Reductase (EC 1.3.1.9)

In mammals and other higher eukaryotes, all reactions in fatty acid synthesis are catalyzed by the type I fatty acid synthase (FAS-I), while bacteria, plants, and algae contain a type II system (FAS-II), in which each reaction is carried out by a monofunctional enzyme. The type II fatty acid biosynthetic pathway has recently been discovered in a number of Apicomplexan parasites, including the malaria parasite, *Plasmodium falciparum*. *Mycobacterium tuberculosis* employs both FAS-I and FAS-II systems. FAS-I is responsible for the synthesis of short-chain FAs, whereas the FAS-II system extends these FAs to very long-chain mycolic acids, important components of the mycobacterial cell wall. The central role of FA biosynthesis and the structural differences between the human and microbial FAS systems render FAS-II as an attractive target for antimicrobial drug discovery.

The FabI (enoyl-ACP reductase) is a crucial enzyme of all FAS-II systems, since it catalyzes the last NADH-dependent reduction step in each elongation cycle. Six known metabolites (**6–11**) and complex fatty acid mixtures (**FAMA-FAMG**) isolated from the Turkish marine sponge *Agelas oroides* were identified as active components in the target (*Pf* FabI)-based antimalarial screening. Compounds **6–11** showed inhibitory activity against *Pf* FabI with IC₅₀ values of >100, >100, 40, 0.30, 5.0, >100, and >100 µg/mL, respectively. Interestingly, TFA salt of **8** showed better inhibitory activity (IC₅₀ 40 µg/mL), while the activity of TFA salt of **9** became weaker (IC₅₀ 5.0 µg/mL). These enzyme inhibitory activities were well correlated with anti-plasmodial activities against *P. falciparum*, except that **10** showed better anti-protozoan activity (IC₅₀ 7.4 µg/mL) compared to its enzyme inhibitory activity.

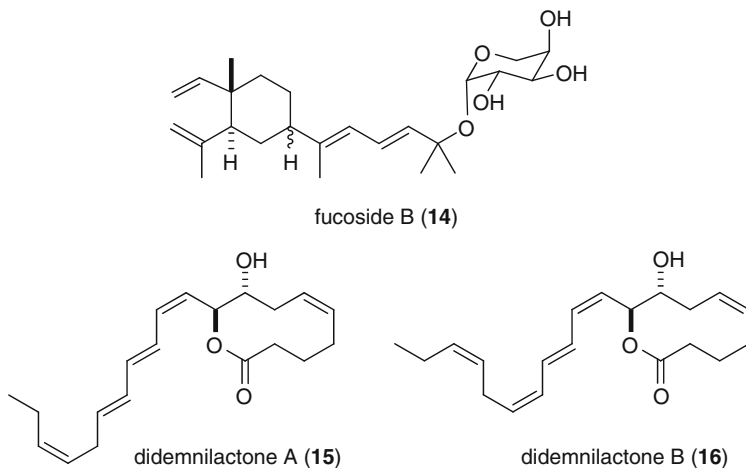
Mixtures of fatty acids showed *Pf* FabI inhibitory activity with IC_{50} s in the range of 0.35–20 $\mu\text{g/mL}$, while they showed anti-plasmodial activities against *P. falciparum* (IC_{50} s 3.4–40.9 $\mu\text{g/mL}$), *Trypanosoma brucei rhodesiense* (IC_{50} s 5.3–42.3 $\mu\text{g/mL}$), *Trypanosoma cruzi* (IC_{50} s 16 to > 30 $\mu\text{g/mL}$), *Leishmania donovani* (IC_{50} s 6.0–14.4 $\mu\text{g/mL}$), respectively. In addition, two mixtures (**FAMA** and **FAMD**) inhibited FabI of *Mycobacterium tuberculosis* (*Mt*FabI, IC_{50} s 9.4 and 8.2 $\mu\text{g/mL}$, respectively) and *Escherichia coli* (*Ec*FabI, IC_{50} s 0.5 and 0.07 $\mu\text{g/mL}$, respectively). FAMA was a mixture of 5,9-dienoic fatty acids of C_{23} (**12**) and C_{24} (**13**), while FAMD contained 10-methylhexadecanoic and palmitic acids as major lipids [4].



23.2.3 Lipoxygenases (EC 1.13.11.12)

Lipoxygenases (LO) mediate hydroperoxidation of polyunsaturated fatty acids (PUFAS), leading to formation of leukotrienes and lipoxins. Selective inhibitors of lipoxygenase isoforms can be useful for pharmacological agents, nutraceuticals,

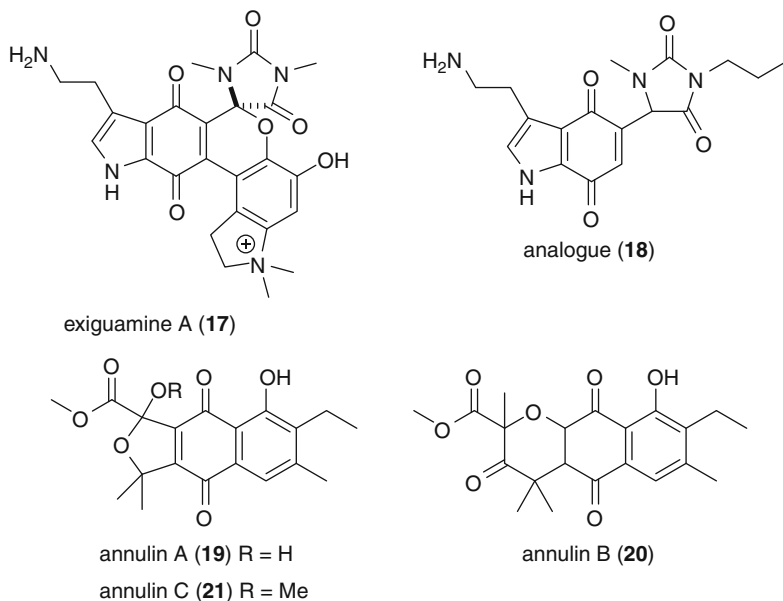
or molecular tools. Fucosides, originally isolated from the Caribbean gorgonian *Eunicea fusca* [5], selectively and irreversibly inhibited leukotriene (LT) formation in murine models of inflammation. Further pharmacological study indicated that fucoside B (**14**) inhibits conversion of arachidonic acid (AA) to leukotriene B₄ (LTB₄) by inhibition of 5-LO with an IC₅₀ of 18 μM [6]. Similarly, didemnilactones A (**15**) and B (**16**) isolated from the tunicate *Didemnum moseleyi* showed inhibition against lipoxygenases of human polymorphonuclear leukocytes with IC₅₀ values of 9.4 and 8.5 μM (**15** and **16**, respectively against 5-LO), and 41 μM (**15** against 15-LO) [7].



23.2.4 Indoleamine 2,3-Dioxygenases (EC 1.13.11.42)

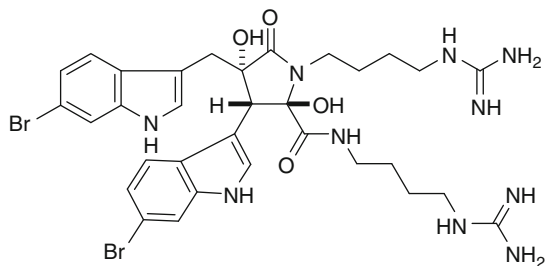
Indoleamine-2,3-dioxygenase (IDO) catalyzes the oxidation of tryptophan to *N*-formylkynurenine at the rate-limiting step in the metabolic degradation of tryptophan. Because T-cells are sensitive to tryptophan depletion, overexpression of IDO in most tumors is thought to cause apoptosis of T-cells and, as the results, leads to immune escape of solid tumors. Significant regression of tumors observed in a mouse model system treated by a combination of relatively poor IDO inhibitor such as 1-methyltryptophan and cytotoxic agents (e.g., paclitaxel) have provided proof of demonstration for the potential value of IDO inhibitors in cancer treatment. Exiguamine A (**17**) was isolated as an IDO inhibitor from the marine sponge *Neopetrosia exigua* collected at Papua New Guinea. The biogenesis of the unprecedented complex hexacyclic alkaloid skeleton of **17** was proposed to be starting from DOPA, tryptophan, and *N,N*-dimethylhydantoin. Exiguamine A has a *K_i* of 210 nM for inhibition of IDO in vitro [8]. Synthetic analogues of **17** were prepared and evaluated their inhibitory activity against IDO. Although all of the synthetic analogues turned out to be less active than **17** (*K_i* 41 nM in the modified

assay system), a simpler analogue **18** showed relatively potent noncompetitive inhibition against IDO (K_i 200 nM) [9]. Four new polyketides annulin C (**21**), 2-hydroxygarveatin, garveatin, and garvin C, as well as known annulins A (**19**) and B (**20**), garveatins A and C, and 2-hydroxy garvin A were isolated from the Northeastern Pacific hydroid *Garveia annulata*. Among these compounds, annulins A–C showed potent submicromolar IDO inhibition with K_i values of 0.14, 0.69, and 0.12 μM , respectively [10].

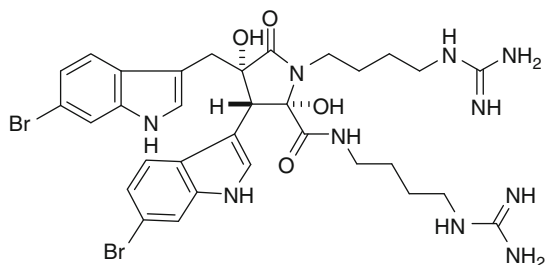


23.2.5 Neuronal Nitric Oxide Synthase (EC 1.14.13.39)

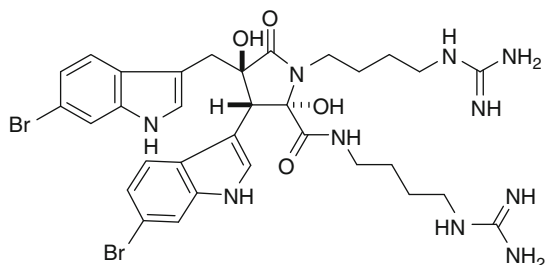
Neuronal nitric oxide synthase (nNOS) represents an important therapeutic target for neuropathological disorders, such as stroke, Alzheimer's disease, Parkinson's disease, AIDS, and dementia, because NO plays an important multifunctional role in the modulation of many neurotransmitters in the brain and its overproduction has been associated with such diseases. Eusynstyelamides A–C (**22–24**) isolated from the Australian ascidian *Eusynstyela latericius* inhibited nNOS with IC_{50} values of 41.7, 4.3, and 5.8 μM , respectively, while they were found to be nontoxic toward the three human tumor cell lines MCF-7 (breast), SF-268 (CNS), and H-460 (lung). Eusynstyelamides A and B were mildly antibacterial against *Staphylococcus aureus* (IC_{50} s 5.6 and 6.5 mM, respectively), and weakly inhibited the C4 plant regulatory enzyme pyruvate phosphate dikinase (PPDK) (IC_{50} values of 19 and 20 mM, respectively) [11].



eusynstyelamide A (22)



eusynstyelamide B (23)



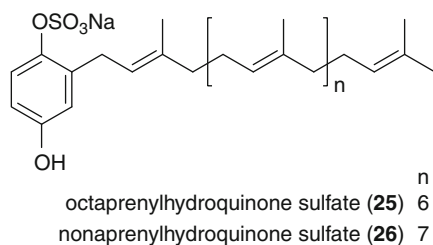
eusynstyelamide C (24)

23.3 Transferases (EC 2.-.-.-)

23.3.1 1 α -1,3-Fucosyltransferases (EC 2.4.1.214)

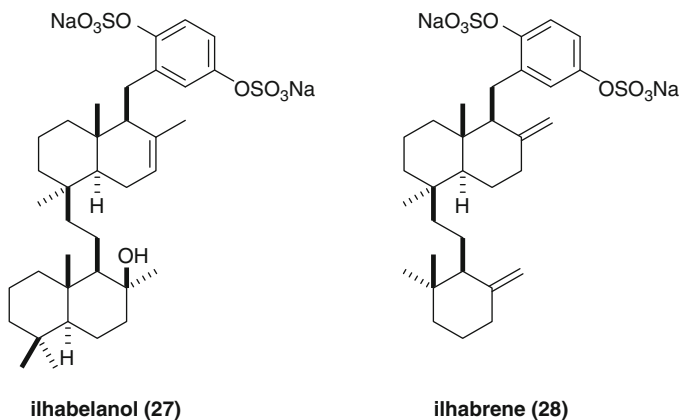
α -1,3-Fucosyltransferases (Fuc Ts, EC 2.4.1.214) which catalyze the transfer of L-fucopyranoside residues from guanosine diphosphate fucose (GDP-fucose) to glycoconjugate acceptors are known to be involved in the biosynthesis of sialyl Lewis X (SLe^X) present on the extracellular surfaces of leukocytes. The E-selectin-SLe^X interaction encourages leukocytes to move from the bloodstream into sites of injury or infection and to cause inflammation, thus indicating that inhibitors

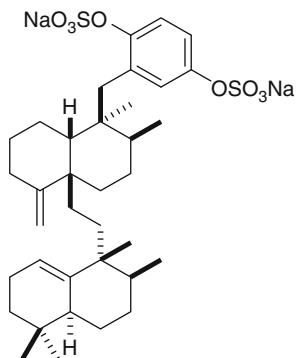
of α -1,3-fucosyltransferase are potential drugs for the treatment of inflammatory diseases [12]. Octa- and nonaprenylhydroquinone sulfates **25** and **26** isolated from an Australian marine sponge *Sarcotragus* sp. inhibited α -1,3-fucosyltransferase VII (Fuc TVII) with IC_{50} values of 3.9 and 2.4 $\mu\text{g/mL}$, respectively, while they showed very weak activity against Fuc TVI [13].



23.3.2 Adenosine Phosphoribosyltransferase (EC 2.4.2.7)

Adenosine phosphoribosyltransferase (APRT) catalyzes the salvage pathway of purine nucleotides. In mammals, there are both *de novo* and salvage pathways for purine nucleotides synthesis, while kinetoplastid parasites such as *Leishmania* spp. lack the *de novo* pathway. Therefore, selective inhibitors of phosphoribosyl transferase should compromise the parasite metabolism selectively. Three new disulfated meroterpenoids, ilhabelanol (**27**), ilhabrene (**28**), and isoakaterpin (**29**) were isolated from a Brazilian sponge *Callyspongia* sp. as *L. tarentolae* adenosine phosphoribosyltransferase (L-APRT) inhibitors. Isoakaterpin (**29**) inhibited L-APRT with an IC_{50} of 1.05 μM , while the accurate IC_{50} values for ilhabelanol (**27**) and ilhabrene (**28**) could not be obtained because of the too small amount of isolated compounds [14].



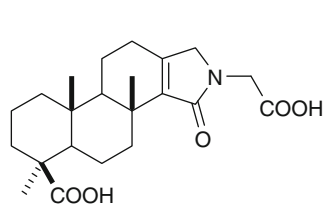
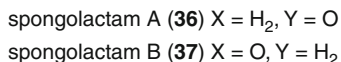
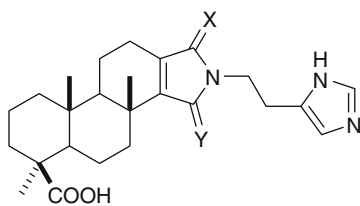
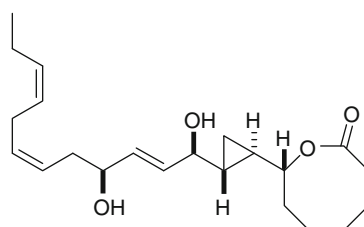
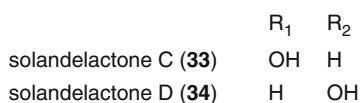
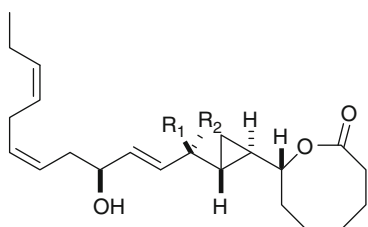
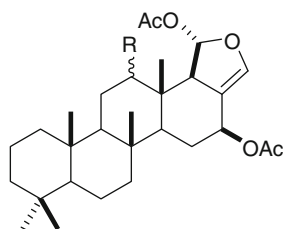
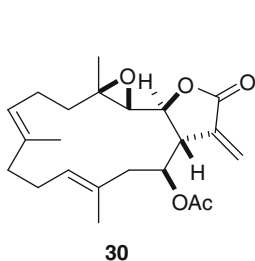


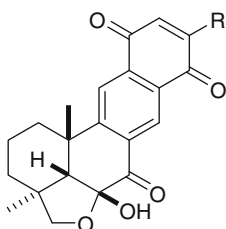
isoakaterpin (29)

23.3.3 Farnesyl Protein Transferase (EC 2.5.1.58)

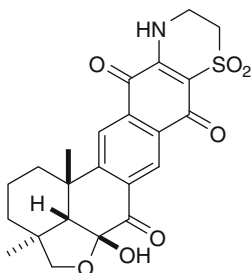
The Ras family of guanine nucleotide binding proteins plays important roles in signal transduction and regulation of cell differentiation and proliferation. The Ras protein requires posttranslational processing in order to associate with the plasma membrane and to function in signal transduction or cellular transformation. The first processing step is catalyzed by farnesyl protein transferase (FPT) which adds a farnesyl group to a cysteine residue near the carboxy terminus of the Ras protein. Inhibition of FPT is a potential therapeutic target for novel anticancer agents. A cembranolide diterpene **30** isolated from the soft coral *Lobophytum cristagalli* showed potent inhibitory activity against FPT at an IC_{50} of 0.15 μM [15]. The bioassay guided isolation of FPT inhibitors from the marine sponge *Hyrtios reticulata* yielded a known sesterterpene, heteronemin (**31**) as the active constituent which inhibited FPT with an IC_{50} value of 3 μM , while its 12-epimer (**32**) did not show any noticeable activity [16]. Solandelactones C (**33**), D (**34**), and G (**35**) were cyclopropyl oxylipins isolated from the hydroid *Solanderia secunda* and exhibited moderate inhibitory activity against FPT (69, 89, and 61% inhibition at 100 $\mu\text{g}/\text{mL}$, respectively) [17]. Spongolactams A–C (**36–38**) were FPT inhibitors isolated from an Okinawan marine sponge *Spongia* sp. by employing newly developed LC/MS-guided assay systems. To study their structure–activities relationships, spongolactams were semisynthesized from the known diterpene. The inhibitory activities of **36–38** against FPT were confirmed as IC_{50} values of 23, 130, and >260 μM , respectively [18]. Four new dual inhibitors, alisiaquinones A–C (**39–41**) and alisiaquinol (**42**), against FPT and plasmoidal kinase Pfnek-1 were isolated from an unidentified New Caledonian deepwater sponge. Compounds **39–42** showed FPT inhibition at IC_{50} values of 2.8, 2.7, 1.9, and 4.7 μM , respectively.

Moreover, alisiaquinone A and alisiaquinol strongly inhibited plasmoidal NIMA-like kinase Pfnek-1 at as low as 1 μM , whereas alisiaquinone C (**41**) showed almost no inhibition at this concentration. However, alisiaquinone C showed a much better inhibitory activity against *P. falciparum* in vitro. These results correlated with a better activity of alisiaquinone C on FPT, as was shown by the dramatic effects of FPT inhibitors on malaria parasites. The in vivo activity of alisiaquinones A and C was investigated on rodent malaria and was shown that they reduced by 50% the parasitemia at 5 mg/kg and displayed relatively high level of toxicity with 100% and 80% mortality, respectively at 20 mg/kg, which precluded further antimalarial development [19].

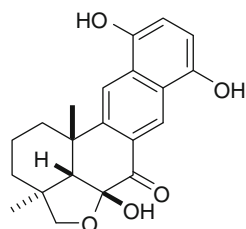




alisiaquinone A (39) R = H
 alisiaquinone B (40) R = OMe



alisiaquinone C (41)



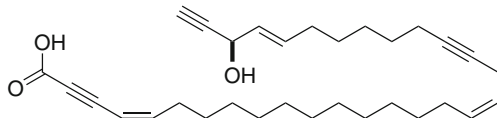
alisiaquinol (42)

23.3.4 Geranylgeranyltransferase Type I (EC 2.5.1.59)

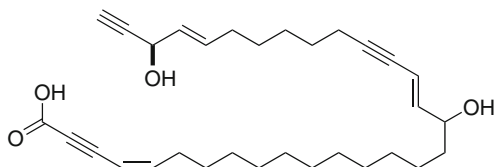
Geranylgeranyltransferase type I (GGTase I) catalyzes the posttranslational attachment of the geranylgeranyl unit on the carboxy terminal cysteine residues of proteins, to promote membrane interaction and biological activities of these proteins [20]. Rho1p, a regulatory subunit of 1,3- β -D-glucan synthesis and the key player in cell wall biosynthesis [21], is known as one of the targets of GGTase I and is essential for viability of *Saccharomyces cerevisiae*. Since there is only 30% sequence homology between the human and pathogenic fungus *Candida albicans* GGTase I [22], its inhibitors are expected to be selective antifungal agents.

Corticatic acids are the polyacetylenic GGTase I inhibitors isolated from the marine sponge *Petrosia corticata*. Corticatic acids A (43), D (44), and E (45) inhibited *C. albicans* GGTase I with IC_{50} values of 1.9, 3.3, and 7.3 μ M, respectively, while corticatic acid A (43) also inhibited the growth of *C. albicans* with an MIC value of 54 μ M [23].

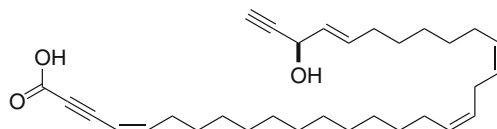
Massadine (46), a highly oxygenated alkaloid isolated from the marine sponge *Stylissa* aff. *massa* as an inhibitor of GGTase I from *C. albicans* inhibited GGTase I with an IC_{50} value of 3.9 μ M [24].



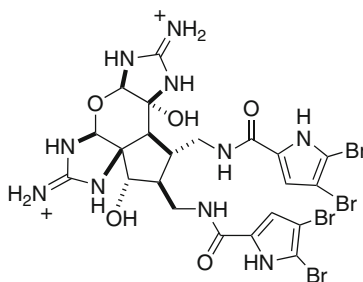
Corticatic acid A (43)



Corticatic acid D (44)



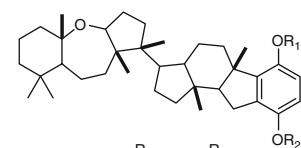
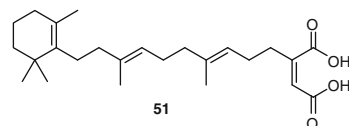
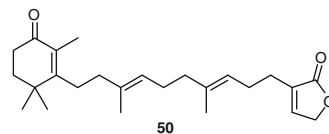
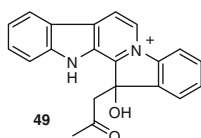
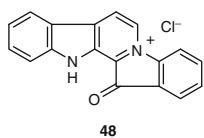
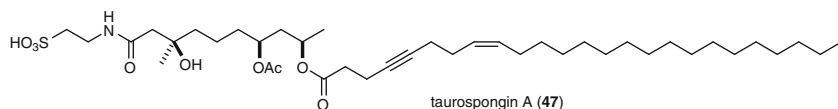
Corticatic acid E (45)



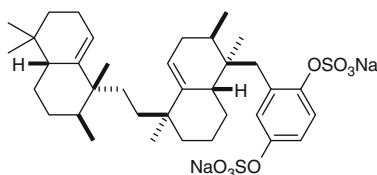
Massadine (46)

23.3.5 HIV Reverse Transcriptase (EC 2.7.7.49)

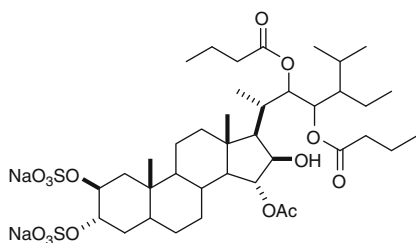
Reverse transcriptase (RT) is the key enzyme in the life cycle of human immunodeficiency virus (HIV). RT is a multifunctional enzyme responsible for the transcription of viral RNA into double-stranded DNA, and exhibits both RNA-dependent DNA polymerase (RDDP) and DNA-dependent DNA polymerase (DDDP) activities as well as an inherent ribonuclease H (RNase H) activity. All the catalytic functions of RT play a pivotal role in HIV replication. Taurospongins A (47), a metabolite of an Okinawan sponge *Hippospongia* sp., is another example of acetylenic compounds which possess HIV RT inhibitory activity (IC_{50} 6.5 μ M, K_i 1.3 μ M), along with inhibitory activity against DNA polymerase β (IC_{50} 7.0 μ M, K_i 1.7 μ M) and c-erbB-2 kinase (IC_{50} 28 μ g/mL), but no cytotoxicity (IC_{50} > 10 μ g/mL) against L1210 and KB cells [25]. Tryptophan-derived pigments 48 and 49 and accompanying sesterterpenes 50 and 51 isolated from the Fijian sponge *Fascaplysinopsis reticulata* showed weak inhibition against HIV RT [26]. Toxicols A–C (52–54) and toxiusol (55), triterpenes isolated from the Red Sea sponge *Toxiclona toxius*, were reported to be inhibitory against HIV RT, but no detailed bioactivities were available [27]. Clathsterol (56) isolated from a Red Sea sponge *Clathria* sp. showed anti-HIV-1 RT at 10 μ M [28]. Polycitone A (57), a general inhibitor of retroviral reverse transcriptases and cellular DNA polymerases, was isolated from an ascidian *Polycitor* sp. It inhibited RDDP and DDDP activity of HIV-1 RT with IC_{50} values of 245 and 470 nM, respectively, while it showed general inhibition against MuLV (murine leukemia virus) RT, MMTV (mouse mammary tumor virus) RT, calf-thymus pol α , human pol β , and KF (*E. coli* DNA polymerase I) with IC_{50} values ranging from 73 to 600 nM [29].



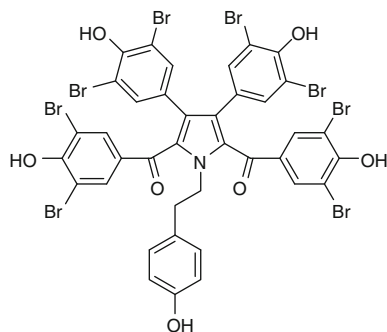
	R ₁	R ₂
toxicol A (52)	SO ₃ Na	SO ₃ Na
toxicol B (53)	H	H
toxicol C (54)	SO ₃ Na	H



toxiosol (55)



clathsterol (56)

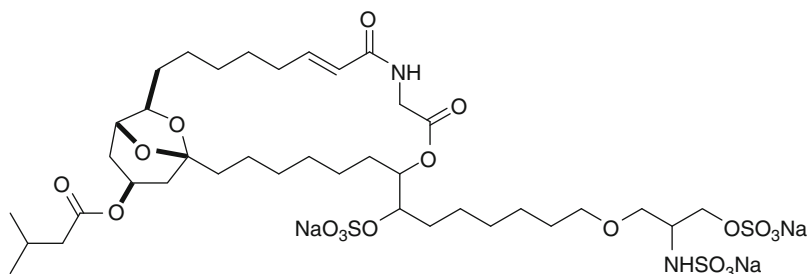
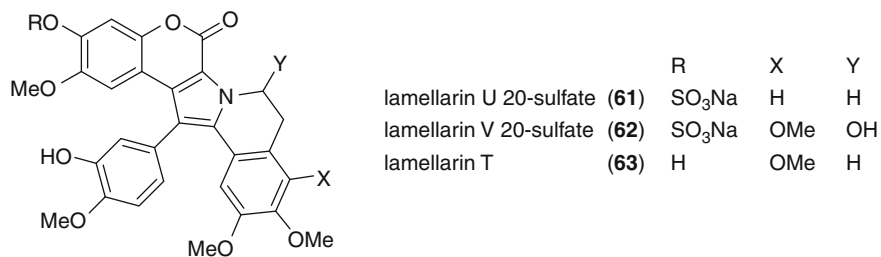
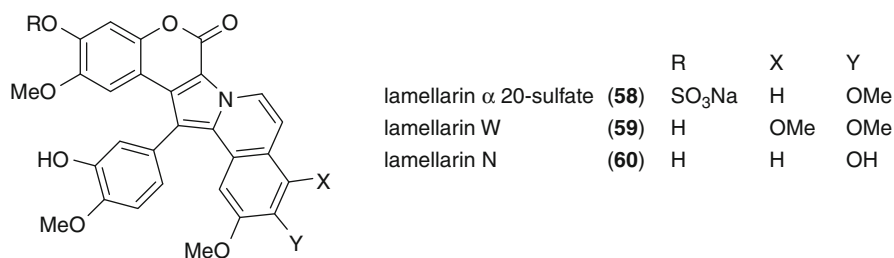


polycytone A (57)

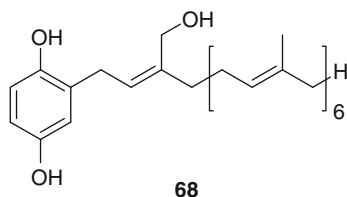
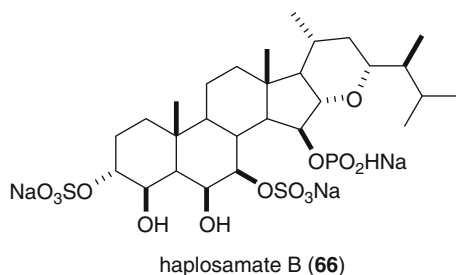
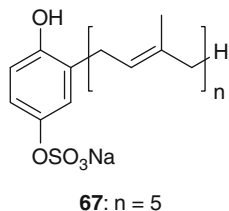
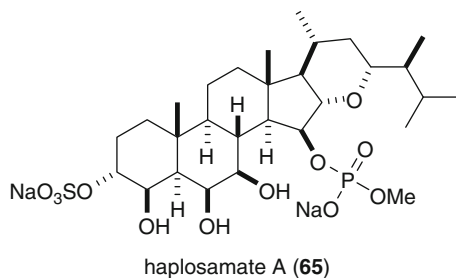
23.3.6 HIV Integrase (EC 2.7.7.-)

HIV integrase catalyzes the initial DNA-breaking and DNA-joining reactions responsible for the attachment of HIV cDNA to host DNA. Since there are no similar proteins known to be important for normal function of cells, HIV integrase

is a promising target for less toxic anti-HIV drugs. A series of ascidian alkaloids, the lamellarins (**58**)–(**63**) showed selective inhibition of HIV integrase with IC_{50} values of 16–73 μM for terminal cleavage and 14–51 μM for strand transfer activities, respectively; lamellarin α 20-sulfate (**58**) showed inhibition in the early steps of replication of HIV-1 in cell culture with an IC_{50} value of 8 μM [30]. Cyclodidemniserinol trisulfate (**64**) isolated from the Palauan ascidian *Didemnum guttatum* showed inhibition against HIV integrase at an IC_{50} of 60 $\mu\text{g/mL}$ [31]. Haplosamates A (**65**) and B (**66**) isolated from two haplosclerid sponges (*Xestospongia* sp. and unidentified sponge) inhibited HIV-1 integrase with IC_{50} values of 50 and 15 $\mu\text{g/mL}$, respectively [32]. Prenylhydroquinone sulfates **67** and **68** from a deepwater sponge *Ircinia* sp. showed HIV-1 integrase inhibition (65% inhibition at 1 $\mu\text{g/mL}$ and 45% inhibition at 5 $\mu\text{g/mL}$, respectively) [33].

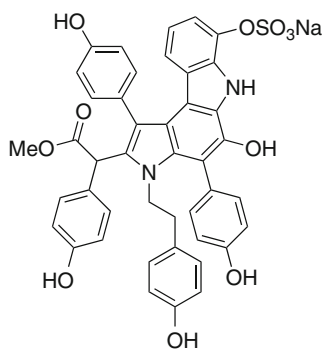


cyclodidemniserinol trisulfate (**64**)

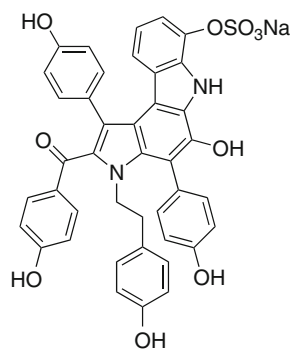


23.3.7 Telomerase (EC 2.7.7.49)

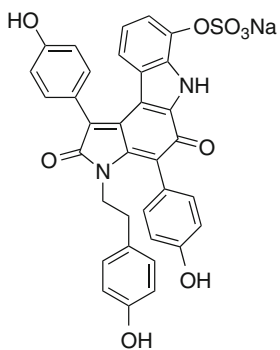
Telomerase is a ribonucleoprotein enzyme that adds repeats of the DNA sequence, TTAGGG, called telomere, onto the 3'-ends of chromosomes [34]. Telomerase activity is found in about 90% of human tumors, but not in normal cells [35]. Thus, inhibitors of telomerase are potential antitumor agents [36]. In fact, some synthetic inhibitors based on the function of telomerase have been successful in clinical trials [37]. From the marine sponge *Dictyodendrilla verongiformis* collected in southern Japan, five telomerase inhibitors, dictyodendrins A–E (**69–73**) were isolated along with the sodium salts of two known compounds (**2** and **3**) which were obtained as aldose reductase inhibitors from a marine sponge of the same genus [3]. All these seven compounds showed 100% inhibition of telomerase activity at the concentration of 50 $\mu\text{g/mL}$, while the desulfated analogue of dictyodendrins C (**71**) was not active at this concentration [38]. Recently, the total synthesis of dictyodendrins B (**70**), C (**71**), and E (**73**) was accomplished [39]. An unprecedented highly sulfated lipopolysaccharide, axinelloside A (**74**), isolated from the marine sponge *Axinella infundibula* showed a potent inhibition against human telomerase (IC_{50} 2.0 $\mu\text{g/mL}$) [40].



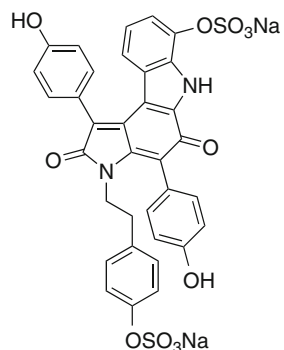
Dictyodendrin A (69)



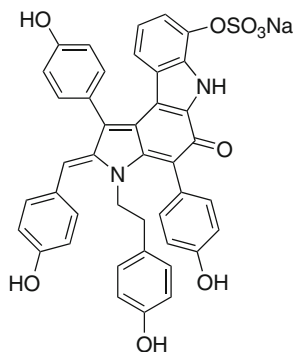
Dictyodendrin B (70)



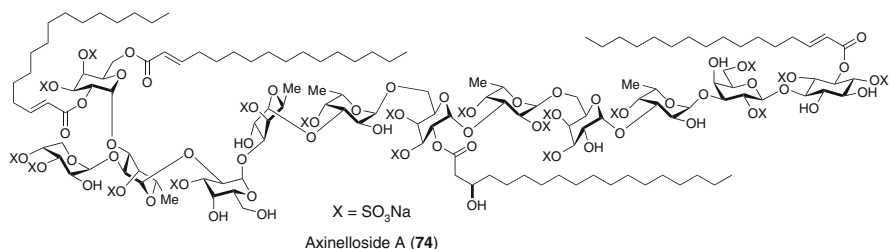
Dictyodendrin C (71)



Dictyodendrin D (72)

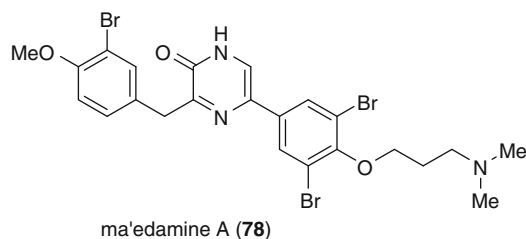
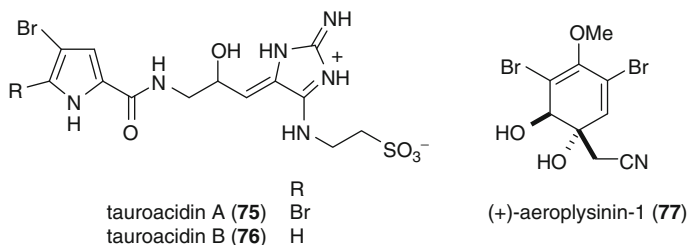


Dictyodendrin E (73)



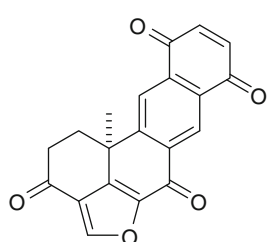
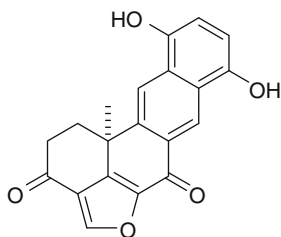
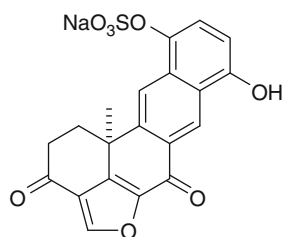
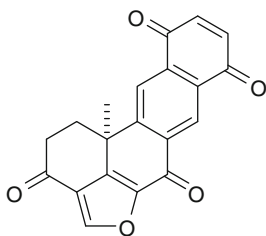
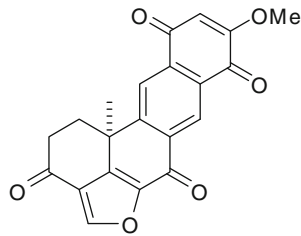
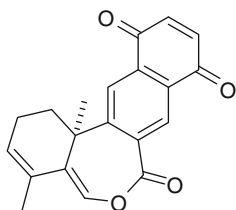
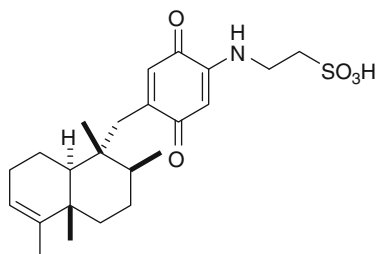
23.3.8 Epidermal Growth Factor Receptor Kinase (EC 2.7.10.1)

Protein tyrosine kinases comprise a large family of enzymes that regulate cell growth and intracellular signaling pathways; inhibitors of these enzymes may be potential anticancer drugs [41]. There are at least four members of the type 1 growth factor receptor gene family, including the epidermal growth factor receptors (EGFR), erbB-1, erbB-2, erbB-3, and erbB-4. Members of this tyrosine kinase receptor family have been implicated in the establishment or progression of human cancer, particularly breast cancer, and enormous amounts of effort have been made to identify specific small molecule inhibitors of EGFR tyrosine kinase [42]. Tauroacidins A (75) and B (76), bromopyrrole metabolites of an Okinawan sponge *Hymeniacidon* sp., exhibited inhibitory activity against c-erbB-2 kinase with an IC₅₀ of 20 μg/mL [43]. (+)-Aeropylsinin-1 (77) isolated from the marine sponge *Verongia aerophoba* inhibited EGF receptor kinase completely at 0.5 μM [44]. Ma'edamine A (78), a cytotoxic bromotyrosine alkaloid isolated from a marine sponge *Suberea* sp., inhibits c-erbB-2 kinase with an IC₅₀ value of 6.7 μg/mL [45].



23.3.9 Tyrosine Kinase pp60^{V-SRC} (EC 2.7.10.2)

A tyrosine kinase, pp60^{V-SRC} is the oncogenic protein encoded by Rous sarcoma virus. Halenaquinone (**79**), halenaquinol (**80**), halenaquinol sulfate (**81**), and xestoquinone (**82**) isolated from the Fijian sponge *Xestospongia* cf. *carbonaria* was found to inhibit the kinase activity of pp60^{V-SRC} with IC₅₀ values of 1.5, 60, 0.55, and 28 μM, respectively [46]. Halenaquinone (**79**) also inhibited phosphatidylinositol 3-kinase with an IC₅₀ value of 3 μM [47]. Two more pp60^{V-SRC} inhibitors, 14-methoxyhalenaquinone (**83**) and xestoquinolide A (**84**) were isolated from the same sponge (IC₅₀ values of 5 and 80 μM, respectively) [48]. Melemeleone B (**85**), a sesquiterpene quinone isolated from two *Dysidea* sponges, showed inhibitory activity against pp60^{V-SRC} with an IC₅₀ value of 28 μM [49].

halenaquinone (**79**)halenaquinol (**80**)halenaquinol sulfate (**81**)xestoquinone (**82**)14-methoxyhalenaquinone (**83**)xestoquinolide B (**84**)melemeleone B (**85**)

23.3.10 Other Tyrosine Protein Kinase

Four prenylhydroquinone sulfates **67–68** and **90–91** obtained from a deepwater sponge *Ircinia* sp. showed inhibitory activity of tyrosine phosphorylation by membrane fraction prepared from HER2 overexpressing 3T3 cells with IC₅₀ values of 8, 4, 8, and 5.9 µg/mL, respectively. Compounds **67** and **68** were also reported to be HIV-1 integrase inhibitors [33].

23.3.11 MSK1 (EC 2.7.11.1) and MAPKAPK-2

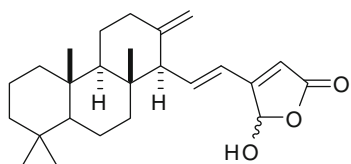
Mitogen- and stress-activated kinase 1 (MSK1) and mitogen-activated protein kinase-activated protein kinase 2 (MAPKAPK2) are two serine protein kinases involved in signal transduction. Both of these enzymes are located in the nucleus and are involved in the late stage of signal transduction pathway, therefore, selective inhibitors of these enzymes are most likely to exhibit highly specific cellular effects. Four cheilanthane sesterterpenoids **86–89** were isolated from a marine sponge *Ircinia* sp. as inhibitors of both MSK1 (IC₅₀s 4 µM for all compounds) and MAPKAPK-2 (IC₅₀ 90 µM for all compounds) [50].

23.3.12 Raf/MEK1/MAPK

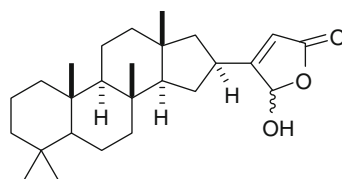
The Ras-MAPK-signaling cascade is found in all eukaryotic organisms and is involved in cellular signaling processes. Since the oncogenic form of Ras is associated with 30% of all cancers, Ras and the downstream kinases represent attractive targets for pharmacological intervention. The Raf/MEK-1/MAPK cascade inhibition assay-guided fractionation of the Philippine marine sponge *Stylissa massa* yielded eight known pyrrole alkaloids, aldisine (**92**), 2-bromoaldisine (**93**), 10Z-debromohymenialdisine (**94**), a 1:1 mixture of 10E- and 10Z-hymenialdisines (**95–96**), hymenin (**97**), oroidin (**98**), and 4,5-dibromopyrrole-2-carbonamide (**99**), among which **93–97** were active with IC₅₀s ranging from 3 to 1288 nM; the most active were **95** and **96** (IC₅₀s 3 and 6 nM, respectively). In addition, all compounds showed essentially identical IC₅₀ values in the MEK-1 to MAPK assay, while none of them showed activity in the Raf to MEK-1 assay [51].

23.3.13 Checkpoint Kinases (EC 2.7.11.1)

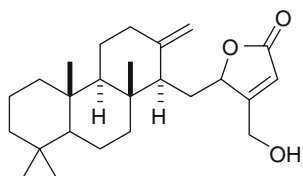
The synthetic 10Z-debromohymenialdisine (**94**) inhibited checkpoint kinases Chk1 and 2 with IC₅₀ values of 3 and 3.5 µM, respectively [52]. Further investigation into its inhibitory activity toward kinases led to identification of 11 new targets including p90RSK, KDR, c-Kit, Fes, MAPK1, PAK2, PDK1, PKCθ, PKD2, Rsk1, and SGK for this class of alkaloids [53].



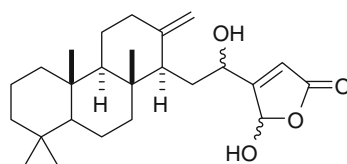
86



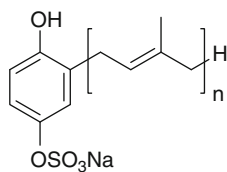
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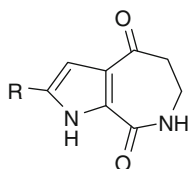


89



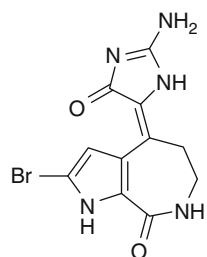
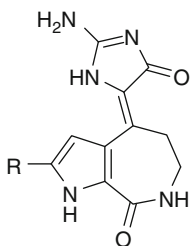
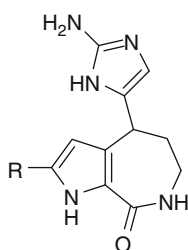
90: n = 6

91: n = 7

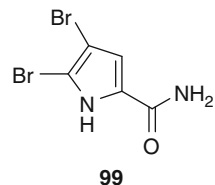


aldisine (92) R = H

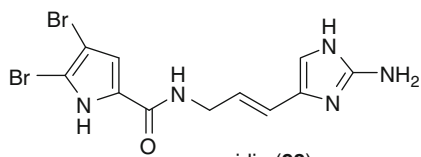
2-bromoaldisine (93) R = Br

10*E*-hymenialdisine (95)10*Z*-debromohymenialdisine (94) R = H10*Z*-hymenialdisine (96) R = Br

hymenin (97)



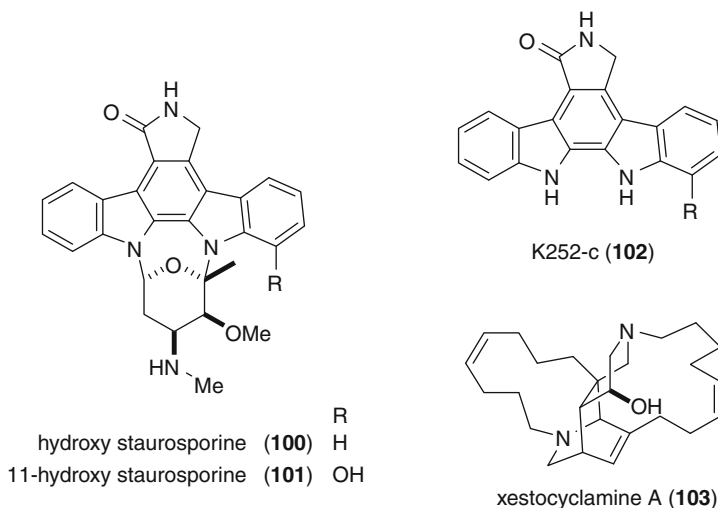
99

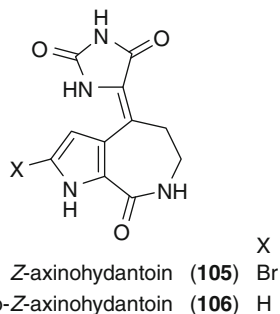
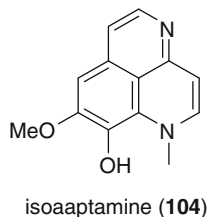


oroidin (98)

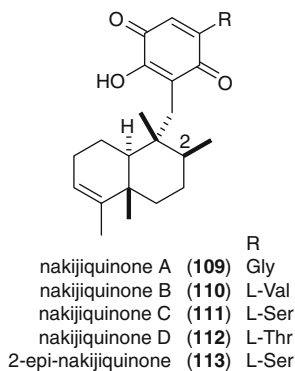
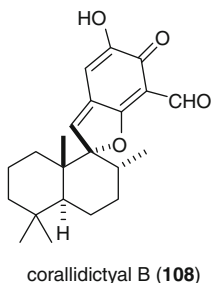
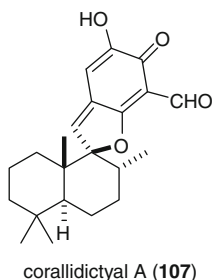
23.3.14 Protein Kinase C (EC 2.7.11.13)

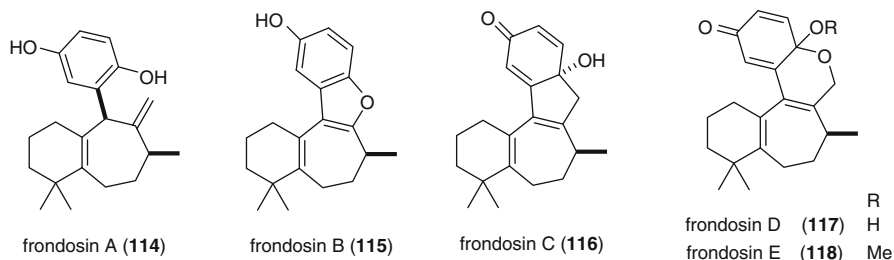
Protein kinase C (PKC), a phospholipid-dependent protein phosphorylating enzyme, is a key player of cellular signal transduction and is believed to be responsible for cancer, cardiovascular and renal disorders, and immunosuppression and autoimmune diseases, such as rheumatoid arthritis. Therefore, inhibitors of protein kinase C (PKC) can be potential drug leads for the treatment of such diseases. Staurosporine (**100**), isolated from *Streptomyces staurosporeus*, is the most famous natural product PKC inhibitor [54]. 11-Hydroxystaurosporine (**101**) isolated from a tunicate *Eudistoma* sp. collected in Pohnpei inhibited PKC with an IC_{50} value of 2.2 nM which is about 30% more active than staurosporine (**100**) [55]. Staurosporine aglycone K252-c (**102**) isolated from another *Eudistoma* sample inhibited eight cloned PKC isoenzymes α , β I, β II, δ , ϵ , η , γ , and ζ with IC_{50} values of 1.3, 0.6, 0.5, 1.2, 1.1, 0.8, 1.5, and >6.4 μ M, respectively [56]. Xestocyclamine A (**103**), bis-alkylpiperadines from a marine sponge *Xestospongia* sp., moderately inhibited PKC ϵ (IC_{50} 4 μ g/mL) [57]. Isoaaptamine (**104**), which was first reported from a suberitid sponge in 1988, was found to be a PKC inhibitor; recent evaluation of PKC inhibitory and antitumor activities for synthetic isoaaptamine and its derivatives disclosed that none of them met the criteria for further evaluation after the primary screen in the NCI tumor cell line panel [58]. Z-axinohydantoin (**105**) and debromo-Z-axinohydantoin (**106**) isolated from the marine sponge *Stylotella aurantium*, moderately inhibited PKC (IC_{50} s 9.0 and 22 μ M, respectively) [59].



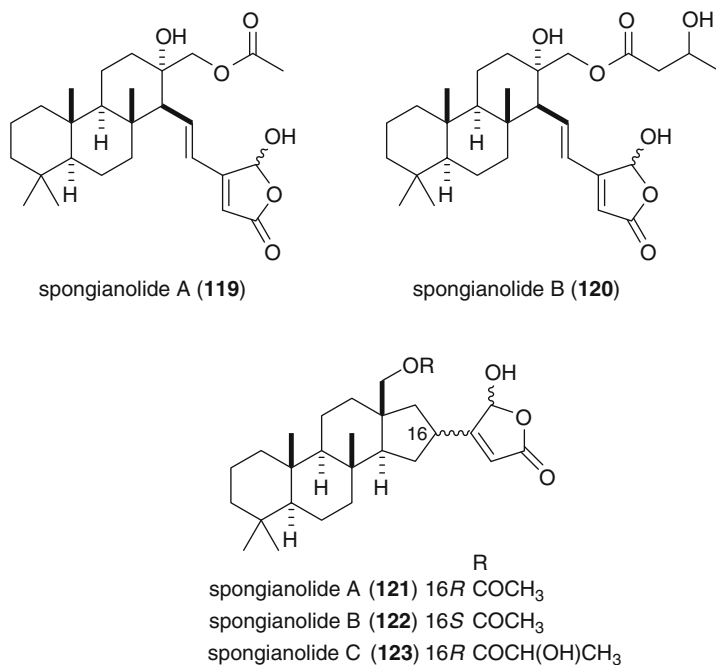


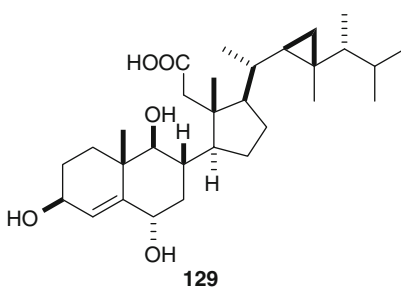
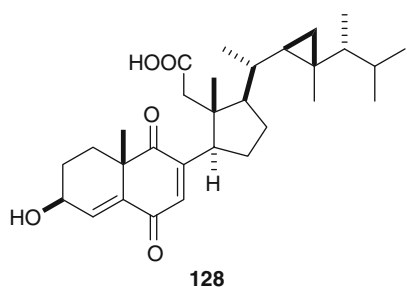
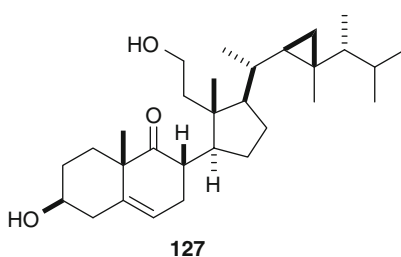
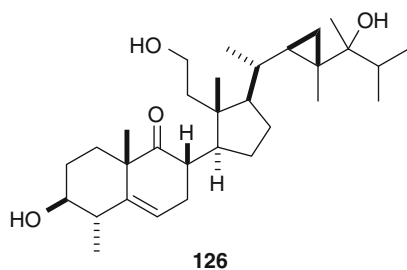
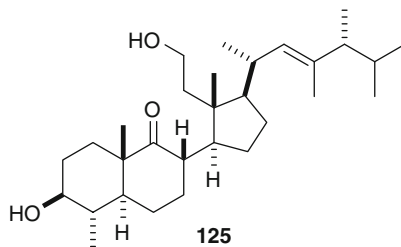
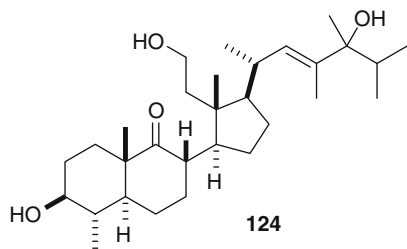
The mixture of corallidictyals A (**107**) and B (**108**), spirosesquiterpene aldehydes isolated from the marine sponge *Aka* (*Siphonodictyon*) *coralliphagum*, inhibited PKC with an IC_{50} value of 28 μ M. Interestingly, the corallidictyral mixture selectively inhibited PKC α with an IC_{50} value of 30 μ M (IC_{50} s 89, >300, and >300 μ M for ϵ , η , and ζ , respectively). In addition, the corallidictyral mixture inhibited the growth of cultured Vero (African green monkey kidney) cells with an IC_{50} value of 1 μ M after continuous exposure (72 h) [60]. Nakijiquinones A–D (**109–112**), sesquiterpene quinones isolated from an Okinawan marine sponge of the family Spongiidae, exhibited inhibitory activity against PKC with IC_{50} values of 270, 200, 23, and 220 μ M, respectively, whereas they were also active against EGF receptor kinases and c-erbB-2 kinase with IC_{50} values of >400, 250, 170, and >400 μ M, and 30, 95, 26, and 29 μ M, respectively [61]. Recently, enantioselective total synthesis of nakijiquinones and closely related analogues was reported [62]. The evaluation of their biological activities disclosed that C-2 epimer of nakijiquinone (**113**) was a potent and selective inhibitor of tyrosine kinase VEGFR2 (KDR) with an IC_{50} value of 21 μ M. Incidentally, VEGFR2 is a receptor for the vascular endothelial growth factor (VEGF) family and is responsible for endothelial cell proliferation and blood vessel permeability, therefore inhibitors of VEGFR2 are potential anti-angiogenic drugs [62]. Frondosines A–E (**114–118**), sesquiterpenoids from the sponge *Dysidea frondosa*, inhibited PKC with IC_{50} values of 1.8, 4.8, 20.9, 26, and 30.6 μ M, respectively [63].



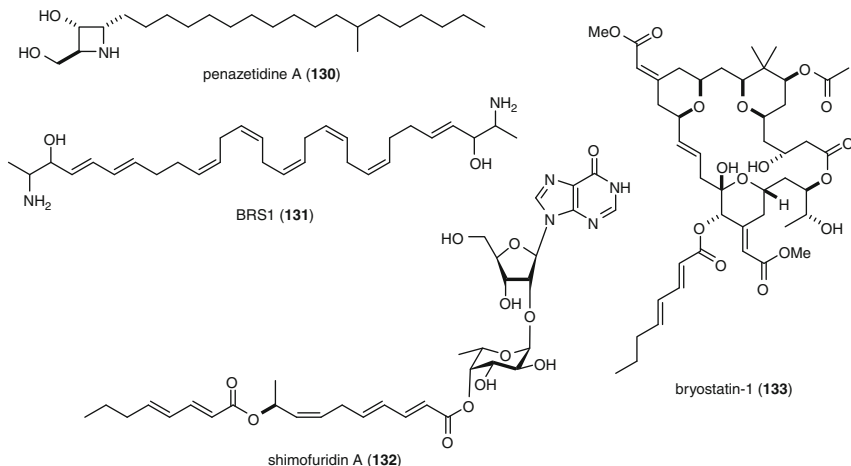


Spongianolides A–E (**119–123**), cytotoxic sesterterpenes isolated from a marine sponge *Spongia* sp., inhibited PKC at IC_{50} values of 20–30 μ M [64]. Three secosterols **124–126** isolated from a gorgonian *Pseudopterogorgia* sp. inhibited the human PKC α , β I, β II, γ , δ , ϵ , η , and ζ with IC_{50} values in the range of 12–50 μ M. The semisynthetic derivatives **127–129** also showed similar activity [42].



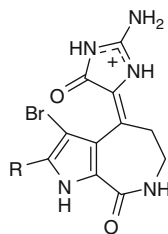
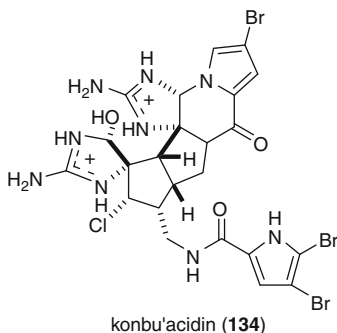


Penazetidine A (**130**), an azetidine isolated from the Indo-Pacific sponge *Penares sollasi*, inhibited PKC with an IC_{50} value of $1 \mu M$ [65]. BRS1 (**131**), a C_{30} bis-amino, bis-hydroxy polyunsaturated lipid from an unidentified Australian sponge of the class Calcarea, inhibited not only PKC (EC_{50} $98 \mu M$) but also radiolabeled phorbol ester binding to the enzyme (EC_{50} $9.2 \mu M$) [66]. Shimofuridin A (**132**) isolated from an Okinawan marine tunicate *Aplidium multiplicatum* inhibited PKC at an IC_{50} of $20.0 \mu g/mL$ [67]. Bryostatin-1 (**133**) which was isolated from the bryozoa *Bugula neritina* as an anticancer agent [68], is known to bind the C1 domain of PKC and regulate its activity [69].

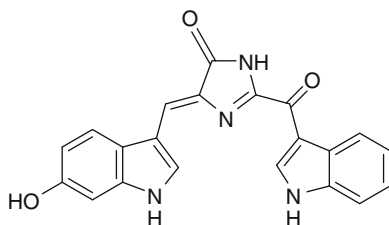


23.3.15 Cyclin-Dependent Kinases (EC 2.7.11.22)

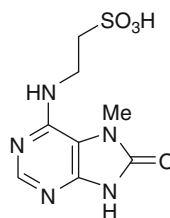
Cyclin-dependent kinases (CDK) are also a family of protein tyrosine kinases, some of which are involved in cell cycles, and their inhibitors are expected to be potential anticancer drugs. Konbu'acidin A (**134**) is a bromopyrrole alkaloid possessing inhibitory activity against CDK4 (IC_{50} 20 $\mu\text{g}/\text{mL}$) isolated from a marine sponge *Hymeniacidon* sp. [70]. Spongiacidins A (**135**) and B (**136**) also isolated from the same sponge inhibited c-erbB-2 kinase (IC_{50} s 8.5 and 6.0 $\mu\text{g}/\text{mL}$, respectively) and cyclin-dependent kinase 4 (CDK4) (IC_{50} s 32 and 12 $\mu\text{g}/\text{mL}$, respectively) [71]. Rhopaladins A–D isolated from an Okinawan tunicate *Rhopalaea* sp. are the first example of bis-indole alkaloids possessing an imidazolinone moiety as tunicate metabolites; rhopaladin B (**137**) inhibited CDK4 and c-erbB-2 kinase with IC_{50} values of 12.5 and 7.4 $\mu\text{g}/\text{mL}$, respectively [72]. Microxine (**138**) from an Australian marine sponge *Microxina* sp. inhibited CDK1 (cdc2) kinase with an IC_{50} value of 13 μM [73].



spongiacidin A (**135**) R = Br
spongiacidin B (**136**) R = H



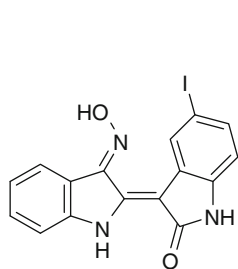
Rhopaladin B (137)



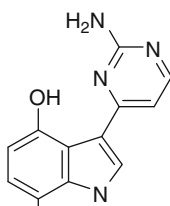
microxine (138)

23.3.16 Glycogen Synthase Kinase-3 (2.7.11.17)

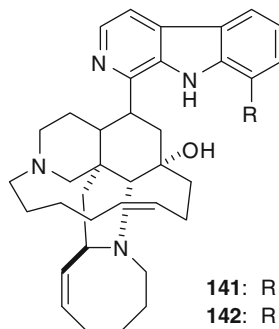
Glycogen synthase kinase-3 (GSK-3) is a serine-threonine kinase ubiquitously expressed and involved in the regulation of many cell functions. GSK-3 phosphorylates glycogen synthase or the microtubule-associated protein tau, being implicated in type-2 diabetes, Alzheimer's disease, or different tau pathologies such as Pick's disease. Hymenialdisine (**96**) [74], indirubine (**139**) [75], and meridianine (**140**) [76] are the known marine-derived GSK-3 inhibitors isolated from several species of marine sponges, the mollusk *Hexaplex trunculus*, and the ascidian *Aplidium meridianum*, respectively. Hymenialdisine (**96**) potently inhibited GSK-3 β (IC₅₀ 10 nM) and plant GSK-3 (ASK- γ) with an IC₅₀ value of 80 nM as well. It inhibited in vivo phosphorylation of specific neuronal proteins by GSK-3 β and CDK5 such as AD-characteristic phosphorylation of tau completely [74]. Indirubin inhibited GSK-3 α/β with an IC₅₀ value of 1.00 μ M [75]. Studies of structure-activity relationship (SAR) in the class of manzamine alkaloids revealed that manzamine A (**141**) inhibited GSK-3 β at an IC₅₀ value of 10.2 μ M; 8-hydroxymanzamine A (**142**) being the most potent analogue (IC₅₀ 4.8 μ M) [77].



139



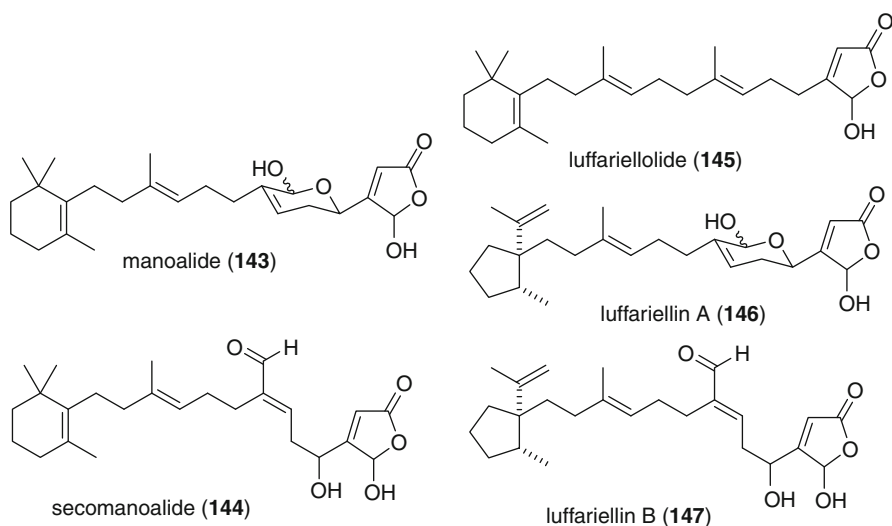
140

141: R = H
142: R = OH

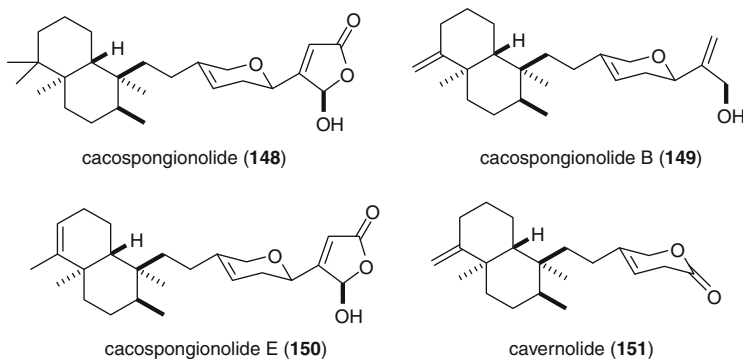
23.4 Hydrolases (EC 3.-.-)

23.4.1 Phospholipase A₂ (EC 3.1.1.4)

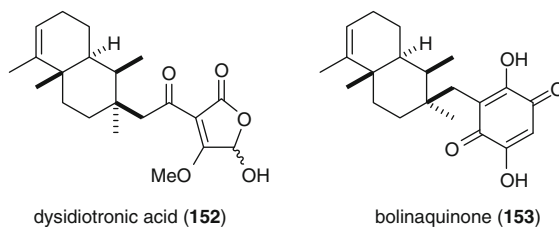
Phospholipase A₂ (PLA₂) cleaves the ester linkage of the β -position of phospholipids to release arachidonic acid which is metabolized to prostaglandins, leukotrienes, and other mediators of inflammation. Prostaglandins are implicated in various forms of pain and inflammation. In biogenesis of prostaglandins, arachidonic acid formation is the rate-determining step, thus, PLA₂ inhibitors are expected to be potential anti-inflammatory drugs. Manoalide (**143**), initially isolated as an antibacterial metabolite from the marine sponge *Luffariella variabilis* [78], was later found to be a potent inhibitor of PLA₂ with an IC₅₀ value of 1.7 μ M [79], which led to synthesis and anti-inflammatory evaluation of more than 100 analogues. Unfortunately, none of them was developed for drugs. Three congeners of manoalide were also obtained from the same sponge [80], of which secomanoalide (**144**) is more potent against bovine pancreatic PLA₂ [81]. Luffariellolide (**145**) isolated from a Palauan sponge *Luffariella* sp. also inhibited the bee venom PLA₂ with an IC₅₀ of 0.23 μ M. The partially reversible and weaker inhibitory activity of **145** was suggesting that the γ -lactol group in **143** was responsible for the irreversible reaction of **143** with Lys residues on PLA₂ [82]. Luffariellins A (**146**) and B (**147**) isolated from *L. variabilis* are very potent against bee venom PLA₂ with IC₅₀ values of 56 and 62 nM, respectively [83]. These sesterterpenes are known to covalently and specifically modify PLA₂ by a Schiff base formation between Lys-56 residue of PLA₂ and the hemiacetal or aldehyde functionality of these terpenoids [84]. According to this mechanism, Katsumura and coworkers designed PLA₂ inhibitors, one of which potently and selectively inhibited bovine pancreas PLA₂ [85].

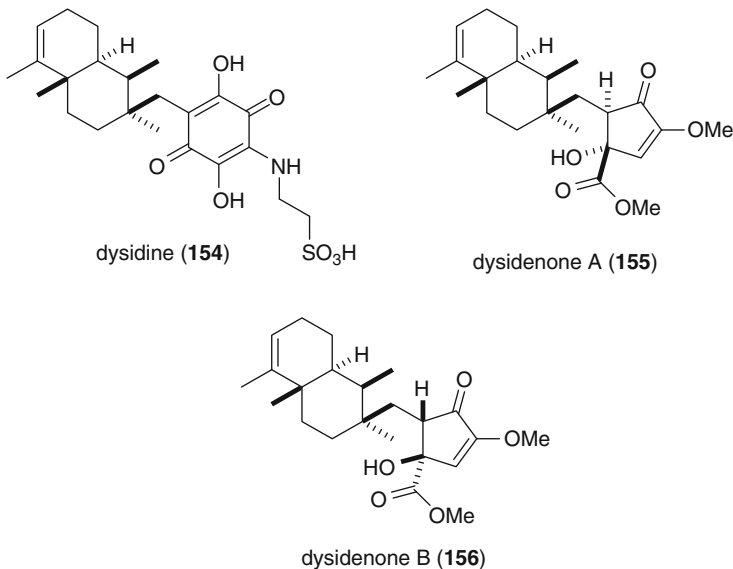


Cacospongionolides (**148–150**), originally isolated as antitumor compounds from the Mediterranean sponge *Fasciospongia cavernosa* [86], preferentially inhibited bee venom and human synovial PLA₂ among PLA₂s of various origins. Cacospongionolide B (**149**) exhibited specific inhibition against human PLA₂ [87], while cacospongionolide E (**150**) was the most potent inhibitor toward human synovial PLA₂ (IC₅₀ 1.4 μM), showing higher potency than manoalide [88]. The structure–activity relationship study on synthetic analogues suggested that **149** has an enantiospecific interaction with the enzyme that is independent of the γ-hydroxybutenolide moiety [89]. Furthermore, cacospongionolide B (**149**) was reported to suppresses the expression of inflammatory enzymes including inducible nitric oxide synthase (iNOS) and cyclooxygenase-2 (COX-2) as well as to reduce tumor necrosis factor-α (TNF-α) [90]. Cavernolide (**151**) isolated from a marine sponge *Fasciospongia cavernosa* selectively inhibited human PLA₂ with an IC₅₀ value of 8.8 μM [91].



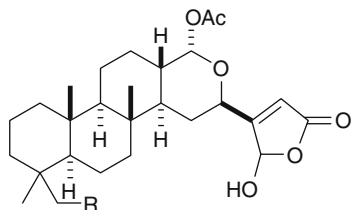
Dysidiotronic acid (**152**), a sesquiterpenoid from a Vanuatu sponge *Dysidea* sp., inhibited human synovial PLA₂ with an IC₅₀ value of 2.6 μM [92], while bolinaquinone (**153**), dysidine (**154**), and a 1:1 mixture of dysideonones A (**155**) and B (**156**) significantly inhibited human synovial PLA₂, among which **153** showed the most potent activity with an IC₅₀ value of 0.2 μM, but was not a selective inhibitor toward this enzyme. On the contrary, dysidine (**150**) showed selective inhibition against this enzyme with an IC₅₀ value of 2.0 μM. However, **153–156** did not inhibit cPLA₂ [93].



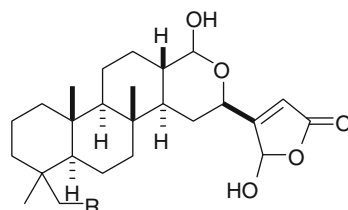


Petrosaspongiolides M–R (**157–161**), sesterterpens from the New Caledonian marine sponge *Petrosaspongia nigra* inhibited PLA₂; the most potent petrosaspongiolide M (**157**) inhibited human synovial and bee venom PLA₂ with IC₅₀ values of 1.6 and 0.6 μM, respectively, while petrosaspongiolide P (**159**) inhibited human synovial PLA₂ (IC₅₀ 3.8 μM) more selectively than bee venom PLA₂ (IC₅₀ >10 μM). Other petrosaspongiolides N (**158**), Q (**160**), and R (**161**) showed only weak activity [94]. Petrosaspongiolide M was shown to form the covalent adduct between PLA₂ and γ-hydroxybutenolide which is essential for the activity [95]. Ironically, a mild non-covalent PLA₂ inhibitor, 25-acetyl-petrosaspongiolide M, was found to be hydrolyzed with PLA₂ to form the potent inhibitor, petrosaspongiolide M [96]. Interestingly, a full characterization of the *bv* PLA₂ adduct with petrosaspongiolide R (**161**), one of the least active and most structurally different among petrosaspongiolides, using LC-MS, MSⁿ, and computational methods, confirmed the same inhibition mechanism and covalent binding site already found for petrosaspongiolide M (**167**). The correct arrangement of the ligand in the active site, induced by non-covalent interactions, is of pivotal importance in the inactivation process [97]. The anti-inflammatory effects of petrosaspongiolide M was suggested to be mediated by inhibition of NF-κB signaling pathway [98].

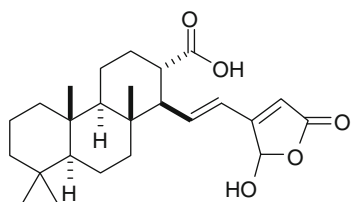
Aplyolide (**162**), a sesterterpene isolated from the marine sponge *Aplysinopsis elegans* inhibited human PLA₂ with an IC₅₀ value of 10.5 μM [99], whereas the related terpenoid, luffolide (**163**) isolated from a Palauan *Luffariella* sp., completely inhibited bee venom PLA₂ at a concentration of 3.5 μM [100].



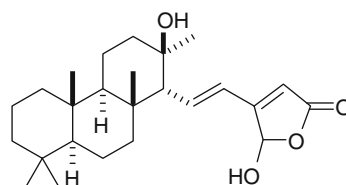
petrosaspongiolide M (**157**)
 R H
 N (**158**) OAc



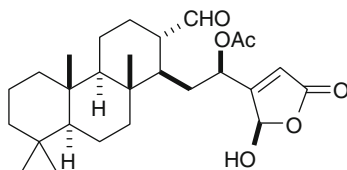
petrosaspongiolide P (**159**)
 R H
 Q (**160**) OAc



petrosaspongiolide R (**161**)

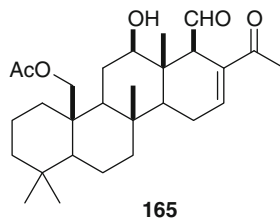
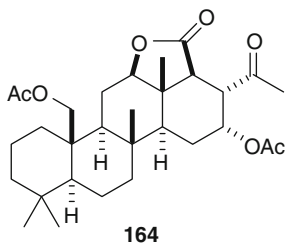


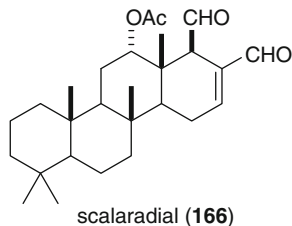
aplyolide A (**162**)



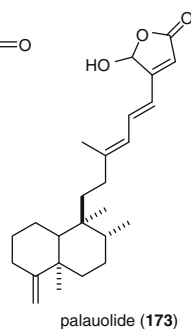
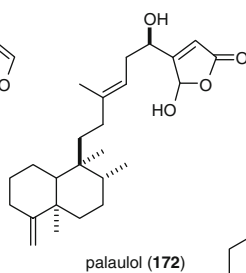
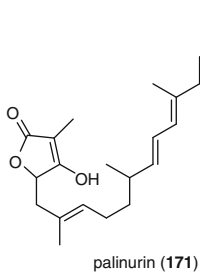
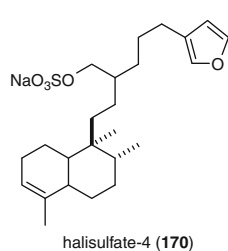
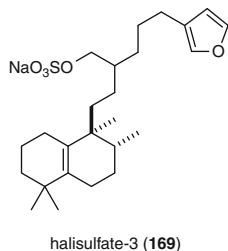
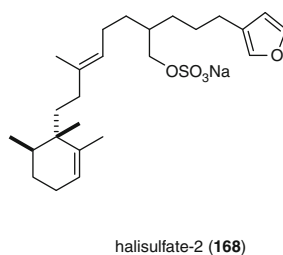
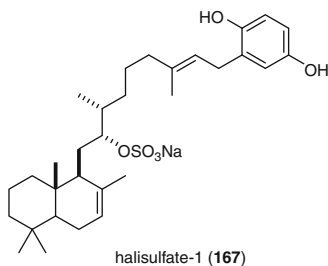
luffolide (**163**)

A homoscalarane sesterterpene (**164**) isolated from a marine sponge *Lendenfeldia frondosa* showed moderate PLA₂ inhibition (35% inhibition at 8 μM) [101]. A sesterterpene, 12-deacetyl-23-acetoxy-20-methyl-12-epi-scalaradial (**165**), from the Pacific nudibranchs *Glossodoris sedan* and *G. dalli* inhibited mammalian cytosolic PLA₂ with an IC₅₀ value of 18.0 μM [102]. The parent compound, scalaradial (**166**) is more potent (IC₅₀ 0.6 μM) [84a, 103].

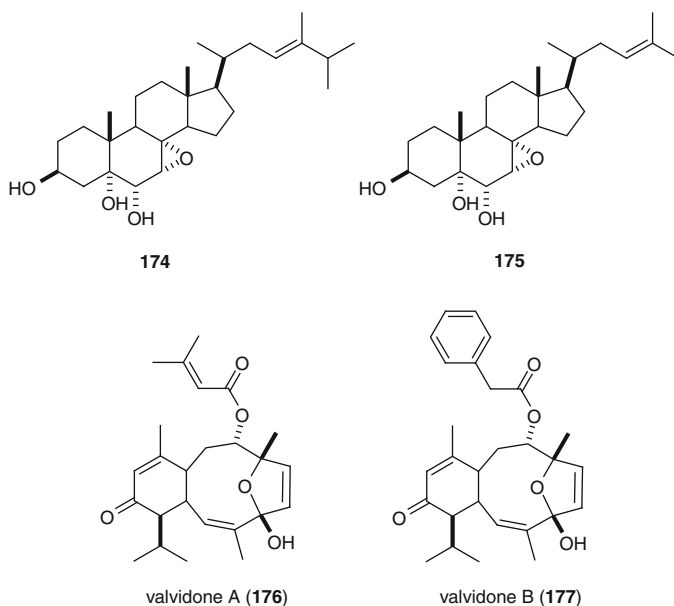




Halisulfate 1 (**167**) from a halichondrid sponge inhibited PLA₂ completely at 16 μg/mL, while a mixture of halisulfates 2–4 (**168–170**) inhibited PMA-induced inflammation in the mouse ear edema assay as well as PLA₂ (data not shown) [104]. Palinurin (**171**), originally isolated from the Mediterranean marine sponge *Ircinia variabilis* [105], was inhibitory against PLA₂ with an IC₅₀ value of 50 μM [2]. Two sesterterpenes, palaulol (**172**) and palaulide (**173**) isolated from a Palauan sponge *Fascaplysinopsis* sp. inhibit bee venom PLA₂ (85% and 82% inhibition at 0.8 μg/mL, respectively) [106].

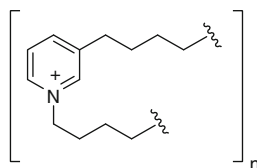


Two polyhydroxy sterols **174** and **175** from the Korean gorgonian *Acabaria undulata* inhibited PLA₂ with IC₅₀ values of 13.8 and 21.5 μM, respectively [107]. Valdivones A (**176**) and B (**177**), diterpenoids isolated from the South African soft coral *Alcyonium valdiviae*, strongly inhibited chemically induced inflammation in the mouse ear assay (93% and 72% inhibition at 50 μg/ear, respectively), but their activity against bee venom PLA₂ was not potent (43% inhibition at 16 μg/mL for both) [108].



23.4.2 Acetylcholinesterase (EC 3.1.1.7)

3-Alkylpyridinium polymers **178** from a marine sponge *Reniera sarai* showed potent inhibitory activity against electric eel acetylcholinesterase (AChE), human erythrocyte AChE, insect recombinant AChE, and horse serum butylcholinesterase (BuChE) with IC₅₀ values of 0.06, 0.08, 0.57, and 0.14 μg/mL, respectively, while it did not inhibit trypsin or alkaline phosphatase [109].



MW 5520 & 18900

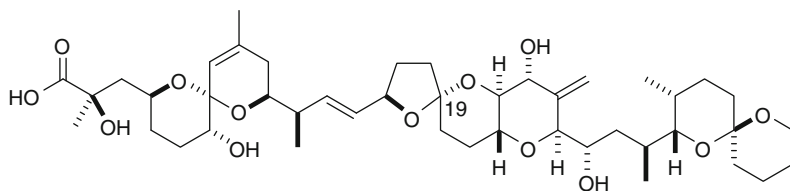
178

23.4.3 Protein Phosphatases (EC 3.1.3.16)

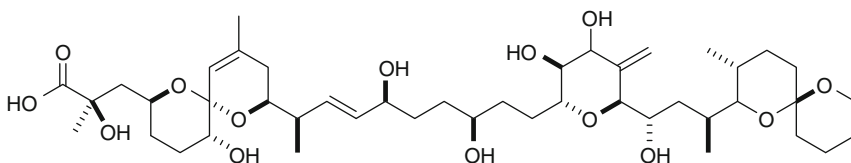
Reversible protein serine/threonine phosphorylation regulates numerous cellular functions, including muscle contraction, neurotransmission, cell proliferation, carcinogenesis, and apoptosis. Although a large number of protein kinases have been well investigated for several decades, it is quite recent that our understanding of protein phosphatases (PPs), namely PP1, PP2A, PP2B, and PP2C, has been considerably deepened by the discovery of natural product inhibitors.

23.4.3.1 PP1 and PP2

Okadaic acid (**179**), the first natural product inhibitor of PP1 and PP2A, is a polyether polyketide isolated as a cytotoxic substance from two sponges, Japanese *Halichondria okadai* and Caribbean *H. melanodocia* [110]. It was succeedingly identified as a causative agent of the diarrhetic shellfish poisoning. Later, **179** was found to show a potent tumor promoting activity caused by potent inhibition of PP1 and PP2A with IC_{50} values of 3 and 0.2–1 nM, respectively, whereas it showed only weak or no inhibition against PP2B or PP2C [111]. It has become a powerful tool for the study of biological processes mediated by protein phosphorylation. The crystal structure of PP1 γ -okadaic acid complex was elucidated in 1995 [112]. A remarkable reduction of inhibitory activity against PP1 (IC_{50} 465 nM) was observed for 19-*epi*-okadaic acid isolated from dinoflagellate *Prorocentrum belizeanum*, whereas the inhibitory activity against PP2A remained as the same level (IC_{50} 0.47 nM) for **179**. It was suggested that the stereochemistry at C19 is crucial for the selectivity between PP1 and PP2A [113]. A new okadaic acid class compound, belizeanic acid (**180**) with an unusual skeleton was isolated from the dinoflagellate *Prorocentrum belizeanum*. Despite its opening of C/D rings, it still retains the potent inhibitory activity against PP1 (IC_{50} 318 nM), slightly reduced potency compared to okadaic acid (IC_{50} 62 nM in the same assay system) [114].

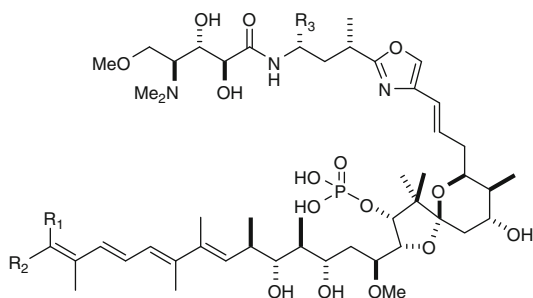


okadaic acid (**179**)

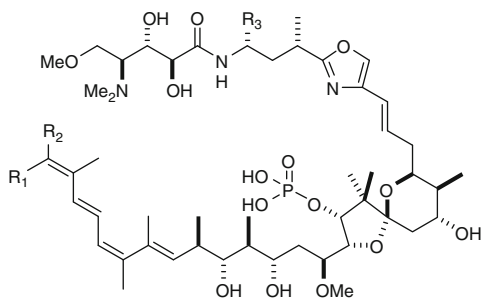


(**180**)

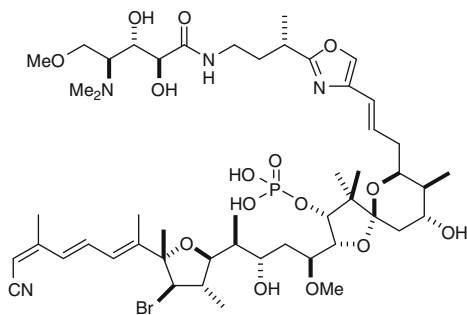
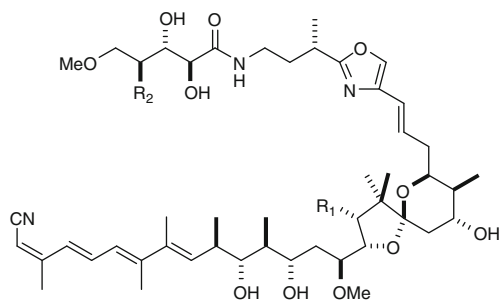
Calyculin A (**181**) was isolated from the Japanese marine sponge *Discodermia calyx* as a potent antitumor agent [115]. Like okadaic acid, it was found to be a potent tumor promoter and to inhibit PP1 and PP2A with IC₅₀ values of 1.4 and 2.6 nM, respectively, while it showed weak inhibition against PP2B [116]. Calyculins B–H (**182–188**), geometrical isomers of **181**, or their 32-methyl derivatives which were succeedingly isolated from the same sponge, were originally reported to have similar inhibitory activity against PP2A (IC₅₀ 1.0–6.0 nM) [117], but this was later found to be not correct; the geometry of the tetraene portion affects the enzyme inhibition significantly [119]. Furthermore, calyculin J (**189**), calyculinamides A (**190**) and F (**191**), des-*N*-methylcalyculin A (**192**) and dephosphonocalyculin A (**193**) were isolated as PP2A inhibitors from *D. calyx* [118]. Later, isolation of hemicalyculin A (**194**) from *D. calyx* and structure-activity relationship studies were reported [119]. Hemicalyculin A (**194**) was equipotent as calyculin A (**181**) against PP1 γ and PP2A with IC₅₀ values of 14 and 1.0 nM, respectively. Interestingly, **194** showed cytotoxicity over 2000 times less than that of **181**. More recently, the crystal structure of the calyculin A-PP1 γ complex was solved by X-ray crystallography [120], which showed that the hydrophobic tail, phosphate, and 13-OH moieties are essential for binding to PP1 γ . These features are the cases of the PP1c/microcystin LR [121] and PP1c/okadaic acid complexes [112]. Clavosines A–C (**195–197**), glycosylated derivatives of C21-*epi*-calyculinamide C, were isolated from the marine sponge *Myriastrra clavosa*. Clavosines A (**195**) and B (**197**) inhibited PP1 γ (IC₅₀s 0.5 and 13 nM, respectively), native PP1c (IC₅₀s 0.25 and 1.0 nM, respectively), and PP2Ac (IC₅₀s 0.6 and 1.2 nM, respectively) [122].



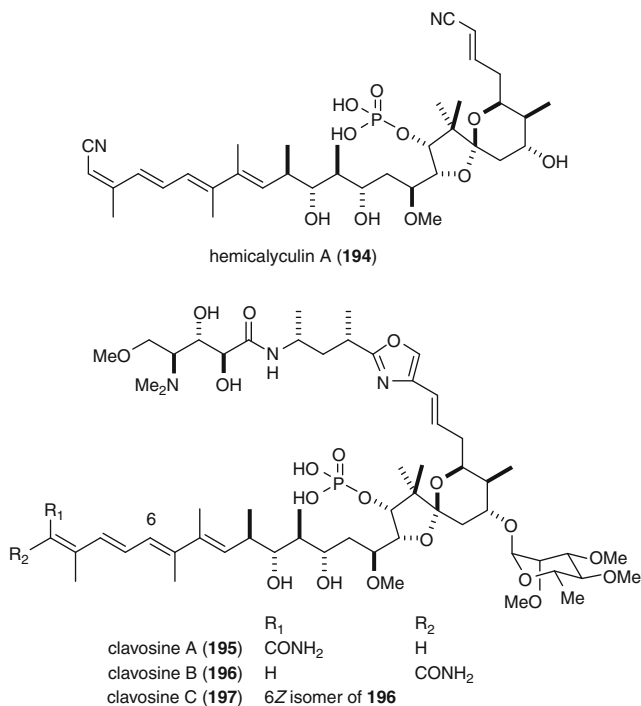
	R ₁	R ₂	R ₃
calyculin A (181)	CN	H	H
calyculin B (182)	H	CN	H
calyculin C (183)	CN	H	Me
calyculin D (184)	H	CN	Me
calyculinamide A (190)	CONH	H	H



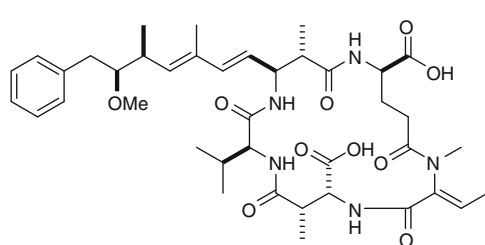
	R ₁	R ₂	R ₃
calyculin E (185)	CN	H	H
calyculin F (186)	H	CN	H
calyculin G (187)	CN	H	Me
calyculin H (188)	H	CN	Me
calyculinamide F (191)	H	CONH	H

calyculin J (**189**)

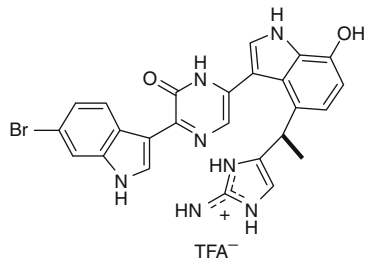
	R ₁	R ₂
des- <i>N</i> -methylcalyculin A (192)	OPO ₃ H ₂	NHMe
dephosphonocalyculin A (193)	OH	NMe ₂



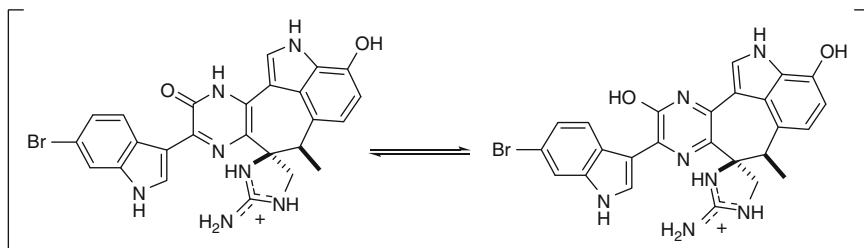
Motuporin A (**198**), one of the most potent PP1 inhibitors known, isolated from the Papua New Guinea sponge *Theonella swinhoei* inhibited PP1 at <1 nM [123]. Dragmacidins D (**199**) and E (**200**) isolated from a southern Australian deepwater sponge *Spongosorites* sp. are potent serine-threonine protein phosphatase inhibitors; **199** selectively inhibited PP1, while **200** inhibited both PP1 and PP2A in the preliminary test (data not shown). Dragmacidin E (**200**) seemed to exist in tautomeric equilibrium between pyrazine and pyrazinone forms [124]. Spirastrellolide A (**201**) was a novel macrolide isolated from the marine sponge *Spirastrella coccinea* as an antimetabolic agent [125]. Recently, its revised structure and selective inhibitory activity against PP2A (IC_{50} 1 nM) were reported [126]. Nagelamides are dimeric bromopyrrole alkaloids isolated from a marine sponge *Agelas* sp., among which nagelamides A–C (**202–204**), G (**205**), and H (**206**) were shown to inhibit PP2A (IC_{50} 13 to >50 μM) [127].



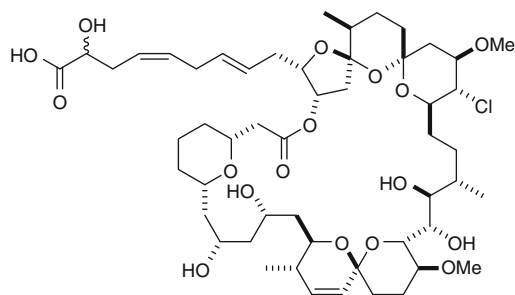
motuporin A (198)



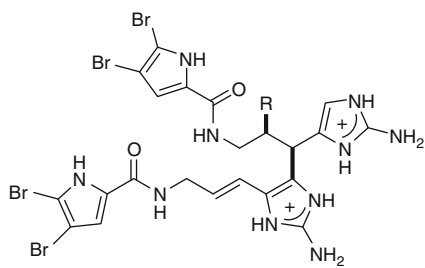
dragmacidin D (199)



dragmacidin E (200)

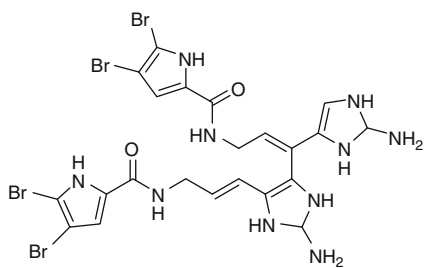


spirastrellolide A (201)

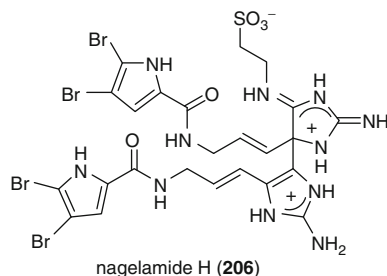
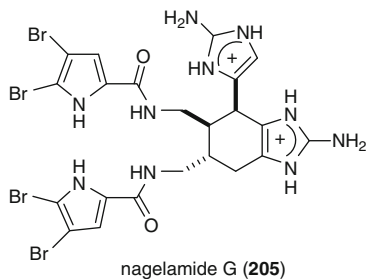


nagelamide A (202) R = H

B (203) R = OH

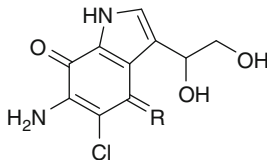


nagelamide C (204)



23.4.3.2 Calcineurin (PP2B)

Calcineurin (CaN), a serine-threonine protein phosphatase (PP2B) involved in signal transduction, is recognized as one of the principal signaling molecules that regulates the immune response [128]. Immunosuppressants such as FK506 and cyclosporin A have been shown to exert their effect through inhibition of CaN following their association with binding proteins [129]. Thus, inhibitors of CaN may be useful as immunosuppressants. Secobatzellines A (**207**) and B (**208**) isolated from a Caribbean deepwater sponge *Batzella* sp. inhibited CaN with IC_{50} values of 0.55 and 2.21 $\mu\text{g/mL}$, respectively. Secobatzelline A (**207**) also inhibited peptidase activity of CPP32 (IC_{50} 0.02 $\mu\text{g/mL}$), a cysteine protease known as caspase-3 which play a major role in the programmed cell death known as apoptosis [130].



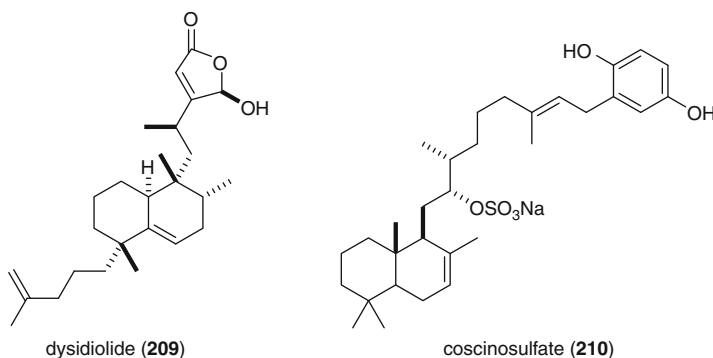
secobatzelline A (**207**) R = NH

secobatzelline B (**208**) R = O

23.4.4 Protein Tyrosine Phosphatases (EC 3.1.3.48)

Cdc25 is a dual-specificity protein tyrosine phosphatase which regulates activation of CDKs (cyclin-dependent kinases) through the dephosphorylations of a threonine and a tyrosine residues of CDKs. Due to their unique substrate selectivity and their essential functions in cell cycle control, cdc25 phosphatases are attractive screening target to identify new antimitotic compounds. Dysidiolide (**209**) is the first natural product inhibitor of cdc25A isolated from the Caribbean sponge *Dysidea etheria*. It inhibited the dephosphorylation of *p*-nitrophenol phosphate by cdc25A phosphatase with an IC_{50} of 9.4 μM [131].

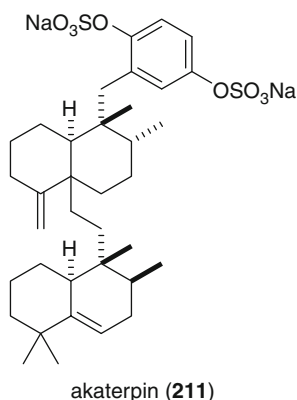
Because of its unusual structure and interesting biological activity, a number of synthetic chemists entered the race of total synthesis of dysidiolide, from which some important structure-activity relationships were provided [132]. Coscinosulfate (**210**), a sesquiterpene sulfate isolated from the New Caledonian sponge *Coscinoderma mathewsi* exhibited selective inhibition against cdc25A phosphatase with an IC_{50} of 3 μ M [133].



23.4.5 Phospholipase C (EC 3.1.4.3)

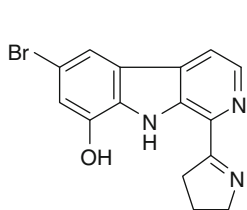
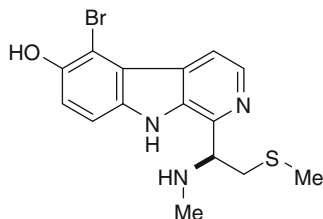
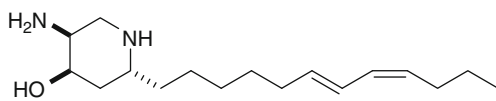
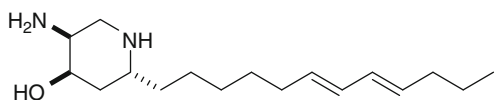
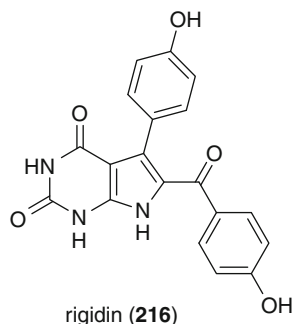
Phosphatidylinositol-specific phospholipase C (PI-PLC) is the rate-limiting enzyme in the phosphatidylinositol turnover. PI-PLC hydrolyzes the phosphate-glycerol linkage of phosphatidylinositol to produce two second messengers, inositol triphosphate and diacylglycerol which play key roles in cellular signal transduction induced by growth factors and hormones [134].

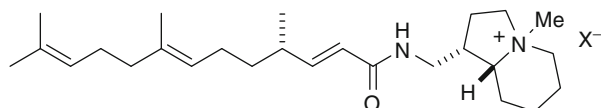
Akaterpin (**211**) isolated from an Okinawan marine sponge *Callyspongia* sp. showed potent inhibition against PI-PLC (IC_{50} 0.5 μ g/mL) as well as weak inhibition against neutral sphingomyelinase with an IC_{50} value of 30 μ g/mL [135].



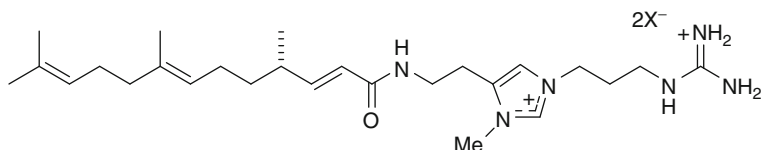
23.4.6 Phosphodiesterase (EC 3.1.4.-)

The Ca^{2+} -calmodulin system plays an important role in the control of cellular proliferation and tumor formation. A calmodulin antagonist, W-7, has been found to inhibit proliferation of Chinese hamster cells and formation of mouse skin tumors. Eudistomin A (**212**), a β -carboline alkaloid isolated from the Okinawan tunicate *Eudistoma glaucus*, inhibited calmodulin-activated brain phosphodiesterase with an IC_{50} value of 20 μM [136], while eudistomin C (**213**) exhibited calmodulin antagonistic activity (IC_{50} 30 μM) [137]. Pseudodistomins A (**214**) and B (**215**), unusual alkyloppiperazines of the Okinawan tunicate *Pseudodistoma kanoko*, inhibited calmodulin-activated brain phosphodiesterase at the same concentration (IC_{50} 30 μM), which is about three times more potent than W-7 [138]. Rigidin (**216**) isolated from an Okinawan tunicate *Eudistoma cf. rigida* inhibited calmodulin-activated brain phosphodiesterase with an IC_{50} value of 50 μM [139]. Stelletamide A (**217**), an unusual indolizidine alkaloid originally isolated from a marine sponge *Stelletta* sp. as an antifungal and cytotoxic compound [140], was found to inhibit Ca^{2+} /calmodulin-dependent phosphodiesterase and $(\text{Ca}^{2+}\text{-Mg}^{2+})\text{-ATPase}$ with IC_{50} values of 52 and 100 μM , respectively [141]. Related alkaloids, stelletazole A (**218**) [142], bistelletadines A (**219**), and B (**220**) [143], from the same sponge showed moderate inhibitory activity against Ca^{2+} /calmodulin-dependent phosphodiesterase (**218**: 45% inhibition at 100 μM , **219** and **220**: 40% inhibition at 100 μM).

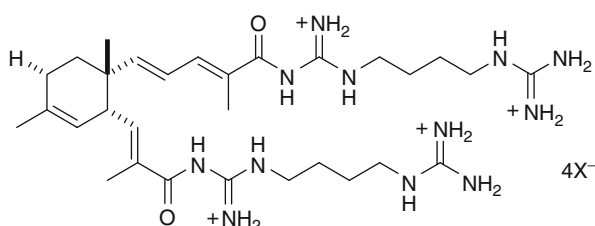
eudistomin A (**212**)eudistomin C (**213**)pseudodistomin A (**214**)pseudodistomin B (**215**)rigidin (**216**)



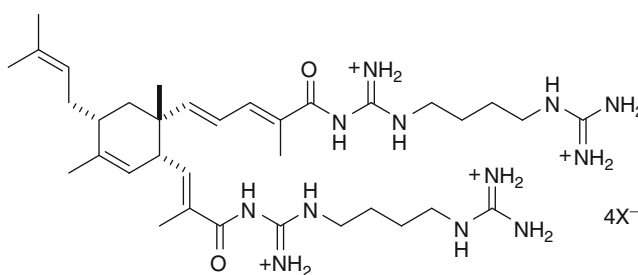
stellettamide A (217)



stellettazole A (218)



bistellettadine A (219)

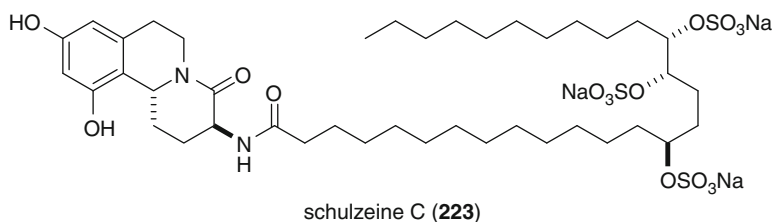
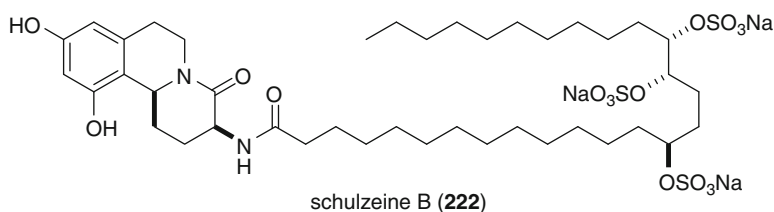
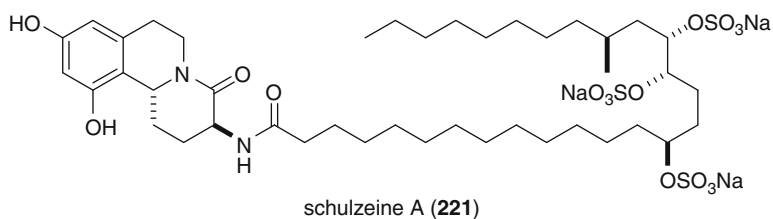


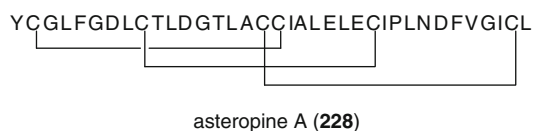
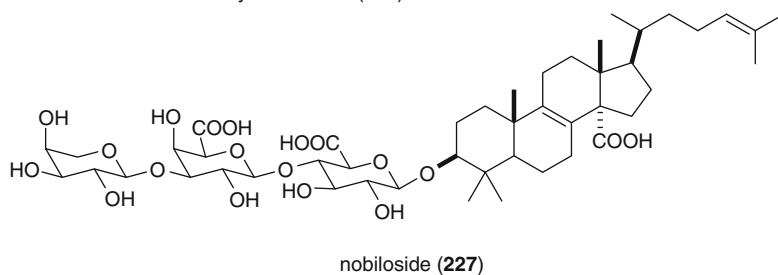
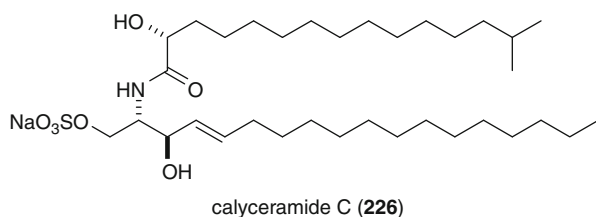
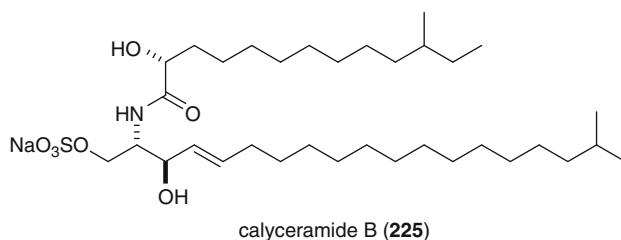
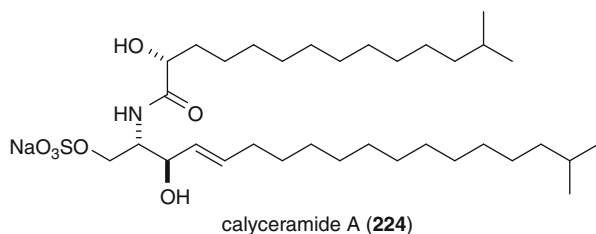
220

23.4.7 Sialidase (EC 3.2.1.18)

Sialidase cleaves an α -linked terminal *N*-acetylneuraminic acid from glycoproteins, glycolipids, and oligosaccharides. In several viral and bacterial infections, neuraminidases play important roles; influenza virus employs this enzyme to detach itself from the infected cell in the budding stage, thus indicating requirement of neuraminidase for replication of the virus. Therefore, selective inhibitors

of sialidase are potential therapeutic agents against influenza. The α -glucosidase inhibitors, schulzeines A–C (**221–223**), were also inhibitory against viral neuraminidase with IC_{50} values of 60 μ M. Calyceramides A–C (**224–226**), sulfated ceramides isolated from the marine sponge *Discodermia calyx*, inhibited sialidase from *Clostridium perfringens* with IC_{50} values of 0.4, 0.2, and 0.8 μ g/mL, respectively [144]. Another example of a marine sialidase inhibitor is nobiloside (**227**), a triterpenoid saponin of the marine sponge *Erylus nobilis*, which inhibited *Clostridium perfringens* sialidase with an IC_{50} value of 0.46 μ g/mL [145]. Asteropine A (**228**) is the first cystine knot of sponge origin isolated from *Asteropus simplex*. Asteropine A showed potent and competitive inhibition against bacterial sialidases (from *Clostridium perfringens*, *Vibrio cholerae*, and *Salmonella typhimurium*) with K_i values of 36.7, 340, and 350 nM, respectively [146].

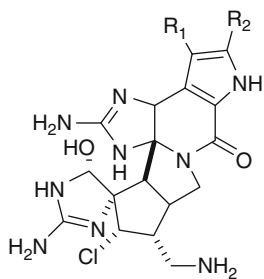




23.4.8 Chitinase (EC 3.2.1.14)

Chitinase plays crucial roles in a wide variety of organisms ranging from nutrition to defence and control of ecdysis in arthropods, thus indicating their potential for antifungal and insecticidal agents. Styloguanidines (**229–231**) isolated from the

sponge *Stylotella aurantium* collected off Yap showed inhibitory activity against chitinase from a bacterium *Schwanella* sp. at the dose of 2.5 $\mu\text{g}/\text{disc}$ by using the “squid chitin agar plate method.”[147].

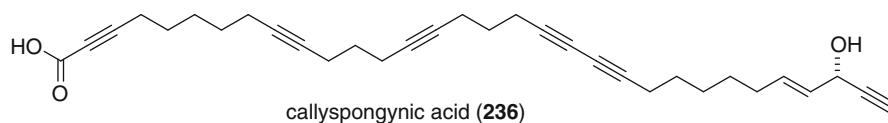
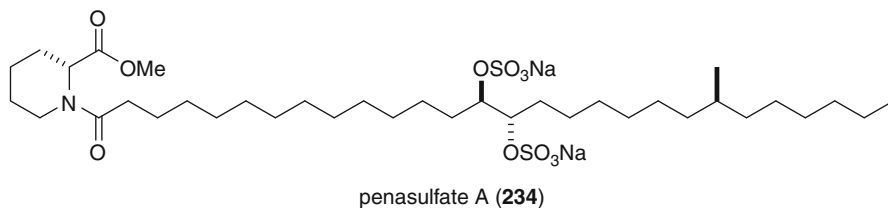
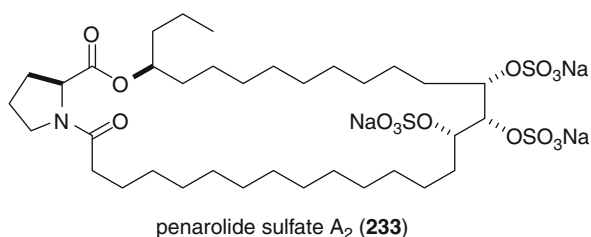
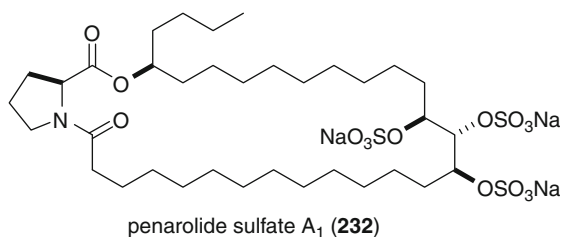


	R ₁	R ₂
styloguanidine (229)	H	H
3-bromostyloguanidine (230)	Br	H
2,3-dibromostyloguanidine (231)	Br	Br

23.4.9 α -Glucosidases (EC 3.2.1.20)

α -Glucosidases are involved in glycoprotein processing and glycogenolysis and, therefore, their inhibitors can be applied for treatment of diabetes, obesity, viral infections, and cancer. Penarolide sulfates A₁(**232**) and A₂(**233**), L-proline containing macrolide trisulfates isolated from a marine sponge *Penares* sp., inhibited α -glucosidase of yeast origin with IC₅₀ values of 1.2 and 1.5 $\mu\text{g}/\text{mL}$, respectively, while they showed only weak or no inhibition against β -glucosidase or β -galactosidase. Penarolide sulfates also inhibited thrombin with IC₅₀ values of 3.7–4.2 $\mu\text{g}/\text{mL}$. Perhaps, the three sulfate groups are responsible for the activity [148]. A linear type congener, penasulfate A (**234**), in which L-proline was replaced by D-pipecolic acid, was isolated from the same sponge. Penasulfate A (**234**) showed about ten times as potent inhibition (IC₅₀ 0.14 $\mu\text{g}/\text{mL}$) as penarolides against the same enzyme, while the inhibitory activity against the enzyme from the different source remained the same level [149]. The known 1,4-dideoxy-1,4-imino-D-arabinitol (**235**) was isolated as an α -glucosidase inhibitor from a marine sponge *Haliclona* sp. collected in Western Australia. Iminopentitol (**235**) strongly inhibited yeast α -glucosidase at an IC₅₀ value of 0.16 $\mu\text{g}/\text{mL}$ [150]. Callyspongynic acid (**236**), a polyacetylenic acid was isolated from the Japanese marine sponge *Callyspongia truncata*. Callyspongynic acid (**236**) inhibited α -glucosidase with an IC₅₀ value of 0.25 $\mu\text{g}/\text{mL}$, but was inactive against β -glucosidase, β -galactosidase, thrombin, and trypsin at 100 $\mu\text{g}/\text{mL}$. Both the carboxylic acid and the allylic alcohol linked to an acetylene are thought to be important for the activity [151]. The Japanese marine sponge *Penares schulzei* afforded three new α -glucosidase inhibitors, schulzeines A–C (**221–223**), which showed potent inhibitory

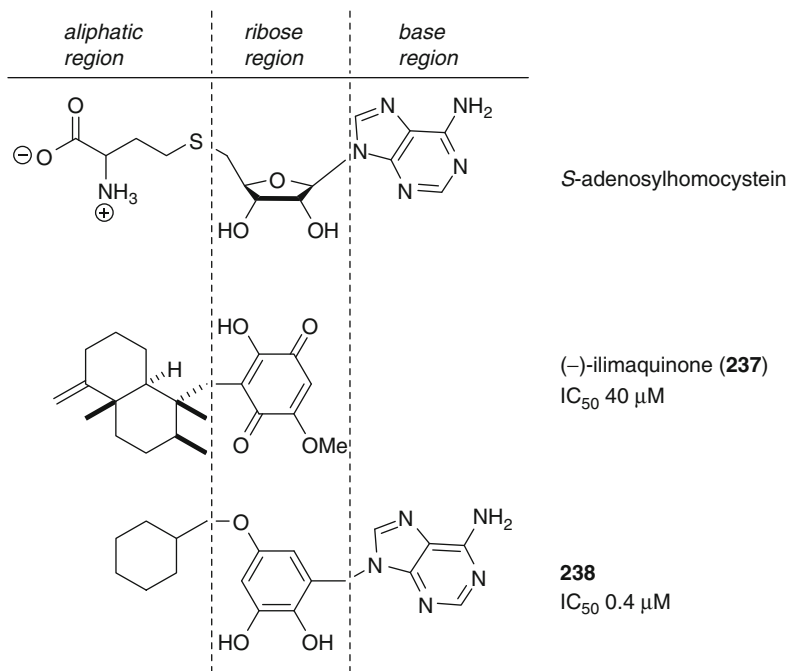
activity against α -glucosidase with IC_{50} values of 48–170 nM. It should be noted that desulfated schulzeines A and B still retained activity (IC_{50} s 2.5 and 1.1 μ M, respectively) [152]. Recently, the stereochemistry at C-20 of **221** was revised on the basis of total chemical synthesis [153].



23.4.10 S-Adenosylhomocysteine Hydrolase (EC 3.3.1.1)

S-adenosylhomocysteine hydrolase that reversibly hydrolyzes S-adenosylhomocysteine to homocysteine and adenosine has been considered an attractive target for the design of antiviral, antiparasitic, antiarthritic and immunosuppressive agents. Ilimaquinone (**237**) has been reported to possess antiviral,

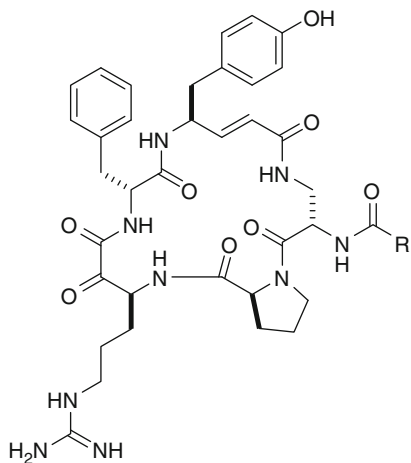
antimitotic, antimicrobial, and anti-HIV activities. It was also shown to vesiculate the Golgi apparatus as well as to protect cells against the toxic effects of ricin and diphtheria. Whole-cell and cytosolic photoaffinity labeling and affinity chromatography studies with chemical probes prepared from **237** converged on *S*-adenosylhomocysteine hydrolase as a cellular target of **237**. Subsequent studies with isolated enzyme indicated that ilimaquinone is a competitive inhibitor of *S*-adenosylhomocysteine hydrolase (IC_{50} 40 μ M). On the basis of SAR studies, pharmacophore modeling, and computer docking studies have allowed for the design and preparation of a simplified structural variant (**238**) possessing a 100-fold greater inhibitory activity than that of natural (–)-ilimaquinone (**237**) [154].



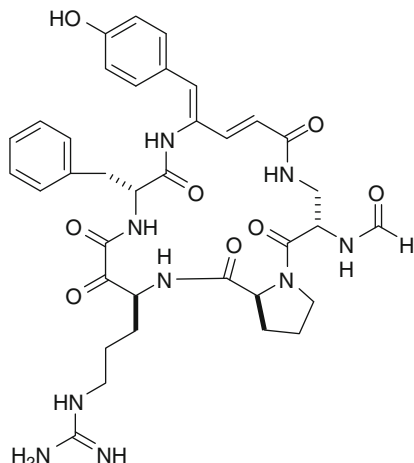
23.4.11 Serine Proteases (EC 3.4.21.-)

Proteolytic enzymes are classified into serine proteases, cysteine proteases, aspartic proteases, and metalloproteases on the basis of their catalytic centers. Trypsin-like enzymes, a group of serine proteases, are associated with many disease states. The hyperproteolytic activities of this homologous family of enzymes are attractive chemotherapeutic targets in pathways of blood coagulation, fibrinolysis, kinin formation, complement activation, digestion, reproduction, and phagocytosis. Thus,

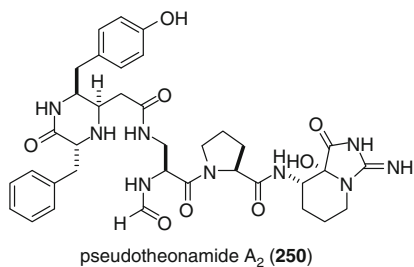
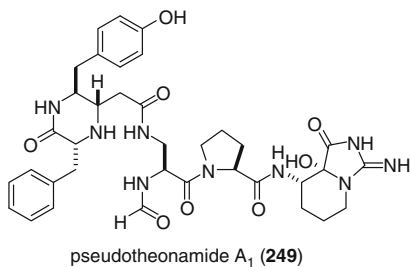
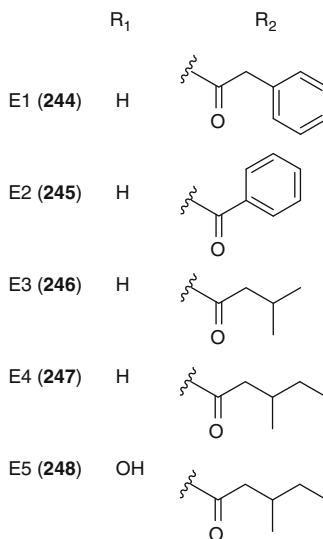
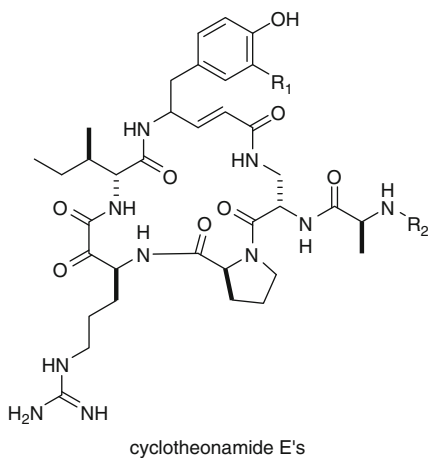
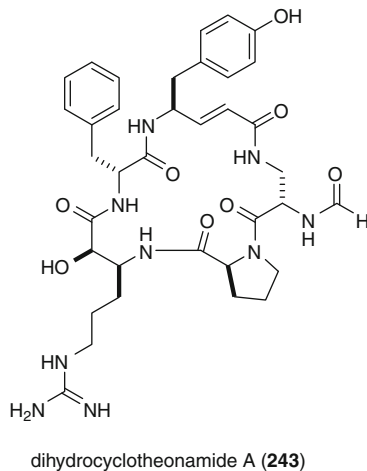
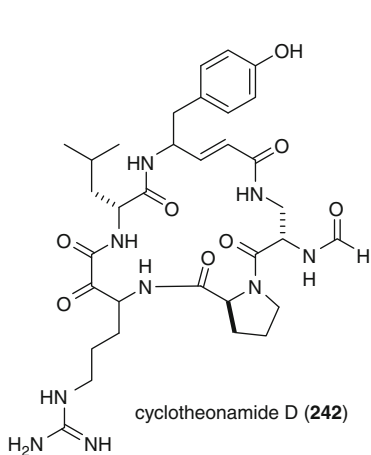
inhibitors of specific serine proteases can be potential drug-leads for many disease status [155]. Cyclotheonamides A (**239**) and B (**240**) from a marine sponge *Theonella* sp. (now known to be *T. swinhoei*) inhibited thrombin, trypsin and plasmin with IC_{50} values of 0.076, 0.2, and 0.3 $\mu\text{g/mL}$, respectively [156]. Further investigation of *T. swinhoei* yielded cyclotheonamides C (**241**) and D (**242**) [157]. Cyclotheonamides E series (**244–248**) were not found from this sponge, but from the other type of *T. swinhoei* whose interior part is white (E1–E3) [158] and from an Okinawan sponge *Ircinia* sp. (E4–E5) [159]. Cyclotheonamides C (**241**), D (**142**), and E1–E5 (**244–248**) showed potent inhibition against thrombin and trypsin with IC_{50} values of 2.9–68 nM and 7.4–55 nM, respectively. Cyclotheonamide E1 (**244**), E4 (**247**), and E5 (**248**) strongly inhibited both mouse and human tryptases (IC_{50} s 6.9, 23, and 84.7 nM for human tryptase, and 17.0, 6.5, and 54.1 nM for mouse tryptase, respectively) [159]. Dihydrocyclotheonamide A (**243**), pseudotheonamides A₁ (**249**), A₂ (**250**), B₂ (**251**), C (**252**), and D (**253**) from *T. swinhoei*, in which α -ketohomoarginine (k-Arg) residues are cyclized, showed only moderate activity against these enzymes with IC_{50} values ranging from 0.19 to 3.0 μM (thrombin) and 3.8 μM (trypsin) [160]. Complexes between cyclotheonamide A and human α -thrombin and between cyclotheonamide A and trypsin were successfully crystalized and their crystal structures were solved, disclosing that cyclotheonamide A binds to the catalytic center of these enzyme; particularly k-Arg which forms the hemiacetal linkage with Ser195 of one of a catalytic triad is important for the binding to the enzyme [161]. From the same *T. swinhoei*, was isolated a thrombin inhibitory linear peptide, nazumamide A (**254**) which inhibited thrombin with an IC_{50} value of 2.8 $\mu\text{g/mL}$, but not trypsin at 100 $\mu\text{g/mL}$ [162]. Retro-binding mode of nazumamide A to human thrombin was demonstrated by X-ray crystallography of the nazumamide A/thrombin complex [163].

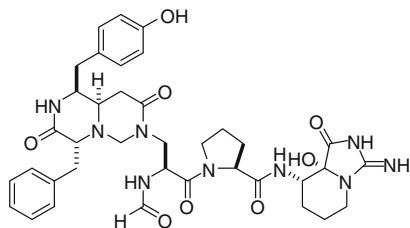
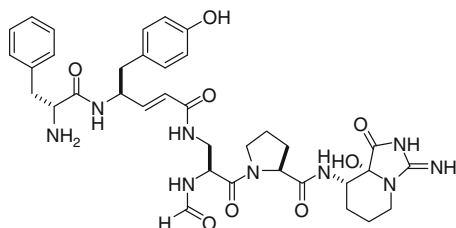
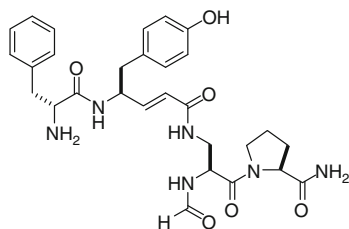
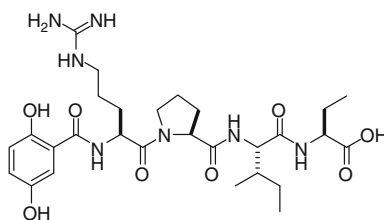


cyclotheonamide A (**239**) R = H
cyclotheonamide B (**240**) R = Ac

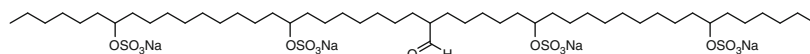
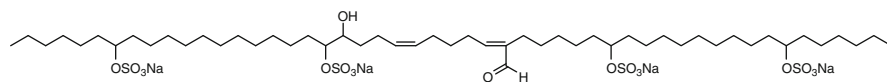
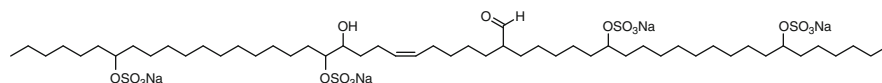
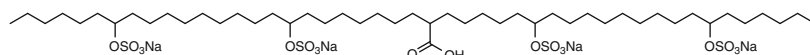


cyclotheonamide C (**241**)



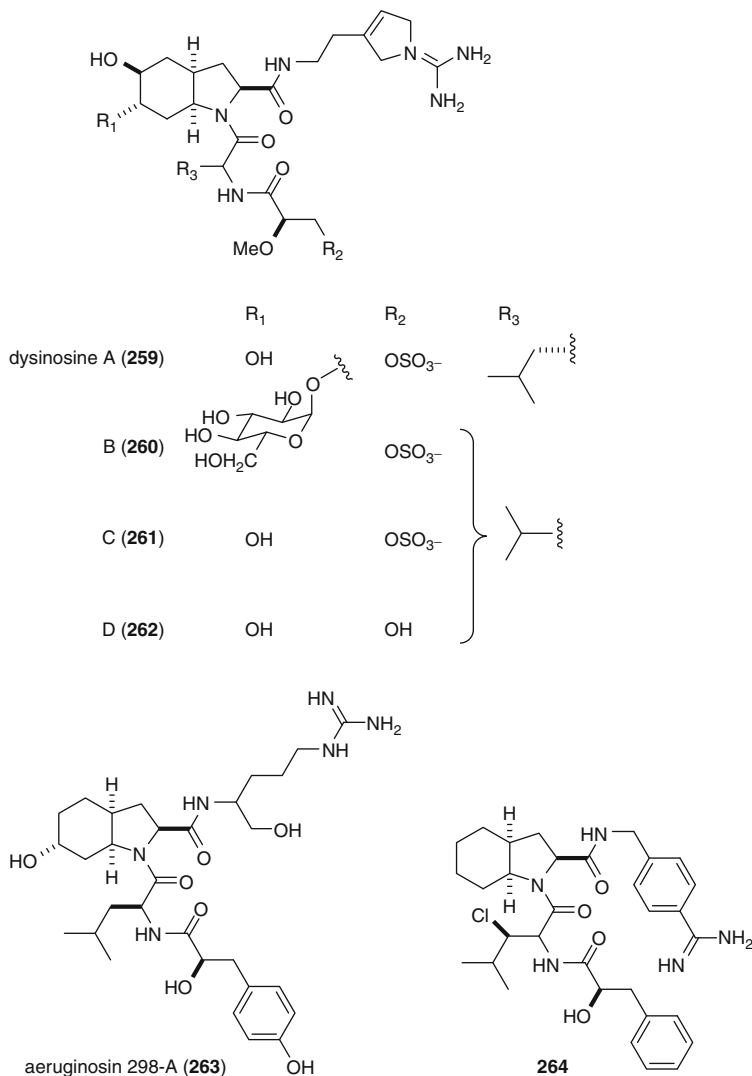
pseudotheonamide B₂ (**251**)pseudotheonamide C (**252**)pseudotheonamide D (**253**)nazumamide A (**254**)

Toxadocials A–C (**255–257**) and toxadocic acid A (**258**) isolated from a marine sponge *Toxadocia* sp., are alkyl sulfate thrombin inhibitors with IC₅₀s of 6.5, 4.6, 3.2, and 2.7 μg/mL, respectively [164]. The mode of enzyme inhibition of toxadocials is not known.

Toxadocial A (**255**)Toxadocial B (**256**)Toxadocial C (**257**)Toxadocic acid A (**258**)

Dysinosins A–D (**259–262**) are inhibitors of factor VIIa and thrombin isolated from the Australian sponge *Lamellodysidea chlorea*. Dysinosins showed potent inhibitory activity against factor VIIa and thrombin with K_i values of 0.090 to 1.32

and 0.17 to $> 23 \mu\text{M}$, respectively [165]. The structural similarity of dysinosins to that of aeruginosins (**263**) which were the serine protease inhibitors isolated from the cyanobacteria *Microcystis aeruginosa* [166] and *Oscillatoria agardhii* [167] implied that they were biosynthesized by symbiotic microbes. Based on X-ray crystallographic data of complexes of chlorodysinosin A with thrombin, a series of analogues were synthesized varying the nature of the P₁, P₂, and P₃ pharmacophoric sites and the central octahydroindole carboxamide core. Introduction of a hydrophobic substituent on the D-Leu amide dramatically improved the inhibitory activity against thrombin (**264**: IC₅₀ 1.6 nM) [168].

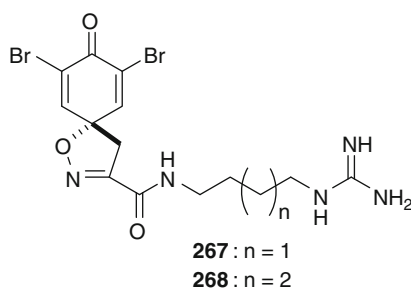
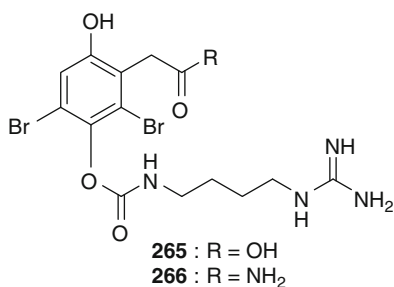


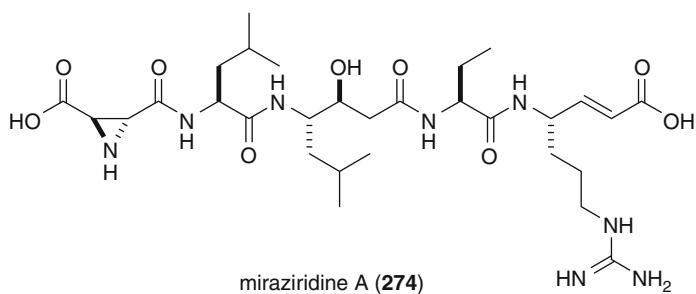
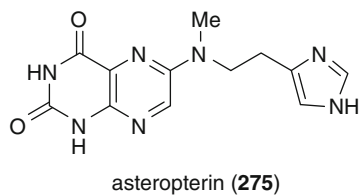
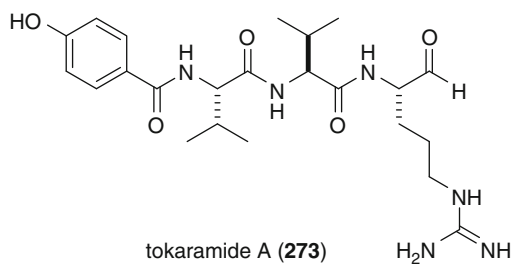
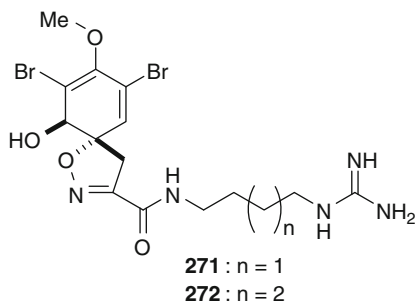
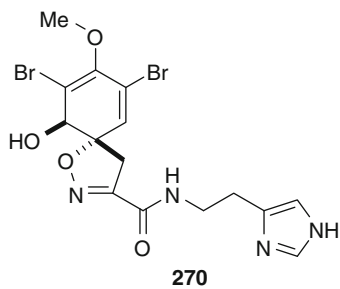
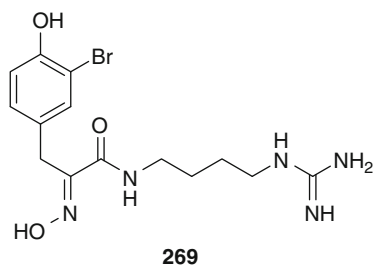
Factor XIa (FXIa) is a trypsin-like serine protease that plays a major role in the amplification phase of the coagulation cascade and in maintaining clot integrity. It is a unique target where specific inhibitors of FXIa might inhibit thrombosis without completely interrupting the function of normal hemostasis and might prevent or minimize the risk of hemostasis complication. Clavatadines A–E (**265–269**) were isolated as FXIa inhibitors from the Australian sponge *Suberea clavata* along with known aerophobin 1 (**270**), purealdin L (**271**), and aplysinamisine II (**272**). Compounds **265** and **266** inhibited FXIa with IC_{50} values of 1.3 and 27 μM , respectively, whereas they did not inhibit FIXa ($< 5\%$ inhibition at 222 μM). The crystal structure obtained by soaking of compound **265** into a single crystal of FXIa showed only the carbamate side chain of **265** covalently bonded to the active site serine residue (Ser 195) [169]. Compounds **267–272** were shown to be weaker inhibitors (12–59% inhibition at 222 μM) [170].

23.4.12 Cysteine Proteases (EC 3.4.22.-)

23.4.12.1 Cathepsin B (EC 3.4.22.1)

Cysteine proteases which have cysteine and histidine as the catalytic center are involved in cytosolic protein metabolisms. Cathepsin B, a cysteine protease, is known to be involved in various disease states, such as inflammation, trauma, muscular dystrophy, and tumors. In particular, its possible roles in cancer metastasis are of major concern in cancer chemotherapy. Two peptidic inhibitors, tokaramide A (**273**) [171] and miraziridine A (**274**) [172] with IC_{50} values of 29 and 1,400 ng/mL were isolated from the marine sponge *Theonella* aff. *mirabilis*. Miraziridine A (**274**) contains three unusual amino acid residues; particularly unusual are vinylogous arginine and aziridine-2,3-dicarboxylic acid. Secobatzelline A (**207**) isolated from a sponge *Batzella* sp. showed inhibition against peptidase activity of CPP32, a member of caspases which are cysteine proteases playing a major role in the programmed cell death mechanism known as apoptosis, with an IC_{50} value of 0.02 $\mu\text{g}/\text{mL}$ as well [130]. Asteropterin (**275**), a unique molecule with a combination of lumazine and *N*-methyl histamine isolated from the marine sponge *Asteropus simplex*, inhibited cathepsin B with an IC_{50} value of 1.4 $\mu\text{g}/\text{mL}$ [173].



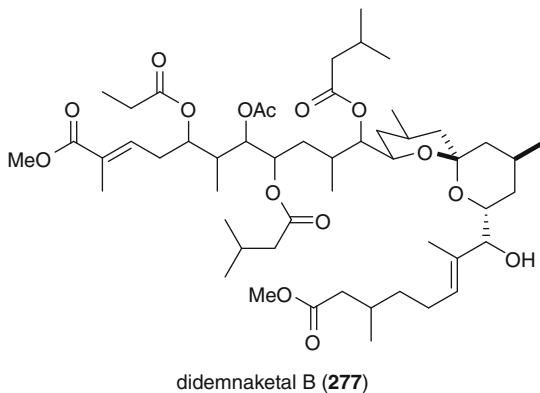
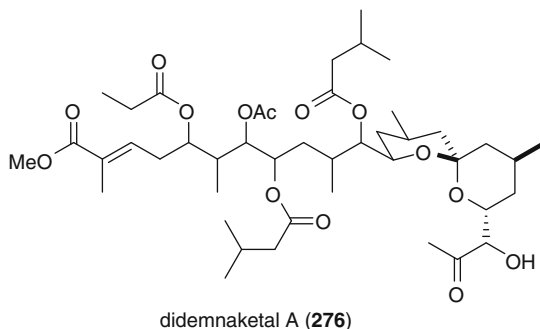


23.4.13 Aspartic Proteases (EC 3.4.23.-)

23.4.13.1 HIV Protease (EC 3.4.23.47)

Replication of HIV involves the expression of several viral polyproteins that requires the presence of a virus-specific protease for their maturation. Inhibition of this enzyme results in immature viral particles; therefore, HIV-1 protease is an ideal target for AIDS chemotherapeutics.

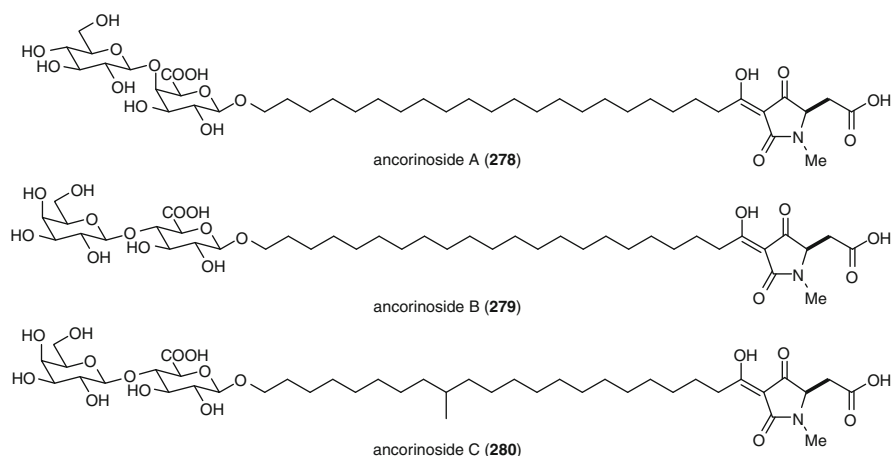
Didemnaketals A (276) and B (277), isolated from a Palauan ascidian *Didemnum* sp., inhibited HIV-1 protease with IC_{50} values of 2 and 10 μ M, respectively [174]. The unusual structures and potent activity of didemnaketals indicated their possibility as attractive synthetic targets [175]. Recently, simplified analogues lacking the spiroketal portion were synthesized, some of which were as potent as didemnaketal A. It was also proposed that didemnaketals inhibit dimerization of HIV-1 protease monomers [176].

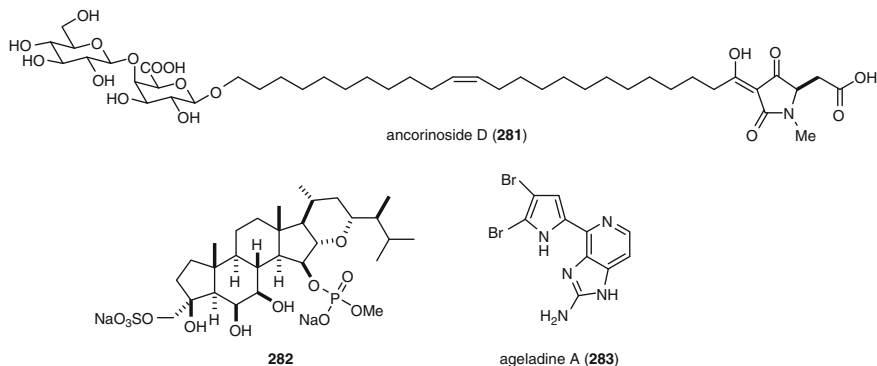


23.4.14 Metalloproteases (EC 3.4.24.-)

Metalloproteases contain metal ions such as Zn^{2+} , Co^{2+} , Mn^{2+} , etc., in their catalytic centers. The matrix metalloproteinases (MMPs), members of a large

subfamily of proteases which contains a catalytic zinc-binding domain, play important roles in the remodeling and degradation of extracellular matrix (ECM). They are linked to a range of physiological and pathological processes, including wound healing, bone remodeling, angiogenesis, inflammation, and tumor progression and metastasis. The membrane-type matrix metalloproteinases (MT-MMPs) are known as key enzymes in tumor metastasis. They activate progelatinase A to the fully matured form which in turn degrades type IV collagen, the major component of the basal membrane which prevents tumor progression. Thus, inhibitors of MT-MMPs are believed to be potential anticancer drugs. Ancorinosides B–D (**279–281**) [177] were isolated as MT1-MMP inhibitors from the marine sponge *Penares sollasi* along with known ancorinoside A (**278**) [178] which was originally isolated as an inhibitor of blastulation of starfish embryos from a marine sponge *Ancorina* sp. Ancorinosides A–D (**278–281**) inhibited MT1-MMP with IC₅₀ values of 440, 500, 370, and 180 µg/mL, respectively. Ancorinoside B (**279**) also inhibited gelatinase A (MMP2) with an IC₅₀ value of 22 µg/mL. Haplosamate A (**65**) and its congener (**282**) were isolated from a Japanese marine sponge *Cribrochalina* sp. as MT1-MMP inhibitors with IC₅₀ values of 150 and 160 µg/mL, respectively; [179] **65** was originally isolated as an HIV integrase inhibitor from Philippine haplosclerid sponges [32]. Ageladine A (**283**) is a fluorescent alkaloid isolated from the marine sponge *Agelas nakamurai*. The IC₅₀ values of **283** against MMPs 1, 2, 8, 9, 12, and 13 were 1.2, 2.0, 0.39, 0.79, 0.33, and 0.47 µg/mL, respectively, while its *N*-methylated derivatives did not inhibit MMP2. Unlike other MMP inhibitors, ageladine A (**283**) was not capable to chelate Zn²⁺ and not a competitive inhibitor against MMP2 [180]. With such interesting aspects of inhibition mode, as well as its anti-angiogenic activity, ageladine A became a target of total synthesis [181].

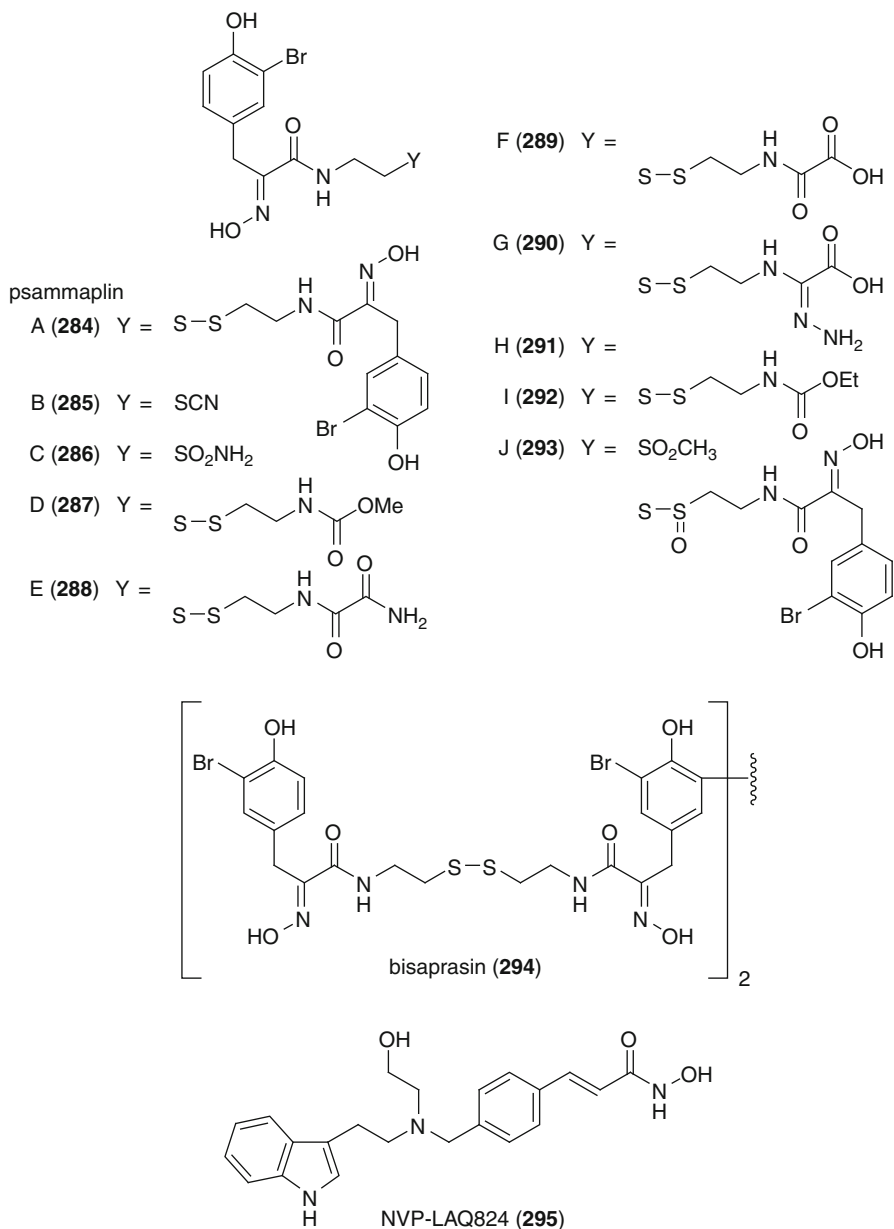


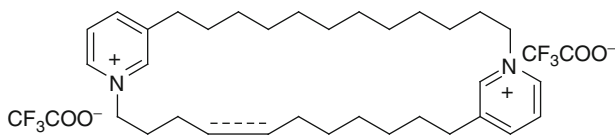


23.4.15 Histone Deacetylases (EC 3.23.-)

Histone acetylation and deacetylation are catalyzed by histone acetyltransferases (HATs) and histone deacetylases (HDACs), respectively, which play important roles in transcriptional regulation [182]. Inhibitors of these enzymes are known to induce cell cycle arrest [183], p53-independent induction of the cyclin dependent kinase inhibitor p21 [184], tumor-selective apoptosis [185], and differentiation of normal and malignant cells [186]. HDAC inhibitors were also demonstrated to exert anti-angiogenic effects through the alteration of vascular endothelial growth factor (VEGF) signaling [187]. These direct and indirect effects on tumor growth and metastasis indicate that HDAC inhibitors are potential anti-cancer agents. Six new psammaplins E–J (**288–293**) were isolated from the marine sponge *Pseudoceratina purpurea* collected in Papua New Guinea along with known psammaplins A–D (**284–287**), and bisaprasin (**294**). These compounds showed potent inhibitory activity against HDAC (IC₅₀s 2.1–327 nM) and cell-based p21 promoter activity (IC₅₀s 0.7–15 μM), in addition to inhibitory activity against DNA methyltransferase (DNMT) [188]. NVP-LAQ824 (**295**) which was developed on the basis of structures of HDAC inhibitors including psammaplins [189] entered phase I clinical trials in patients with solid tumors or leukemia [190]. Three new cyclostellettamines, cyclostellettamine G (**297**), dehydrocyclostellettamines D (**298**) and E (**299**), were isolated together with the known cyclostellettamine A (**296**) from a marine sponge of the genus *Xestospongia*. These compounds inhibited HDAC with IC₅₀ values of 17–80 μM [191]. Five new cyclic tetrapeptides, azumamides A–E (**300–304**) were isolated from the marine sponge *Mycale izuensis*. Azumamides showed inhibitory activity against human HDAC at IC₅₀ values of 0.045–1.3 μM. In the cell-based assay using K562 cells, azumamide A (**300**) inhibited deacetylation of Ac-H3 (Lys9 and Lys 14) and Ac-H4 (Lys 8) in a dose-dependent manner

(0.19–19 μM). Furthermore, azumamide A inhibited angiogenesis in the in vitro vascular organization model using mouse ES cells [192].



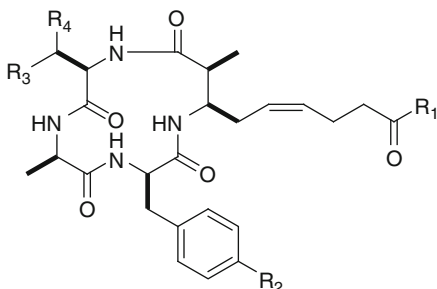


cyclostelletamine A (**296**) : $m = 1, n = 2$

G (**297**) : $m = 1, n = 1$

dehydrocyclostelletamine D (**298**) : $m = 1, n = 4, \Delta^{13}$

E (**299**) : $m = 2, n = 4, \Delta^{13}$



	R ₁	R ₂	R ₃ = R ₄
azumamide A (300)	NH ₂	H	Me
B (301)	NH ₂	OH	Me
C (302)	OH	OH	Me
D (303)	NH ₂	H	H
E (304)	OH	H	Me

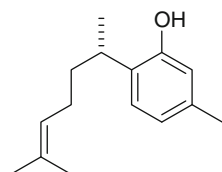
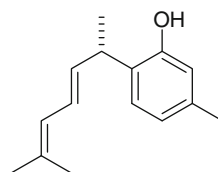
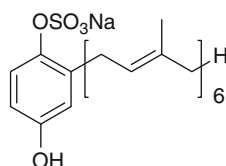
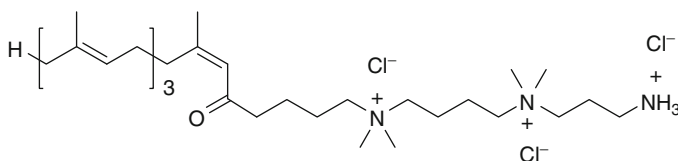
23.4.16 ATPases (EC 3.6.1.3)

23.4.16.1 H,K-ATPase

H,K-ATPase mediates acid secretion from gastric wall cells. Thus, excess activation of this enzyme leads to hyperacidity, causing gastric ulcer. In order to discover potential antiulcer leads, a number of Japanese marine invertebrates have been screened for inhibition of porcine H,K-ATPase which resulted in isolation of several inhibitors.

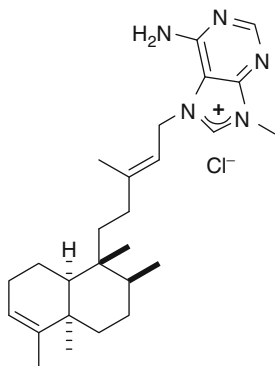
S-(+)-curcuphenol (**305**) and dehydrocurcuphenol (**306**), isolated from a Japanese marine sponge *Epipolasis* sp., inhibited porcine H,K-ATPase with IC₅₀s of 8.3 and 23 μM, respectively, while hydroxycurcuphenol was inactive [193]. It should be noted that the *R*-(-)-curcuphenol had already been reported from the Caribbean gorgonian *Pseudopterogorgia rigida* [194]. Hexaprenylhydroquinone sulfate (**307**) obtained from a marine sponge *Dysidea* sp. inhibited

H,K-ATPase with an IC_{50} of $4.6 \mu\text{M}$ [195]. Since **307** showed promising activity, a number of its analogues were synthesized and evaluated for inhibition of acid secretion and antiulcer activity, however, the results were disappointing [2]. Sinulamide (**308**) derived from a soft coral *Sinularia* sp. inhibited the enzyme activity with an IC_{50} of $5.5 \mu\text{M}$ [2]. The structure of **308** was recently refined by synthetic approach [196].

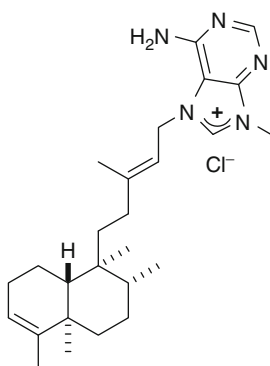
S-(+)-curcuphenol (**305**)dehydrocurcuphenol (**306**)hexaprenylhydroquinone sulfafte (**307**)sinulamide (**308**)

23.4.16.2 Na,K-ATPase

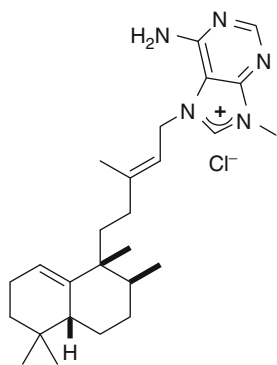
Na,K-ATPase regulates Na^+ transport through cell membranes and is directly related to contraction and relaxation of smooth muscles, thus indicating that inhibitors of the enzyme are potential drug leads for cardiovascular diseases. Agelasines A–F (**309–314**), 9-methyladenine derivatives of diterpenes, isolated from the Okinawan marine sponge *Agelas nakamura*, were reported to inhibit Na,K-ATPase, though their detailed activity is not available [197]. Two hypotaurocyamine derivatives of diterpene, agelasidines B (**315**) and C (**316**) from the same sponge inhibited not only Na,K-ATPase with IC_{50} values of $10\text{--}50 \mu\text{M}$, but also contraction of smooth muscle [198].



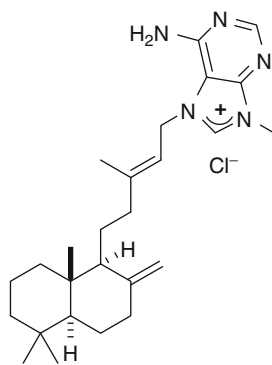
agelasin A (309)



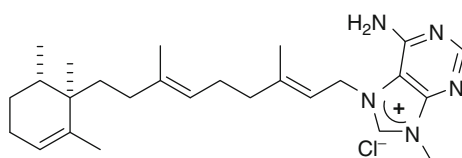
agelasin B (310)



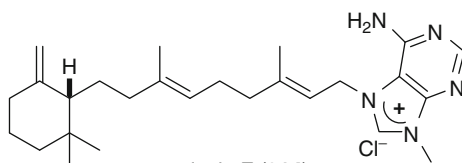
agelasin C (311)



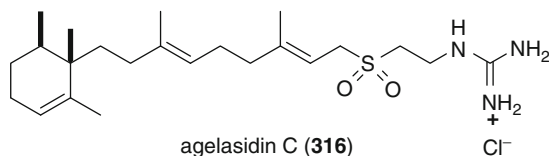
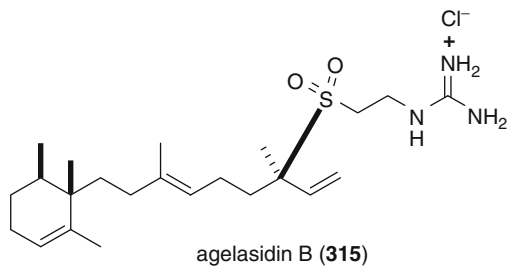
agelasin D (312)



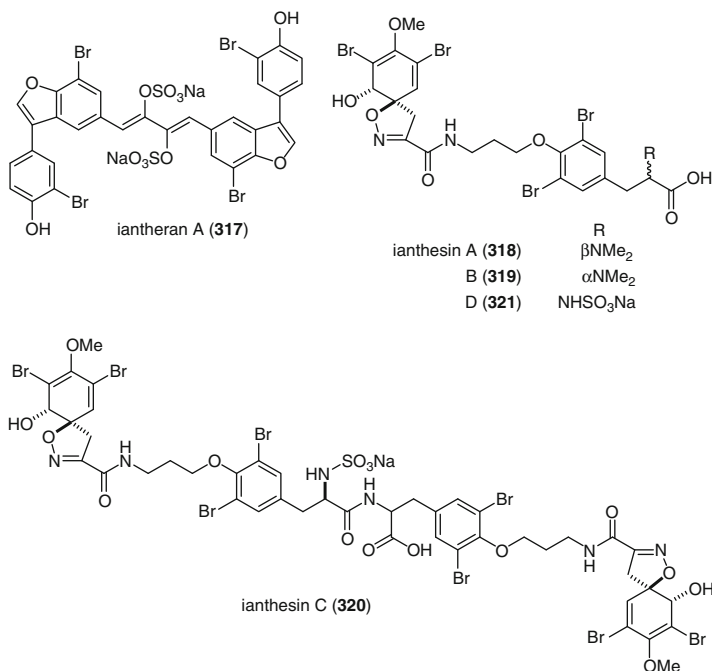
agelasin E (313)



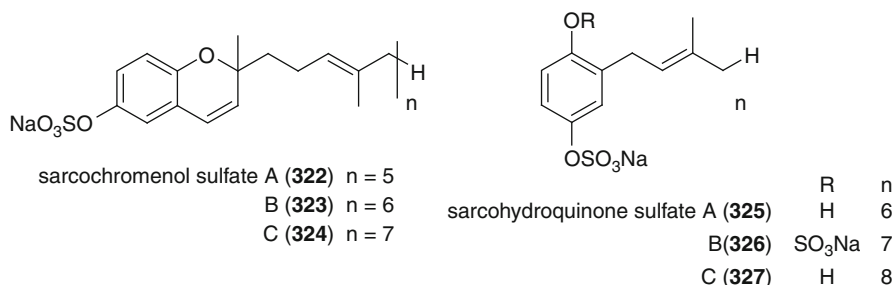
agelasin F (314)



Iantheran A (**317**), its diacetate, and α -hydroxy enone derivatives, isolated from an Australian marine sponge *Ianthella* sp. showed moderate inhibitory activity against Na,K-ATPase with IC_{50} values of 2.5, 5.0, and 10 μ M, respectively [199]. This sponge also yielded ianthesins A–D (**318–321**), of which ianthesins B–C inhibited dog kidney Na,K-ATPase with IC_{50} values of 440, 50, and 280 μ M, respectively [200].



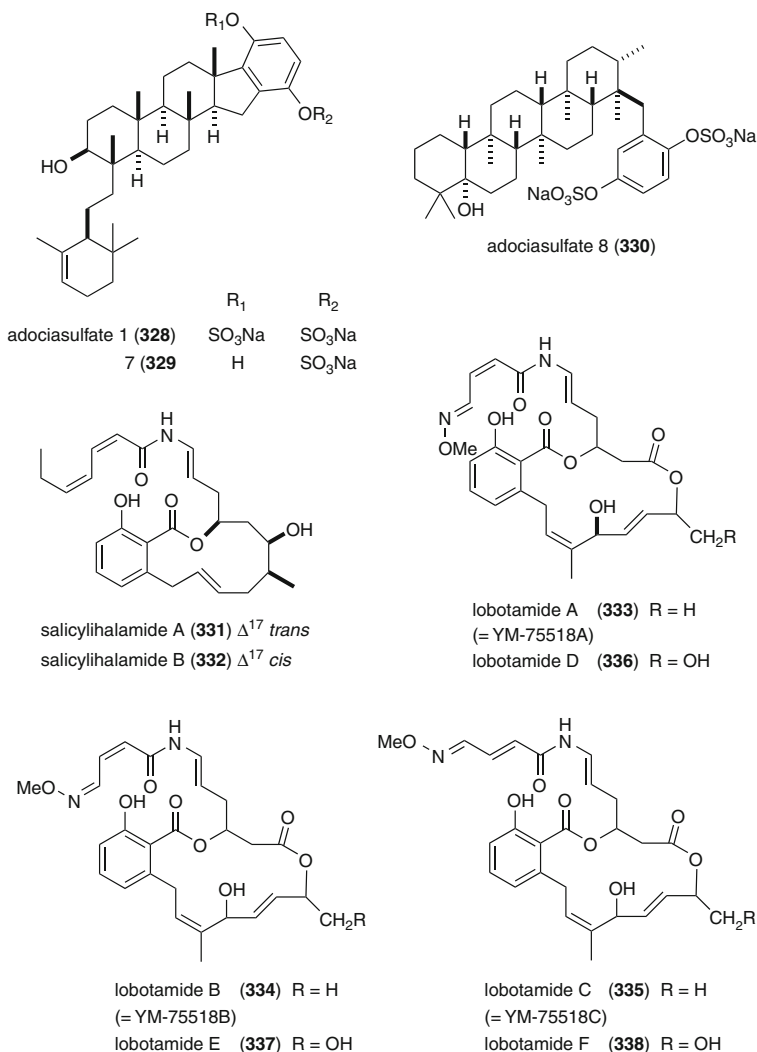
Xestoquinone (**82**), a polycyclic quinone, which was isolated together with the known antimicrobial substance halenaquinone (**79**) [201], from the Okinawan marine sponge *Xestospongia sapra*, inhibited Na,K-ATPase. Xestoquinone was the first example of marine natural products having parallelism between the inotropic action and Na,K-ATPase inhibition. Halenaquinol (**80**) [202], a natural cardioactive pentacyclic hydroquinone, from the marine sponge *Petrosia seriata*, was found to be a powerful inhibitor of the rat brain stem and cortex Na,K-ATPases and the rabbit muscle sarcoplasmic reticulum Ca^{2+} -ATPase with IC_{50} values of 0.70, 1.3, and 2.5 μM , respectively [203]. Sarcochromenol sulfate A (**322**) and sarcohydroquinone sulfates A–C (**325**–**327**) isolated from the New Zealand sponge *Sarcotragus spinulosus* inhibited the rat brain Na,K-ATPase with IC_{50} values of 1.6, 1.6, 1.4, and 1.3 μM , respectively, while sarcochromenol sulfates B (**323**) and C (**324**) were inactive [204].

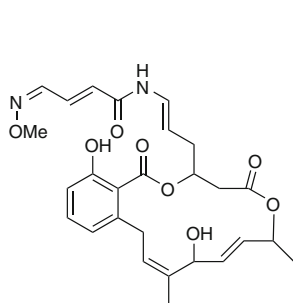


23.4.16.3 Vacuolar ATPases

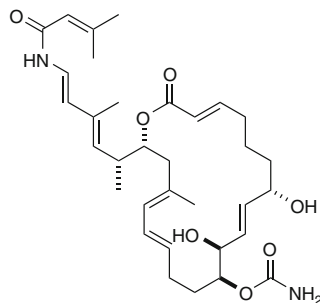
Vacuolar H^+ -ATPases, a class of proton pumps present in all eukariotic cells, are responsible for proton transport in bone-derived membrane vesicles, and the process of osteoclast-mediated bone resorption is directly dependent on H^+ -translocating ATPases. Inhibition of osteoclast vascular H^+ -ATPase may be effective for reducing the rate of bone resorption in pathological conditions such as osteoporosis. Adociasulfate 1 (**328**), a sesterterpenoid isolated from an Australian marine sponge *Adocia* sp., reduced proton pump activity in hen bone-derived membrane vesicles with an IC_{50} value of 3.6 μM and proton pumping in brain-derived vesicles with an IC_{50} value of 4.69 μM , while adociasulfates 7 (**329**) and 8 (**330**) were less active (IC_{50} 30 μM and 55% inhibition at 100 μM , respectively) [205]. Recently, antitumor polyketides, salicylihalamides A (**331**) and B (**332**) isolated from a marine sponge *Haliclona* sp. [206] and lobotamides A–F (**333**–**338**) from the tunicate *Aplidium lobatum* [207], both of which share the core structure with YM-75518 (**339**), an antifungal metabolite of *Pseudomonas* sp. Q38009 [208], were found to be a potent and selective inhibitors of mammalian V-ATPases (IC_{50} s 0.40–14.0 nM) [209]. Palmerolide A (**340**) isolated from the Antarctic tunicate *Synoicum adareanum* is a cytotoxic macrolide. It showed 3 orders of magnitude greater sensitivity (LC_{50} 18 nM) against melanoma relative to other cell lines tested in the NCI 60 cell line panel.

Palmerolide A displayed a 60-cell-line activity profile which correlated, using the NCI COMPARE algorithm, to several vacuolar ATPase inhibitors. Indeed, it inhibited V-ATPase with an IC_{50} of 2 nM and to be active in NCI's hollow-fiber assay [210]. Following study on its stereochemistry by degradation [211] or total synthesis [212] revised its stereochemistry at C7, C10, and C11. The SAR study of palmerolides using synthetic analogues showed that a phenyl substitution on side chain and removal of the C7 hydroxy group enhanced the potency, while the selectivity against melanoma of **340** was not reproduced [213].





YM-75518D (339)

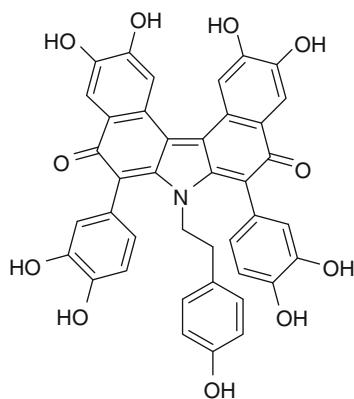


palmerolide A (340)

23.5 Lyases (EC 4.-.-.-)

23.5.1 ATP Citrate Lyase (EC 4.1.3.8)

Since the very-low-density lipoproteins (VLDL) are metabolic precursors of low-density lipoproteins (LDL) which play a key role in hypercholesterolemia, intervention of VLDL synthesis has provided a strategic target for hypercholesterolemia therapy. Inhibitors of ATP-citrate lyase (ACL) are anticipated to reduce the production of acetyl CoA and can affect both lipogenesis and cholesterologenesis, and as a result, expected to reduce VLDL synthesis. Purpurone (341), a poly catecholic pyrrole isolated from a marine sponge *Iotrochota* sp., inhibits ATP-citrate lyase in a dose-dependent manner with an IC_{50} value of 7 μ M [214].



purpurone (341)

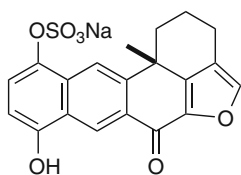
23.6 Isomerases (EC 5.-.-.-)

23.6.1 Topoisomerase

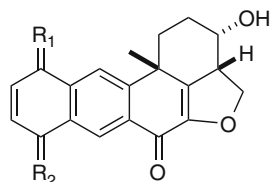
DNA topoisomerases are nuclear enzymes that catalyze DNA breaking and unwinding during cellular replication and RNA transcription. In eukaryotic cells, DNA topoisomerases I (topo I) and II (topo II) play distinct roles in DNA unwinding. Topo I catalyzes single-strand “nicking” to allow supercoiled DNA to unwind, whereas topo II facilitates chromosomal duplication by relaxing and unwinding the DNA duplex. Thus, inhibitors of topo I and topo II are expected to control cancer cell proliferation and thought to be important targets for cancer chemotherapy.

23.6.1.1 Topoisomerase I (EC 5.99.1.2)

Xestoquinol sulfate (**342**) and xestosaprols A (**343**) and B (**344**), as well as a known compound **345** and halenaquinol sulfate (**81**), were isolated as topo I inhibitors from the Okinawan sponge *Xestospongia sapra*; **342–344** inhibited DNA topo I with MICs of 10, 12.5, and 12.5 $\mu\text{g/mL}$, respectively, while **345**, xestoquinone (**82**), and halenaquinone (**79**) were more potent with MICs of 2.5, 2, and 0.4 $\mu\text{g/mL}$, respectively [215]. Interestingly, halenaquinol sulfate (**81**) was not active in this assay. Makaluvamine G (**346**), a cytotoxic pigment which was isolated from an Indonesian sponge *Histodermella* sp., inhibited topo I with an IC_{50} value of 3.0 μM [216]. Two ceramide 1-sulfates **347** and **348** from the Japanese bryozoa *Watersipora cucullata* inhibited human topo I with IC_{50} s of 0.4 and 0.2 μM , respectively [217]. Similarly, amphimic acids A (**349**) and related long-chain fatty acids from an Australian sponge *Amphimedon* sp. showed topo I inhibition with IC_{50} s ranging from 0.47 to 6.7 μM [218].



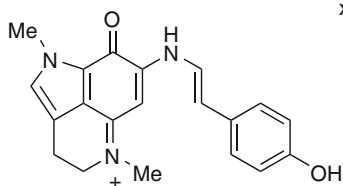
xestoquinol sulfate (**342**)



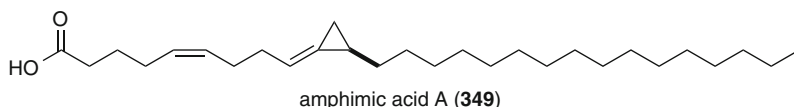
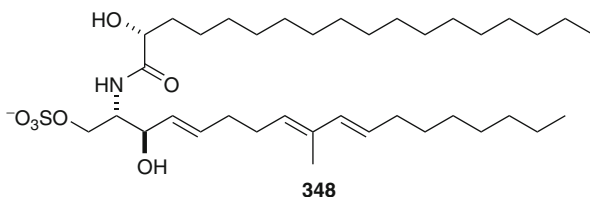
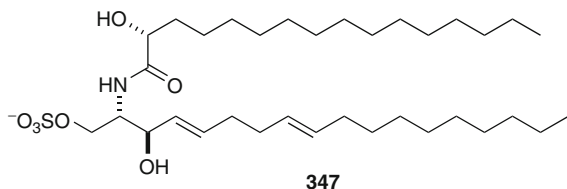
xestosaprol A (**343**) $R_1 = \text{H, OH}; R_2 = \text{O}$

xestosaprol B (**344**) $R_1 = R_2 = \text{H, OH}$

(**345**) $R_1 = \text{O}; R_2 = \text{H, OH}$

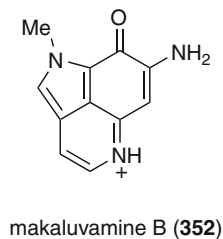
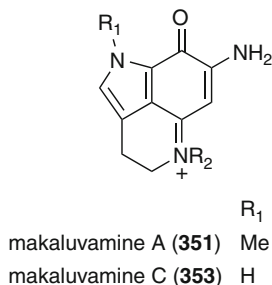
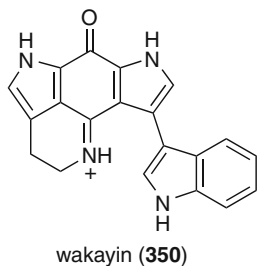


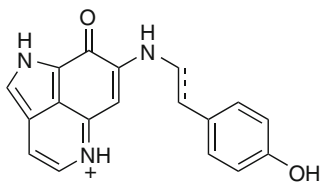
makaluvamine G (**346**)



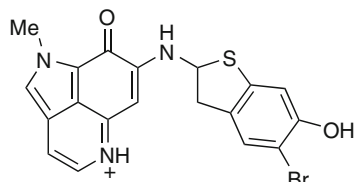
23.6.1.2 Topoisomerase II (EC 5.99.1.3)

Wakayin (**350**), a cytotoxic pyrroloiminoquinone alkaloid, isolated from the ascidian *Clavelina* sp., inhibited topo II at 250 μM [219]. Pyrroloiminoquinones, makaluvamines A–F (**351**–**356**) which were isolated from Fijian sponges of the genus *Zyzzya*, showed topo II inhibition with IC_{50} s of 41, >500, 420, 320, 310, and 25 μM , respectively, while related makaluvone and damirone B were not active. The makaluvamines showed differential toxicity toward the topo II-sensitive CHO cell line xrs-6; makaluvamines A (**351**) and C (**353**) exhibited *in vivo* antitumor activity against the human ovarian carcinoma Ovar3 implanted in athymic mice [220]. Similarly, makaluvamine N (**357**) isolated from the Philippine sponge *Zyzzya fuliginosa* exhibited greater than 90% inhibition of topo II at 5 $\mu\text{g}/\text{mL}$ [221]. Other makaluvamines G–H did not show inhibitory activity against topo II [222], whereas only makaluvamine G showed moderate inhibition against topo I [189]. Bengacarboline (**358**), a β -carboline alkaloid isolated from a marine ascidian *Didemnum* sp., inhibited topo II at 32 μM [223].

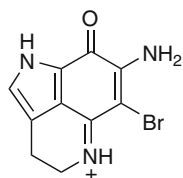




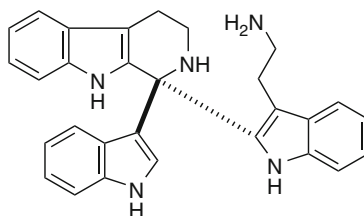
makaluvamine D (354)
makaluvamine E Δ (355)



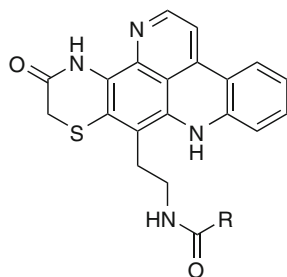
makaluvamine F (356)



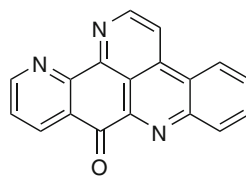
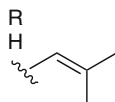
makaluvamine N (357)



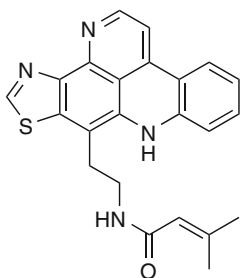
bengacarboline (358)



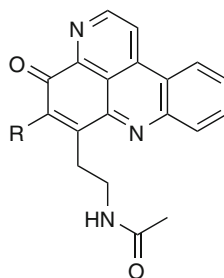
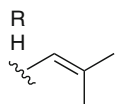
shermilamine B (359)
shermilamine C (362)



ascididemin (360)



dehydrokuanoniamine B (361)
kuanoniamine D (364)

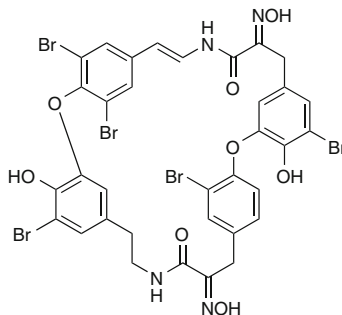
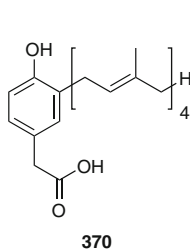
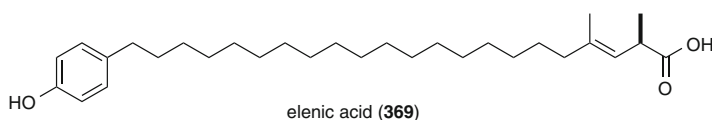
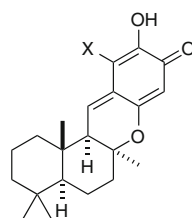
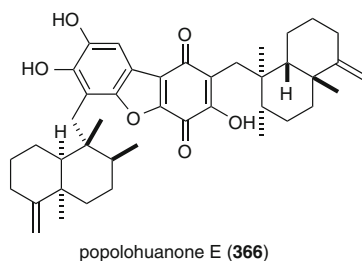


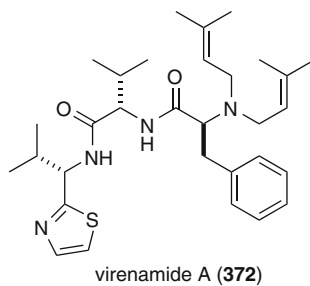
cystodytin J (363)
diplamine (365)



Two aromatic alkaloids, shermilamine B (**359**) [224] and ascididemin (**360**) [225] were reported to inhibit topo II at 30 and 75 μM , respectively [226]. Similarly, dehydrokuanoamine B (**361**), shermilamine C (**362**), cystodytin (**363**), kuanoniamine D (**364**), and diplamine (**365**) from an ascidian *Diplosoma* sp., inhibited topo II with IC_{50} values of 115, 138, 8.4, 127, and 9.2 μM , respectively [227]

Popolohuanone E (**366**), an oxidatively dimerized arenarol derivative isolated from a Pohnpei sponge *Dysidea* sp., was reported to be inhibitory against topo II with an IC_{50} of 400 nM and selectively cytotoxic against the A549 non-small-cell human lung cancer cell line (IC_{50} 2.5 $\mu\text{g}/\text{mL}$) [228]. Puupehenone (**367**) and 21-chloro-puupehenone (**368**), sesquiterpene hydroquinones isolated from a verongid sponge, were tested for a wide variety of biological activities including inhibitory activity against topo II, adenosine deaminase (ADA), glutathione reductase (GR), dihydrofolate reductase (DHFR), and thymidylate synthetase (TS), which disclosed that **367** inhibited topo II with an IC_{50} value of 1 $\mu\text{g}/\text{mL}$, in addition that **367** and **368** inhibited ADA at IC_{50}s >25 and > 25 $\mu\text{g}/\text{mL}$, respectively, GR with an IC_{50} of 6 $\mu\text{g}/\text{mL}$ for **368**, DHFR with IC_{50}s of 5 and 5 $\mu\text{g}/\text{mL}$, respectively, and TS with IC_{50}s of 8 and 3 $\mu\text{g}/\text{mL}$, respectively [229].





Elenic acid (369), an unusual metabolite of an Indonesian sponge *Plakinastrella* sp., inhibited topo II with an IC_{50} value of 0.1 $\mu\text{g/mL}$ [230], while 3-tetraprenyl-4-hydroxy benzylic acid (370) isolated from the marine sponge *Ircinia muscarum* had an IC_{50} of 0.5 $\mu\text{g/mL}$ [231]. Bastadin 14 (371) from the marine sponge *Psammaphysilla purpurea* showed inhibitory activity against topo II and dehydrofolate reductase with IC_{50} values of 2.0 and 2.5 $\mu\text{g/mL}$, respectively [232]. Virenamide A (372), a cytotoxic linear peptide from the Australian ascidian *Diplosoma virens*, exhibited topo II inhibitory activity with an IC_{50} of 2.5 $\mu\text{g/mL}$ [233].

23.7 Conclusions

More than 370 metabolites derived from marine invertebrates have been shown to inhibit various enzymes. These enzymes play pivotal roles in many aspects of the biological processes; therefore, inhibitors are useful for understanding complicated biological phenomena. These inhibitors fall into a wide range of biogenetic classes, ranging from simple terpenoids or polyketides to complex polyketides and oligopeptides. Therefore, there are still good chance to find structurally unique new enzyme inhibitors such as okadaic acid, calyculins, and cyclotheonamides. However, at the same time, we should make efforts to find new activities of trivial known compounds to maximize the potentials of marine natural products. As mentioned in the introduction, one of the trends of marine natural products will be the discovery of new biological activities.

While this chapter was being prepared, a huge earthquake (M 9.0) occurred at the Northeastern part of Japan. Tsunami and nuclear pollution have damaged quite seriously the coast and marine organisms of the wide areas. Since these areas are bountiful of marine organisms, this damage will give considerable limitation to study marine natural products from this part. We hope the environment will be recovered in the near future.

23.8 Study Questions

1. Is there any room for new findings in marine natural products chemistry?
2. How far have we understood the potentials of marine natural products?

3. Which should we attach more importance, to new structures or to new activities?
4. What is the status of our understanding on the mechanisms of action for marine natural products?
5. How can marine natural products chemistry contribute to the upcoming trend of life sciences?

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Fluorescent Proteins from the Oceans: Marine Macromolecules as Advanced Imaging Tools for Biomedical Research

24

Edward G. Smith, Cecilia D'Angelo, Franz Oswald,
G. Ulrich Nienhaus, and J. Wiedenmann

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E.G. Smith • C. D'Angelo • J. Wiedenmann (✉)

National Oceanography Centre Southampton, University of Southampton, European Way,
Southampton, UK

e-mail: e.smith@soton.ac.uk, C.D'angelo@soton.ac.uk, joerg.wiedenmann@noc.soton.ac.uk

F. Oswald

Department of Internal Medicine I, University of Ulm, Albert-Einstein-Allee 23, Ulm, Germany

e-mail: franz.oswald@uni-ulm.de

G.U. Nienhaus

Center for Functional Nanostructures, Karlsruhe Institute of Technology, Wolfgang-Gaede-Str. 1 a,
Karlsruhe, Germany

and

Department of Physics, University of Illinois at Urbana-Champaign, 1110 West Green Street,
Urbana, IL, USA

e-mail: uli@uiuc.edu

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Abstract

Fluorescent proteins (FPs) of the green fluorescent protein (GFP)-like protein family are not only responsible for the spectacular colors of some reef corals, but they can be also found in several other marine invertebrate taxa. The chromophore of these proteins resides in the center of an 11-stranded β -barrel and is formed by autocatalytic reactions in the presence of oxygen. In some proteins, photochemical reactions are involved in the maturation of the chromophore. The variability of the chromophore structures and the interactions with the surrounding protein scaffold are responsible for the diverse emission colors, ranging from cyan to green and yellow to red. FPs develop their fluorescence also upon expression in recombinant cells which allows their use as genetically encoded markers. Application examples include the labeling of cells, cellular compartment or proteins, studies of gene activity, and sensor studies. Recently, photoactivatable FPs enabled live-cell imaging with a resolution beyond the diffraction barrier of optical microscopy. Nevertheless, before their potential as advanced markers can be fully exploited, FPs often need to undergo extensive protein engineering to alter some detrimental properties such as the tendency to form stable multimers.

24.1 Introduction

Fluorescent proteins have become an indispensable component of the biomedical imaging toolbox [15, 51, 103]. The first representative of this protein family, the green fluorescent protein (GFP), emerged from a study of bioluminescence in the hydrozoan *Aequorea victoria* by Osamu Shimomura and colleagues [77]. Further studies of bioluminescent cnidarians identified more GFPs from marine bioluminescent organisms such as the seapen *Renilla* and hydrozoan polyp *Obelia* [52, 53]. In bioluminescent cnidarians, GFP acts as secondary emitter in the bioluminescence reaction during which the chromophore of GFP is excited as result of a radiationless energy transfer from the photoprotein aequorin [52, 54]. Shimomura and colleagues were the first to propose the structure of the GFP chromophore [13, 76].

It took about 30 years from the discovery of GFP until the potential of this protein as a genetically encoded fluorescence marker was fully realized. The first important step towards its application as an imaging tool was the cloning of GFP-encoding DNA by Prasher et al. [66]. Subsequently, Chalfie and coworkers succeeded in expressing the protein functionally in the nematode worm *Caenorhabditis elegans* [9]. These groundbreaking studies transformed GFP from a scientifically interesting marine pigment to a fluorescence marker with enormous application and commercial potential. Studies soon thereafter began to focus on engineering of the GFP to provide new colors and to render the protein more suitable

for cellular imaging applications, for instance, by enhancing its brightness or by producing blue, cyan, and yellow variants [86]. The tremendous impact of GFP technology on life science research was recognized by the award of the 2008 Nobel Prize for Chemistry to Osamu Shimomura, Martin Chalfie, and Roger Tsien [15, 55].

Despite extensive efforts to create novel color variants of GFP, red fluorescent proteins (RFPs) appeared elusive during the early years of GFP research [47]. These longer wavelength markers are particularly desirable for imaging applications because of reduced cellular autofluorescence in this spectral region, reduced phototoxicity of the excitation light, and the better penetration of long wavelength light in tissue [103]. Furthermore, RFPs were in demand for novel fluorescence resonance energy transfer (FRET) applications [17, 32].

Ultimately, it was nature that provided the first sources of RFPs. The search for natural FPs had originally focused on bioluminescent organisms as the discovery of GFPs in these animals suggested a strict coupling of FPs to bioluminescence reaction. Contrary to this common notion, Wiedenmann [96] proposed the existence of red-emitting GFP-like proteins and nonfluorescent homologues in the sea anemone *Anemonia sulcata* and other cnidarians [96]. Subsequent studies confirmed the presence of GFP-like proteins in numerous nonbioluminescent anthozoans [18, 43, 99, 100] while uncovering the RFPs DsRed and eqFP611; the latter being the natural RFP with the most red-shifted emission [43, 100]. These studies revealed nonbioluminescent anthozoans as a rich source of natural FPs, giving access to a broad palette of emission colors [56]. In particular, the diversity of RFPs among anthozoans was exploited to create advanced marker proteins with optimized biochemical and spectral properties [8, 32, 36, 72].

Interestingly, anthozoans, especially reef corals, harbor a variety of photoactivatable FPs (PAFPs) [3, 4, 37, 40, 61, 101]. While the basic chromophore forms in an autocatalytic reaction as in GFP from *Aequorea victoria*, the final emission color is determined by the exposure to distinct light quantities and qualities [56]. The chromoprotein asulCP (synonym asFP595), for instance, combines reversible “on”/“off” switching of red fluorescence in response to alternating irradiation with low intensities of green and blue light with an irreversible “on” switching under high levels of green light [5]. In contrast, photoconvertible FPs such as Kaede and EosFP first develop a green fluorescent chromophore that is irreversibly converted into a red fluorescent state under illumination with violet light [57]. PAFP have a high application potential as markers in pulse-chase experiments, whereby the fate of a certain subset of labeled cells or cellular components can be monitored independently by selective excitation after targeted photoactivation [97]. Moreover, photoactivatable proteins were key tools in the realization of imaging concepts that enable light microscopy with a resolution beyond the diffraction barrier [6, 28].

24.2 Sources of GFP-like Proteins

The first GFP was found in the bioluminescent hydromedusa *A. victoria* [77]; subsequent studies discovered GFPs also in other bioluminescent organisms

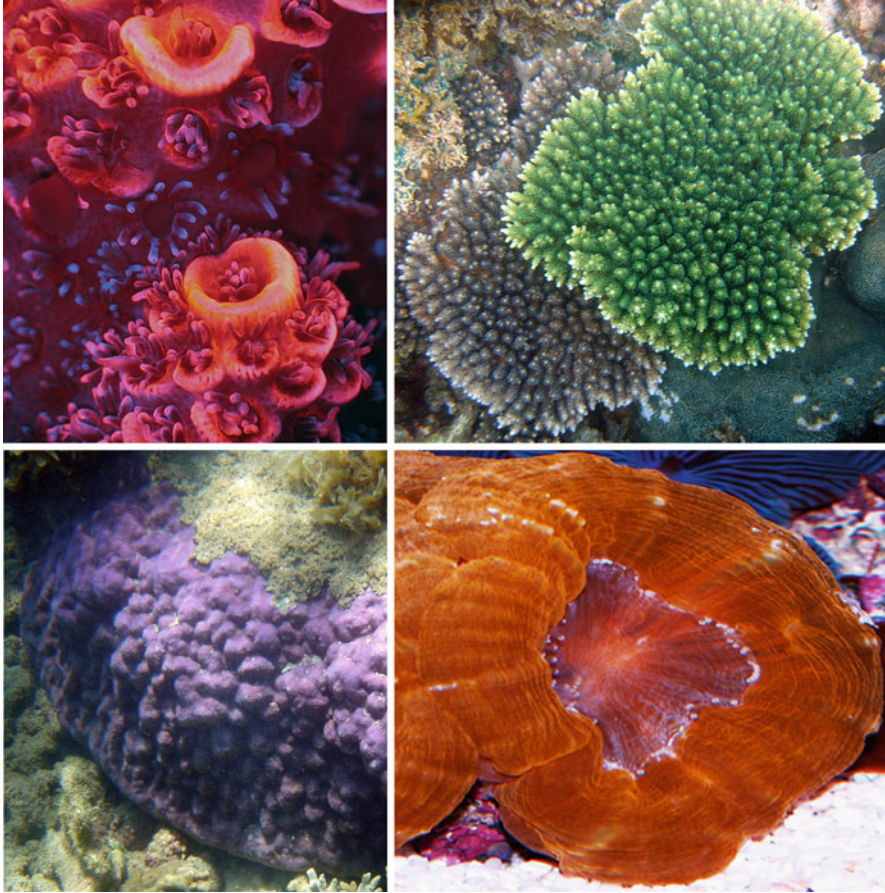


Fig. 24.1 Sources of GFP-like proteins. Anthozoa, particularly scleractinian corals, harbor a huge variety of GFP-like proteins. *Left panel:* Localization of red and cyan fluorescent proteins in the tissue of *Acropora millepora*. Fluorescence was excited under the microscope and photographed through a dual bandpass filter. The emission of cyan fluorescent protein appears blue under these conditions. *Upper right panel:* Color polymorphism among *Acropora* sp. GFPs lend the green color to the upper colony, whereas the dominant brown tones of the lower colony are caused by the photosynthetic pigments of symbiotic alga (zooxanthellae). *Lower left panel:* The purple color of the *Porites* sp. colony is due to high-level expression of a nonfluorescent, GFP-like chromoprotein. *Lower right panel:* The orange colour of *Lobophyllia hemprichii* is produced by a green-to-red photoconvertible protein

including *Renilla* and *Obelia* [52, 53]. The studies of FPs in anthozoans showed that FPs are expressed throughout all major taxa of the anthozoans including sea anemones, corals, ceriantharians, octocorals, and disk anemones (Fig. 24.1). The GFP-like pigments in these organisms show emission colors ranging from cyan green over yellow to red [56]. Some individuals also contain chromoproteins (CPs), yet another subpopulation within the family of GFP-like proteins which are intensely colored but essentially nonfluorescent [40, 67]. In fact, several

anthozoans, particularly corals, express more than five different GFP-like proteins within a single individual [14, 99]. Different expression levels of both FPs and CPs are primarily responsible for the color polymorphism that can be frequently observed among reef-building corals (scleractinia) and sea anemones (Actiniaria) [38, 61, 98]. Fluorescent proteins are often present in the tentacles and in other light-exposed body parts of corals and sea anemones [38, 98]. This can be partially explained by the finding that numerous FP- or CP-encoding genes are upregulated in response to elevated light intensities in their habitat. In this context, D'Angelo et al. found that blue light is most effective in regulating the tissue content of GFP-like proteins [14]. However, several species of sea anemones and corals show a constitutive high-level expression of CPs or FPs that is only minimally or not at all regulated by the environmental light [33, 61]. Taxonomic variability is also found concerning the tissue in which the proteins are expressed. In *Anemonia sulcata*, expression is limited to ectodermal cells, whereas both *Lobophyllia hemprichii* and *Montastrea cavernosa* express FPs in ectodermal and gastrodermal cells [38, 99]. GFP-like proteins may contribute up to 14% of the total soluble protein content in the tissue [37]. However, the slow turnover of these proteins facilitates the maintenance of such high tissue concentration [37].

GFP-like proteins are not only confined to the taxon Cnidaria, but have also been identified in other phyla such as Ctenophora, Crustacea, and even Chordata [16, 25, 71]. Interestingly, a non-fluorescent, colorless structural homologue of GFP, the G2 domain of the extracellular matrix protein nidogen, is present even in mammals [29].

While FPs have been found in a range of organisms other than anthozoans, this animal group remains the most promising source for novel marker proteins due to the vast diversification that the GFP homologues experienced in the course of the evolution of this taxon.

24.3 Structural Aspects of GFP-like Proteins

24.3.1 The Three-Dimensional Structure

GFP-like proteins have a distinct structure comprising of an 11-stranded β -barrel with a helix running along the central axis of the protein [56, 105]. Close to the geometric center of the molecule, the central helix is interrupted by the chromophore (Fig. 24.2). The chromophore is formed from a tripeptide sequence in an autocatalytic reaction in the presence of molecular oxygen [27]. The chromophore is primarily responsible for the spectral characteristics of the GFP-like proteins, with the wavelength of absorption and emission increasing with the number of the conjugated π bonds [69]. Interactions with adjacent amino acids, however, can shift the absorbance and emission spectra by up to 20 nm [69].

GFP exists in a predominantly monomeric form at concentrations below 1 mg/mL [95]. In contrast, GFP from *Renilla* exists as a stable dimer [95]. Most anthozoan FPs form tight tetrameric assemblages, although a number of dimeric variants have also been described in corals and sea anemones [57, 59, 60] (Fig. 24.2).

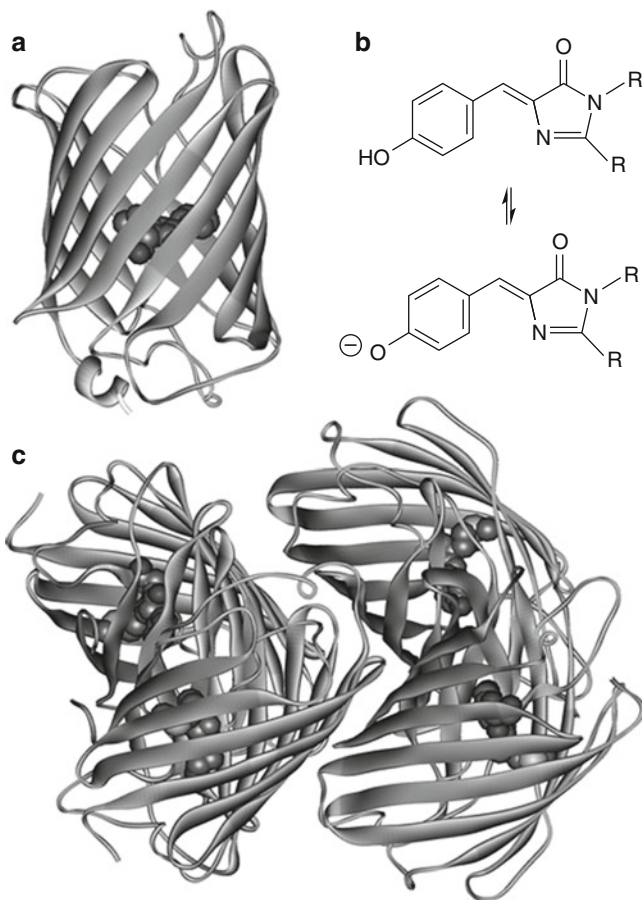


Fig. 24.2 Structural aspects of GFP-like proteins. (a) Ribbon diagram of GFP exhibiting the arrangement of the 11 β -sheets around the central helix. The position of the chromophore in the center of the molecule is represented by Van der Waals spheres. (b) The p-HBI chromophore of GFP in its neutral (maximal absorption at 395 nm; *upper structure*) and deprotonated state (maximal absorption at 475 nm; *lower structure*). (c) Typical assembly of protomers in a tetramer of an anthozoan FP as “dimers of dimers.” The β -can fold of GFP is highly conserved

24.3.2 Chromophore Structures

The amino acid triad that forms the GFP chromophore, Ser65-Tyr66-Gly67, undergoes a three-step process of cyclization, dehydration, and oxidation to form the functional chromophore [78]. Firstly, the amide of Gly67 attacks the carbonyl of Ser65 to form imidazole. Dehydration converts the imidazole to imidazolinone and subsequent oxidation of the $C\alpha$ - $C\beta$ bond of Tyr66 extends the conjugated π electron system from the imidazolinone to the aromatic group of Tyr66 to yield the final 4-(p-hydroxybenzylidene)-5-imidazolinone (p-HBI) chromophore [78].

The GFP chromophore features two states depending on the protonation of the hydroxybenzyl group (Fig. 24.2). The neutral (protonated) chromophore absorbs maximally at 395 nm, whereas the anionic (deprotonated) form is excited best by blue light at 475 nm [86]. The interesting phenomenon that both states emit mostly green fluorescence can be explained by an excited-state proton transfer that occurs upon excitation of the neutral chromophore [10].

The color diversity of natural FPs is derived from modifications of the green fluorescent p-HBI chromophore (Fig. 24.3), which is considered to be the ancestral form [2]. In the following paragraphs, an overview of the chromophore types responsible for the different photophysical properties of GFP-like proteins will be presented.

24.3.2.1 Cyan/Green Emission

Cyan/green emission of GFP-like proteins results from p-HBI chromophores [59, 60]. Emission maxima of cyan/green FPs have been recorded in the range from 470 to 520 nm [2]. The cyan FPs (CFPs) are characterized by wider excitation/emission bands and larger Stokes shifts compared to the green FPs [2]. The chromophore environment plays an important role in the spectral properties of these proteins. For example, it is responsible for the blue shift in the CFP emission relative to GFP. Fluorescence of both the anionic and the neutral forms of the chromophore are observed in some members of this group, for instance, in asFP499 [60] (Fig. 24.3).

24.3.2.2 Yellow Emission

To date, only two naturally occurring yellow FPs have been discovered, phiYFP [71] and zFP538 [43] (Fig. 24.3). These two proteins have an emission maxima of 537 and 538 nm and excitation maxima of 525 and 528 nm, respectively. They achieve yellow fluorescence through different modifications of the p-HBI chromophore. The yellow fluorescence of zFP538 results from a three-ringed chromophore, whereas phiYFP's fluorescence results from π -stacking interactions of the tyrosyl moiety of p-HBI with the chromophore environment [65].

24.3.2.3 Red Emission

Numerous natural orange/red FPs have been identified, and many more engineered, with emission wavelengths up to 611 nm (Table 24.1) [56, 100]. There are two classes of red fluorescent proteins, distinguished by the pathway in which the red fluorescent chromophore is achieved. Each class is named after the protein for which the type of chromophore was described: DsRed-type chromophores and Kaede/EosFP-type chromophores.

Maturation of the DsRed-type chromophore begins with the formation of the neutral chromophore. At this point, the chromophore can follow one of two possible pathways. There have been different pathways proposed for the formation of the mature red chromophore but both acknowledge that it is a result of the formation of a double bond between the C(α) and the amide N of Gln66 [82, 89]. DsRed-type chromophores usually adopt a *cis* conformation [106] (Fig. 24.3). An exception is eqFP611 in which the red-shifted natural emission is produced by a DsRed-type chromophore in *trans* conformation [64] (Fig. 24.3).

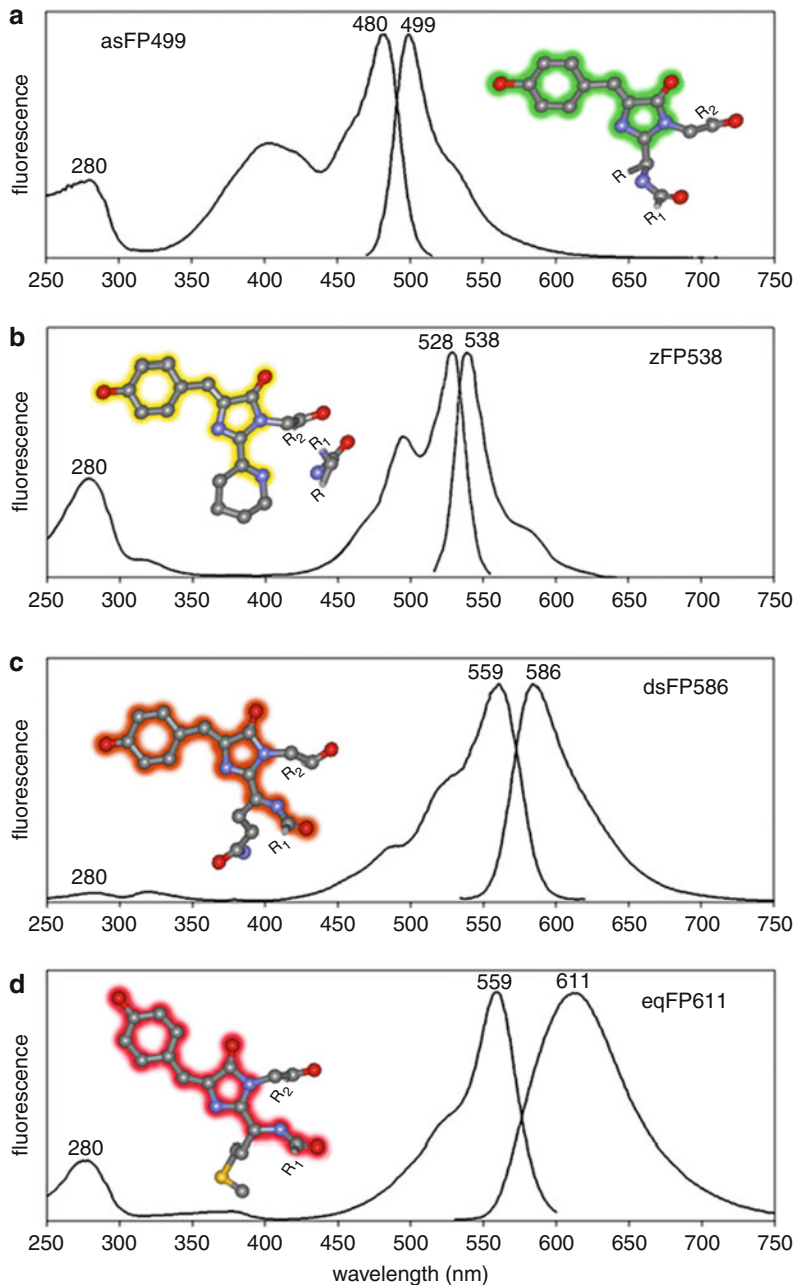


Fig. 24.3 Chromophore structures of major FP color classes. Excitation and emission spectra are shown with the position of the peak maxima in (nm) indicated above the peaks. Structural models of the different chromophore types were constructed using representative GFP-like proteins (protein data bank code A: 1W7S, B: 2OGR, C: 1GGX, D: 3E5T). The extension of the conjugated

Once expressed in cells, both Kaede, EosFP, and related proteins form a green fluorescent p-HBI chromophore that exists predominantly in the deprotonated state [57, 101]. However, illumination of the neutral p-HBI chromophore with violet light (~ 390 nm) causes cleavage of the peptide backbone at the $N\alpha$ - $C\alpha$ bond of the first chromophore-forming residue, which is always a histidine in these photoconvertible proteins [3, 61, 101]. The red emission arises from the extension of the conjugated π -electron system into the imidazole group of the histidine [50].

24.3.2.4 Chromoproteins

Nonfluorescent chromoproteins absorb between ~ 550 and ~ 600 nm and are characterized by purple, lilac, and blue hues [14]. Emission is virtually absent from the chromoproteins. However, a chromoprotein from the sea anemone *Anemonia sulcata* becomes brightly fluorescent upon intense green-light irradiation [40]. The absence of fluorescence in chromoproteins is attributed to the nonplanarity and *trans* conformation of the DsRed-type chromophore [67, 68].

24.4 Isolation of Novel GFP-like Proteins

Anthozoans are currently considered to be the most promising source of novel marker proteins because of the vast diversification of these proteins within this taxon [2]. This notion is supported by the numerous anthozoan proteins that have been already rendered into valuable imaging tools [103]. The wide taxonomic distribution of GFP-like proteins, however, suggests that pigment proteins can be discovered from virtually any taxonomic group. Therefore, broad screening might yield further variants with new properties. The spectral properties of the organism can be used to guide the choice for subsequent analysis. It is important to note, though, that many variants are expressed at very low levels and might be difficult to detect, especially in the presence of high levels of GFP-like protein with different spectral properties. The discovery of eqFP611 is an example for which an analysis of the whole complement of pigments in a heterologous system helped identify underrepresented variants with interesting properties [100]. As exemplified by EosFP, the proteins can exist in a mature state in the source organism, and the photochemical reactions that make them interesting as marker proteins may not be easily detected [101]. Prior to the selection of an organism, tests on the tissue extract with organic solvents can help prevent nonprotein pigments becoming the subject of unsuccessful cloning attempts [102].

The cloning of the gene coding for a protein of interest begins with the creation of a cDNA library. The library can subsequently be probed for the presence of the



Fig. 24.3 (continued) π -bond system is marked by colors symbolizing the emission color. (a) asFP499: The secondary excitation maximum at ~ 400 nm of the cyan-green FP results from the neutral p-HBI chromophore undergoing excited-state proton transfer. (b) The chromophore of the yellow fluorescent zFP538 features a 3-ring structure. (c) The DsRed-type chromophore of dsFP586 is extended along the peptide backbone. (d) The red-shifted emission of eqFP611 is associated with a DsRed-type chromophore adopting a *cis* conformation

Table 24.1 Properties of engineered orange-red-emitting FPs derived from cnidarian pigments

FP variant	Source organism	Oligomerization degree (# protomers)	Excitation maximum (nm)	Emission maximum (nm)	Stokes shift	QY	E_{mol} ($\text{M}^{-1} \text{cm}^{-1}$)	Relative brightness ^a (% of EGFP)
EGFP [63]	<i>Aequorea victoria</i>	1	488	507	19	0.6	53,000 ^b	100
mKO2 [70]	<i>Fungia concinna</i>	1	551	565	14	0.62	63,800 ^b	124
td-Tomato [72]	<i>Discosoma</i> sp.	2	554	581	27	0.69	69,000	150
mOrange2 [73]	<i>Discosoma</i> sp.	1	549	565	16	0.60	58,000 ^c	109
TurboRFP [45]	<i>Entacmaea quadricolor</i>	2	553	574	21	0.67	92000 ^c	194
TagRFP-T [73]	<i>Entacmaea quadricolor</i>	1	555	584	29	0.41	81,000 ^c	104
mRuby [36]	<i>Entacmaea quadricolor</i>	1	558	605	47	0.35	Not applicable ^c 112,000 ^d	123
DsRed-Express2 [81]	<i>Discosoma</i> sp.	4	554	591	37	0.42	35,600	47
eqFP611 [100]	<i>Entacmaea quadricolor</i>	4	559	611	52	0.45	116,000 ^c 146,000 ^d	164 ^c 207 ^d
mCherry [72]	<i>Discosoma</i> sp.	1	587	615	28	0.22	72,000 ^c	50
mKeima [34]	<i>Montipora</i> sp.	1	440	620	180	0.24	14,400 ^b	11
mRaspberry [94]	<i>Discosoma</i> sp.	1	598	625	27	0.15	86,000 ^c	41

RFP630 [35]	<i>Entacmaea quadricolor</i>	4	583	630	47	0.35	50,000 ^c	55
mKate2 [75]	<i>Entacmaea quadricolor</i>	1	588	635	47	0.4	62,500 ^c	79
Katushka [74]	<i>Entacmaea quadricolor</i>	2	588	635	47	0.34	65,000 ^c	70
RFP637 [35]	<i>Entacmaea quadricolor</i>	4	587	637	50	0.23	72,000 ^c	52 ^c
							141,300 ^d	102 ^d
RFP639 [35]	<i>Entacmaea quadricolor</i>	4	588	639	51	0.18	69,000 ^c	39 ^c
							110,400 ^d	63 ^d
hcRed [23]	<i>Heteractis crispata</i>	2	594	645	51	0.05	70,000 ^c	11
mPlum [94]	<i>Discosoma</i> sp.	1	590	649	59	0.1	41,000 ^c	13 ^c
							143,400 ^{d,f}	45 ^d
AQ14(52)	<i>Actinia equina</i>	4	595	663	68	–	–	–

^aProduct of QY and E_{mol} of purified proteins compared to the brightness of EGFP ($53,000 \text{ M}^{-1} \text{ cm}^{-1} \times 0.60$)

^bConcentration of the red chromophore deduced from the protein concentration as determined by colorimetric methods

^cConcentration of the red chromophore determined by the alkaline denaturation method [22]

^dConcentration of the red chromophore determined by the *dynamic difference method* [35]

^eDetermined from expression in HEK293 cells

^fV values from Ref. [35]

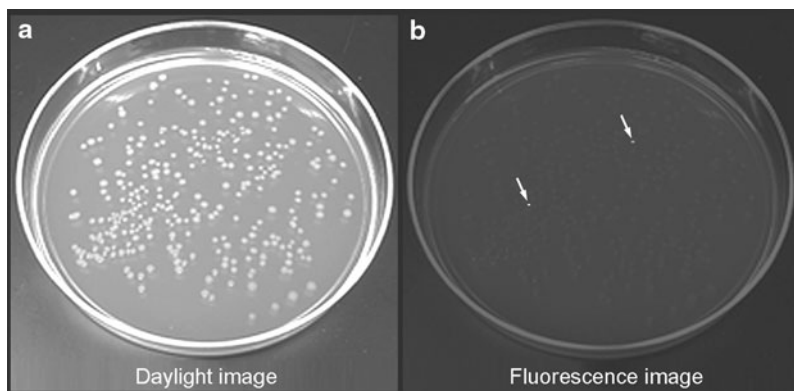


Fig. 24.4 Isolation of novel GFP-like proteins. (a) *Escherichia coli* was transformed with expression plasmids containing a cDNA library from the fluorescent tentacles of the sea anemone *Entacmaea quadricolor* and spread on agar plates. After growth of the bacterial colonies, the plates were incubated at 4°C for several days to allow maturation and accumulation of the expressed proteins. (b) When viewing the plates under UVA (~366 nm) or blue light (~450 nm) through suitable green or red long pass filters, colonies containing potential proteins of interest (arrows) can be identified by their fluorescence

GFP-coding genes by using one of two methods. The choice of method depends on a multitude of factors including knowledge of the target protein, availability of homologous sequences, and quality of the cDNA.

The first method involves PCR amplification of cDNA fragments using degenerate primers based on conserved regions of the GFP-like protein genes. The main advantages of this method are: its sensitivity, which allows isolation cDNAs expressed at low transcript levels; the applicability to cDNA samples of limited quality; and the relative speed of the process [2]. However, the method hinges on the performance of the degenerate primers which can become a major limitation when screening for novel FPs in taxonomic groups only remotely related to the source organisms that provided the templates for primer design. An alternative method to the direct PCR amplification is the functional expression of the cDNA library in recombinant systems such as bacteria [100]. Subsequently, bacterial colonies can be screened quickly and efficiently by their color or fluorescence on agar plates for the presence of interesting candidate proteins (Fig. 24.4). Toxicity of the FP may compromise the success of the method; however, the method is ideally suited for the search of GFP-like proteins in new taxonomic groups as it is not constrained by the primer design.

24.5 Applications of Fluorescent Proteins from Marine Invertebrates

GFP-like proteins have revolutionized the field of cellular imaging over the past two decades [15, 103]. The autocatalytic formation of the functional chromophore

without the requirement for cofactors, their diverse spectral characteristics, and the *in vivo* stability of the chromophore over a range of physiological conditions has resulted in their widespread popularity as live-cell markers. As the chromophore can be expressed, matured, and maintained *in vivo*, FPs represent unrivaled tools with which, for instance, complex biochemical pathways can be studied within the living cell. Fluorescent proteins belonging to the GFP-like family have been used for various studies including gene expression, protein localization, protein–protein interactions, and monitoring of intracellular biochemistry [15, 103]. In addition, photoactivatable proteins have enabled super-resolution optical imaging beyond the diffraction limit through techniques such as photoactivated localization microscopy (PALM) or reversible saturable optical fluorescence transitions (RESOLFT) [6, 28]. This section aims to provide an overview of the applications of fluorescent protein technology.

24.5.1 Gene Expression

The suite of genes expressed by a particular cell is a fundamental aspect of cell differentiation. Interpreting the patterns of gene expression, both spatially and temporally, is therefore key to understanding the functioning of different cells, under different stimuli and different stages of development. FPs offer the opportunity to monitor gene expression in living organisms [9]. For this purpose, the FP of choice is expressed in the cells of interest under the control of the target promoter. An adequate stimulation of the experimental promoter can be detected by the increase in cellular fluorescence (Fig. 24.5). Although the *in vitro* maturation of many FPs is fairly swift, it often takes several hours until significant amounts of the reporter have accumulated in the cells. Protein engineering helped accelerate the maturation times of several FPs, but there is presently still further demand for natural or engineered variants with faster maturation rates [7]. Monitoring of the downregulation of a gene is often complicated by the long half-decay time of FPs [37]. The long persistence in the cell can be attributed to the stability of the β -can fold. Biotechnological manipulation such as the introduction of PEST sequences can be used to create variants with faster turnover rates that can be used to determine the time when genes are switched off [42]. Fluorescent timer proteins were created from anthozoan FPs by mutagenesis [84, 85]. In these variants, the ratio of blue-, green-, and red-emitting states of DsRed-type chromophores changes over time and can be used to backtrack the onset of gene expression. The oligomerization degree (monomeric vs. tetrameric) of the protein is less important for the successful application as long as the FPs do not form unspecific aggregates [103].

24.5.2 Labeling of Proteins and Subcellular Compartments

Proteins are involved in essentially all processes in a living organism, and the knowledge of their location within the cell is an important part of understanding their function. FPs provide an invaluable tool with which to tag proteins within

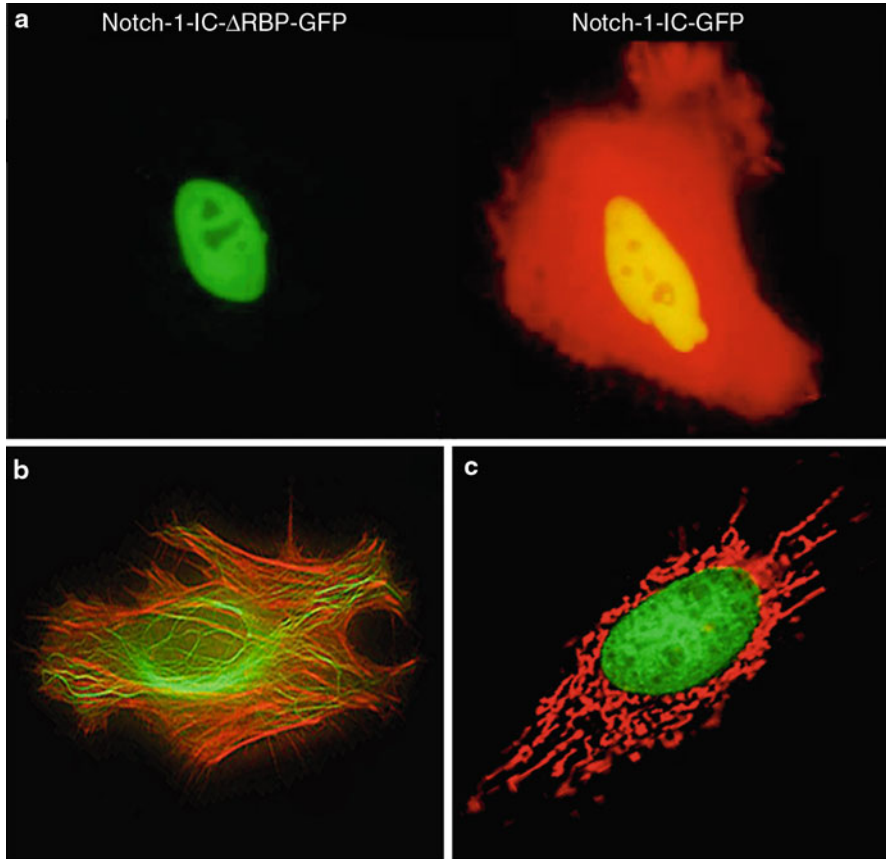


Fig. 24.5 Applications of fluorescent proteins from marine invertebrates. (a) Combined application of FPs as markers of subcellular compartments and gene expression. A Notch1-responsive promoter element was cloned upstream of the cDNA encoding mRuby, the monomeric variant of eqFP611. Cells were cotransfected with this reporter construct and expression vectors encoding truncated forms of the Notch1 receptor fused to GFP. The presence of the receptor is indicated by the green fluorescence of the nucleus (appearing yellow in the right cell due to the overlay with red fluorescence). Truncated Notch1 forms lacking the binding site for the recombination signal-binding protein (Notch1-IC-ΔRBP-GFP) fail to stimulate the expression of the reporter protein (*left cell*). The red fluorescence of the right cells indicates activity of the reporter gene and therefore the presence of a functional RBP binding site – the construct encoding the complete intercellular domain of Notch1 (Notch1-IC-GFP). (b) Dual color labeling of the cytoskeleton. Tubulin fibers are stained green by the tubulin-binding protein RITA expression in fusion with GFP. Actin fibers are labeled red by the fluorescence of mRuby fused to the actin-binding peptide Lifeact. (c) The mitochondrial network of a HeLa cell is highlighted in red by mRuby fused to a mitochondrial targeting signal from subunit VIII of cytochrome c oxidase. The nucleus is stained green by the presence of histone 2B expressed in fusion with GFP

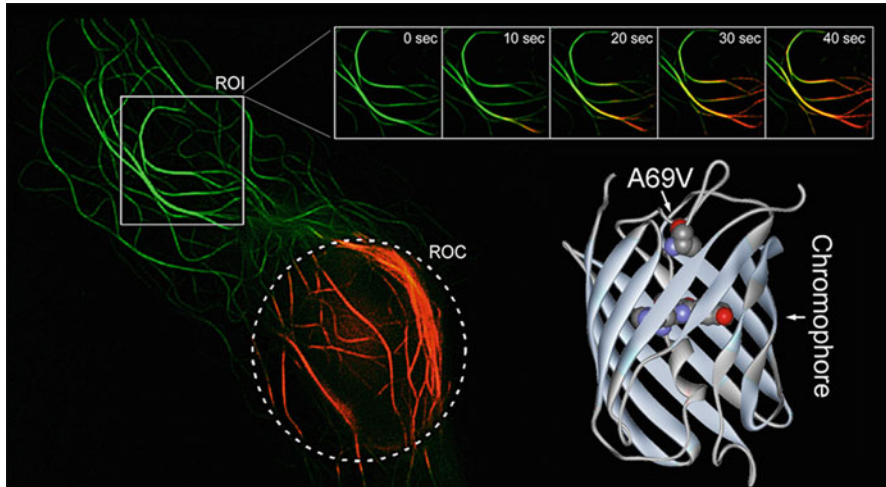


Fig. 24.6 Pulse-chase experiments using green-to-red photoconvertible mEosFPthermo. The ribbon diagram on the *right side* shows the localization of the amino acid A69 exchanged for a valine (represented by Van der Waals spheres) that improves functional expression of the protein at 37°C. The *background image* shows the tubulin skeleton of a HeLa cell highlighted by the green fluorescence of mEosFPthermo fused to the tubulin-binding protein RITA. Local photoconversion was induced by illumination of the region of conversion (ROC) with violet light. Subsequently, the movement of mEosFPthermo-RITA along the tubulin fibers can be followed by the red fluorescence in the region of interest (ROI)

cells [15]. The FP-encoding DNA can be coupled with another fragment coding for the protein of interest, but it is important to remove any stop codon that might be present between the two DNAs. Consequently, the FP is expressed in the cells in tandem together with the protein of interest. In most cases, FPs behave neutral in terms of their cellular localization as long as no unspecific aggregates are formed [103]. The location of the fluorescent tandem will be dominated by the protein of interest, allowing insights in its whereabouts in the cell at distinct time points (Fig. 24.5). The correct localization of fusion proteins can be impaired by an existing oligomerization tendency of the FP. For instance, the correct localization of the tubulin-binding protein RITA is strongly promoted by the monomeric character of the label. Here, the monomeric RFP mRuby and the thermostable monomeric EosFP variant, mEosFPthermo, were used to visualize the close association of RITA with tubulin fibers [92] (Figs. 24.5 and 24.6). Therefore, considerable efforts have been invested to create monomeric versions of multimeric anthozoan proteins [8, 31, 36, 45, 72].

The oligomerization tendency of the label is usually not of concern if they are used to label whole cells or cellular organelles (Fig. 24.5). The short-signaling peptides required for correct targeting in a distinct subcellular compartment are usually not affected in their functionality. The aforementioned applications may use multiple FPs to monitor different targets at the same time.

24.5.3 Protein–Protein Interactions

Studies of protein–protein interactions are very important to assess the function of certain proteins and understand the pathways that these proteins are involved in. A co-localization of two proteins as determined by dual-color labeling techniques using standard fluorescence microscopy does not prove their interaction at the molecular level.

Fluorescence resonance energy transfer (FRET), the radiationless transfer of energy from one chromophore to the other is only possible at distances that are usually provided by molecular interactions [48]. Hence, FRET can be used to determine whether or not two colocalized proteins are indeed interacting. FRET applications require two differently colored FPs, where the emission spectrum of the donor FP needs to overlap with the excitation spectrum of the acceptor FP [20, 32]. These markers are used to label the two proteins under study. Only if the target proteins bring the FPs close enough to be indicative of molecular interactions, FRET will occur and an excitation of the donor will result in an increased emission of the acceptor FP [88].

24.5.4 Sensors

The exact knowledge of molecular changes, post-transcriptional modifications, and the resulting structural changes within the target molecules is an important prerequisite for the development of reliable biosensors.

Fluorescent protein-based sensors have been designed to allow visualization of changes in intracellular conditions (Fig. 24.5). The FRET-based sensors of intracellular calcium levels were among the first sensors based on fluorescent proteins [48, 49]. These so-called chameleons represent a fusion between two FPs that are connected by a linker comprising of calmodulin (CaM) and a 26-residue CaM-binding peptide, called M13, from the myosin light-chain kinase. Upon binding to calcium ions, the linker induces a conformation change in the fusion, bringing the two FPs close enough together for FRET to occur. Consequently, fluctuations of the intracellular calcium levels can be inferred from changes in the ratio of donor and acceptor fluorescence [49]. In another FRET-based sensor for kinase activity, the linker between the donor and acceptor FPs is composed of the SH2 domain of c-Src kinase, a flexible linker region, and an Src substrate peptide from p130cas. Upon phosphorylation, the substrate peptide interacts strongly with the SH2 domain and induces a conformational change within the sensor. In contrast to the above-mentioned chameleons, FRET efficiency decreases in response to increases of the analyte concentrations [93].

Another approach to visualize the presence of analytes is based on monitoring changes in the subcellular localization of FP fusions as a consequence of cellular signal transduction processes. G-protein-coupled receptor (GPCR) signaling leads to cAMP production and subsequent release of intracellular Ca^{2+} . High Ca^{2+} in turn activates the Ca^{2+} /calmodulin-dependent phosphatase calcineurin.

Dephosphorylation of the transcription factor NFAT (nuclear factor of activated T-cells) by calcineurin induces its nuclear translocation and activation of NFAT target genes. Therefore, the rapid migration of an NFAT–FP fusion protein from the cytoplasm to the nucleus can also be used as a calcium sensor in living cells [104].

In addition, FP sensors that report the presence of analytes/ligands by fluorescence changes induced by interactions with the target molecules are available. The fluorescence emission of sensors for transition metal ions and chloride, for instance, anions, are altered by the structural impact of binding in proximity to the chromophore. The anion-sensitive GFP-based YFP-H148Q is an example of an FP whose emission characteristics are altered by interaction with a target molecule of interest, i.e., chloride. The fluorescence of the protein decreases with increasing chloride concentration due to a halide-binding site near the chromophore resulting in a promising tool for high-throughput drug screening for cystic fibrosis [30, 41]. Changes in pH of FP solution can result in changes of the absorption and emission properties of the dye molecules. Some pH-sensible FPs were successfully applied as probes to measure for instance the pH of different compartments in living cells [26, 39, 46].

A fluorescence-based endoplasmic reticulum (ER) stress sensor exploits the activity of a specific ribonuclease. Upon accumulation of misfolded proteins in the endoplasmic reticulum, the so-called *unfolded protein response* (UPR) leads to the activation of the ER transmembrane protein IRE-1. Active IRE-1 targets the mRNA of a transcription factor called XBP-1 and excises exactly 26 nucleotides in a particular cytoplasmic splicing reaction. The excision produces a reading frame shift within the XBP-1 mRNA and a different, now highly active XBP-1 transcription factor variant is produced to activate the transcription of UPR proteins (for example heat shock proteins, HSPs) [107]. An engineered XBP-1–FP fusion construct was developed which becomes fluorescent when the splicing reaction and the resulting frame shift occurs during ER stress [108].

An elegant tension sensor was constructed by linking to FPs suitable to form a FRET couple via an elastic part of the spider silk protein flagelliform [21]. The FRET efficiency decreases gradually under tension and recovers upon relaxation, enabling measurements of forces in the piconewton range.

24.6 Photoactivatable GFP-like Proteins (PAFPs)

PAFPs allow the willful manipulation of their fluorescence by controlled illumination with light of specific quantities and qualities. Subsequently, the optically marked fraction can be independently monitored among the whole population of the marker molecules. Three major responses of PAFP can be distinguished: reversible on/off switching, irreversible activation, and irreversible conversion from one emission color to another. A few natural FPs including asulCP and cerFP505 show pronounced photoactivation responses [40, 90]. In contrast, a number of FPs such as Kaede and EosFP feature green-to-red photoconversion as part of the chromophore maturation [97]. Protein engineering succeeded in

creating numerous variants in which reversible on/off switching or irreversible on switching was strongly enhanced (Table 24.2). Monomeric derivatives were also created to satisfy the demand for PAFPs useful for protein labeling (Table 24.2). IrisFP and its monomeric form are markers that join reversible switching responses with irreversible photoconversion of the chromophore [1, 19]. The two major application fields of PAFPs, pulse-chase experiments, and super-resolution microscopy are described in the following paragraphs.

24.6.1 Pulse-Chase Experiments

Once the markers are expressed and matured, a small subsample of the population is activated with a light pulse. Subsequently, the movement of the activated target proteins can be tracked in real time [97] (Fig. 24.6). Photoconvertible proteins such as Kaede, EosFP, and their derivatives have been proven particularly useful for pulse-chase imaging due to the exceptionally high optical contrast that is generated between the activated and the nonactivated form. Moreover, the use of spectrally well-separated light colors for activation and detection of the markers largely reduces the risk of undesired activation during the tracking phase of the experiment: blue and green light is used for detection, whereas violet light is used to induce photoconversion. Pulse-chase experiments can be performed at the level of cells or tissue, for instance, to monitor the fate of cells during embryonic development [91]. When targeted to subcellular compartments, PAFPs allow the tracking of movement and fusion or fission processes of organelles [97]. In these applications, the oligomerization degree of the marker proteins is usually not an issue as long as no unspecific aggregates are formed. Consequently, the excellent optical properties of tetrameric proteins such as EosFP can be exploited. In contrast, protein-tracking studies might be impaired by the size of the label, so the use of tandem dimer or monomeric variants is often advisable [44, 58] (Fig. 24.6).

24.6.2 Super-Resolution Microscopy

PAFP have also enabled the realization of imaging concepts that achieve resolutions beyond the diffraction barrier of standard optical microscopy. This allows the visualization of structures which are separated less than 200 nm from each other [6, 28]. Here, the photoactivated localization microscopy (PALM) shall be explained in greater detail. Firstly, proteins are labeled with the PAFP of choice. Secondly, the sample is illuminated briefly at low intensity with light that induces activation. Consequently, only a few molecules are activated that are far enough apart for their blurred images to be captured with a conventional microscope. The center of the blurred spots is determined for each molecule, and all loci of the molecules are recorded. Subsequently, the activated molecules are either switched off or photobleached to erase the screen for a new round of activation and localization. Over numerous cycles, a large number of marker molecules are registered until enough data are accumulated to allow reconstruction of an image from the

Table 24.2 Properties of engineered photoactivatable FPs derived from cnidarian pigments

FP variant	Source organism	Oligomerization degree (# protomers)	Type of fluorescence activation	Wavelengths (nm) required for fluorescence activation	Excitation maximum (nm)	Emission maximum (nm)	Molar extinction coefficient	Quantum yield	Relative brightness ^a (% of EGFP)
PA-GFP [62]	<i>Aequorea victoria</i>	1	Off-On	488	504	517	17,400	0.79	43
PS-CFP [11]	<i>Aequorea coeruleus</i>	1	Cyan-green conversion	405	402/490	468/511	34,000/27,000	0.16/0.19	17/16
Kaede [3]	<i>Trachyphyllia geoffroyi</i>	4	Green-red conversion	~400	508/572	518/580	98,800/60,400	0.88/0.33	273/63
KikGR [87]	<i>Favia favius</i>	4	Green-red conversion	~400	507/583	517/593	53,700/35,100	0.70/0.65	118/72
EosFP [101]	<i>Lobophyllia hemprichii</i>	4	Green-red conversion	~400	506/571	516/581	72,000/41,000	0.70/0.62	159/80
Dendra2 [12]	<i>Dendronephthya</i> sp.	1	Green-red conversion	~400	490/553	507/573	45,000/35,000	0.50/0.55	71/61
mKikGR [24]	<i>Favia favius</i>	1	Green-red conversion	~400	505/580	515/591	49,000/28,000	0.69/0.63	106/56
tdEosFP [58]	<i>Lobophyllia hemprichii</i>	1	Green-red conversion	~400	506/569	516/581	84,000/33,000	0.66/0.60	174/62
mEosFP [101]	<i>Lobophyllia hemprichii</i>	1	Green-red conversion	~400	505/569	516/581	67,200/37,000	0.64/0.62	135/72
mEosFP2 [44]	<i>Lobophyllia hemprichii</i>	1 ^b	Green-red conversion	~400	506/573	519/584	56,000/46,000	0.84/0.66	148/96
Dronpa [4]	<i>Pectiniid coral</i>	1	Reversible on/off switching	~400/~488	503	518	95,000	0.85	254
rsFastLime [79]	<i>Pectiniid coral</i>	1	Reversible on/off switching	~400/~488	496	518	39,000	0.77	94

(continued)

Table 24.2 (continued)

FP variant	Source organism	Oligomerization degree (# protomers)	Type of fluorescence activation	Wavelengths (nm) required for fluorescence activation	Excitation maximum (nm)	Emission maximum (nm)	Molar extinction coefficient	Quantum yield	Relative brightness ^a (% of EGFP)
rsCherry [80]	<i>Discosoma</i> sp.	1	Reversible on/off switching	~450/~550	572	610	80,000 ^c	0.005 ^c	5.
rsCherryRev [80]	<i>Discosoma</i> sp.	1	Reversible on/off switching	~450/~550	572	608	84,000 ^c	0.02 ^c	1.3
PAmCherry [83]	<i>Discosoma</i> sp.	1	Reversible on/off switching	390–440/570	570	596	18,000	0.46	26
IrisFP [1]	<i>Lobophyllia hemprichii</i>	4	Green–red conversion, rev. on/off switching	405 (conversion) ~400/~488 (green) ~440/532 (red)	488/551	516/580	52,200/35,400	0.43/0.47	71/52
mIrisFP [19]	<i>Lobophyllia hemprichii</i>	1	Green–red conversion, rev. on/off switching	405 (conversion) ~400/~488 (green) ~440/532 (red)	486/546	516/578	47,000/33,000	0.54/0.59	80/62

^aDetermined for purified proteins^bDimerization tendency [44]^cData from Ref. [80]

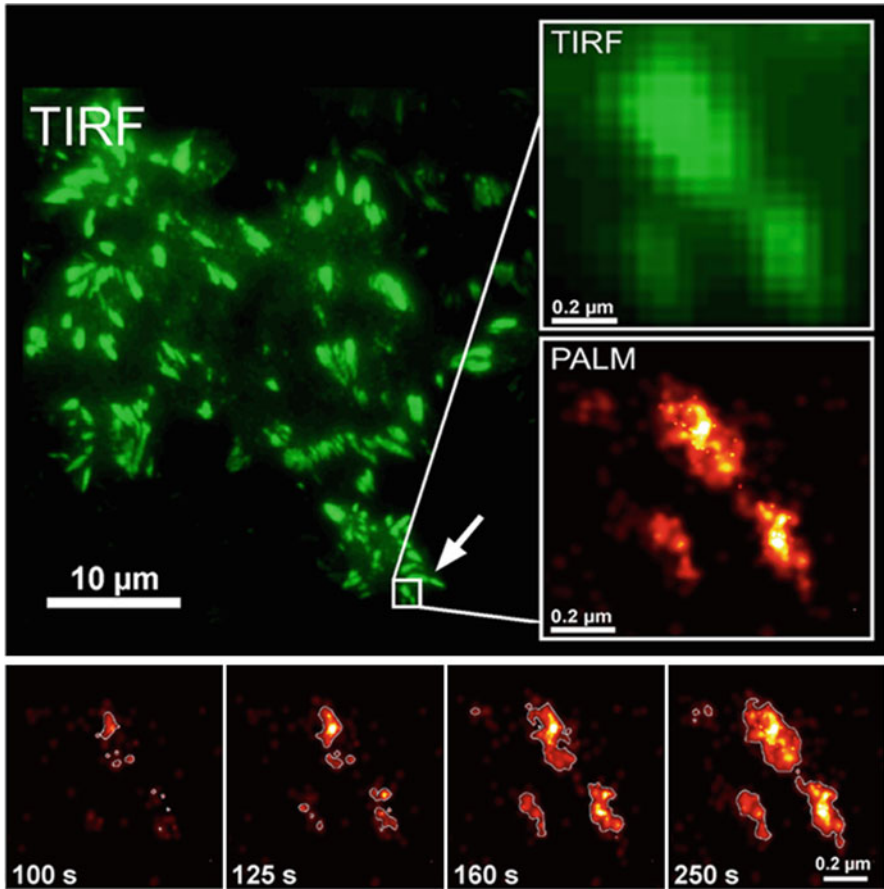


Fig. 24.7 Applications of PAFPs for PALM imaging. mIrisFP was expressed in fusion with paxillin in a HeLa cell. *Upper panel:* The green fluorescent mIrisFP-paxillin accumulates predominantly in focal adhesions. Insets: exploiting the reversible photoswitching of mIrisFP for PALM, images can be constructed with a significantly higher resolution compared to those obtained by conventional TIRF microscopy. *Lower panels:* Pulse-chase experiments with super-resolution. mIrisFP-paxillin was photoconverted by illumination with violet light. PALM images were acquired by photoswitching of the red form of mIrisFP in intervals of 0–100, 0–125, 0–160, and 0–250 s. The increase of molecules over time indicates the growth of the focal adhesions

individual loci. Resolutions between 30 and 100 nm can be regularly achieved by this method. With the recent advent of mIrisFP, it is now also possible to perform pulse-chase experiments at super-resolution [19] (Fig. 24.7).

24.7 Conclusion

Fluorescent proteins from marine organisms revolutionized biomedical research by enabling completely new approaches to study live cells. The vast majority of

fluorescent proteins that can be found in the oceans are yet unstudied. Hence, the combination of “gene hunting” in the marine realm and “protein engineering” in the laboratory will certainly lead to exciting discoveries also in the future. In summary, fluorescent proteins hold a great promise to meet the increasing demand for optical research tools.

24.8 Study Questions

1. In which taxa of marine invertebrates can fluorescent proteins be found?
2. What is the tertiary structure shared by all FPs?
3. How can the diversity of emission colors be explained?
4. Which property of FPs enables their use as genetically encoded markers?
5. What are major applications of FPs and how are they related to their biochemical and photophysical properties?
6. Which properties of FPs can hamper the application as markers?
7. How can the properties of FPs be altered?

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From Biosilica of Sponges (Demospongiae and Hexactinellida) to Fabricated Biomedical Materials

25

Xiaohong Wang, Heinz C. Schröder, Matthias Wiens, Lu Gan, Wolfgang Tremel, and Werner E. G. Müller

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X. Wang

National Research Center for Geoanalysis, 26 Baiwanzhuang Dajie, Beijing, China and

Institute for Physiological Chemistry, Medical Center of the Johannes Gutenberg University, Duesbergweg 6, Mainz, Germany

e-mail: wxh0408@hotmail.com

H.C. Schröder • M. Wiens • W.E.G. Müller (✉)

Institute for Physiological Chemistry, Medical Center of the Johannes Gutenberg University, Duesbergweg 6, Mainz, Germany

e-mail: wmueller@uni-mainz.de

L. Gan

National Research Center for Geoanalysis, 26 Baiwanzhuang Dajie, Beijing, China

W. Tremel

Institute for Chemistry, Johannes Gutenberg University Mainz, Duesbergweg 10-14, Mainz, Germany

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Abstract

Only 13 years after realizing, during a repair of a telegraph cable pulled out from the deep sea, that the bottom of the ocean is plentifully populated with a highly diverse fauna and flora, the Challenger expedition (1873–1876) treasured up a rich collection of vitreous sponges (Hexactinellida). They have been described by Schulze and represent the phylogenetically oldest class of siliceous sponges (phylum Porifera); they are eye-catching because of their distinct body plan, which relies on a filigree skeleton. It is constructed by an array of morphologically determined elements, the spicules. During the German Deep Sea Expedition “Valdivia” (1898–1899), Schulze could describe the largest siliceous hexactinellid sponge on Earth, the up to 3 m high *Monorhaphis chuni*, which likewise forms the largest biosilica structure, the giant basal spicule. Using such spicules as a model, basic knowledge on the morphology, formation, and development of the skeletal elements could be acquired. They are formed by a proteinaceous scaffold (composed of a 27-kDa protein), which mediates the formation of siliceous lamellae that encase the protein. The 27-kDa protein represents an enzyme that forms polysilicate from silicic acid monomers. The silica matrix is composed of almost pure silicon and oxygen, providing it with unusual optophysical properties that are superior to those of man-made waveguides. Experiments suggest that the spicules function in vivo as a nonocular photoreception system. In addition, the spicules are provided with exceptional mechanical properties, combining mechanical stability with strength and stiffness. These basic insights, obtained from the spicule formation in sponges, will surely contribute to a further applied utilization and exploration of silica in biomaterial/biomedical science.

25.1 Introduction: Sponges

The sponges (phylum Porifera) have occupied – since Aristotle (384–322 BC) – a distinguished position among the animals because of their biomedical potential, their beauty, and their enigmatic evolutionary origin. Difficulties in their systematic positioning and in the elucidation of their relationship to other multicellular organisms have resulted in their designation as “zoophytes” or “plant-animals” (a taxon placed between plants and animals) until they were finally recognized as genuine metazoans, which diverged first from the animal ancestor, the urmetazoan [1]. By then it became clear that sponges are not “simple blobs of cells” but contain and express a variety of metazoan-like transcription factors and in turn form sophisticated tissue assemblies [2]. After the discovery/appreciation of the glass sponges [3], the sponges have been grouped into three classes: Demospongiae, Hexactinellida (both have a siliceous skeleton), and Calcarea (calcareous skeleton) [4].

Figure 25.1 gives examples of hexactinellids (*Hyalonema sieboldi*, Fig. 25.1A; *Monorhaphis chuni*, Fig. 25.1F) and one example of demosponge (*Suberites domuncula*, Fig. 25.1G). Sponges were united to the phylum Porifera due to the characteristic and distinct pores on the surface of the animals. They represent the evolutionary oldest, still extant taxon which testifies the developmental level of animals living in the Neoproterozoic Eon (1,000–520 million years ago [MYA]); hence they can be termed “living fossils” [5].

The Hexactinellida are the oldest group of sponges in fossil records of the Sansha section in Hunan (Early Cambrian; China), where more or less completely preserved sponge fossils, like *Solactiniella plumata* (Fig. 25.1B), have been found [6]. This fossil is noteworthy since it shows, besides an unusual body preservation, also very intact siliceous spicules (skeletal elements). The approximately 40-mm-large specimen comprises 0.5–5-mm-long spicules with a diameter of 0.1 mm (Fig. 25.1C); some of them are broken and present the open axial canals. It should be mentioned that high-resolution scanning electron microscopic (HR-SEM) analyses (Fig. 25.1C), coupled with energy-dispersive X-ray, identified those spicules of *S. plumata* as to be composed of the original amorphous silica. In contrast, the characteristic fossil hexactin spicules from hexactinellids found in the Xinjiang Province from the Tarim basin, and dated back to the Ordovician (510–445 MYA), have not conserved their silica state but have been diagenetically converted to calcite microcrystals (Fig. 25.1D, E).

The siliceous sponges disclosed – after application of modern molecular biological and cell biological techniques – a hitherto unknown biochemical reaction, the synthesis of a polymeric inorganic molecule (silica) via an organic molecule, an enzyme (reviewed in [7–9]). Such an activity/reaction was not known before. A thorough elucidation of this process resulted in a paradigm shift which might contribute also to new directions in biomaterial sciences.

25.2 The Power of “Nature as Model” in Bioinorganic Material Science: Shift of a Paradigm

In 1828 Wöhler [10] succeeded to copy nature by producing an organic compound from inorganic reactants. He synthesized urea from the inorganic ammonium cyanate, establishing the first rules in organic chemistry. However, to copy organic (bio)synthetic reactions comprehensively, the existence of enzymes had to be discovered, an important step which dates back to Pasteur [11]. He found that lactic acid is a fermentation product, and thus proved the basis for the discipline biochemistry. In fact, already in 1784 Spallanzani [12] described that gastric juice, soaked into a horny sponge that he had swallowed and subsequently removed from his own stomach, had the potency to digest meat. This experiment can be taken as a first demonstration of (enzymatic) reactions inside living organisms. The causal-analytical understanding of organic reactions in biological systems became possible after the deciphering of the genetic code and the subsequent elucidation and application of molecular biological, recombinant techniques.

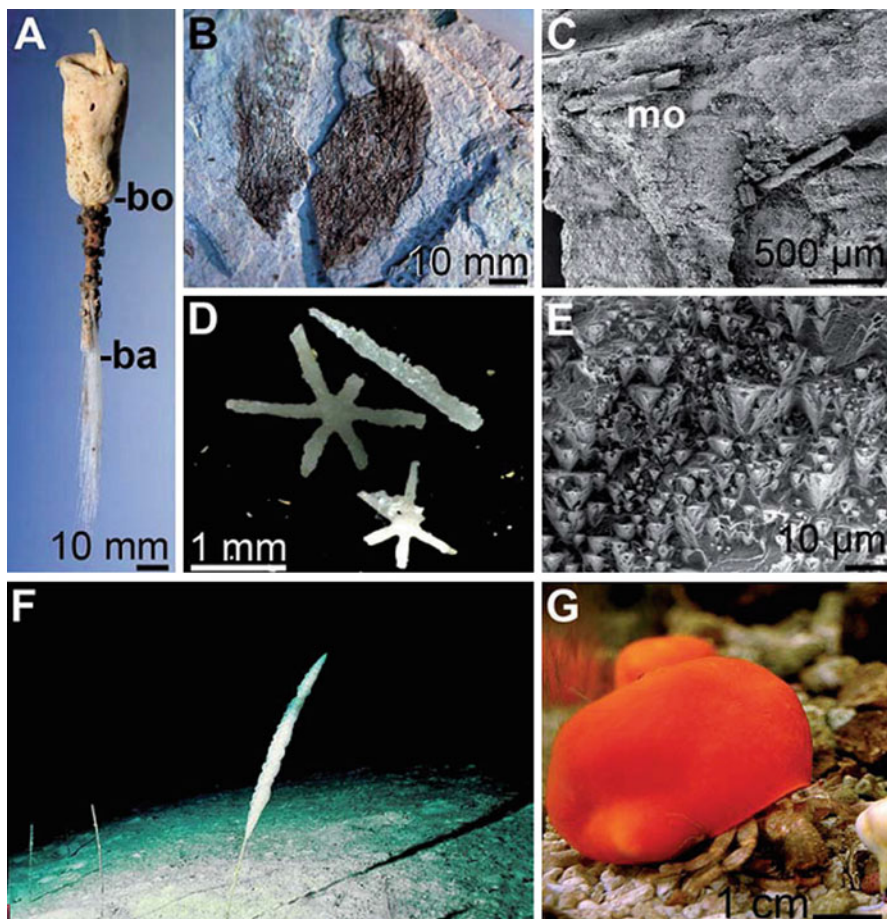


Fig. 25.1 Fossil and present-day siliceous sponges. (A) Hexactinellida: *Hyalonema sieboldi*. Lateral view of a specimen showing the body and the stalk (size 500 mm). Specimens of this hexactinellid can be morphologically divided into the cylindrical upper body (bo) which is attached to 30-cm-long basal stalk spicules, also termed basalia (ba), that fix the specimens to the substratum. (B) Earliest sponge in body preservation, *Solactiniella plumata* (Lowermost Cambrian Sansha section [Hunan, China]) (size 40 mm). (C) High-resolution scanning electron microscope (HR-SEM) analysis was performed to visualize the monaxial spicules (mo) from *S. plumata*. (D) Characteristic fossil hexactin spicules from a hexactinellid, found in the Tarim basin (Xinjiang Province, China); Ordovician (510–445 million years). (E) The silica material in these spicules had been diagenetically converted to calcite microcrystals; HR-SEM. (F) *Monorhaphis* in its natural soft bottom habitat of bathyal slopes off New Caledonia (Photograph taken by Michel Roux, University of Reims; reproduced with permission). (G) Demospongiae: example *Suberites domuncula*. This specimen lives on the hermit crab *Paguristes oculatus* which resides in shells of the mollusk *Trunculariopsis trunculus*; size 30 mm

However, only recently first strategies could be formulated and experimentally proven, to outline the biosynthesis of inorganic structures formed in uni- and multicellular organisms. At present, in a self-accelerating progress, the matrices (templates), e.g., collagen, and the organic catalysts (enzymes, e.g., silicatein) required for the synthesis of such inorganic structures and skeletal elements have been illuminated with the help of inorganic/organic chemists, biochemists, molecular biologists, and material scientists. These interacting and cooperating activities established the discipline of “bioinorganic material science.” The first opportunities have been touched in biomedicine and electronics, providing us with a first indication about the power and potential of this new technology [13–16].

25.3 Levels of Biomineralization

Biomineralization describes processes by which living organisms produce minerals. These widely discovered reactions include also the formation of silica (biosilica) in algae, plants, and invertebrates or of calcium phosphates and carbonates in vertebrates [17–20]. The biologically mediated reactions result in the formation of sea shells or the bones in mammals and birds. Less frequently than silicon- and calcium-based skeleton formation occurs the biomineral formation using copper, iron, and gold deposits. It is one current challenging task to mimic the natural ways of producing minerals/“inorganic polymers” (biomimetics). While related man-made processes, performed by chemical reactions only, require elevated temperatures and strong chemicals, the organisms are able to lay down and form mineral structures at ambient temperatures. Most frequently, those mineralization processes in biological systems allow the formation of composites which comprise, in addition to the inorganic polymer, an organic part, often proteins, which controls those reactions (biomineralization; [19, 20]).

It is the achievement of Lowenstam and Weiner [17] to have systematized processes of biomineralization into the following two categories: the biologically induced mineralization and the biologically controlled mineralization. These two groups are distinguished by the properties of the guiding functions of the organic components. In biologically induced mineralization processes, organic surfaces act as nucleation for the biomineralization. The processes are driven either by the chemical and/or physical properties of organic surfaces only (Fig. 25.2, left), or involve also biochemical reactions (Fig. 25.2, middle). An example for biomineralization processes, occurring on organic surfaces and mediated by their chemical and/or physical properties, is the formation of ferromanganese crusts on marine basaltic seamounts. The deposition of the minerals is facilitated by the pH and redox environment in the vicinity of the coccolith/coccolithophore algae. The formation of manganese nodule involves a biochemical reaction which is based on exoenzymes. Those enzymes facilitate the oxidation of manganese and iron under formation of insoluble reaction products. Finally, the biologically

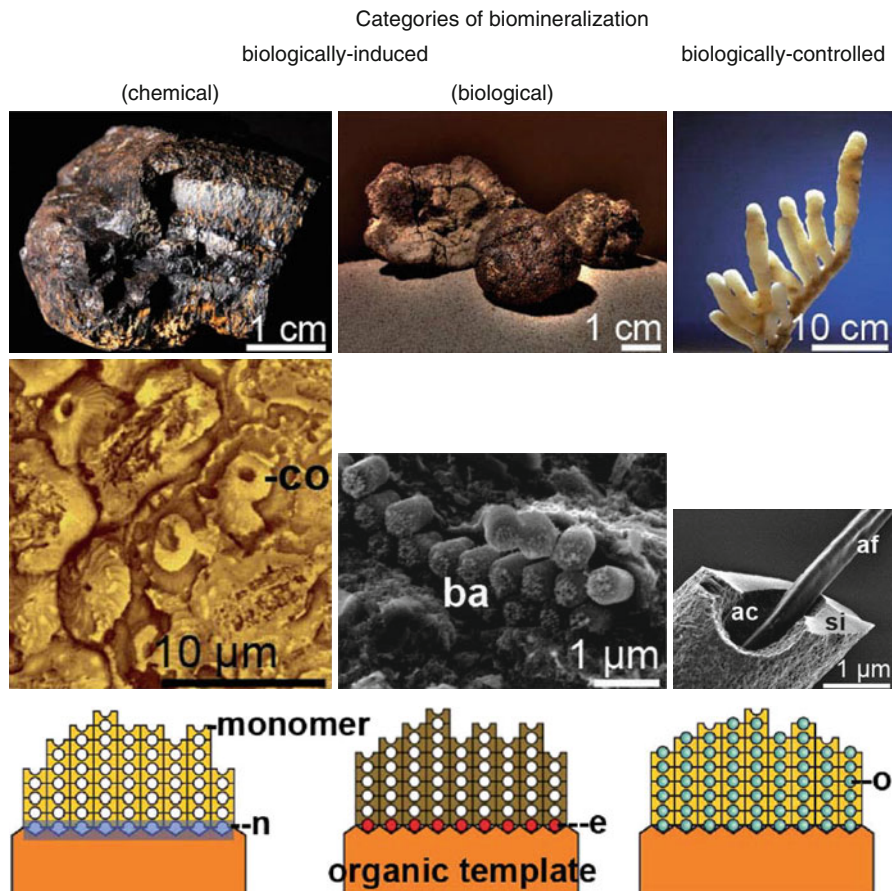


Fig. 25.2 Categories of biomineralization. *Left:* Biologically induced mineralization (based on chemical and physical properties of organic surfaces). Those processes had been elucidated in ferromanganese crusts, formed on basaltic seamounts in the deep sea (*top*). The formation of those mineral deposits is (passively) initiated by the surfaces of calcareous algae, the coccoliths/coccolithophores (co) (*middle*). These organisms act with their surfaces in the initial stage of mineral formation, the induction phase of nucleation (n). The inorganic monomers are deposited, after the nucleation phase, without help of an organic component (*bottom*). *Middle:* Biologically induced mineralization (based on biochemical reactions, which proceed on organic surfaces). In manganese nodules (as likely examples), exoenzymes (e) mediate oxidation of Mn(II) to Mn(IV) and/or Fe(II) to Fe(III) (*top*). The insoluble reaction products precipitate onto organic surfaces. Those oxidation reactions occur on S-layers of bacteria (ba) (*middle*). The further growth of the mineral is independent of organic components (*bottom*). *Right:* Biologically controlled mineralization (the deposition of the minerals is guided by an organic scaffold). This type of mineralization is controlled by an organic matrix and results in the formation of a composite biomineral. The organic component (o) is intimately involved in the formation of polymeric inorganic molecules (*bottom*). Prominent examples for an enzymatically, biologically controlled mineralization are the siliceous skeletons from sponges (*top*) with an example of *Lubomirskia baicalensis*. The enzymatic/proteinaceous matrix is composed of silicatein, which forms the axial filament (af), that resides in the axial canal (ac) and mediates the formation of the silica layers (si) of the spicules (*middle*)

controlled mineralization (the deposition of the minerals guided by an organic scaffold) must be highlighted since in this category the morphology of the inorganic deposition is controlled by an organic matrix. Hence those biominerals represent a composite, formed from the inorganic polymer and an organic component (protein, polysaccharide, glycoprotein). The associations of inorganic monomers are linked together by organic polymers (Fig. 25.2, right). A prominent/unique example of this category is represented by the siliceous sponges. In these organisms the skeletal siliceous elements is enzymatically formed by association of the silicic acid monomers to amorphous biosilica (Fig. 25.2, bottom right).

25.4 Spicule Network in Siliceous Sponges: A Unique Skeleton

In living organisms four major groups of biominerals exist: (1) iron compounds, which are restricted primarily to Prokaryota; (2) calcium phosphates, found in Metazoa; (3) calcium carbonates, used by Prokaryota, Protozoa, Plantae, Fungi, and Metazoa; and (4) silica (opal), present in sponges and diatoms [21]. The formation of the skeleton is a multifaceted process and can be explained in an exemplary way for the siliceous sponges. Even though these animals comprise the simplest body plan, their biomineral structure formation is already highly complex and by far not completely understood. Like the skeletons in triploblasts, the skeleton formation in the diploblastic Porifera also is intimately connected with morphogenesis [8, 22].

The formation of siliceous spicules in sponges is a genetically controlled process that initiates the morphogenesis phase. Data demonstrated that suitable silicate concentrations induce genes, e.g., those encoding collagen, silicatein, or myotrophin [23]. A major step to elucidate the formation of the siliceous spicules on molecular level was the finding that the “axial organic filament” of siliceous spicules is in reality an enzyme [24–26], silicatein, which mediates the apposition of amorphous silica and hence the formation of spicules.

The skeletal framework of the sponges is highly ordered. In the examples of the demosponge *Suberites domuncula* (Fig. 25.1G) and the hexactinellid *Monorhaphis chuni* (Figs. 25.1F and 25.3A, B), as well as the freshwater sponge *Lubomirskia baicalensis* (Fig. 25.2, upper right), it can strikingly be seen that the growth of the sponges proceeds in a highly organized architecture, mostly in a radiate accretive manner. Most siliceous sponges comprise larger megascleres (>100 μm long) (Fig. 25.3F), and smaller microscleres (<100 μm) (Fig. 25.3D). Some microscleres have bizarre shapes (Figs. 25.3D and 25.4G), while the megascleres usually have a long central rod (Fig. 25.3A). Importantly, the spicules (Fig. 25.4) contain, both in the central hole and within the outer concentric silica layers, the enzyme silicatein. The silica shell of the spicules is synthesized in the initial stage by the silicatein fiber which exists in the central hole, the axial canal. Around this canal a >3- μm -thick siliceous hollow fiber is finally formed (Fig. 25.4B, C, H) [27, 28].

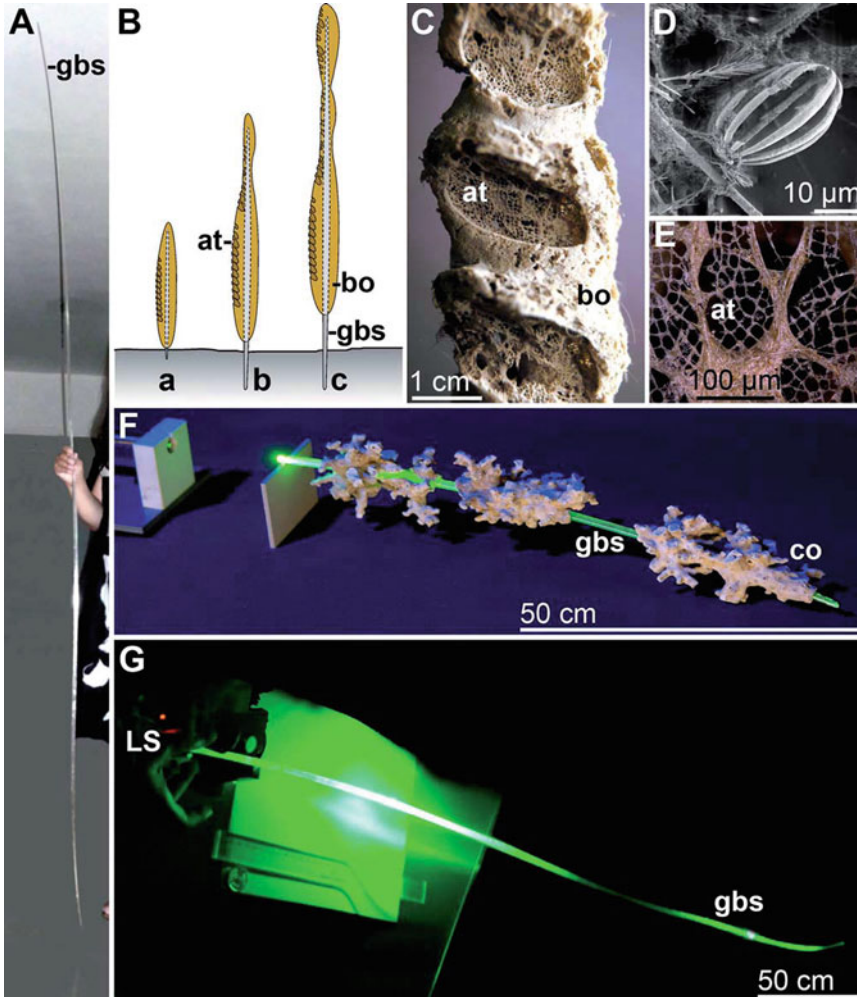


Fig. 25.3 Extreme size and morphology of the spicules in the hexactinellid sponge *Monorhaphis*. (A) A 270-cm-long giant basal spicule (gbs) having a diameter of up to 11 mm. (B) Schematic representation of the growth phases of the sessile animals with their giant basal spicule (gbs) which anchors them to the substratum and holds their surrounding soft body (bo). The characteristic habitus displays linearly arranged large atrial openings (at) of approximately 2 cm in diameter. With growth the soft body dies off in the basal region and exposes the bare giant basal spicule (a–c). (C) Part of the body (bo) with its atrial openings (at). The body surface is interspersed with ingestion openings allowing a continuous water flow through canals in the interior which open into oscules that are centralized in atrial openings, the sieve plates. (D) An ornate mesamphidisk. (E) Grilles forming the atrial openings (at) are composed of different types of spicules, tauactines, framing of lattices, on which the pentactines are arranged in a phalanx. (F) Giant basal spicule (80 cm long), collected 1898/1899 at a depth of 1,079 m off the coast of Somalia (06° 18.800'N–049° 32.500'E) (Museum für Naturkunde Berlin, Germany; ZMB Por 12700). The spicule (gbs) is surrounded by stony corals (co). (G) The 270-cm-long giant basal spicule was used as an optical waveguide; green light was used as a light source (LS)

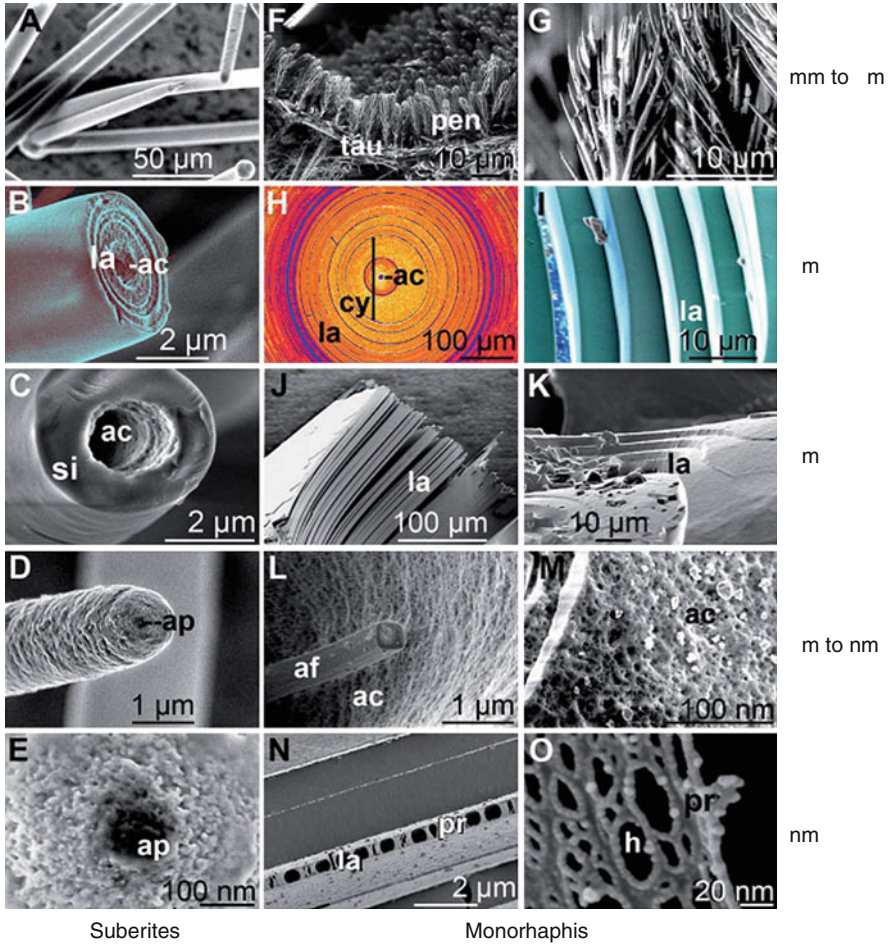


Fig. 25.4 Morphology of the spicules from *S. domuncula* (A–E) and *Monorhaphis* (F–O), as analyzed by their top-down hierarchical organizations. Sequentially, images from the cm to μm level, then around the μm range, proceeding from the μm to nm scale and finally from the nm level are given. *Organization of the S. domuncula tylostyles* ($\leq 400 \mu\text{m}$): (A) nest of some tylostyles. (B and C) Cross breaks through tylostyles. In (B) a lamellar organization (la) of the silica spicule becomes visible after etching with hydrofluoric acid (HF) vapor. This zonation of the siliceous mantle (si) is absent in those spicules which remained native (C). In both samples the axial canal (ac) is seen. (D) Young tylostyle, approximately $20 \mu\text{m}$ in length, displays an open aperture (ap) which runs into the axial canal. (E) Higher magnification of the apical aperture (ap). *Monorhaphis spicules*: (F) HR-SEM image of the lattice of a grille. The pentactines (pen) are oriented toward the exterior of the body thus forming a mechanical and relative sealing of the atrial opening. The strutting columns are formed from tauactines (tau). (G) Tip of a dermal pentactine pinnule. (H and I) Structural arrangement of the lamellae in the giant basal spicules; cross sections. In the center of the spicule, the axial canal (ac) is surrounded by the axial cylinder (cy), a region formed from electron-dense homogeneous silica. The third and major part of the spicules is composed of the outer 300–800 concentrically arranged lamellae (la) (H). (I) Higher magnification of the image in (H), taken from the lamellar region. (J and K) Cross breaks through a spicule, showing the piled

25.4.1 Spicule Diversity: Case Study Hexactinellid *Monorhaphis*

The sponge *Monorhaphis chuni* is distributed in the Indo-West Pacific region and is found in depths between 516 and 1,920 m. For most of the studies, specimens dredged from 800 m in the Okinawa Trough and from 1,000 m in the South China Sea have been used. *Monorhaphis* inhabits muddy substrata and is fixed there by a single giant basal spicule. Photographs taken from the natural environment by Roux et al. [29] are available (Fig. 25.1F). Young specimens have been imagined to comprise a continuous body; one giant basal spicule anchors the specimen to the substratum and carries the cylindrical body (Fig. 25.3B). The body is interspersed with many atrial openings which are located along one side (Fig. 25.3B, C, E). Special dermal pinnular pentactine spicules exist (Fig. 25.4F, G) that are aligned along tauactines that frame the atrial openings, the sieve plates (Figs. 25.3E and 25.4F). These tauactines form the grille of the atrial openings and are armed by pentactines, allowing a mechanical sealing of the body toward the aqueous environment. The size of a mesamphidisk (microsclere) is approximately 100 μm (Fig. 25.3D). The diameter of the body reaches in larger specimens 8 cm. During growth the specimens elongate together with an extension of their giant basal spicules (Fig. 25.3B). Older specimens apparently lose the basal portions of their soft body and expose the bare giant basal spicule. While recently giant basal spicules of a size of 1.7 m in maximum have been discovered, now giant spicules with a length of 2.7 m have been collected that are used by the author for the studies. The maximum diameter of that spicule is at its middle 12 mm and at its base 3 mm [27, 30].

25.4.2 Giant Basal Spicules from *Monorhaphis*: The Largest Bio-Silica Structure on Earth

The spicules consist of an organic scaffold and an inorganic silica layer/mantel. The silica mantel is formed from individual lamellae. These lamellae had been analyzed mainly by SEM. The morphological description here proceeds from the millimeter to the nanometer scale. Initial studies on the morphology of siliceous spicules were performed with the spicules from *S. domuncula* [26]. This demosponge comprises only one type of spicules, the tylostyles. They reach in the outer layer of the animals a size of $200 \times 5 \mu\text{m}$ and in the center of the specimens $300\text{--}500 \times 5\text{--}8 \mu\text{m}$ (Fig. 25.4A). All spicules have a $0.3\text{--}1.6\text{-}\mu\text{m}$ -wide axial canal in their center. As shown in SEM images (Fig. 25.4B, C), the central canal is surrounded by lamellated



Fig. 25.4 (continued) lamellae (la) (J). (K) A tangential view to a cross break of a giant basal spicule displaying the stepwise layering of the silica lamellae. (L and M) In the axial canal (ac) the square axial filament (af) is seen (L). (M) Higher magnification of the wall of the axial canal toward the center of the spicule. (N and O) Appearance of the proteinaceous palisade-like scaffold (pr) within one lamella (la) after exposure of the spicule to HF vapor. The fibrous structures are interrupted by holes (N). (O) The proteinaceous palisade-like scaffold protein (pr) is composed of fibers that are interconnected and leave open holes (h) whose rims are reinforced

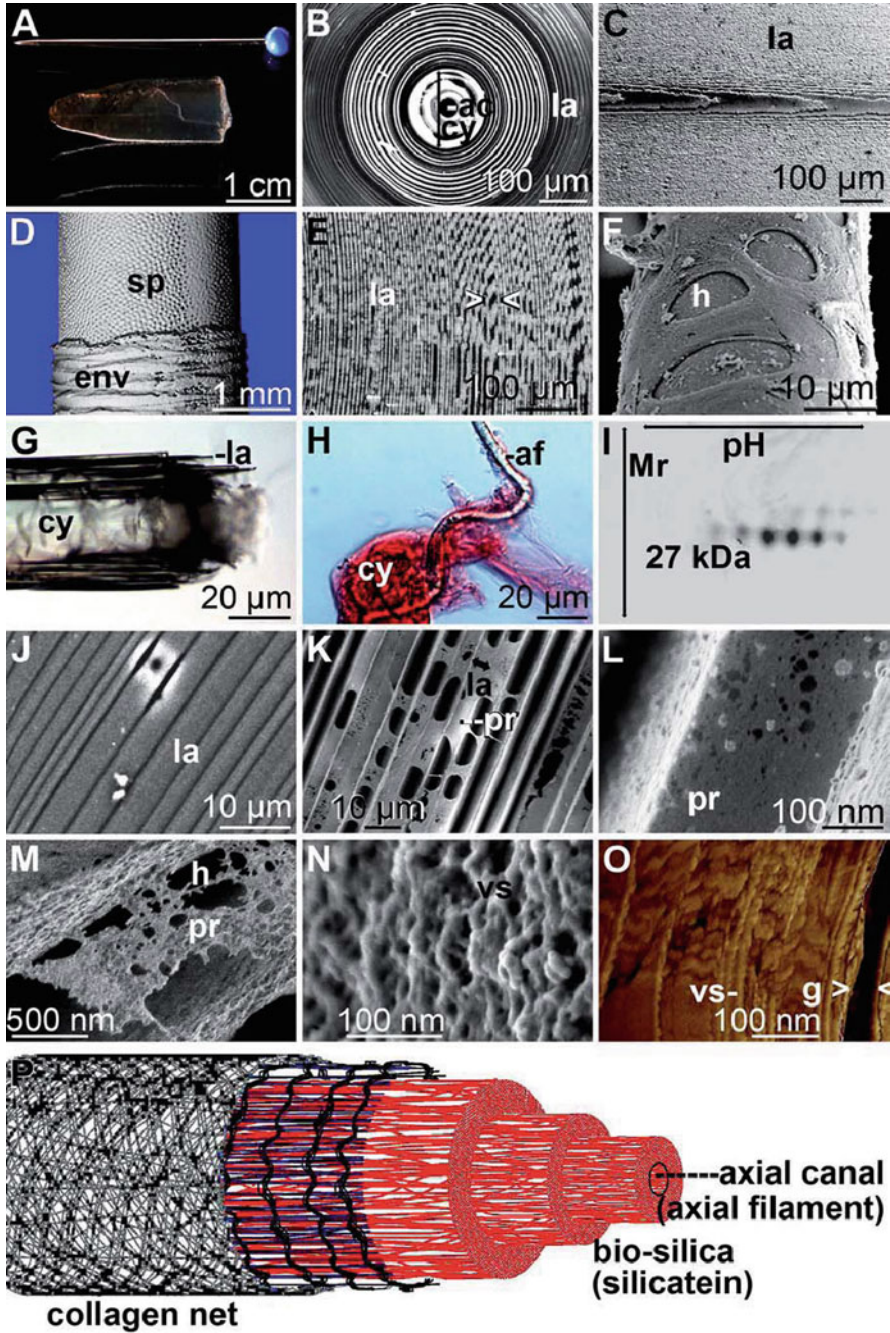


Fig. 25.5 Composite characteristics of the giant basal spicule (*Monorhaphis*). (A) Comparison between the tip of a giant basal spicule (diameter of 7 mm) and a pin/needle. (B) Polished cross

silica layers (Fig. 25.4B). In young, just growing spicules, their tips are open and display an aperture of a size of 100 nm (Fig. 25.4D, E). Based on these exploratory studies, a detailed analysis of the giant basal spicules from *Monorhaphis* became possible [27, 30, 31].

A view of a broken giant basal spicule from *Monorhaphis*, with a large diameter of up to 12 mm (Fig. 25.5A), discloses at the fracture surface the lamellar-wise organization of the silica mantel. A cut through a giant basal spicule shows that the lamellae are arranged in perfect concentric rings around the central axial cylinder (Fig. 25.4H, I).

Millimeter to micrometer scale: Studies were performed by high-resolution scanning electron microscopy (HR-SEM), allowing a resolution of the morphology of the giant basal spicules. A diagonal SEM analysis of a polished cross section of a spicule shows the structural division of the spicule into three zones (Fig. 25.4H). In the center of the spicules lies the axial canal which is surrounded by a region of electron-dense homogeneous silica constituting the axial cylinder of a diameter of 100–150 μm (Fig. 25.4H). The major part of the spicules is composed of 300–800 regularly and concentrically arranged lamellae (each 3–10 μm thick; Fig. 25.4H, I, as well as Fig. 25.5B, C, E). Cross breaks of those spicules show piles of lamellae that open like pages of a book (Fig. 25.4J). A lateral view opens the stepwise arrangement of the layers, reminiscent of the



Fig. 25.5 (continued) section through a giant basal spicule, displaying its three parts, the axial canal (ac), the axial cylinder (cy), and the lamellar region (la). (C) A longitudinal cut through the spicule shows the foliate, lamellar (la) piling of the layers within a spicule. (D) MicroCT analysis of a giant basal spicule. 3D reconstruction of the spicule close to the tip. There, the spicule (sp) is surrounded by an organic envelope (env). The surface of the lamellae shows that protrusions are regularly arranged on the spicule. (E) Polished cross section through a spicule pointing to the discontinued gaps between the lamellae (la). It appears that the connections between the lamellae have an ordered arrangement. One of those connections is marked (> <). (F) A collagen net, perforated with holes (h), surrounds the spicules. (G) During the process of stepwise dissolution of the silica shell around the axial filament (by HF), the lamellar zone (la) starts already after 1–3 min to dissolve. (H) In a later phase the proteins in the axial cylinder (cy) are released that surrounds the axial filament (af); stained with Sirius red. (I) Analysis of the proteins in total extract of the spicules by two-dimensional gel electrophoresis (first isoelectric focusing and then size separation). The gel has been stained with Coomassie brilliant blue. A set of ≈ 27 kDa proteins are stained reflecting their different phosphorylation status. (J–L) Stepwise release of the protein matrix within the lamellae (la), giving rise to the palisade-like proteinaceous scaffold (pr); exposure to HF for 1 min (J), 30 min (K), or 180 min (L). (M) Higher magnification of the fibrous structure from the lamellae, the palisade-like scaffold (pr), disclosing holes (h). (N) A slightly etched cross section through a spicule. Vermicular structures (vs) within the lamellae are disclosed. (O) Analysis of those spicular surfaces by atomic force microscope (AFM), displaying the vermicular structures (vs) as concentric arranged cables. In addition, one gap between two lamellae is visible (g). (P) Scheme summarizing the morphological zones of the giant basal spicules, outlining their composite property. The axial canal harbors the organic axial filament. This structure is surrounded by the silica mantel which comprises within its lamellae the protein/enzyme, silicatein. This silica mantel is surrounded by a collagen net

seat rows in an amphitheater (Fig. 25.4K). The interlamellar space of the spicules does surprisingly not constitute a continuous open slit. The slit is in average 0.1–0.2 μm wide and is composed of alternating fusion zones and open gaps; apparently the fusion zones allow a continuum between silica lamellae (Fig. 25.5E). The axial canal harbors the organic axial filament which has a characteristic rectangular shape (Fig. 25.4L). The wall of the axial canal is not completely smooth but displays a fine-structured network, composed of 20–40-nm-large silica granules (Fig. 25.4M).

Nanometer scale: Studies, to obtain an insight into the structural organization of the spicules at the nm scale, have been performed after mild, partial, and limited dissolution of the silica material by hydrofluoric acid (HF). Under such conditions the organic matrix is released from the interior of the lamellae (Fig. 25.4N, O). In light microscopic studies it could be shown that the dissolution kinetics (caused by HF) is different in the region of the axial cylinder and the lamellar region. The dissolution starts from cracks in the spicule, primarily following the gaps between the lamellae (Fig. 25.5G). During this process the lamellar zone can be distinguished from the axial cylinder by the protruding ends of dissolving individual lamellae (Fig. 25.5G). The dissolution of the axial cylinder proceeds from the periphery without revealing individual lamellae (Fig. 25.5H). Application of different dyes allows a differential visualization of the proteinaceous components. While Coomassie brilliant blue stains the released protein from the lamellae and the axial cylinder, the polypeptides released from the axial cylinder react selectively with Sirius red (Fig. 25.5H).

Next the HR-SEM technique was applied to detect/identify the proteinaceous scaffold that is released after HF treatment (Fig. 25.5J–L). In the transition phase, until a complete dissolution by HF is reached, the siliceous surfaces of the lamellae remain visible (Figs. 25.4N and 25.5K); they are held up by palisade-like pillar structures composed of proteinaceous material. The individual pillars have a diameter of 0.1–0.2 μm and a length of 5–10 μm (Figs. 25.4O and 25.5M). The proteinaceous material obtained was characterized biochemically as one distinct protein with an apparent size of ~ 27 kDa. Slightly etched spicules show on the surfaces vermicular structures of diameters of 20–30 nm (Fig. 25.5N), likely to represent the proteinaceous matrix. The different mechanical properties of these vermicular structures within a lamella can be visualized by atomic force microscope (AFM) analysis (Fig. 25.5O); these structures follow the concentric arrangement/orientation of the lamellae [8].

25.4.3 Chemical Composition

The gross chemical composition of sponge spicules has been described both for Demospongiae and for Hexactinellida. Already Schulze [32] determined that besides Si (silicon) and O (oxygen) (96%), only trace amounts of Na and K contribute to the inorganic material. Hence the silica (opal) of the spicules possesses quartz glass quality [33].

25.4.4 Giant Basal Spicules – Protein Scaffold

Surprisingly it was found that the siliceous lamellae, composing the spicules from *Monorhaphis*, contain also a proteinaceous scaffold. The proteinaceous material obtained was characterized by NaDodSO₄-PAGE and found to represent one distinct protein with an apparent size of ≈ 27 kDa (Fig. 25.5I) [31, 34, 35]. If such a protein sample is subjected to two-dimensional gel electrophoresis, the proteins are separated into acidic and alkaline sets of protein (Fig. 25.5I). Work had been focused especially on the identification of the function of the ≈ 27 -kDa protein. By applying biochemical and immunobiochemical techniques, it could be established that this ≈ 27 -kDa protein represents the silica-forming enzyme, silicatein. This molecule constitutes the axial filament as well as the matrix of the silica lamellae. Hence, the “inorganic” silica material of the spicules represents a composite, formed of protein and silica (Fig. 25.5P).

Collagen is surely, also in sponges, an important component in the morphogenesis of the spicules. These fiber polypeptides surround the spicules as a fibrous sheath. By application of the SEM technique, the collagen net was found to be regularly interrupted by circular holes (7–10 μm ; Fig. 25.5F). Microtomography (MicroCT) analysis revealed that this organic envelope (collagen fibrils) surrounds the inorganic spicule (Fig. 25.5D). In addition, it could be visualized that the surface of the silica spicule is not even but has a serrated relief structure. The protrusions are arranged in an organized pattern, an almost regular helical succession of small projections (Fig. 25.5D, P) [36].

25.4.5 Biochemical Properties and Intracellular Localization of Silicatein

The kinetic parameters for silicatein follow those of usual enzymes; the Michaelis constant (K_m) for silicatein was determined to be 22.7 μM , and the corresponding V_{max} (maximal velocity) was 9.6 nM/min [9].

The spicules are formed in the first stage intracellularly and are completed extracellularly. Silicic acid is taken up intracellularly via a $\text{Na}^+/\text{HCO}_3^-$ [$\text{Si}(\text{OH})_4$]-cotransporter system [37]. There silicic acid is accumulating in special organelles, the silicasomes (Fig. 25.6). Within this compartment, the first immature spicules are formed from silicic acid under formation of polysilica around the silicatein/axial filament (Fig. 25.6A). Subsequently those immature spicules are extruded into the extracellular space where the spicules are completed by the (also) extracellularly existing silicatein. This biomineralization pathway, enzymatic formation of intracellular polysilica structures and subsequent extracellular completion of the spicules by silicatein, is unique and found only in sponges (Fig. 25.6A).

These data, first the selective uptake of silicic acid by membrane-associated transporters and then formation of polysilica structures by the enzyme silicatein, allows also a biochemical explanation of the ability of sponges to form high-quality

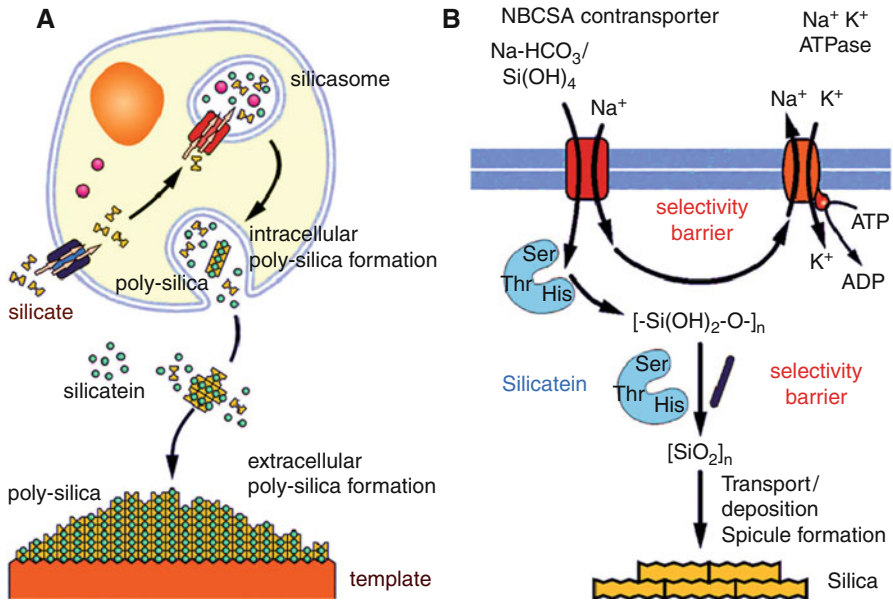


Fig. 25.6 Schematic outline of the enzymatic synthesis of polysilica structures (biosilica) and of the transport of silicic acid into sponge cells. **(A)** Orthosilicate (silicic acid) is taken up by a membrane-associated transporter. From there the silicic acid monomers are transported into the silicasomes and undergo association with the silicatein enzyme. After formation of the first silica structures, the immature spicules are released from the cells and completed extracellularly by the existing silicatein molecules and silicic acid. **(B)** Scheme outlining the two selectivity barriers that control the synthesis of the pure biosilica product. The Na⁺-bicarbonate⁻/silicic acid cotransporter mediates the uptake of silicate, allowing a strong selective enrichment of silicate in the cells and in the tissue of the sponges (first selectivity control). Na⁺ is pumped out via the Na⁺/K⁺ ATPase transporter under the consumption of ATP. The second selectivity control is on the level of silicatein, which will accept – substrate specifically – only silicate under formation of biosilica

quartz glass spicules. This high purity is the result of a selective uptake [Si(OH)₄-cotransporter system] and selective deposition of polysilica (silicatein) (Fig. 25.6B).

25.4.6 Cloning of the Hexactinellid Silicatein cDNA

Only sponges are provided with the polysilica-forming enzyme, silicatein. After cloning of the silicateins from demosponges, it became obvious that silicatein belongs to the class of cathepsins, with cathepsin L as the most prominent member [23, 25]. This lysosomal enzyme belongs to the family of papain-like peptidases that are characterized by the catalytic triad of cysteine (Cys), histidine (His), and asparagine (Asn). The silicateins are distinguished from the cathepsins by the exchange of the first amino acid (aa) residue in the catalytic triad, Cys by Ser. In addition, the silicateins are distinguished from the cathepsins by the presence of

a Ser stretch that precedes the second aa in the catalytic triad, His. Like demosponges (Fig. 25.7), also hexactinellids contain the silicatein enzyme. Recently, also the gene encoding this enzyme in Hexactinellida has been isolated from *Crateromorpha meyeri* [34].

25.5 Modeling of the Morphology of the Spicules

The determination of the spicule morphology remains one of the most enigmatic processes in sponges. Surely, the sizes and forms of the spicules are under species-specific control. However, only little information is presently known to define those control systems, governing the growth and form processes. The basis of the spicule formation is defined by the axial filament that elongates by a controlled interaction of silicatein molecules. Silicatein, especially if it is extracted from the spicules under mild, nonharsh conditions, readily forms dimers through noncovalent linkages. Subsequently, filaments/aggregates are formatted from monomeric silicatein, suggesting a reassembly through fractal-like structures [28, 38, 39]. Those native protein samples reveal after NaDodSO₄-PAGE (one-dimensional separation) analysis only one band of a size of 27 kDa (Fig. 25.8A-a). If the sample is subjected to two-dimensional gel electrophoresis, the proteins are separated into a series of isoenzymes, due to different phosphorylation states. The number of silicatein spots on the gel is considerably larger if extracts obtained by mild (short) HF dissolution (Fig. 25.8A-b) are analyzed, than with extracts obtained after extensive (>24 h) HF dissolution (Fig. 25.8A-c). This finding reflects the fact that during HF treatment, phosphate groups are split off from the protein.

We ascribe to the axial filament a major role as a form factor for the determination of the morphology of the spicules. From the *S. domuncula* silicatein it is known that the enzyme exists in at least two isoforms, transcribed from two different genes, silicatein- α and silicatein- β [28, 38, 39]. These proteins readily form dimers, tetramers, as well as hexamers. Furthermore, it could be worked out that the two isoforms associate in a defined stoichiometric ratio: four molecules of silicatein- α with one molecule of silicatein- β . It has been suggested that the four silicatein- α molecules form a platform with serine clusters directed to the center. These serines of the coaxially arranged silicateins interact with silicatein- β . In order to attribute a function to the obviously crucial phosphate units linked to the silicatein, it is proposed that the orientation of the 4:1 silicatein assembly undergoes alterations driven by different phosphorylation levels of the enzyme (Fig. 25.8C). The first support came from studies with the different silicatein molecules isolated from the demosponge *Geodia cydonium*. This species comprises two types of spicules, sterrasters (which are microscleres) and anatriaenes (megascleres) (Fig. 25.8D, E). It could be shown that these spicules comprise not only a different set of silicateins but also silicateins with a distinct and different phosphorylation pattern. We propose that cells adjacent to the spicules secrete both silicatein and collagen that forms a well-controlled proteinaceous tube into which the axial cylinder and the lamellar zone are imbedded.

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SILCAa SUBDO MLVTVVILGILGFASAA-----OPKFEVEVEWQIAKSTHSMIEISQIMLELERHL 49
SILCAb SUBDO MSALKFVVALCVVHTSLGIAE SVGKSTAGLSDDGNYTAVTKSVRLTPVLFEEEDKQMTDHRKVIYSDVRERVRYKT 78
CATL SUBDO MKVLIILSIVALVSAAF-----DPEEVAVKOEHSKSEYIELEELRRHT 45
CATL_HUMAN MNPFTLILAAFCILGASA-----ILTFDHSLEAQITFKKAMENELGMAN-EEGWERRA 50
{ ~-signal-~ }
(-propeptide-~)

SILCAa SUBDO TPLSNKKYIEOHNVNSH-IFGETLANNFGDLSELEMANVLYGXRIEDKKSNYSKTFORDPLO----- 112
SILCAb SUBDO VLRANKYEDOHNAQA--RLGYTLKANKFGDLITKEFIEGYHCVDYDQIPFNASHENKHKTHAFVDYGDVFRGGTGE 154
CATL SUBDO LWQSNKREIDSHNSVSD--KEGYTLKANKFGDLISGVEFKQIYNGYLDQERANDTKLFLFASPYME----- 107
CATL_HUMAN VKEKMKYTELHNQEYREGKHSFTLRANNAFGDITSEEFKQVMNGFQNRKPKGVQFPLFYE-----propeptide-~}
~-propeptide-~}

SILCAa SUBDO -----DYPEAVDWRKGA VTA VKDQDCGASAFSAAMGLEGANLAKGNVLSSEONLIDCSIPYGNHCGHGMXY 184
SILCAb SUBDO GYRGVGNPEITMDVRTSGVTKVKDCLRCGSSAFSAAMALEGINALYGSIVLSEONLIDCSVYGNHCGACGVN 232
CATL SUBDO -----PAASVDWRKGVSEVKNKCCGSCGAFSATGELGOMFRKTRGLISLSEONLIDCSGFGNREGCGGLD 178
CATL_HUMAN -----APRSVDWREKGYVTFVKNQCCGSCGAFSATGELGOMFRKTRGLISLSEONLIDCSGFGNREGCGGLD 184
[~-mature chain-~]
[~-rec-silicatein-~]

SILCAa SUBDO DAEFLVLANEGVDQDSAYFVVG-----KQSSQVNSKYKGTSMGMSVSKGSESDTQAANVSNVGPVSVAILDGANSAE 257
SILCAb SUBDO RALLVYIENDGVDITWKGYPSCGDPYRSKQYSCKYERQYRGASARGIVSIAAGDENTLITAVANSQPVSVVVDATSTSE 310
CATL SUBDO DAEFYVLSNHGVDTES SYPYTA-----KDGYSRENQNVGATETSYRDIARGSESLTCAASQIGPISVAIDASHRES 251
CATL_HUMAN YAFQYVQDNGLDSEESYPYEA-----TEESCAYNPKYSVANDTGFVDIPK-CEKALMKAVATVGPISVAIDAGHESF 256
[~-mature chain-~]
[~-rec-silicatein-~]

SILCAa SUBDO REWYSGVDSSRCCSSLSLHNAVVTGYGSLNGK-----KWLAKNSMGTNWNSGYVAVARKNKVCCGLIADASYPT 330
SILCAb SUBDO QEFSDGVLNVFPCSSSTLSHMLVVIIGLYKYSGQ-----DHWLVKNSWGNPNTVYFGIQRANKNKCCGLIADASYPT 383
CATL SUBDO QEFKGVYEPSCSSRLDHCVLAVGYGTGGGQ-----DFFYIVKNSWGTWGDGYIMSRNRKNNCGIASCASYPY 324
CATL_HUMAN IEFYKEGIFPEPCSSEDYDHCVLAVGYGFESTSDNNKWLVLKNSWGEWGGYGVYVAKDRRNHCGLIASASYPT 333
[~-mature chain-~]
[~-rec-silicatein-~]

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Fig. 25.7 Silicatein: sequence. The silicatein protein from the hexactinellid *C. meyeri* was deduced from the isolated cDNA and aligned with silicatein- α from *S. domuncula* (SILCAa_SUBDO) and silicatein- β from *S. domuncula* (SILCAb_SUBDO) and one isoform of silicatein- α from *L. baicalensis* (α -3) (CATL SUBDO) as well as with the cathepsin L sequences from *S. domuncula* (CATL_SUBDO) and human (CATL_HUMAN). Residues conserved (similar or related with respect to their physicochemical properties) in all sequences are shown in white on black, and those in at least four sequences in black on gray. The characteristic sites in the sequences are marked; the catalytic triad (CT) amino acids, Ser in silicateins and Cys in cathepsin, and His and Asn. The borders within the mature silicatein (mature peptide), the signal peptide as well as the propeptide are given. The stretch of the enzymatically active silicatein molecule has been used for the preparation of recombinant, active silicatein. The “conventional” serine cluster (Ser) is marked. Finally the potential phosphorylation sites within the sequences are listed above the alignment

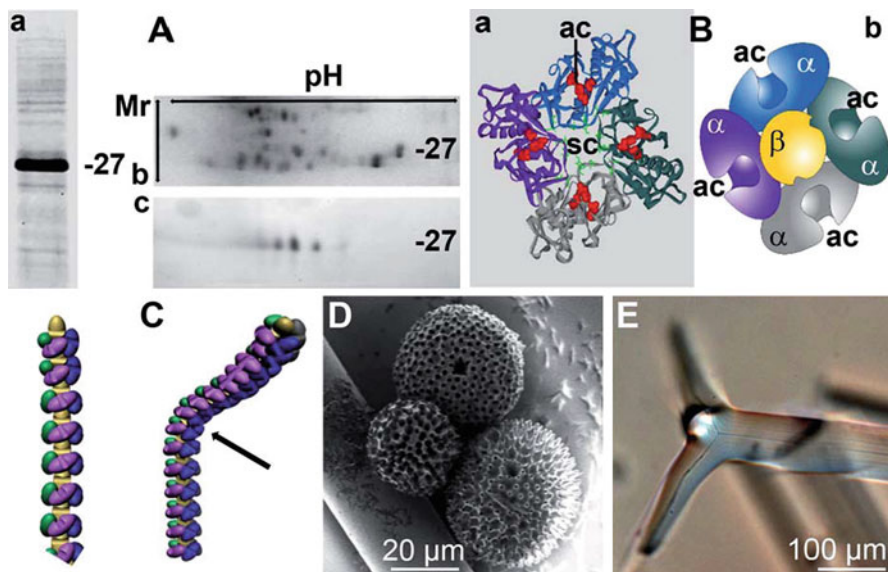


Fig. 25.8 Silicatein protein, space model and backbone for the synthesis of the diverse silica structures, giving rise to the spicules. (**A-a**) Analysis of the total spicule extract by one-dimensional gel electrophoresis. The line marks the position of the 27 kDa protein. The gel was stained with Coomassie brilliant blue. (**A-b** and **A-c**) Analysis of a total spicule extract by two-dimensional gel electrophoresis (first isoelectric focusing and then size separation). Protein extract was collected after mild (short) (**A-b**) or extensive (>24 h) (**A-c**) HF-dissolution. The lines mark the positions of the 27-kDa polypeptides. (**B**) Schematic representation of planar-oriented silicatein- α tetramer (α ; green-gray-blue-pink) with one silicatein- β (β) in the center (yellow). The amino acids involved in the active centers (ac) of the silicateins are marked. In this orientation the Ser-rich clusters (sc) are directed toward the center of tetramer (**B-a**). (**B-b**) Graphical model of the silicatein- α tetramer with the silicatein- β in the center. (**C**) Working model proposing that the orientation of the 4:1 silicatein assembly is changed by an alteration of the level of phosphorylation state of the enzyme molecules (arrow). (**D**) Sterrasters (microscleres) from the demosponge *Geodia cydonium*. (**E**) The tip of a megasclere (anatriaene)

25.5.1 Phases of Silica Deposition During Spicule Formation

The process of spicule formation can be divided into the following phases: the initial intracellular steps and the extracellular final and shaping phase.

The intracellular phase in the sclerocytes: In the first steps silicatein is synthesized as a proenzyme and processed via the 34.7-kDa form (propeptide-mature enzyme) to the 23-kDa mature enzyme [26, 27]. Very likely during the transport through the endoplasmic reticulum and the Golgi complex, silicatein undergoes phosphorylation and is transported into silicasomes where it forms rods, the axial filaments (Fig. 25.6A). After assembly to filaments the first layer(s) of silica is (are) formed. Silica deposition occurs in two directions: first from the axial canal to the surface (centrifugal orientation) and second from the mesohyl to the surface of the

spicule (centripetal). Finally the spicules are released into the extracellular space where they grow in length and diameter by appositional growth.

Extracellular phase (appositional growth): Silicatein is present also in the extracellular space. It came surprising that also there the silicatein molecules are organized to larger entities. The immunogold electron microscopical analysis showed that the silicatein molecules are arranged along strings, which are organized in parallel to the surfaces of the spicules. In the presence of Ca^{2+} , silicatein associates with galectin and allows the appositional growth of the spicules (Fig. 25.9). Since the surface of a new siliceous spicule is also covered with silicatein, the appositional growth/thickening of a spicule hence proceeds from two directions (centrifugal and centripetal). In the next step, the galectin-containing strings are organized by collagen fibers to net-like structures. It is very likely that collagen, which is released by the specialized cells the collencytes, provides the organized platform for the morphogenesis of the spicules. The longitudinal growth of the spicules can be explained by the assumption that at the tips of the spicules, the galectin/silicatein complexes are incorporated into deposited biosilica under formation and elongation of the axial canal [39].

25.5.2 Giant Basal Spicules – Mechanical Properties

Inspired by studies with *Monorhaphis*, a new concept of natural composite material in rigid biological systems was born and fundamentally outlined by Mayer [40]. The organic phase controls energy dissipation especially in systems that are interspersed by very thin organic layers. In continuation of this topic, it had been proposed from their load–displacement studies that breakage of hexactinellid spicules follows a telescope-like pattern [30, 31].

Images from a typical load–displacement experiment with spicules from *Monorhaphis* are given in Fig. 25.10. The pattern of fractures within the spicule was correlated with the organization of the lamellar zone and the axial cylinder, since both areas are characterized by different bioorganic/inorganic hybrid compositions (Fig. 25.10A–D). With increasing load, a sequential breakage of the lamellae occurred. At first the outer, concentrically arranged silica layers burst, followed by the more inwardly located layers. If a sample from an unbroken, nontreated spicule was subjected to the classical bend test, the resulting load–displacement curve showed at first a linear increase reflecting the elastic response of the outer lamellar layers of the spicule. The following deflection does not drop to zero but is fixed according to the viscoelastic view by the more central lamellar layers.

The stepwise breakage of an untreated giant spicule (from the hexactinellid *Hyalonema sieboldi*; diameter of 0.8 mm) is shown in Fig. 25.10E–L. The spicule was inserted into a traction device between two moving rubber wheels, and continuous pulling was achieved by a motor. If the breaking process is recorded with a high-speed camera, the first crack of the outer lamellae is not visible even if the spicule has been completely bent by one circumvolution, leaving a diameter of the circular, wrapped-around spicule of 4.5 cm (Fig. 25.10E). However, after

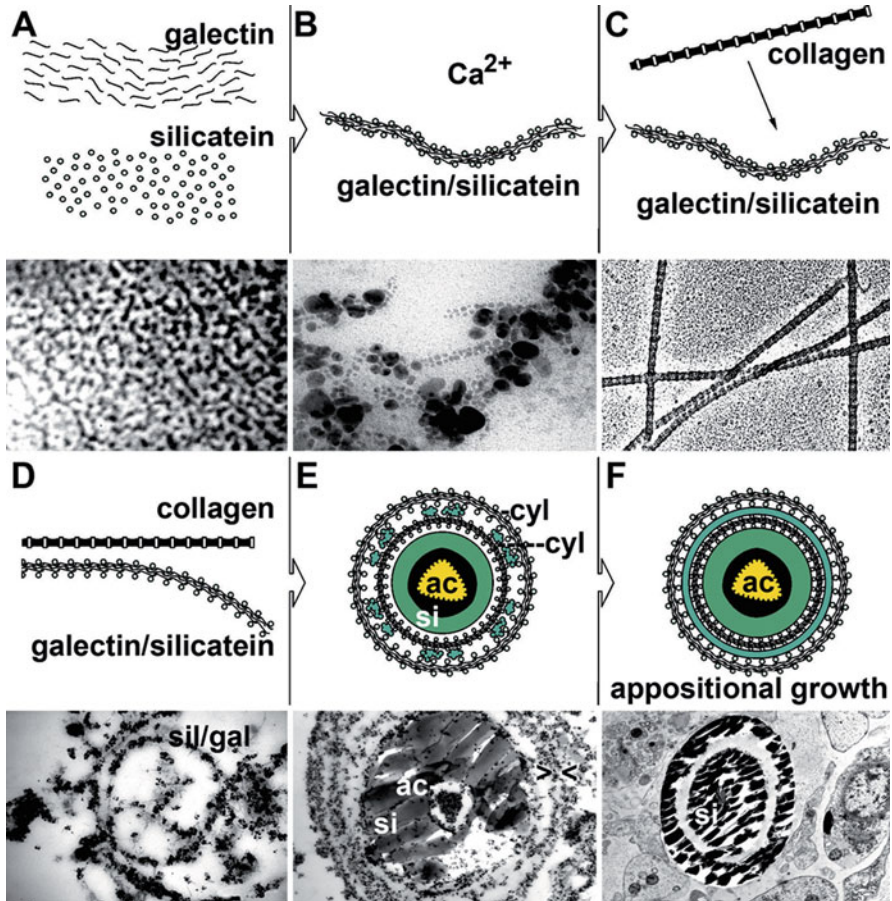


Fig. 25.9 Schematic outline of the appositional spicule formation in sponge (example *S. domuncula*). The process of the appositional growth of the spicules occurs in the extracellular space (mesohyl). (A and B) There, galectin molecules associate in the presence of Ca^{2+} to strings (nets) that allow binding of silicatein molecules. (C) Collagen fibers orient the silicatein-galectin strings concentrically round the growing spicules. (D–F) In the last steps, the silicatein-galectin strings oriented by collagen fibers circle and allow biosilica deposition within the formed cylinder (> <). After completion of one biosilica lamella (si), the next biosilica lamella starts in the same manner by apposition onto the previous lamella (E). The initial biosilica layer is formed around the silicatein rod (axial filament), existing in the axial canal (ac) of the spicules. Below the graphs the corresponding electron microscopic images are given

pulling the circle down to 4 cm, the first set of the outer lamellae blasts off (Fig. 25.10F). Then another period of flexible bending proceeds until the second breakage point is reached (Fig. 25.10H). Again, a further flexible bending phase takes place until a third spalling of the lamellae occurs, followed by a final fracture of the spicule (Fig. 25.10K). In comparison, the breakage of a quartz glass fiber of

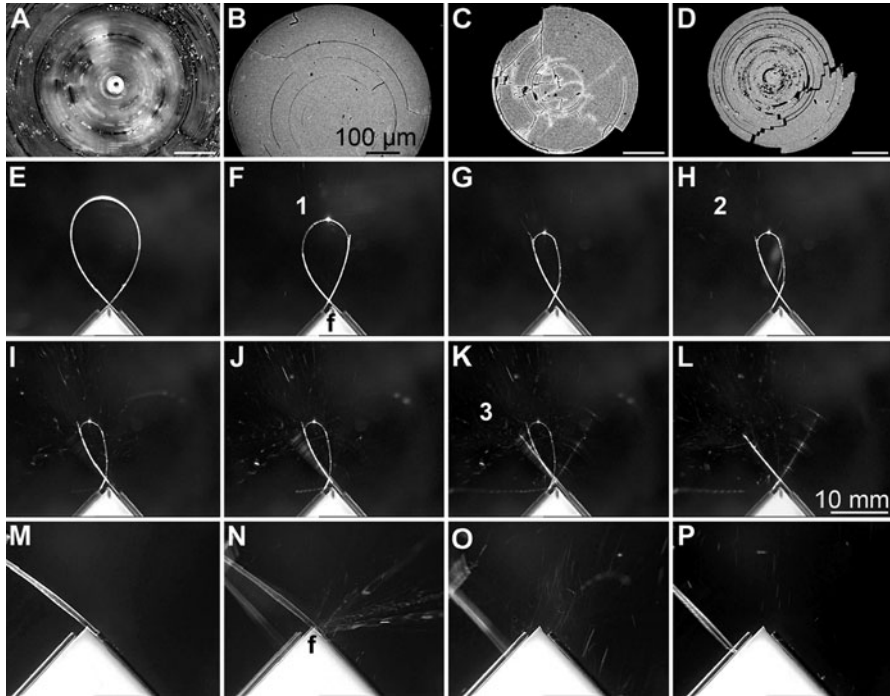


Fig. 25.10 Force displacement relationship of a giant basal spicule, as measured in a 3-point bending assay. (A) SEM analysis of a partially noncracked spicule. (B–D) After increased loading, the silica layers crack starting from the surface of the spicules. (E–L) Flexible breakage of a giant spicule (from *H. sieboldi*), (M–P) in comparison to quartz glass fibers. The diameter of both fibers was about 0.8 mm. The fibers were inserted into a traction device between two moving rubber wheels and were continuously pulled toward the fixation point (F) using a motor. The breakage was recorded with a high-speed camera. The spicule had been completely bent by one circumvolution; the diameter of the circular, wrapped-around spicule was initially 4.5 cm. After proceeding traction, three stepwise breaking steps can be recorded (F, H, and K) which are interrupted by phases of flexible bending. In contrast, an abrupt and total fracture of a quartz glass fiber is recorded. Even before a complete circle could be wound, the fiber blasted

a similar diameter has been recorded (Fig. 25.10M–P). As expected, the glass fiber cannot even be bent to a large circle but cracks almost immediately after an inflection of about 30°.

25.5.3 Giant Basal Spicules – Optophysical Properties

Sponges can react fast to physical stimulation from the environment with contraction or expansion. These observations could imply that the coordinate reactions are governed by a nerve system. However, until now no nerve fibers or synapses could be identified in sponges. Nevertheless, our previous studies showed that the siliceous demosponges *S. domuncula* and *G. cydonium* contain and express genes coding for neuronal molecules, e.g., a metabotropic glutamate/GABA

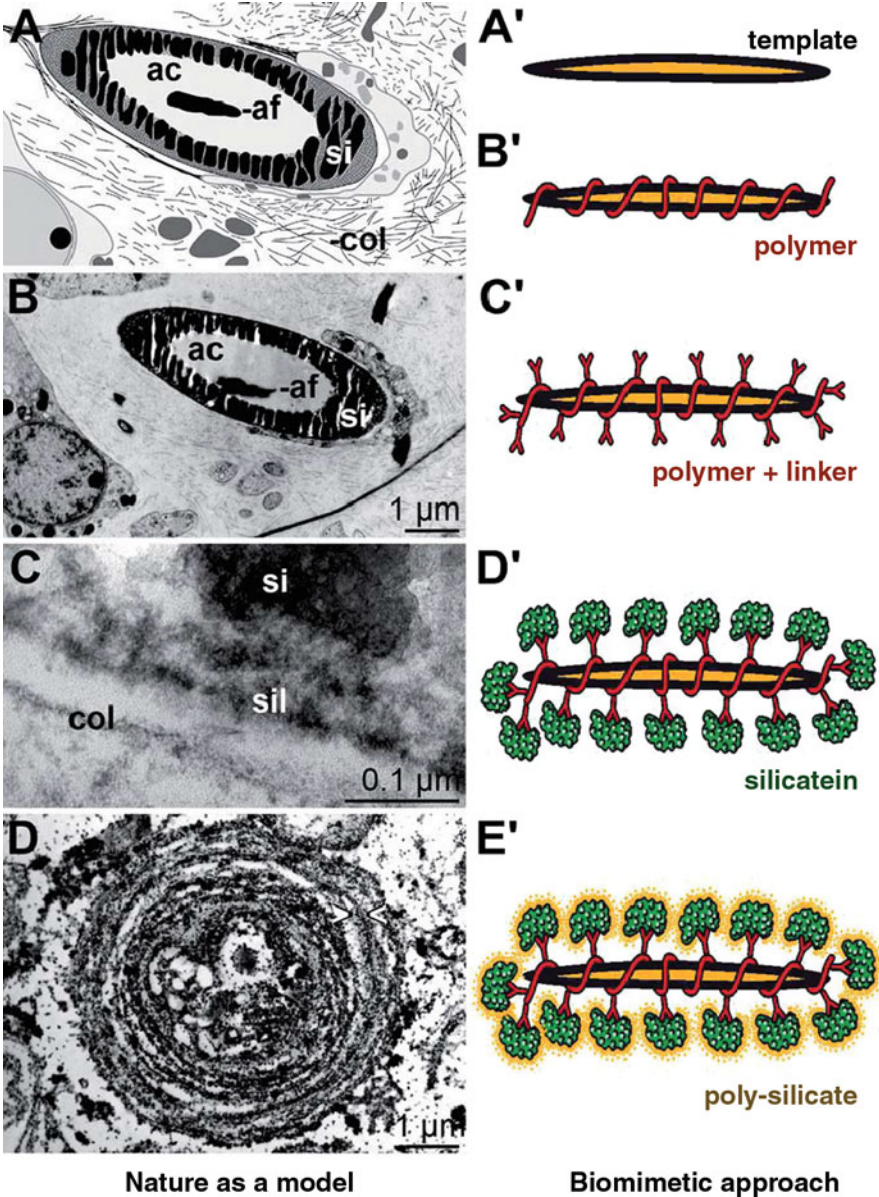


Fig. 25.11 “Nature as a Model” – a biomimetic approach. (Left panel: A–D) Synthesis of spicules in the extracellular space. (A) Scheme; cross section through a growing spicule with the silica mantle (si) which surrounds the axial canal (ac) that harbors the axial filament (af). In the extracellular space collagen (col), fibers are indicated. (B and C) SEM images showing the respective sections; silicatein molecules are marked (sil). (D) Immunogold labeling with antibodies raised against silicatein to visualize the organic cylinders which guide and mediate the synthesis of the silica layers in an appositional manner (marked > <). (Right panel: A’–E’) The

(γ -aminobutyric acid)-like receptor. Furthermore, it is well established that sponge embryos and adult sponges react to light. So far all attempts to identify photosensory cells in sponges failed. Therefore, the question was raised, if noncellular structures, like spicules, might function as biological receiver for light energy. The first prerequisite was already discovered to a great extent by the findings that spicules from sponges can transmit light. In these elegant studies, the hexactinellids *Rossella racovitzae* and *E. aspergillum*, *H. sieboldi*, and *Monorhaphis* (Fig. 25.3G) were used. It could be demonstrated that these large spicules transmit light with high efficiency. The blue light with a wavelength between 400 and 600 nm is filtered out. Based on this finding, it has been suggested that the spicules from hexactinellids act as an optical absorbent in a novel photo-reception. This assumption has been supported by the recent finding that sponges possess the luciferase enzyme [41].

25.6 Biomimetic Approaches

Electron microscopy studies revealed that spicule formation occurs by appositional layering. In the extracellular space, the spicules grow through apposition of lamellar silica layers up to their final size of 450 μm (Demospongiae) or 2.5 m (Hexactinellida). Based on the experimental studies on the extracellular growth of the spicules, the natural principle (“Nature as a Model”) was applied in a biomimetic way. As mentioned, growth of the spicules is guided by an organic cylinder formed from silicatein and galectin that results in the formation of biosilica lamellae (Fig. 25.11; left panel) [15, 16].

This concept from the elucidation of the different phases of spiculogenesis and the molecules involved in it allows a wide application of silicatein in the field of nanobiotechnology. This principle has been utilized by the group of Tremel to synthesize on an “inert” surface (matrix), biosilica from monomeric precursors [42–44]. The matrix used had been activated by cysteamine to allow binding to a reactive polymer; in turn this polymer is able to chemisorb the nitrilotriacetic acid ligand. Finally, this architecture allowed the binding of recombinant histidine-tagged silicatein (Fig. 25.11, right panel). Surprisingly enough, silicatein immobilized onto this matrix has the capacity to catalyze biosilica and even biotitania and biozirconia from the monomeric precursors. This is a further striking example to show that nature can be used as a biological blueprint for nanobiotechnological applications. In addition, this technology introduces a new concept, the synthesis of inorganic polymers by an organic molecule (silicatein). Just in opposite, in 1828, Wöhler succeeded with his epochal experiments on the synthesis of



Fig. 25.11 (continued) biomimetic approach. (A' and B') The template is functionalized with a reactive ester polymer and (C') then with the NTA linker. (D') The recombinant silicatein is bound via the His-tagged to the NTA polymer. (E') The recombinant silicatein mediates polysilica formation and forms a silica lamella like nature does in sponge spicules

urea, an organic compound, from inorganic basic materials (“die künstliche Erzeugung eines organischen, und zwar animalischen, Stoffes aus unorganischen Stoffen”).

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D.J. Newman (✉) • G.M. Cragg
Natural Products Branch, Developmental Therapeutics Program, National Cancer Institute,
NCI-Frederick, Frederick, MD, USA
e-mail: newmand@mail.nih.gov, gmcragg@verizon.net

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Abstract

Perhaps the major perception both in the general medical and scientific communities, and also to some extent in the natural products community, is that marine natural products are of interest but not directly feasible for further development. This perception was fundamentally correct up through roughly the early 1990s, due to major physical difficulties in obtaining enough raw materials from which to isolate the compound of interest. In this chapter, we will show how application of novel techniques in growth and isolation processes, increased knowledge of genomics, and major advances in chemical synthesis have made observers alter their perceptions to the extent that, nowadays, production of marine natural product molecules is a combination of many techniques, each adding their quota of experience. We will use a case study mechanism to demonstrate how these methods evolved and have now enabled marine natural products to be serious contenders as drug candidates.

26.1 Introduction

Marine natural products with significant activities in many pharmacologic areas have been well documented over the years, particularly in the extensive reviews initiated by the late Dr. John Faulkner and now continued by the New Zealand marine group [1]. However, there was a perception, based on reality prior to the middle to late 1990s, that the development of marine-based compounds would require immense efforts from the aspect of recovery and processing of large amounts of biomass in order to obtain even enough material for initial *in vivo* screening. Added to this was that very large amounts would be necessary for further drug development processes, where requirements might well be in the hundreds of grams to multikilogram levels of pure compound produced under current good manufacturing practices (cGMP).

These perceptions were not aided by the fact that most of the agents reported from marine sources were exquisitely potent, often with IC_{50} values in the nanomolar range and present at very low levels in the invertebrate. For example, when reports indicated that 18 g of bryostatin 1 was isolated from over 13 metric tons of *Bugula neritina* or 300 mg of halichondrin B from 1 metric ton of a deep water *Lyssodendoryx* sp., it did not help sell the concept of “drugs from the sea” to pharmaceutical houses. Although these figures were true at the time of publication, nowadays thanks to advances in biology and chemistry over the last 10 plus years the situation has undergone a “sea change,” with combination methods and routes

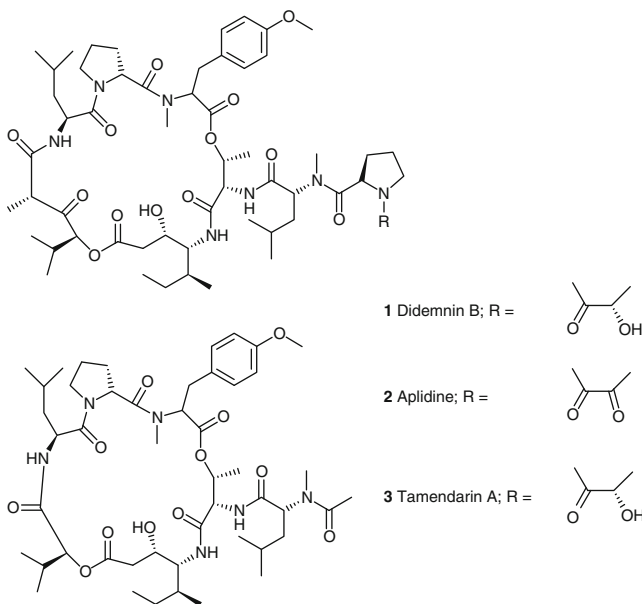
such as microbial biosynthesis, aquaculture (in sea or on land) coupled to potential chemical syntheses, now being considered as part and parcel of the initial discovery/development process.

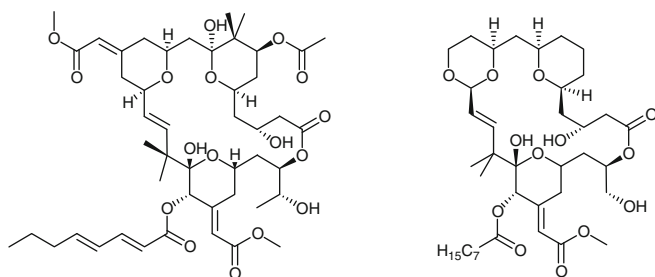
In order to put the recent advances in perspective, we will discuss a series of marine-sourced agents being evaluated in anticancer therapies, mainly due to the initial funding coming from the National Cancer Institute (NCI) or its European equivalents. These case studies in general have been chosen in order to demonstrate how the initial large-scale harvesting methods, necessary in some cases due to the time frame of the initial discovery, have been transformed as knowledge from many sources were applied to the situations as time progressed.

26.2 Case Study 1: Didemnin B and Dehydrodidemnin B (Aplidine)

26.2.1 Didemnin B

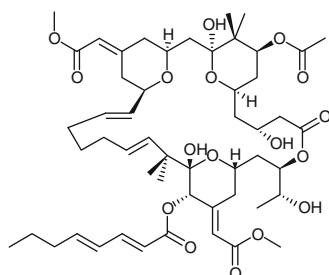
The first compound entered into human clinical trials directly from a marine source was the cyclic depsipeptide, didemnin B (**1**), isolated by the Rinehart group from the encrusting tunicate *Trididemnum solidum* [2, 3]. This was one of a number of very similar compounds isolated from the same organism and included a very close analogue differing by only two hydrogens, dehydrodidemnin B (DDB) now known as aplidine (**2**). This compound subsequently followed DB into human clinical trials [4] approximately 15 years later.



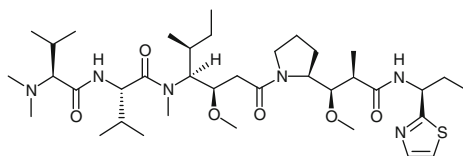


4 Bryostatin 1

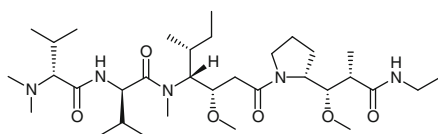
5 Wender's Bryolog



6 Ring Expanded Bryostatin 1



7 Dolastatin 10



8 TZT-1027

Due to the paucity of the producing organism, the level of didemnin B and the multiple derivatives coproduced by the invertebrate, plus the requirement for the production of materials for clinical trials under “current good manufacturing practice (cGMP)” for human trials, synthetic methods were the only viable route at that time for production of compound. In 1987, the Rinehart group published a synthetic method to three of the didemnins, A, B, and C [5] followed the same year with a publication from the Joullie group demonstrating how to synthesize further derivatives of the unusual amino acid “statine” found in the didemnins [6].

In 1991, the Jouin group in France reported on synthesized derivatives that had the linear lipophilic peptide side chain modified. They showed that except for a derivative where palmitic acid was substituted for the lactyl group of didemnin B, the biological activities both in vitro and in vivo were not significantly changed when compared with the natural product [7]. However, the palmityl derivative lost effectively all cytotoxic activity, though no immunosuppressive assays were reported as didemnin B and other congeners exhibited significant immunosuppressive activities [8].

Seven further syntheses by the Schmidt, Shioiri, Joullie, and Jou groups were later discussed in detail in a 2002 review by Vera and Joullie [9]. These, together with the 1996 paper from the Rinehart group referred to above [8], yielded a very significant number of enantiomerically pure analogues together with the required didemnin B. As an example of what can be done, using modern techniques once the materials are available in purity is the report in 2004 by Marco et al., where the probable target for cytotoxicity of the didemnins was shown to be elongation factor eLF1A [10].

Didemnin B was placed into a significant number of clinical trials by the NCI working through a variety of groups but was taken off trials in the middle 1990s due to (cardiac) toxicities [11], with the last published example being the report from a phase II trial in brain carcinomas by Mittelman et al. in 1999 [12]. What is of potential significance, however, were the retrospective comments made by Vera and Joullie (2002) on the methods of delivery used in these early trials – a single bolus dose at close to the maximum tolerated dose (MTD). From later work with aplidine [4], the use of different dosing schedules and a modicum of other supportive medications avoided the significant toxicities seen previously with didemnin B.

26.2.2 Dehydrodidemnin B (Aplidine)

This compound was reported as being isolated from the Mediterranean tunicate *Aplidium album* in a review on the 1990 USA-Japan Seminar on Bioorganic Marine Chemistry by Schmitz and Yasumoto [13], and it was also reported in a US patent in 1994 [14] and in a citation to an application for a UK patent in 1989 in the synthetic paper by Sakai et al. [8] with the initial report of formal activity of dehydrodidemnin B (DDB or aplidine) in animals being the paper in 1996 by Urdiales et al. [15].

Just as in the case of its very close analogue, didemnin B, the amounts required for both initial preclinical studies and then for any future studies precluded the use of wild collections; thus total synthesis was the only viable route to production of this agent, even though there had been reports in some of the very early papers on these agents implying production by a symbiotic interaction between the blue-green alga *Synechocystis trididemni* and the invertebrate [7, 16, 17].

The method used for the production of aplidine was a route based upon the liquid phase peptide synthesis described in 1997 by Jou et al. [18] in which synthetic didemnin A was coupled with the side chain “pyruvate-proline-OH” to give DDB.

Two routes to produce a protected didemnin A were investigated by Jou et al. The first used macrocyclization of a linear seven-membered peptide containing the first extracyclic amino acid of the didemnin side chain. This gave an overall yield of 4% of the protected didemnin A. The other approach, initial formation of the basic didemnin macrocycle followed by coupling of the first extracyclic amino acid, used a six-membered linear peptide that led to the didemnin macrocycle on cyclization. Following addition of the first amino acid of the side chain, the overall yield of the protected didemnin A was 27%. Irrespective of the methods used to derive didemnin A, the subsequent coupling step to yield DDB proceeded with a 62% yield.

These methods will have been further optimized in order to produce materials under cGMP conditions for the clinical development of the agent but as is usual, the information that is given in the chemical and manufacturing controls (CMC) section for an investigational new drug application (INDA) for the FDA, or its equivalent section in any submission to the EMEA in the European Union, is not available for public dissemination nor have any publications with such information been published as far as can be determined to date.

Aplidine (DDB or plitidepsin) is currently in phase I/II clinical trials predominately in blood-based carcinomas, including multiple myeloma where a phase II trial (NCT00229203) has just completed and a phase II trial (NCT00884286) has just commenced studying its activity in non-Hodgkin’s lymphoma, with a new phase III trial (NCT01102426) beginning to recruit patients for a comparison of aplidine plus dexamethasone versus dexamethasone in relapsed/refractory myeloma (ADMYRE trial). In addition, over the years, it has been in trials against a variety of cancers in the EU, Canada, and the USA with a significant number of publications listed through the middle of 2005 [4, 11], and eight more reports from phase I/II shown in a current search of the Scopus database from late 2005 to date.

26.2.3 Lessons from Case Study 1

As a result of the very low yields of material from the natural sources (encrusting didemnin invertebrates), though the possibility of a symbiotic production from a cyanobacterium (blue-green alga) of metabolites was suggested as early as 1979 [16], the only viable method of production was total chemical synthesis. The initial work of the Rinehart group led to the very successful application of liquid-phase methods by the Jou group, leading to the current clinical trials of DDB.

The lessons learned from these compounds were aptly demonstrated by two other investigators involved in the didemnin story, and led to a report in 2007 of variations in the synthetic approaches to the didemnin analogues, the tamandarins (**3**) [19]. These synthetic variations compared to those originally reported [20, 21]

led to significantly increased synthetic yields and production of analogues with *in vitro* antitumor activity, thus, extending the structure activity relationships in this very active series.

26.3 Case Study 2: Bryostatin 1 and Derivatives

26.3.1 Bryostatin 1 from Natural Sources (Wild Collections and Aquaculture)

After didemnin B, the next “direct from the sea” compound to go into clinical trials was bryostatin 1 (**4**); currently it has been in over 80 clinical trials, with six phase I/II trials in cancer still being listed in the NIH clinical trials database, of which five are still active but not recruiting further patients, and the remaining one is a phase I trial involving bryostatin 1 in concert with temsirolimus. In addition, a phase II trial in Alzheimer’s is listed but not yet recruiting patients.

That this compound ever made it from a biological discovery to human clinical trials can be ascribed to the determination of G. Robert (Bob) Pettit, who first reported this class of compounds in 1970 [22]. The subsequent work, leading to the identification of 19 variations on the same basic structure, mainly as a result of Pettit’s group at Arizona State University (ASU) and collaborators in multiple other institutions has been reported in a large number of papers and reviews [23, 24]. The latest “variation” on the basic structure from a natural source was the new bryostatin derivative (bryostatin 20) reported from an Atlantic *Bugula neritina* by Lopanik et al. in 2004 [25], and on comparison with the known 19 earlier molecules, its structure is effectively the ring-closed version of bryostatin 10.

As a result of the initial preclinical and clinical (phase I) responses to bryostatin 1 [26, 27], it was necessary to produce gram quantities of the compound for initial trials. No synthetic method was available so the NCI contracted a small California company, Marinus Inc., in Long Beach to collect close to 13 metric tonnes of wet *Bugula neritina* from depths between 3 and 30 m off the coast of Southern California. Since this particular animal is a large-scale fouling organism and is ubiquitous in the waters off California, no significant effect on the environment was anticipated.

Following shipment of the 40,000 L of wet organism in isopropanol to NCI-Frederick, the US Government contractor who ran the NCI-Frederick Cancer Research Center, then Program Resources Incorporated together with scientists from NCI and Bristol Myers Squibb (who had licensed the bryostatin patent from ASU), produced 18 g of cGMP quality bryostatin 1 in 10 months of work [28]. A later small-scale rework of the process using supercritical fluid extraction rather than conventional liquid–liquid extraction, followed by large-scale chromatography reduced the processing time from 10 months to under a month assuming scaling would be relatively linear [29].

From the raw material supply problems that arose in the case of Taxol[®] [30, 31], NCI decided in the early 1990s to “plan for success” when natural product-sourced

compounds entered preclinical/clinical trials. Therefore, as a result of the volumes of wild-collected material that would be involved if bryostatin 1 was successful as an antitumor drug, a very large amount of raw material would be required in order to produce enough of the compound for clinical use, NCI funded a competitive SBIR phase I and a subsequent phase II contract with the small California biotechnology company, CalBioMarine.

The aim of this initial contract (phase I), and its subsequent extension (phase II), was to grow *Bugula neritina* using both in-sea and on-land aquaculture in order to avoid the problems of seasonal variation in both levels of this bryozoan and, as learned later, in the levels of bryostatin in the animal. The goals of the contract were successfully met, demonstrating that the organism could be produced by either in-tank aquaculture or via seeded screens suspended in the Pacific Ocean off La Jolla, California. The levels of bryostatin were high enough to obtain a useful supply of the compound, though significant optimization of feeding protocols and recovery methods would have been necessary. The work involved was subsequently described by one of the CalBioMarine principals, Dominick Mendola [32].

26.3.2 Bryostatins by Chemical Synthesis

From the initial reports on the structures of the bryostatins, chemists recognized the base molecule as a challenge for their synthetic skills. A significant number of syntheses of parts of the bryostatin 1 molecule and total syntheses of various members of the complex were reported, with the first being the enantiomeric synthesis of bryostatin 7 in 1990 by Masamune's group [33], followed by papers from the Evans' group giving details of an enantiomeric synthesis of bryostatin 2 in the 1998–1999 time frame [34, 35]. The third in the initial series was the synthesis of bryostatin 3 by Nishiyama and Yamamura in 2000 [36]. These earlier syntheses together with partial syntheses of other bryostatins were reviewed in detail through 2002 by Hale et al. [37]. Following a break of 8 years, in 2008, Trost and Dong published [38] their relatively simple and quite elegant synthesis of bryostatin 16 involving some novel metal-linked catalysis steps [39], including a ruthenium tandem alkyne-enone coupling and then a palladium catalyzed alkyne-ynoate macrocyclization to give the cyclized precursor of bryostatin 16.

In spite of all of these elegant methods, to date, no de novo synthesis of bryostatin 1 has been published, though in the early days of studying the bryostatins, Pettit et al. demonstrated that bryostatin 2 could be converted to bryostatin 1 and bryostatin 12 [40]. Thus, one could argue that a formal synthesis of bryostatin 1 has been achieved by using the Evans et al. bryostatin 2 asymmetric synthesis [34, 35] and then applying the Pettit conversion method. Very recently, an excellent review of the synthetic chemistry surrounding the bryostatins was published by Hale and Manaviazar [41], which should be consulted by those interested in the specific methodological differences between the various syntheses.

26.3.3 Bryostatin Analogues/Mimics by Chemical Synthesis

From the early days of the bryostatins, Wender's group postulated that if one could synthesize a simpler analogue with comparable activity, then chemical production of such an agent might well be a viable option. Over the years, Wender and his colleagues have successfully synthesized a significant number of what they have named "bryologs"; nominally simpler molecules that have pharmacologic characteristics similar to bryostatin 1. These were originally designed by modeling bryostatin 1 on to the binding site of the phorbol esters on protein kinase C and over the years, a significant number have been published with the latest variations being those reported in 2008 [42, 43], with a representative molecule being shown in (5). Other synthetic groups have also produced synthetic modifications that are different from the Wender bryologs, but still have significant biological activities. One example is the ring-expanded molecule (6) where five extra carbon atoms have been inserted between the C₁₆ and C₁₇ carbon atoms of bryostatin 1 [44] while maintaining bryostatin-like activity. However, other more subtle modifications where only four changes were made on the periphery of the bryostatin 1 molecule, converted the bryostatin 1 structure to a molecule that had biological activities that mimicked those of the phorbol ester tumor promoters rather than those of the parent molecule [45]. Thus, one has to be very careful in assessing the actual activities of what appear to be small modifications to the base molecule.

26.3.4 Putative Microbial Source(s) of Bryostatins

One of the discoveries made from the collections made by Calbiomarine of wild *Bugula neritina* when they were collaborating with the Haygood group at the Scripps Institution of Oceanography was that there appeared to be two potential subspecies, one from deep (below ~10 m) and one from shallow (above ~7 m). However, the bacterial symbionts of the invertebrate were investigated [46], and suggested that the actual producer of the bryostatins was a previously unrecognized and, as yet, noncultured bacterium.

Over the next 10 plus years, in conjunction with experts in gene identification and cloning, Haygood and her collaborators have been able to identify and clone, but not yet express in a heterologous host, the putative biosynthetic cluster that should produce what they are calling bryostatin 0, that would then be further elaborated by as yet unidentified tailoring enzymes. Thus, Haygood and her collaborators investigated the potential sources of bryostatins in both the adult animal and in the larvae. In a series of excellent investigations, they demonstrated that within the larvae of bryostatin-producing animals there were as yet uncultured bacteria (given the name of *Candidatus Endobugula sertula*) in the first report by Davidson and Haygood in 1999 [47] and extended in 2001 [48].

A series of later papers included a review of the possibilities of identification and expression of genes from symbionts [49], the identification of different symbionts from other *Bugula* species that produced bryostatins and contained similar gene constructs [50], together with the identification of a putative *bryA* cluster [51]. Further work by Lopanik et al. on Atlantic-sourced, rather than Pacific or Gulf Coast-sourced *Bugula neritina*, has confirmed the presence of *bryA*-like fragments from this geographic area's organisms as well [52].

It should be emphasized that in none of the cases described does the identification of the *bryA* cluster in these organisms prove the absolute production of bryostatins by the symbiont, but the evidence is highly suggestive. Currently the complete putative genomic sequence has been identified and sequenced but not yet expressed [53] including the recognition of an unusual transacylase [54]. Finally, in addition to the genomic work related to the biosynthesis in a variety of *Bugula* species and locations, work from an ecological perspective has also been reported by Haygood and collaborators, demonstrating that bryostatins are important molecules from an ecological as well as a pharmacological perspective [54, 55].

26.3.5 Lessons from Case Study 2

Just as in the case of didemnin B, bryostatin 1 was present in vanishingly small amounts in what was thought to be the producing organism, the encrusting and fouling bryozoan, *Bugula neritina*. Unlike didemnin B, due to the massive amounts of organism available off the California coast, it proved ecologically feasible to isolate 18 g of cGMP quality material from 13 metric tonnes of wet organism, and methods were also developed on a small scale for a much faster isolation process using supercritical fluid extraction.

Due to the obvious problems of very low levels and massive collection programs if bryostatin became a potential drug, NCI, who had learned their lesson from the problems of sourcing enough *Taxus* bark for clinical trials of Taxol[®], commissioned aquacultural methods and directly and indirectly through the NIH grants programs, aided in funding synthetic approaches to both bryostatins and their "simpler" modifications, the "bryologs."

Basic ecological studies coupled to the massive advances in the study of biosynthetic gene processes led to the recognition that an as yet uncultured symbiotic microbe may be a potential source of bryostatin precursors; these may be modified by either chemistry or genomic methods to produce the desired chemical skeletons for further development.

Finally, although bryostatin is not a particularly viable antitumor agent at the present time, it may well have utility in Alzheimer's disease as shown in the work by researchers at the University of West Virginia [56–58] and the approval from the FDA for a phase II clinical trial of bryostatin 1 in patients with Alzheimer's under the ClinicalTrials.gov identifier number NCT00606164.

26.4 Case Study 3: Dolastatin 10 and Derivatives

26.4.1 Dolastatin 10, Original Source and Syntheses

In the same time frame as the bryostatins, the Pettit group also reported on the dolastatins, a series of cytotoxic linear and cyclic peptides that were originally isolated in very low yield from the Indian Ocean gastropod mollusk *Dolabella auricularia*. The history and work-up of the dolastatins, in particular the tubulin interactive linear peptide dolastatin 10 (**7**) through early 2005, were reported in detail by Flahive and Srirangam in a 2005 book chapter [59].

Similarly to the case of didemnin B, the original discoverers realized from the beginning that only total chemical synthesis would yield the necessary amounts of material to even pursue advanced preclinical and hopefully clinical studies. Thus, the Pettit group devised synthetic methods for the large-scale enantiomeric syntheses of the unusual γ -amino- β -methoxy-acid residues dolaproline and dolaisoleucine, each of which contained three chiral centers, and the novel C-terminal residue, dolaphenine, which contains a thiazole and is derived from phenylalanine. Their approach was described in a paper in 1989 [60] and fuller details of this and other syntheses were reported in an excellent review by Pettit in 1997 [61].

Due to the potency, at the time it was the most potent agent tested by the NCI, and mechanism of action as a tubulin-interactive agent binding close to the *Vinca* domain [62–64], dolastatin 10 entered phase I clinical trials in the 1990s under the auspices of the NCI. It progressed through to phase II trials as a single agent, but although tolerated at the doses used, which were high enough to give the expected levels in vivo to inhibit cell growth, it did not demonstrate significant antitumor activity in a phase II trial against prostate cancer [65], nor in metastatic melanoma [66].

26.4.2 Auristatin PE/TZT-1027; Dolastatin 10 Derivatives

Although the natural products did not succeed in demonstrating activity in humans, the syntheses described by Pettit and others led the way to a series of other molecules based upon the natural product but with modifications to the base linear peptide. Numbers of these have been discussed in the literature including a compound simultaneously synthesized by both the Pettit group under the name of auristatin PE [67] and a group from the Japanese company Teikoku Hormone (**8**) under the name TZT-1027 [68]. This compound under the names, TZT-1027, auristatin PE, and soblidotin, depending on the particular organization sponsoring the compound, went into phase I/II trials with mixed results and is not currently listed as being in active trials in the NIH clinical trials site.

However, demonstrating how compounds that exhibit interesting activities can be further optimized by clever chemistry and biology, the compound with a small linker was used as a warhead by Seattle Genetics. Two variations differing in the

antibody and the specific linker are currently in phase II (glembatumumab vedotin) and phase III (brentuximab vedotin) with another (anti-CD19-vcMMAE) in preclinical trials. Using the auristatin PE derivative, auristatin F (where the C-terminal amino acid is now phenylalanine), a third monoclonal antibody-warhead combination (1 F6-MMAF) is currently in phase I clinical trials and unlike the other two, it does not have a cleavable linker. Up-to-date discussions of the rationale behind the use of such methods with both cleavable and noncleavable linkers are presented by Senter's group from Seattle Genetics [69, 70] and by Teicher from Genzyme [71].

In addition to the linked molecules referred to above, auristatin PE itself was shown to be a vascular disruption agent with three relatively recent papers discussing the possibilities of such agents as antitumor treatments as they cause the internal vasculature of the tumor to collapse [72–74]

26.4.3 Actual Source(s) of the Dolastatins

Similarly to the situation with the bryostatins and the didemnins, there was always a potential question with the dolastatins as to whether or not they were microbial in origin, as peptides with unusual amino acids have been well documented in the literature as coming from the Cyanobacteria. In the last few years, this supposition has been shown to be a fact. Thus, in 1998, workers at the Universities of Guam and Hawaii reported the isolation and purification of simplostatins 1 [75] from the marine cyanobacterium *Simploca hynoides*. This molecule differed from dolastatin 10 by the addition of a methyl group on the first *N*, *N*-dimethylated amino acid. Subsequently, in 2001, the same groups reported the direct isolation of dolastatin 10 from another marine cyanobacterium that was known to be grazed on by *D. auricularia* [76]. Dolastatin 10 was in fact isolated from the opisthobranch following feeding of the cyanobacterium, thus confirming the original hypothesis (Paul 2006, #145).

26.4.4 Lessons from Case Study 3

As with didemnin B, recognition that collections of the raw material source was not a feasible method led to the derivation by Pettit's group of synthetic methods on a large scale (for an academic institution) for the intermediates. These individual syntheses then allowed the synthesis of dolastatin 10 with its multiple chiral centers and three very unusual amino acids in its short peptide structure. From these initial studies came the capability to produce novel molecules such as auristatin PE. Modifications around that structure combined with clever utilization of monoclonal antibody technologies have led to currently active agents in phases I to III clinical trials.

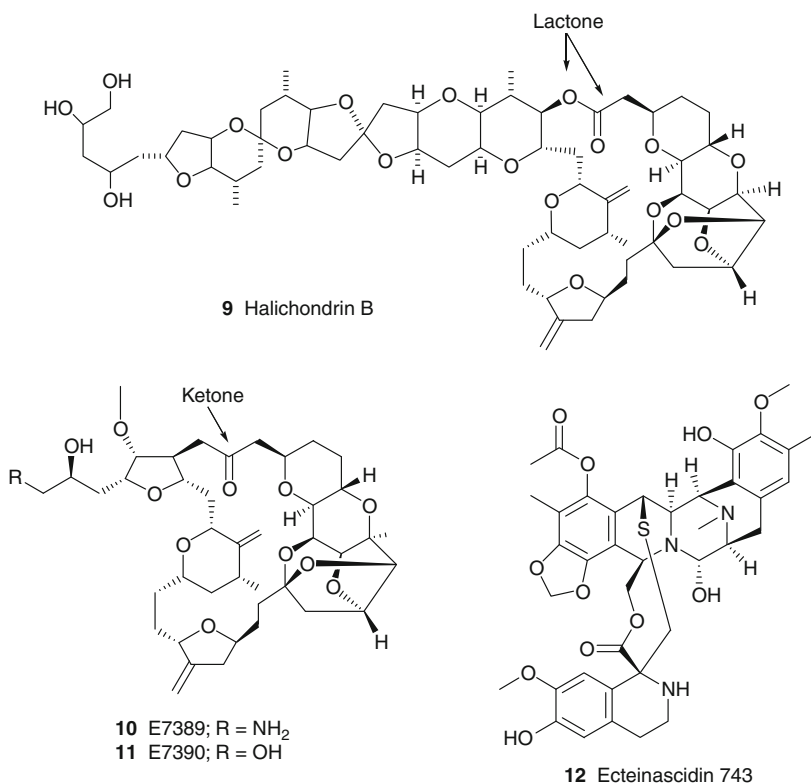
The work in the late 1990s by the Hawaii and Guam groups demonstrating that, as suspected for many years, the agents were linked to cyanobacterial diets of the opisthobranchs, leads to the possibility that in due course the biosynthetic gene

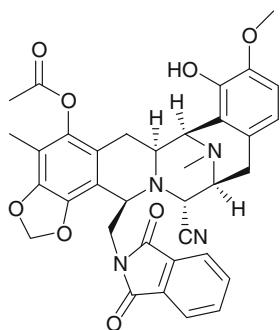
clusters may be identified. If this can be done, then there is the possibility that the metabolites might be expressed in a heterologous host. Examples of this technique were reported simultaneously by two groups with *Prochloron* peptide metabolites using the heterologous host *E. coli*. One used shotgun cloning of the gene clusters [77] and the other identification of the cluster(s) followed by cloning and subsequent expression [78].

26.5 Case Study 4: Halichondrin B and Eribulin

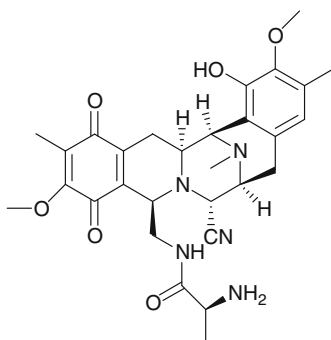
26.5.1 Halichondrin B from Natural Sources (Wild Collections and Aquaculture)

Halichondrin B (**9**) was first reported from the Japanese sponge *Halichondria oakdai* by Uemura's group in 1985 [79] and 1986 [80], and, subsequently, halichondrin B or congeners were reported over the next few years from a variety of other sponge sources. These initial reports were then followed by two papers that made this series of agents very interesting for development as antitumor agents.

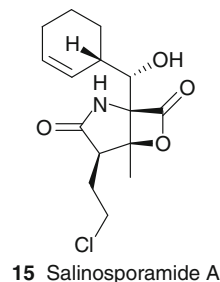




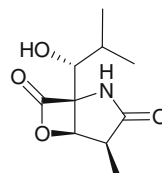
13 Phthalascidin



14 Cyanosafraclin B



15 Salinosporamide A



16 Omuralide

The first, in 1991, showed that halichondrin B acted as a tubulin interactive agent (TIA) potentially binding close to the *Vinca* site [81]. The other, in 1992 from Kishi's group at Harvard (funded by NCI), presented a synthetic route to halichondrin B [82]. As a result of the first of these reports and other work at NCI, the NCI's Decision Network Committee decided in early 1992 to recommend further preclinical development of halichondrin B.

Although recommended for development, there was no natural source of the material reported to that time that had the potential to provide enough material for even initial preclinical studies. Thus, the NCI's Natural Products Branch (NPB) put out a general request to the natural products worldwide community asking for potential sources. The New Zealand groups at the University of Canterbury (Munro and Blunt) and the New Zealand Government's National Institute of Water and Atmospheric Research (Battershill) responded with information that had not been published on the presence of halichondrins in a deepwater sponge identified as a species of *Lissodendoryx* that had been collected by dredging off the Kaikoura peninsula at a depth of ~100 m.

The NCI first funded an environmental assessment of the extent of the sponge field and using this data, were able to obtain a permit from the New Zealand government that permitted up to 1 tonnes of sponge to be dredged, extracted, and processed in a joint operation between the New Zealand collaborators and the NCI. Direct funding was provided by the NCI with (predominately) payment in kind by the New Zealand operations. The raw materials were harvested over the next 4 years and processed in New Zealand to yield 300 mg of 98% pure halichondrin B.

Contemporaneously, NCI financed a series of significant in-sea aquaculture experiments in New Zealand waters that demonstrated for the first time that

a deepwater sponge could be cultured in shallow water and still produce a significant amount of the desired secondary metabolite. The initial reports were given in abstract format, covering the experiments in mussel farms in South Island, New Zealand at depths up to 30 m and also in waters as shallow as 10 m in Wellington harbor. These results were then used as the basis for a larger series of experiments, and the results were published as a case study by the New Zealand scientists who were directly involved [83].

By the end of 1997, NCI had samples from a very significant supply of pure halichondrin B and used it to compare activities of the pure halichondrin B versus materials that had only been isolated in very small amounts (3–5 mg) from other sources. These were reported in abstract format at the American Association for Cancer Research (AACR). Thus, the stage was set to use the sponge-derived materials to perform early preclinical studies and optimistically, to be able to produce material via in-sea aquaculture in order to provide material for later development [83].

26.5.2 Synthetic Production of Halichondrin B and Derivatives

In 1992, at the same time as the decision by NCI to develop halichondrin B, Kishi's group at Harvard reported the total synthesis of halichondrin B [82], a study funded via an NCI grant. Because of the relationship between the Eisai Research Institute (ERI) in the USA and Professor Kishi, this organization investigated the potential of the Kishi synthesis, having licensed the essential patent from Harvard [84].

Kishi's group had shown, in patent form, that the required portion of the molecule for maintenance of bioactivity was the macrolide ring, whereas other groups had been modifying the "tail" part of the molecule. The Eisai chemical group realized that they could convert the macrolide ring into a ketone by changing the oxygen to a methylene group while still maintaining the basic activity. In addition, truncation of the "tail" and changes to the oxygen heterocycle next to the macrocyclic ring led to two very similar compounds E7389 and E7390.

Fortuitously, the head of ERI's oncology group happened to see the work that NCI's Developmental Therapeutics Program (DTP) scientists reported in abstract form on the *in vitro* activity of pure halichondrin B at the 1998 AACR meeting. This led to a collaborative project between ERI/Kishi and DTP, comparing the NCI's pure halichondrin B with two truncated, fully synthetic molecules that they had made, E7389 (**10**) and E7390 (**11**). This preliminary work demonstrated that E7389 was more active *in vivo* and with a better therapeutic index than either halichondrin B or its chemical precursor, E7390. ERI then provided sufficient E7389 synthesized under cGMP conditions that permitted NCI to perform preclinical studies including INDA-directed toxicology and led to approval in 2001 by the then NCI Decision Network Committee for human clinical trials.

The compound was approved by the NCI for clinical development in 2001, entered clinical trials soon thereafter and as of January 2010, was in phase III clinical trials against refractory breast carcinoma under the Eisai Metastatic Breast

Cancer Study Assessing Physician's Choice versus E-7389 (the EMBRACE studies, ClinicalTrials.gov Identifier NCT00388726). In addition to the global studies under the EMBRACE consortium, eribulin is in other trials at the phase II level in different carcinomas. Applications were made to both Switzerland and Singapore for marketing approval in 2009 on the preliminary results from the global studies and were followed in early 2010 by simultaneous submissions to the US FDA, the EU's EMEA, and the Japanese Ministry of Health, Labor and Welfare (MHLW) for approval for the treatment of inoperable or recurrent breast cancer. As of mid 2010, the FDA and the MHLW have given priority review status to these submissions.

A short paper presenting the basic chemistry was published by the ERI group in 2004 [85], whereas a thorough discussion of the details of the synthetic and base biological information was published by the leaders of the studies at ERI in 2005 [86]. In 2007, a short article covering the basic details but with later clinical citations was published by Wang [87], and recently Kishi's group have published novel and simpler routes to the macrocyclic ring of halichondrin and eribulin [88, 89].

The molecule, like its parent, is a tubulin-interactive agent with very potent activity at the nanomolar level in *in vitro* studies [90] and binding at or close to the *Vinca* site from modeling studies [91]. In a recent paper from Jordan's group, the mechanism of action is defined as: "The strong correlation between suppression of kinetochore-microtubule dynamics and mitotic arrest indicates that the primary mechanism by which eribulin blocks mitosis is suppression of spindle microtubule dynamics" [92].

26.5.3 Lessons from Case Study 4

This is an example of where the base molecule was the initial active agent, and a source had to be identified with the political agreements necessary for collections of the deepwater sponge negotiated at government to government levels. Once permission had been obtained, then large-scale collection and extraction processes had to be developed. At the same time, methods of large-scale production had to be considered, even before the first large-scale deepwater collection had been made, because if the compound was successful, multiple grams of material would be required. Thus, aquaculture methods ran in concert with the large-scale recovery and purification.

NCI had funded, via a competitive grant mechanism quite distinct from the NPB-directed work, a total synthesis of the base halichondrin B molecule which was reported at the same time as the initial decision to go forward with the compound in preclinical studies at NCI. The synthesis was not judged by DTP to be feasible under their restricted chemical synthetic capabilities as a substitute for the natural product. What was not known by DTP/NCI at the time was the relationship between Professor Kishi and the ERI. ERI licensed the Harvard patents that demonstrated the viability of the truncated halichondrins (realized from biological assays of the intermediates in the synthesis at ERI).

Once DTP reported their *in vitro* work with the pure halichondrin B at the 1998 AACR meeting, discussions were held between the ERI scientists, Prof. Kishi, and

DTP in the late summer of 1998, at which time the two compounds ultimately known as E7389 and E7390 were tested by DTP biologists against a series of cell lines *in vitro* and *in vivo*. The compounds tested were the last samples that ERI had as their synthetic tour de force (over 200 variations had been synthesized at ERI) was winding down. When the DTP data was reported to ERI, they began a synthesis of the most active compound with the highest therapeutic index and produced enough cGMP grade E7389 by total synthesis for NCI to proceed with the necessary pre-IND directed studies in toxicology, culminating in the entry into phase I clinical trials in early 2002, 10 years after the Decision Network Committee had approved further development of the natural product.

Thus, this particular example demonstrates how modern synthetic chemistry can build extremely complex molecules that have clinical potential, based upon the natural product structure, and in quantities sufficient for clinical use. However, it must not be forgotten that eribulin or its congeners would not have entered clinical trials in the absence of the massive effort across the globe to obtain enough of the natural product to use as both a standard and as a comparator. Another beneficial spin-off was the knowledge gained in how to aquaculture deepwater sponges in shallow water and maintain metabolite production.

26.6 Case Study 5: Ecteinascidin 743 (Yondelis®)

26.6.1 Ecteinascidin 743 from Natural Sources (Wild Collections and Aquaculture)

The antitumor activity of extracts of *Ecteinascidia turbinata* was first reported in 1969 [93], and the isolation and structure of ET743 was independently reported by the groups of Wright [94] and Rinehart [95] in back to back papers in 1990. Evaluation of the structures showed that they contained the essential aspects of the saframycins, known terrestrial microbial tetrahydroisoquinoline antitumor antibiotics, and that there were other marine natural products of a similar basic structure in the literature. For further information on this general class of molecules, the 2002 review by Scott and Williams should be consulted [96].

ET743 (**12**) was licensed in the very early 1990s to PharmaMar for development, and over the next 10 or so years, a whole variety of methods were utilized in order to obtain enough biomass to isolate the compound of interest. These included wild collections in the Caribbean where three production periods were usually seen [97], and the Mediterranean sea where temporal variation due to temperature meant that only in the summer could the Mediterranean stocks be sampled [98, 99], as well as in-sea and lake-based aquaculture [100]. Using multiple sites in addition to major operations in the Spanish Balearic island Formentera and surrounding areas, PharmaMar in the years between 1998 and 2004 produced approximately 100 tonnes of biomass, from which enough material was purified to carry preclinical and clinical trials to phase II [101]. The overall approximate yield to purification was $\leq 1.0 \mu\text{g}\cdot\text{g}^{-1}$, or 100 g from 100 metric tonnes.

26.6.2 Ecteinascidin 743 from Chemical Synthesis

In order to provide enough material for advanced clinical trials and then commercial production, it became apparent that none of the then-current methods would suffice. Although Corey et al. had reported an enantioselective synthesis inspired by the proposed biosynthesis [102] of the natural product in 1996 [103], it was not amenable to large-scale production. Martinez and Corey then published a revised synthetic method that was designed to increase yields significantly, but it was still not adequate for industrial-scale production [104]. However, it did demonstrate a method of production of a simpler analogue named phthalascidin (**13**) that had similar activity to ET-743 [105].

Since these methods were not satisfactory for multigram production under cGMP conditions, the PharmaMar group published [106] a semisynthetic method starting with a microbial product, cyanosafracin B (**14**), produced by large-scale fermentation of *Pseudomonas fluorescens* [107, 108]. The capabilities of this particular method were demonstrated by the preparation of a large number of natural ecteinascidins [109], together with a process that also permitted production of “unnatural” analogues [101]. A more detailed discussion of the developments through early 2005 was reported by Henriquez et al. in 2005 [4] and extended recently by Cuevas and Francesch in an excellent review in 2009 [101].

Et743 was approved by the EMEA in September 2007 for treatment of sarcoma and was launched in Sweden, Germany, and the UK by the end of 2007, thus becoming the first marine natural product used as an antitumor drug. Currently, mid-2010, there are 25 clinical trials listed in the NIH clinical trials database, with three recruiting at the phase III level, and recently it was approved in the EU for ovarian carcinoma treatment in conjunction with liposomal doxorubicin.

26.6.3 Lessons from Case Study 5

Just as in the case of bryostatin, enough material was obtained from a combination of wild collections and very extensive aquaculture in a number of in-sea and on-land operations to produce enough material for preclinical and clinical trials up through some early phase II trials. Although academic groups had produced enantiomeric syntheses of both the natural product and an active derivative that was similar in concept to the bryologs, it was realized that these were not amenable to the large-scale production necessary for further clinical trials and hoped for commercialization.

PharmaMar then decided to use a semisynthetic method based upon modification of a known microbial metabolite, cyanosafracin B, which could be obtained by fermentation on a very large scale, and thus a low overall yield could be tolerated [110]. This method was optimized and modified permitting the synthesis of unnatural derivatives by a relatively simple modification of one of the synthetic steps [101]. Thus, the methods developed were designed to increase the number of potential derivatives to “expand the franchise” where or when necessary.

26.7 Case Study 6: Salinosporamide A

In this particular case, the paradigm is quite different, in that rather than wild collections, syntheses and other methods of large-scale production, including identification of the actual rather than the potential producer, the producing organism was known at the beginning of the work as a prokaryote, in this case a marine-sourced actinomycete. Though we will use the same format in the previous five case studies, this one will be a simpler story as it has taken only 3–4 years from recognition of the molecule and its potential mechanism of action (MOA) to a first use in human phase I clinical trial.

26.7.1 Discovery of Salinosporamide A

In the late 1980s, Fenical and Jensen at Scripps Institution of Oceanography began their systematic investigation of the microbial diversity of marine habitats and its potential relationship to marine natural products. In late 1989, the SIO group investigated the distribution of actinomycetes in near-shore sediments in the Bahamas and discovered a number of organisms that required seawater for growth, and that the majority of such organisms were possibly new genera within the family *Micromonosporaceae* [111]. Although some cursory inspection of the secondary metabolites was performed at that time, no further work was done with these samples until in 1999, a reassessment of their phylogeny at the molecular level suggested that these were a new genus, originally named *Salinospora* within the *Micromonosporaceae* [112]. Further work confirmed this postulate and the genus was renamed *Salinispora* [113].

A reinvestigation of the secondary metabolite profile of these organisms led rapidly to an organism known as CNB-440, which when fermented on a 20-L scale, yielded a very potent cytotoxin named as salinosporamide A (**15**), whose structure was reminiscent of omuralide (**16**) but with significant variations, including a chlorine substituent that was required for the activity [114]. The final confirmation of the structure and proof of its MOA as a proteasome inhibitor was obtained via X-ray crystallographic techniques as described in detail by Groll et al. [115].

26.7.2 Large-Scale Fermentation/Isolation of cGMP Product

Salinosporamide A and other variants were licensed to San Diego Nereus Pharmaceuticals for further development as a cytotoxin. Nereus scientists, in concert with the now defunct fermentation group at Industrial Research Limited (IRL) in Lower Hutt, North Island, New Zealand, were able to produce the necessary cGMP product for clinical trials by fermentation in a saline environment, the first time that this task had been successfully performed on any significant (1,000 L) scale with a marine-sourced microbe. This work included the proof required for the production of a Drug Master

File (DMF), that such fermentation processes could be performed in a saline/alkali metal ion environment. The reason for concern was that such media would “pit” stainless steel fermentation vessels and, therefore, would need quite different cleaning/validation techniques in order to maintain the FDA requirements for cGMP production of the active pharmaceutical intermediates (APIs). This was successful, and the material obtained was satisfactory for advanced toxicology and then clinical trials in man. A series of reports on the fermentation media and on some of the other metabolites produced during the large scale isolation processes have begun to appear in print in the last few years [116–120], and fermentation modifications demonstrating that differing formulations with lower sodium ion concentration [121] or substitution by sodium sulfate can still maintain production but reduce corrosiveness of the medium [122], and in a later paper the same year, the same authors demonstrated that the ionic strength is a major determinant in growth and production [123]. In addition, an excellent discussion of the entire salinosporamide A story was published by Fenical et al. in 2009 [124].

26.7.3 Synthetic Processes

Even though the supply of material for clinical trials is from fermentation (a replacement for IRL was identified by Nereus in Eastern Canada so the supply of material was assured), chemists rose to the challenge and a number of groups including Nereus chemists have published total syntheses of salinosporamide A and analogues [125–134], thus demonstrating if one has a novel structure, chemists will devise syntheses for it as rapidly as possible. As mentioned earlier, the method of production is fermentation for the clinical candidate, but it is possible that derivative production may utilize some form of semisynthesis via the chemistries described above in due course.

26.7.4 Genomic Methods

Although some of the possibilities for genomic modifications/production were alluded to in the discussions on bryostatin (Sect. 26.3, Case 2) and dolastatin (Sect. 26.4, Case 3) where the producing microbe has been “identified,” salinosporamide, in addition to all of its other “firsts,” is the first antitumor agent whose biosynthetic pathway has been described and worked on contemporaneously with the late preclinical and early clinical studies. The genomic sequence of the producing actinomycete was investigated and 17 (plus) genomic clusters, one of which was the salinosporamide cluster, were reported by the SIO group of Moore in collaboration with the Fenical/Jensen group in 2007 [135]. The impact of this information from just the biosynthetic control of salinosporamide microbial synthesis can be seen by the papers that have been published using this basic information in the last 2 or so years. Thus, the biosynthetic route to the very unusual chlorinase that is essential for salinosporamide A’s activity has been reported [136]

together with methods of extending the polyketide synthons to give “unnatural derivatives” [137, 138] and a discussion on more general aspects of bioengineering from the organism itself [139, 140].

26.7.5 Lessons from Case Study 6

This example is quite different from the previous five in that the time frame has been very significantly compressed, from 18 to 20 plus years to less than 3 from realization that the microbes were a new marine-sourced genus, to identification of the metabolites and their potential. Thus, there was no large-scale method necessary except for development of fermentation processes to proceed with this compound. It should also be realized that the fermentation of marine-based microbes had never been attempted in regular fermentation systems prior to this work, let alone produce cGMP quality materials from such a process.

What also needs to be borne in mind is that there have been massive advances in genomic analyses in the last 5 plus years with the first actinomycete genomic sequence being published in 2002. The rapid development of recognition methods by earlier workers for defining the biosynthetic potential of gene clusters enabled the SIO discoverers and their collaborators in Nereus Pharma and SIO, in particular Moore’s group, to be able to use chemistry, knowledge of biosynthetic processes and the fermentation capabilities of Nereus to explore the producing microbe(s) extremely rapidly.

It is obvious from this example that the essential factors, aside from timing, are the dramatic interplay of scientists from many areas of chemistry and biology. Thus, a true multidisciplinary effort is absolutely essential for success.

26.8 In Conclusion

The examples used here for teaching purposes were chosen to show how scientists had to adapt to what was feasible rather than what might make sense using the knowledge of today. Thus, except for case study 6, a wide variety of collection and production methods were used as the time and funds permitted with recognition that at times, chemical synthesis was the only feasible route. Thus, the dolastatins were the product of total synthesis, as was aplidine. Initially, PharmaMar had developed a series of productive aquacultural methods that were used to produce Yondelis[®] for some of the earlier clinical trials and then moved to semisynthesis from a microbial secondary metabolite for large-scale clinical production.

With eribulin, Eisai used a modification of the natural product, halichondrin B, that relied upon an academic exercise in total synthesis of the natural product, during which the active pharmacophore was identified, although published only in a patent. It required a head-to-head comparison with the wild-collected natural product by NCI before Eisai was willing to commit to full scale synthetic production.

In case study 6, we have shown how the dramatic scientific advances in genomics and the influence of these techniques coalesced around a marine microbial metabolite that is currently the fastest natural product agent (and maybe even the fastest compound irrespective source) to go from discovery to clinical trials in under 4 years.

Thus, in the second decade of the twenty-first century, once an “active” agent has been identified as a potential drug lead, all methods for obtaining large-scale production are “on the table” for discussion and if/when the necessity arises for the production of significant amounts, the examples given above show what is currently available and investigators will mix and match as necessary, now that the pioneering work has been performed and evaluated. However, one can predict that new, currently unimagined technologies will come into being, and assist in the ever problematic issue of “meeting the supply needs of marine natural products.”

26.9 Study Questions

1. You have discovered a novel agent from a mixture of marine invertebrates. How would you determine if it was the product of an individual invertebrate? If it is, what are your next obvious steps? If it is not, what could be your best options?
2. You think that you have a small peptide as your active agent. What could be the various methodologies that could be used to produce larger quantities of the material in question, and why?
3. You have an active but quite toxic agent that you want to consider as a potential drug. How might you deliver this agent and why might one method be superior to another?
4. You have a very potent but complex structure as your discovery. What possible method(s) could you use to optimize the discovery for investigation as a potential drug?
5. You think that you have the producing microbe identified. How would you utilize current knowledge to prove that this is the case?

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G.M. Cragg (✉) • D.J. Newman
Natural Products Branch, Developmental Therapeutics Program, National Cancer Institute,
NCI-Frederick, Frederick, MD, USA
e-mail: gmcragg@verizon.net, newmand@mail.nih.gov

F. Katz • J. Rosenthal
John E. Fogarty International Center, National Institutes of Health, 31 Center Drive, MSC 2220,
Bethesda, MD, USA
e-mail: katzf@mail.nih.gov, Joshua_Rosenthal@nih.gov

Abstract

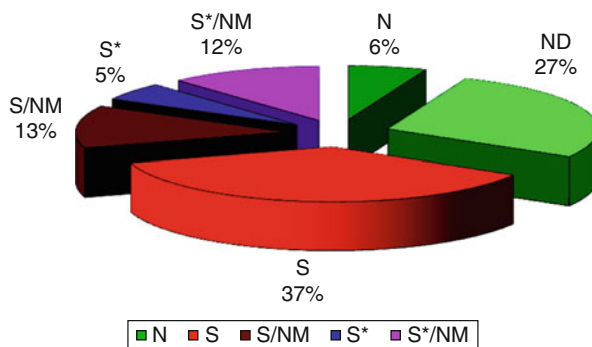
The discovery and development of novel, biologically active agents from natural sources, whether they be drugs, agrochemicals, or other bioactive entities, involve a high level of interdisciplinary as well as international collaboration. Such collaboration, particularly at the international level, requires the careful negotiation of collaborative agreements protecting the rights of all parties, with special attention being paid to the rights of host (source) country governments, communities, and scientific organizations. While many biodiversity-rich source countries currently might not have the necessary resources for in-country drug discovery and advanced development, they provide valuable opportunities for collaboration in this endeavor with research organizations from more developed nations. This chapter discusses the experiences of the US National Cancer Institute and the US government-sponsored International Cooperative Biodiversity Groups program in the establishment of international agreements promoting fair and equitable collaboration with source countries in the investigation of their rich biological resources, and includes recommendations for achieving such collaboration.

27.1 Introduction

Natural products have made, and continue to make, an indispensable contribution to the discovery and development of effective drugs for the treatment of many of the diseases afflicting humankind. A recent review [1] summarizes all approved agents during the past 25½ years from January 1981 to June 2006 for all diseases worldwide (Fig. 27.1).

In the analysis, new drugs were classified as N (an unmodified natural product), ND (a modified natural product), S (a synthetic compound with no natural product conception), S/NM (a synthetic compound showing competitive inhibition of the natural product substrate), S* (a synthetic compound with a natural product pharmacophore), and S*/NM (a synthetic compound with a natural product pharmacophore showing competitive inhibition of the natural product substrate). While 66% of the 974 small-molecule new chemical entities (NCEs) are formally synthetic, the analysis indicated that 17% correspond to synthetic molecules containing pharmacophores derived directly from natural products (classified as S* and S*/NM). Furthermore, 12% were considered to actually model a natural product inhibitor of the molecular target of interest or mimic (i.e., competitively inhibit) the endogenous substrate of the active site, such as ATP (S/NM). Thus, only 37% of the 974 NCEs were considered as truly synthetic (i.e., devoid of natural inspiration) in origin (S). In considering disease categories, close to 70% of anti-infectives (antibacterial, antifungal, antiparasitic, and antiviral) were classified as naturally derived or inspired (N, ND, S*, S*/NM, S/NM), while in the cancer treatment area, 77.8% were in this category, with the figure being 63% if the S/NM category is excluded.

Fig. 27.1 Small-molecule new chemical entities. January 1981–June 2006, by source (N = 974)



The importance of marine-derived secondary metabolites in chemical ecology, and as a source of leads for the development of potential new drugs or agrochemicals, is amply illustrated in the discussions contained in many of the chapters of this book. Indeed, in the area of cancer treatment, an impressive number of marine-derived agents have advanced into clinical development [2, 3].

While natural products are a proven source of novel, bioactive molecules, the actual compound isolated from the natural source often is not suitable for development into an effective drug or agrochemical product, but may, however, be regarded as a lead molecule which can form the basis for further chemical or biochemical modification. The discovery of promising bioactive molecules always involves close collaboration with biologists in the provision of suitable disease-oriented screens, while the optimization of the lead molecule often requires significant input from medicinal and synthetic chemists. The preclinical development of an agent always requires close collaboration with pharmacologists and toxicologists in the determination of the optimal pharmacodynamic and toxicological parameters suitable for advancement of the agent into clinical trials with human patients.

As discussed above, effective discovery and development of novel drugs require multidisciplinary collaboration. In the area of natural product bioactive lead discovery, close international collaboration is an additional, important requirement. Much of the world's biological diversity resides in low- and middle-income countries located in tropical and subtropical regions. The United Nations Law of the Sea (LOS) Treaty allows for open access in international waters or the high seas (<http://www.un.org/Depts/los/index.htm>). However, most accessible marine biodiversity and the vast majority of marine natural product collections come from territorial waters or those that fall under the exclusive economic zones of countries. As such, marine collections of biodiversity for natural products fall under the United Nations Convention on Biological Diversity (CBD); (<http://www.biodiv.org/convention/articles.asp>). The CBD has established a general framework for "access and benefit-sharing" that is being negotiated in more detail and may eventually become binding international law. The objectives as stated in the CBD are "the conservation of biological diversity, the sustainable use of its components and the fair and

equitable sharing of the benefits arising out of the utilization of genetic resources, including by appropriate access to genetic resources and by appropriate transfer of relevant technologies, taking into account all rights over those resources and to technologies, and by appropriate funding.” Irrespective of the legal trajectory of this central component of the CBD, dozens of countries have already implemented the objectives in national laws or policies, and the general expectation today in the international community is that productive interaction between these biodiversity-rich source countries and the more “science and technology-rich” countries is guided by the CBD principles and strives to conduct itself in a fair and equitable framework including access and benefit-sharing. Many of the naturally derived bioactive leads are isolated from organisms located and collected in these biodiversity-rich source countries, and it is incumbent on scientists involved in the biodiscovery process (often called bioprospecting) to establish collaborative agreements meeting the requirements of the CBD with the scientific communities and government agencies in these countries before proceeding with such programs.

Over the past 20 years, a number of international organizations have issued declarations or resolutions urging greater international collaboration and coordination in efforts to promote the conservation of biological and cultural diversity worldwide. Among these have been the Goteborg Resolution [4], and guidelines issued by the American Society of Pharmacognosy [5, 6] and the International Union of Pure and Applied Chemistry [7]. In addition, several books dealing with the commercial and legal aspects have been written [8–12]. The central theme of these publications is the fact that the source countries (mainly low- and middle-income) and their indigenous peoples are the custodians of the majority of the world’s genetic resources and that conservation of these resources requires fair and equitable collaboration and compensation in the development of their resources, as well as just recognition of the inventive and intellectual contributions of the indigenous peoples to the knowledge of the use of these resources. Emphasis is given to training, the exchange of ideas, results and technology, the promotion of traditional health care systems, and the completion of species and traditional knowledge inventories, with the dissemination of this information to all interested parties, including where possible in native languages.

It is clear that, without suitable economic, intellectual, and technological incentives for sustainable development, the genetically rich source countries and their communities will be unable to preserve these valuable resources for research into their beneficial uses for humankind. Although the focus to date has been on the depletion of plant resources, similar arguments apply equally well to the conservation of other organisms, such as those of marine origin.

In order to illustrate the application of the principles of the CBD to the collection and study of genetic resources, the following sections will discuss the experiences of the US National Cancer Institute (NCI) and the International Cooperative Biodiversity Groups (ICBG) program coordinated and administered by the Fogarty International Center (FIC) of the US National Institutes of Health (NIH).

27.2 The NCI Experience

The NCI has been involved in drug discovery and development for close to 50 years and has made significant contributions to the development of many of the anticancer drugs currently used clinically. The success of much of this effort has depended on close collaboration with organizations worldwide, and international collaboration continues to be an important feature of the NCI programs [13].

27.2.1 Achievements: 1955–1982

The NCI (<http://www.nci.nih.gov>) was established in 1937, its mission being “to provide for, foster and aid in coordinating research related to cancer.” In 1955, NCI set up the Cancer Chemotherapy National Service Center (CCNSC) to coordinate a national voluntary cooperative cancer chemotherapy program, involving the procurement of drugs, screening, preclinical studies, and clinical evaluation of new agents. The responsibility for drug discovery and preclinical development at NCI now rests with the Developmental Therapeutics Program (DTP; <http://dtp.nci.nih.gov>), a major component of the Division of Cancer Treatment and Diagnosis (DCTD). Thus, NCI has for the past 50 years provided a resource for the preclinical screening of compounds and materials submitted by scientists and institutions, public and private, worldwide, and has played a major role in the discovery and/or development of many of the available commercial and investigational anticancer agents. During this period, more than 500,000 chemicals, both synthetic and natural, have been screened for antitumor activity.

Initially, most of the materials screened were pure compounds of synthetic origin, but the program also recognized that natural products were an excellent source of complex chemical structures with a wide variety of biological activities. The original plant collections from 1960 to 1982 were performed by the US Department of Agriculture (USDA) through an interagency agreement with NCI and involved the random collection of over 35,000 plant samples, mainly from temperate regions. These collections led to the discovery of paclitaxel (Taxol[®]) and camptothecin which formed the basis for the semisynthesis of several clinically effective drugs. Marine invertebrates were generally collected by academic investigators, mainly funded through grants from the NCI, while microbial samples were obtained from pharmaceutical companies and research institutes, such as the Institute of Microbial Chemistry in Japan, some of which were funded through contracts with the NCI. From 1960 to 1982, over 180,000 microbial-derived, some 16,000 marine organism-derived, and over 114,000 plant-derived extracts were screened for antitumor activity, mainly by the NCI, and as mentioned above, a number of clinically effective chemotherapeutic agents have been developed [14].

27.2.2 Contract Collections: 1986–Present. The NCI Letter of Collection

The systematic collection of marine invertebrates and terrestrial plants was initiated in 1986 and is coordinated by the DTP Natural Products Branch (NPB; <http://dtp.nci.nih.gov/branches/npb/index.html>). Marine organism collections originally focused in the Caribbean and Australasia but, in 1992, were expanded to the Central and Southern Pacific and to the Indian Ocean (off East and Southern Africa) through a contract with the Coral Reef Research Foundation, which is based in Palau in Micronesia. With the renewal of the contract in 2002, collections are now performed worldwide. Terrestrial plant collections have been carried out in over 25 countries in tropical and subtropical regions worldwide through contracts with the Missouri Botanical Garden (Africa and Madagascar), the New York Botanical Garden (1986–1996; Central and South America), the University of Illinois at Chicago (Southeast Asia), the Morton Arboretum, and World Botanical Associates (USA mainland and territories).

The NCI collection contractors are required to obtain all of the necessary permits, including visas and collecting shipping and export permits, from the appropriate source country agencies or departments. The NCI provides the contractors with the NCI Letter of Collection (LOC; <http://ttc.nci.nih.gov/forms/>) [15] for transmission to the appropriate source country authorities and scientific organizations. The LOC states NCI's willingness to collaborate with local scientists and/or authorities in the discovery and development of novel drugs from organisms (plants, marine invertebrates, microbes) collected in their countries and/or territorial waters, and if requested, the NCI will enter into formal agreements based on the LOC with the relevant source country government agency or organization. Fourteen such agreements have been signed (Table 27.1); there are also 24 countries which have not, as yet, signed formal agreements with the NCI (Table 27.2). These countries, however, are fully aware of the terms of the LOC and granted the necessary permits for NCI contractor activities without requiring a formal agreement. In this respect, the NCI is totally committed to the terms of the LOC irrespective of whether or not a formal agreement has been signed [16]. Marine collections have been performed in the territorial waters of Australia, Federated States of Micronesia, Indonesia, Maldives, Marshall Islands, Mauritius, Palau, Papua New Guinea, Tanzania, and Thailand.

This absence of formal agreements has not been due to lack of effort on the part of the NCI contractors and/or NCI staff to solicit formal agreements from the source countries involved. Indeed, NPB staff has interacted with source country government representatives and scientists, both in their countries, or more frequently during NCI-sponsored visits to NCI and contractor US-based home facilities. The purpose of these visits is to provide opportunities for source country officials and scientists to observe the NCI drug discovery facilities and the processes to which their raw materials are subjected, and to discuss collaboration in the drug discovery process. During the past 20 years, over 65 source country officials and scientists have visited NCI, either to discuss participation in NCI contract collections or to discuss direct collaboration in the drug discovery process.

Table 27.1 Source countries with which NCI has collaborated in the collection of plants and marine organisms. Collaborating countries with which NCI had a Letter of Collection agreement

Source country	Source country organization	Year of agreement
Australia	Museum of the Northern Territories	2002
Bangladesh	Bangladesh National Herbarium, Dhaka	1994
Cambodia	Forest and Wildlife Research Institute, Department of Forestry and Wildlife, Phnom Penh	2000
Ecuador	The AWA Peoples Federation	1993
Gabon	Centre National de la Recherche Scientifique et Technologique (CENAREST), Libreville	1993
Ghana	University of Ghana, Legon	1993
Laos	Research Institute of Medicinal Plants, Ministry of Public Health, Vientiane	1998
Madagascar	Centre National D'Applications des Recherches Pharmaceutiques, Antananarivo	1990
Palau	Government of Palau	2002
Papua New Guinea	University of Papua New Guinea, Port Moresby	2001
Philippines	Philippines National Museum, Manila	1992
Sarawak, Malaysia	State Government of Sarawak: State Department of Forests	1994
Sarawak, Malaysia	Sarawak Biodiversity Council (marine collections)	2002
Tanzania	Traditional Medicine Research Institute, Muhumbili University College of Health Sciences, University of Dar Es Salaam	1991
Vietnam	Institute of Ecology and Biological Resources, National Center for Natural Science and Technology, Hanoi	1997

Table 27.2 Collaborating countries with no Letter of Collection agreement with NCI^a

Bahrain	Dominican Republic	Maldives	St. Lucia
Belize	Federated States of Micronesia (e.g., Chuuk, Yap)	Marshall Islands	Thailand
Bolivia	Guatemala	Martinique	Tonga
Cameroon	Guyana	Mauritius	–
Central African Republic	Honduras	Nepal	–
Colombia	Indonesia	Paraguay	–
Dominica	Malaysia	Peru	–

^aNCI is totally committed to LOC terms irrespective of whether or not an official agreement has been signed

27.2.3 Source Country Collaboration

In carrying out collections, the NCI contractors work closely with qualified organizations in each of the source countries. Botanists and marine biologists from source country organizations (SCOs) collaborate in field collection activities and taxonomic identifications, and their knowledge of local species and conditions is indispensable to the success of the NCI collection operations. SCOs provide

facilities for the preparation, packaging, and shipment of the samples to the NCI's Natural Products Repository (NPR) in Frederick, Maryland. The collaboration between the SCOs and the NCI collection contractors, in turn, provides support for expanded research activities by source country biologists, and the deposition of a voucher specimen of each species collected in the national herbarium or repository is expanding source country holdings of their biota. NCI contractors also provide training opportunities for local personnel through conducting workshops and presentation of lectures, both in-country and at the contractor's US facilities.

In addition, through its Letter of Collection and agreements based upon it, the NCI: (1) sponsors visits by scientists nominated by SCOs to its facilities, and/or equivalent facilities in other approved US or local organizations, for 1–12 months to participate in collaborative natural products research involving disciplines pertaining to drug discovery, such as the screening and bioassay-directed fractionation of extracts (over 20 such visits have been sponsored), and (2) dictates arrangements for benefit-sharing and use of source country resources in the event of the licensing and development of a promising drug candidate. Successful licensees of patented agents discovered from NCI contract collections are required to negotiate agreements with the relevant source country government agencies or organizations dictating terms of collaboration and compensation. The terms apply irrespective of whether the potential drug is the actual natural isolate or a product structurally based upon the isolate, a synthetic material for which the natural product material provided a key development lead, or a method of synthesis or use of any aforementioned isolate, product, or material. The terms (e.g., percentage of royalties) negotiated as payment, however, might vary depending upon the relationship of the marketed drug to the originally isolated product.

The formulation of the NCI policies for collaboration and compensation embodied in the Letter of Collection predated the drafting of the United Nations Convention on Biological Diversity signed in Rio de Janeiro by some 4 years. It must be stressed that the NCI abides by the terms of the LOC even if the collaborating source country has not signed a formal agreement. In addition, the NCI and the ICBG US-based collaborating organizations respect the terms of the CBD even though the US has not ratified the treaty, as yet in 2010.

27.2.4 Direct Collaboration with Source Country Organizations. The NCI Memorandum of Understanding

As discussed above, the collections of plants and marine organisms have been carried out in over 25 countries through contracts with qualified botanical and marine biological organizations working in close collaboration with qualified SCOs, and all collections are performed subject to the terms of the NCI Letter of Collection. Particularly in the area of plant-related studies, source country scientists and governments are becoming increasingly committed to performing more of the drug discovery operations in-country, as opposed to the export of raw materials. The NCI has recognized this fact for several years, and contract collections of plants have been

de-emphasized in favor of establishing direct collaborations with qualified organizations in the source countries where the necessary expertise and infrastructure exist.

The NCI has established collaborative agreements [Memoranda of Understanding (MOUs); <http://tc.nci.nih.gov/forms/>] with over 20 SCOs suitably qualified to perform in-country processing (Table 27.3).

In establishing these agreements, the NCI undertakes to abide by the same policies of collaboration and compensation as specified in the LOC. NCI also assists the SCOs to establish their own drug discovery programs through training in techniques of antitumor screening and natural product isolation. NCI has sponsored long-term visitors from 18 countries for purposes of such collaboration and training. Where suitable infrastructure is available at source country institutions, the NCI will provide human cancer cell lines, as well as the appropriate cell line and virus (genetically modified to be noninfectious) for a cell-based anti-HIV screen, at minimal cost to those institutions to enable them to set up screens for their own in-house drug discovery programs.

It is anticipated that the discovery of novel anticancer drugs will be performed by the SCO at its own expense, with assistance from the NCI in terms of free secondary in vitro and in vivo testing. All results from such secondary testing are considered the sole intellectual property of the SCO (NCI regards such testing as a routine service to the scientific community) and can be used by the SCO in the application for patents covering sufficiently promising inventions. The NCI will devote its resources to collaborating with the SCO in the preclinical and clinical development of any SCO-discovered drug which meets the NCI selection criteria and will make a sincere effort to transfer any knowledge, expertise, and technology developed during such collaboration to the SCO, subject to the provision of mutually acceptable guarantees for the protection of intellectual property associated with any patented technology.

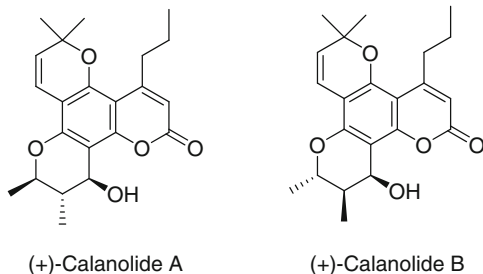
Through this mechanism, collaborations in the collection and study of marine organisms have been established with organizations in Australia, Brazil, Fiji, New Zealand, Papua New Guinea, and South Africa.

27.2.5 Case Study. The Calanolides

An extract of the leaves and twigs of the tree, *C. lanigerum*, collected in Sarawak, Malaysia, in 1987, yielded (+)-calanolide A (Fig. 27.2) which showed significant anti-HIV activity [17]. Efforts to relocate the original tree failed, and collections of other specimens of the same species gave only trace amounts of calanolide A. A detailed survey of *C. lanigerum* and related species discovered that latex of *C. teysmanii* yielded extracts with significant anti-HIV activity. The active constituent was found to be an isomer, (–)-calanolide B (Fig. 27.2), which was isolated in yields of 20–30%. While (–)-calanolide B is slightly less active than (+)-calanolide A, it has the advantage of being readily available from the latex which is tapped in a sustainable manner by making small slash wounds in the bark of mature trees without causing any harm to the trees. The calanolides were licensed by NCI/NIH

Table 27.3 MOUs between NCI and source country organizations: direct collaborations

Source country	Source country organization	Year of agreement
Australia	Australian Institute of Marine Sciences, Townsville, Queensland	1999
Bangladesh	The University of Dhaka	1998
Brazil	Fundacao Oswaldo Cruz – FIOCRUZ, Rio de Janeiro	1999
	South American Organization for Anticancer Drug Development, Canoas	1995
	Universidade do Paulista, Sao Paulo	1997
	Universidade Federal do Parana	1998
China	Universidade Federal do Ceara, Fortaleza	2001
	Hong Kong University of Science and Technology	1998
	Kunming Institute of Botany, Yunnan	1995
	Peking University and State Key Laboratory, Beijing	2001
Costa Rica	Instituto Nacional de Biodiversidad (INBio)	1994
Fiji	University of the South Pacific, Suva	1999
Iceland	The University of Iceland, Reykjavik	1998
Republic of Korea	Korean Research Institute of Chemical Technology (KRICT)	1995
Mexico	Instituto de Quimica, Universidad Nacional Autonoma de Mexico, Mexico City	1995
New Zealand	National Institute of Water and Atmospheric Research (NIWA), Wellington	1996
Nicaragua	Universidad Nacional Autonoma de Nicaragua, Leon	1999
Pakistan	HEJ Research Institute of Chemistry, University of Karachi	1994
Papua New Guinea	University of Papua New Guinea, Port Moresby	2001
Panama	University of Panama	1996
South Africa	Council for Scientific and Industrial Research (CSIR), Division of Food, Biological and Chemical Technologies (BIO/CHEMTEK), Pretoria	1996
	Rhodes University, Grahamstown	1998
Zimbabwe	Zimbabwe National Traditional Healers Association (ZINATHA)	1994

**Fig. 27.2** Potential anti-HIV agents. Calanolides A and B

to Medichem Research, Inc., (now Advanced Life Sciences) which, as required by the NCI LOC [15], negotiated an agreement with the Sarawak State Government. The drugs were initially being developed by Sarawak Medichem Pharmaceuticals, a joint venture company formed between the Sarawak State Government and Medichem Research, Inc., but the lead role in the development is now being undertaken by Craun Research Sendirian Berhad, a company incorporated in Sarawak. Medichem Research had synthesized (+)-calanolide A, and it is currently headed for Phase II clinical trials, while (–)-calanolide B is in preclinical development. The earlier development of the calanolides has been reviewed as a “Benefit-Sharing Case Study” for the Executive Secretary of the CBD by staff of the Royal Botanic Gardens, Kew, UK [18]. It is interesting that subsequent to the discovery of the calanolides, Sarawak established the Sarawak Biodiversity Center (<http://www.sbc.org.my/>) which performs an in-country bioprospecting program as well as other biodiversity-related activities.

27.3 The International Cooperative Biodiversity Groups (ICBG) Program

The International Cooperative Biodiversity Groups (ICBG) Program, in its original conception, adopted several key elements of the NCI experience described above, but is a much broader effort with multiple goals. Initiated in 1993 as a US Government (USG) interagency initiative led by the Fogarty International Center of the NIH, the ICBG program aims to discover new bioactive molecules from nature while providing incentives for sustainable biodiversity conservation. It is based on the premise that biodiscovery, scientific capacity building, and biodiversity conservation are fundamentally interdependent and can yield synergistic benefits from an integrated program that returns economic and scientific benefits to the host countries.

At a basic level, the ICBG program, like that of the NCI programs, is one of international collaboration that pays particular attention to benefit-sharing. However, the ICBGs differ in structure and scope in that they are a competitive grants program through which international research consortia assemble in response to a solicitation to build partnerships between at least one US academic research institution and at least one non-US host organization in biodiversity-rich, low- and middle-income countries (http://www.fic.nih.gov/programs/research_grants/icbg/index.htm; <http://www.icbg.org/>). Because of the multiple goals of the program, consortia typically include between three and ten organizations with different missions and expertise, all collaborating toward joint, interdependent goals.

The first round of the program was jointly sponsored by components of the National Institutes of Health, the National Science Foundation, and the Agency for International Development. The initial focus of the ICBG program was on the identification of compounds and extracts that might lead to the development of new drugs or botanicals in a wide variety of therapeutic areas. With the addition of

Table 27.4 Cosponsors of the ICBG program

USG Agency	Period of participation	Program interest
<i>National Institutes of Health</i>		
Fogarty International Center	1993–present Administrative lead, financial support	Global health, international collaborations, scientific capacity building
National Cancer Institute	1993–present Technical and financial support	Anticancer agents
National Heart, Lung, and Blood Institute	1993–2002	Cardiovascular agents
National Institute of Mental Health	1993–present Technical and financial support	Agents for psychiatric disorders
National Institute of Allergy and Infectious Diseases	1993–2008 Technical and financial support	Anti-infective agents
National Center for Complementary and Alternative Medicine	2003–present Technical and financial support	Ethnomedical remedies
Office of Dietary Supplements	2003–present Technical and financial support	Botanical analysis
National Institute on Drug Abuse	1997–2008 Technical and financial support	Anti-addiction agents
National Institute of General Medical Sciences	2003–present Technical and financial support	Novel bioactive molecules and new chemistry
<i>National Science Foundation</i>		
Directorate of Biological Sciences	1993–present Technical and financial support	Biodiversity inventory and conservation; microbial diversity
Directorate of Geosciences	2003–present Technical and financial support	Marine Biology
<i>US Agency for International Development</i>		
	1993–1996 Technical and financial support	Biodiversity conservation and economic development
<i>US Department of Agriculture</i>		
Foreign Agriculture Service	1997–2003 Technical and financial support	Sustainable use of biodiversity, crop protection
Forest Service	1997–2003 Technical support	Sustainable use of biodiversity, conservation
Cooperative State Research, Extension and Education Service (Current name: National Institute of Food and Agriculture)	2008–present Technical and financial support	Sustainable use of biodiversity, crop protection and animal health
<i>Department of Energy</i>		
Office of Biological and Environmental Research	2008–present Technical and financial support	Biological sources of energy conversion and CO ₂ assimilation

(continued)

Table 27.4 (continued)

USG Agency	Period of participation	Program interest
<i>National Oceanic and Atmospheric Administration</i>		
Oceans and Human Health Initiative	2009–present Technical and financial support	Health products from the ocean; training in marine biotechnology for health; healthy oceans and marine conservation

the US Department of Agriculture (USDA) in 1997 and the Department of Energy (DOE) in 2008, this mandate has expanded further to include discovery of leads for agrochemicals, animal health agents, bioenergy agents, and biofuels. Increased focus on marine research has brought the National Oceanographic and Atmospheric Administration into the partnership. Currently, the program is jointly sponsored by five USG agencies, including six components of the NIH. [Table 27.4](#) outlines the history of USG agency participation and the interest of each component in the program.

Over the history of the program, there have been 7 planning grants and 14 ICBGs, several of which have been competitively renewed for multiple 5-year cycles. In total, these latter have involved multiyear collaborative efforts in 20 countries. While the emphasis in the earlier ICBGs was largely on tropical plants, the projects were encouraged to expand efforts to involve marine and microorganisms in 2003 (NIH Guide: RFA TW-03-004, [19]) and in subsequent competitions. There are currently eight funded ICBGs operating, of which six include significant marine collections. These six are outlined in [Table 27.5](#).

27.3.1 Agreements Governing Collaborative Research and Nature of Benefits

The ICBGs have negotiated viable agreements for collections, research, and the sharing of benefits with organizations in 20 collaborating countries. The collaborating countries include Suriname, Peru, Chile, Argentina, Mexico, Costa Rica, Panama, Vietnam, Laos, Papua New Guinea, Philippines, Indonesia, Fiji, Madagascar, Cameroon, Nigeria, Uzbekistan, the Kyrgyz Republic, Tajikistan, and Kazakhstan. In each of these countries, the projects vetted the agreements with national authorities and local authorities and obtained permission to proceed under the prevailing access-and benefit-sharing policies available at the time. As mentioned above, until recently, most of these have been terrestrial projects. For projects that have had multiple cycles, these agreements and associated permits have evolved and been renewed with the project multiple times.

ICBG marine collections have largely been confined to internal and territorial waters, or fall within the exclusive economic zones of the participating nations and are subject to the same national laws regulating terrestrial collections, as outlined in

Table 27.5 ICBG projects that include marine collections and research

Project (principal investigator: project period)	Organismal focus	Principal participating institutions (current and former)
Biodiversity Conservation and Drug Discovery in <i>Madagascar</i> (David G. I. Kingston: 1993–present)	Tropical plants, microbes, and marine organisms	Virginia Polytechnic Institute and State University Missouri Botanical Garden; Conservation International; Madagascar National Centers for Pharmaceutical, Environmental and Oceanographic Research; University of Maryland Biotechnology Institute; Eisai Research Institute; Dow AgroSciences
ICBG: Training, Conservation and Drug Discovery using <i>Panamanian</i> Microorganisms (Phyllis Coley: 1998–2002; William H. Gerwick: 2003–present)	Tropical plants; endophytic fungi; marine algae, microbes, and marine invertebrates	Smithsonian Tropical Research Institute University of California San Diego; University of Panama Santa Cruz; Oregon State University; University of Panama; National Secretariat for Science, Technology and Innovation (Panama); Novartis Institutes for Biomedical Research; Dow AgroSciences; Eisai Research Institute
Conservation and Sustainable Use of Biodiversity in <i>Papua New Guinea</i> (Louis R. Barrows: 2003–present)	Tropical and medicinal plants, marine and terrestrial microbes, marine invertebrates	University of Utah Smithsonian Institution; University of Minnesota; University of Papua New Guinea; Natural History Museum, London; National Forest Research Institute (PNG); PNGBioNET; Wyeth Research Laboratories
Discovery of Natural Product-based Drugs from <i>Costa Rican</i> Biota (Jon Clardy: 2004–2007; David H. Sherman: 2008–present)	Endophytic fungi, lichens, marine actinomycetes and cyanobacteria, marine invertebrates, insect microbial endosymbionts	University of Michigan Harvard Medical School Instituto Nacional de Biodiversidad (INBio, Costa Rica), Broad Institute of Harvard and MIT, Novartis Institutes for BioMedical Research
Exploration, Conservation, and Development of Marine Biodiversity in <i>Fiji</i> (Mark E. Hay: 2004–present)	Coral reef organisms and marine microbes	Georgia Institute of Technology Scripps Institution of Oceanography; University of the South Pacific (Fiji); Bristol-Myers Squibb
Diverse drug lead compounds from bacterial symbionts in tropical marine mollusks (<i>Philippines</i>) (Margo Haygood: 2008–present)	Marine mollusks and their bacterial symbionts	Oregon Health & Science University University of Utah; University of the Philippines (Quezon City, Philippines); Academy of Natural Sciences of Philadelphia; Ocean Genome Legacy Foundation

the Convention on Biodiversity. Beyond these limits, collections would fall under the United Nations Law of the Sea Treaty (<http://www.un.org/Depts/los/index.htm>).

ICBG projects are governed by legal agreements that must be negotiated individually by the participants in each Group, sometimes including participants from three or more countries. The ICBG Request for Applications lays out a set of

“Principles for accessing genetic resources, the treatment of intellectual property and the sharing of benefits” including requirements to develop fair and equitable agreements that include sharing of diverse and substantial benefits with host country (equivalent to “source country” used in the discussions of NCI programs) partners and to obtain legal access permits, before proceeding (<http://grants.nih.gov/grants/guide/rfa-files/RFA-TW-08-010.html>). These principles or guidelines are very similar to those that have emerged in the CBD process over the past decade and have been modified slightly to accommodate evolution in that arena.

The original ICBG Guidelines drew heavily on the NCI experience with their Letter of Collection program, and the NCI programs have been influenced by ICBG experiences. However, because the programs are operationally distinct and the goals are different in scope, there are a few important differences in how agreements have been developed. The root of these differences derives from the fact that in the ICBGs, the funding agencies are not party to the access and benefit-sharing agreements. Beyond requiring that the project agreements address the general guidelines mentioned above, the agencies do not specify the form or specific terms the agreements should take. Rather, each consortium must develop agreements that meet the needs of its partners and respond to the guiding principles of the program. These agreements and associated host country permits are then submitted to the Fogarty International Center for review and approval in order to receive continued funding past the first year and before any collections can take place or materials can be sent outside the host country.

Consequently, the ICBG agreements have followed a variety of models. The legal documents involved include permits to make collections, community prior informed consent from the owners of the biodiversity, material transfer agreements, benefit-sharing agreements, trust funds, license option agreements, and memoranda of understanding that govern the general conduct of the research and general terms for commercialization of any products discovered by the consortium [20–22]. Often, a partnership involves several of these components in separate but linked documents. The agreements that structure an ICBG are typically organized as a series of bilateral agreements between partner organizations, sometimes in a hub and spoke arrangement around the prime grantee, or a consortium agreement in which three or more of the organizations are parties to one jointly negotiated contract [20]. Most often, an ICBG entails some combination of consortium and bilateral agreements. ICBG agreements are generally among institutional partners, including academic, governmental, and industrial organizations; some include community organizations, especially where traditional knowledge is involved or collections involve land or coastal waters controlled by the communities [20, 23].

Although agreements commonly take 1 year or longer to negotiate, the core criteria developed and benefits sought have many common features. The agreements typically outline the responsibilities of all the parties, establish the principle of full and equal collaboration, limit third-party transfer of materials without written consent of all relevant parties, establish terms of confidentiality and publication of results, and address near-term benefits that accrue to the host country for

access to materials. These benefits most importantly include training of host country scientists in the various disciplines needed to carry out a biodiversity program (field biology, taxonomy, chemistry, bioassays, and others) and access to technology. When industrial partners are included in the consortium, there is sometimes an agreement to provide additional up-front funds from the industrial partner to host country institutions or a local trust fund to further enhance laboratory capability or support community conservation and development efforts beyond the terms of the grant.

Longer-term benefits associated with commercialization of a discovery, such as milestone or royalty payments, may be included as contingent benefits, with discussions of who gets what in a variety of scenarios based on relative contributions to the discovery or other metrics. Negotiating these scenarios was more common in the early years of the ICBG program. However, given the rarity of commercial development and the added transaction costs of these more difficult negotiations, this practice is less common today than a “two-stage” approach. The two-stage approach is generally to negotiate the initial agreements in the context of academic research, with a stipulation that further agreements must be negotiated should discoveries move into a commercialization pathway. This two-phase approach often incorporates a commercial agreement trigger, and tends to ease the burden and speed up negotiation at the outset, and, very importantly, creates more flexibility for the scientists to carry out basic research and training (see [Sect. 27.4.3](#) below).

An increasing emphasis on microbial collections in the last 5 years has created additional challenges in negotiating agreements. Several countries, for example Madagascar and the Philippines, have laws or policies that prohibit export of self-replicating organisms because their provenance may be hard to trace and commercial development may not materially require recollection in the original host country. Consequently, some ICBG agreements specify that all microbes must first be isolated and identified in the host country before they can be tested in bioassays, and only chemical extracts or isolated compounds can leave the country. In other agreements, a host country scientist is required to accompany the microbes and participate in the research if they do need to leave the country to move the research forward. Not infrequently, the authorization for transfer of culturable microbial samples is feasible after a project has had a year or two of collaborative work and an opportunity to develop more trust among partners and host country authorities.

One positive result of microbial transfer restrictions may be the development of microbial technology and expertise in the host country, a benefit in keeping with the goals of the ICBG program. But ultimately, it is often necessary to engage more sophisticated analyses than are possible in a relatively small- or low-resource country even with additions of state-of-the-art equipment. Furthermore, as molecular systematics, molecular diversity analysis, and molecular taxonomy become increasingly common for microbial collections, export of DNA for genomic, metagenomic, and PCR sequencing has recently become an issue. Government officials that oversee biodiversity permits and agreements in many low- and

middle-income countries may be only familiar with the general concept of DNA and anxious about the traceability issues mentioned above. However, because of the increasingly fundamental role of these techniques in modern academic microbiology, this is changing rapidly. Our experience is that clear presentations of the science by the researchers involved to local government officials, especially when it occurs in the context of a project based on equitable partnerships and transparency, are often an effective means of addressing this problem.

Despite the most painstakingly negotiated agreements, there are unique challenges to projects working in low- and middle-income countries that each ICBG must navigate. Countries are implementing access and benefit-sharing policies in diverse ways depending on their preexisting legal environment. Many still have none in place. Even clear regulations can shift with the changing political landscape. In the past 17 years, the ICBGs have been faced with coup d'états (Madagascar, Fiji, Kyrgyz Republic), changes of governments and associated policy changes that temporarily paralyzed parts of the research program (Suriname, Panama), changes in political relations with the USA that forced suspension of international projects (Uzbekistan), and traditional knowledge disputes that temporarily halted one project (Peru) and shut down another (Chiapas, Mexico). Despite these disruptions, with the exception of the Chiapas project and the Uzbekistan component of the Central Asia project, the ICBGs have generally managed to adjust and continue their research, conservation, and capacity building activities.

27.3.2 Achievements

Despite the challenges of negotiating and maintaining these complex research partnerships, the ICBGs have been successful in producing exciting new science and providing benefits both locally and nationally to host countries. From 1993–2009, the ICBGs screened over 83,000 extracts (1.3 million primary screening events) from approximately 10,630 uniquely identified species (of which about 10% were of marine origin) and 50,000 isolated microbial strains in over 78 therapeutic and agrochemical assay areas. These materials, collected specifically for biodiscovery, were largely derived from plant sources during the first 10 years of the program, but since 2003 have increasingly included terrestrial and marine microbes, endophytic fungi, and marine invertebrates and their microbial symbionts (see [Table 27.5](#)). Over 1,400 unique bioactive molecules have been isolated, many of which are new to science. Approximately 20 molecules are currently considered active leads for potential new therapeutics or agrochemicals. Overall, the achievements of the program have been described in over 600 publications, mostly by the investigators themselves.

In addition to biodiscovery, the ICBGs have made significant contributions to building research capacity in host countries. Most critically, over 4,000 individuals have been trained in biodiversity and biodiscovery sciences. These included 350 long-term (1 year or longer) training opportunities, resulting in 135 Masters and

PhD degrees. Approximately 70% of long-term trainees are from host countries. ICBGs have also helped to upgrade collaborating laboratories in host countries through provision of chemistry- and bioassay-related equipment, such as liquid chromatography devices, nuclear magnetic resonance (NMR) technology, spectrometers, microscopes, and PCR machines, computers, and others. The projects have helped to modernize local laboratory, culture, and museum facilities and in some countries have contributed to the creation of national laboratories for chemistry and biological screening.

Biodiversity conservation contributions have been substantial. The scientific basis for conservation has been enhanced by developing or enhancing publicly available bioinventory records for all ICBGs. In addition, bioinventory activities have resulted in the publication in print or on the web of national and regional taxonomy and identification guides, such as the Atlas of Seed Plants of Cuc Phuong National Park (<http://fm2.fieldmuseum.org/plantatlas/>), descriptions of medicinal plants in the public domain [24], and deposition of voucher specimens in national and international repositories. At least two dozen new species and genera of plants have been identified, as well as hundreds of microbes and fungi. ICBG efforts have led to the creation of new protected areas in Panama (see below), Laos, Suriname, and Madagascar and have strengthened existing reserves in many other countries. These contributions have formed a basis for local and regional collaborations and new economic activities in most of these countries.

Finally, the ICBGs have informed policy in many of the countries in which they have worked. As an on-the-ground test of the CBD goal of providing equitable benefits to host countries in return for access to genetic resources, their challenges and lessons learned have been closely observed and extensively documented in academic and policy literature and in multiple CBD forums. For instance, a search on ICBG in the CBD website (<http://www.cbd.int/>) turns up 116 documents including numerous case studies and third-party reports written or translated in multiple languages.

27.3.3 Case Studies

The ICBG Requests for Application that have structured the program require that every Group develop a proposal to address the three major goals of biodiscovery, biodiversity conservation, and return of benefits in the form of scientific capacity and/or economic development, preferably by undertaking activities that integrate these goals and allow them to be mutually reinforcing. Examples of how these goals have been integrated in two projects that currently focus on marine collections are described below.

27.3.3.1 The Panama ICBG

The Panama ICBG (see [Table 27.5](#)), first awarded in 1998, originally focused on plant collections throughout Panama. In 2003, however, in the second cycle of their ICBG, they expanded to include marine collections and began to focus many of their activities around Coiba Island off the Pacific coast of Panama in the Gulf of

Chiriqui. Due to the historical presence of a penal colony on the island since 1919, the vegetation and surrounding waters were exceptionally well conserved. However, when the Panama ICBG began working there in 2003, the penal colony was closing down, and the future of the island was a topic of national debate.

The ICBG project supported extensive bioinventory and drug discovery collections on and around Coiba Island. From both terrestrial and marine species, some of which are endemic to the island, the team has isolated promising bioactive molecules in therapeutic areas important to the population of Panama including novel compounds active against parasitic diseases [25] and cancer [26].

Based in part on this scientific evidence, the Panamanian parliament gave the area National Park protection in 2004 [27]. Working together with the government and other interested parties, the Park and a surrounding special zone of marine protection was proposed to UNESCO as a World Heritage Site, a status that was granted in 2005 (<http://whc.unesco.org/en/list/1138>). This is likely to serve as a basis for expanded tourism and economic revenue for Panama for years to come and creates a clear valuation for national biodiversity conservation, a major goal of the CBD. Conservation of the island and surrounding waters also allows for continued research in relatively pristine areas that would otherwise be rapidly transformed by commercial development and exploitation.

A key feature of the Panama ICBG has been the investment in Panamanian researchers as major collaborators. The philosophy of the project has been that by doing as much of the work as possible in Panama with Panamanian scientists, they are most likely to leave a sustainable research base in the country. The scientific and conservation activities outlined above and many others were used to train University of Panama students in field and marine biology, drug discovery, and chemistry. Some of the Panamanian students were subsequently selected by the Panamanian government for scholarships to undertake MSc and PhD studies abroad and are now returning to Panama to join the project as investigators. Meanwhile, Panamanian scientists working in Spain and the USA have been attracted back to work on the ICBG as investigators at the University of Panama or its Institute for Advanced Studies. Because much of the scientific research of the ICBG has been concentrated in Panamanian institutions throughout the project period, the ICBG has built significant laboratory infrastructure and human capacity for research in biodiversity and biodiscovery sciences [28, 29]. They have also developed bioassays suitable for working in low-resource countries [30, 31].

Together, these capabilities should contribute to the ability of Panama to continue to explore and reap the benefits of its biodiversity in the years ahead.

27.3.3.2 The Fiji ICBG

The goals of the Fiji ICBG (see [Table 27.5](#)) include the discovery of pharmaceutical and bioenergy leads from coral reef organisms and marine microbes, promotion of marine biodiversity conservation through understanding the ecological processes that result in reef degradation and by working with local communities to help protect community reefs, and development of scientific capacity at the University of the South Pacific.

A memorandum of understanding and material transfer agreements were negotiated, and national collection permits were obtained. However, the coral reefs in Fiji are effectively owned by local communities [32]. Consequently, beginning with a planning grant in 2002, the team developed a partnership with a local community to determine appropriate benefits that would accrue to the community in return for access to their coral reefs to conduct scientific research. The negotiations with the village chief in their first intensive collection site were greatly facilitated by the long-term village relationships built by team members from the University of the South Pacific.

Degradation of the reefs and declining fish catch were major concerns of the community. While many factors are involved, both of these problems are exacerbated by the commercial harvesting and sale of living coral (live rock) for the international aquarium trade. Fiji is one of the few countries in the world where this practice is legal, and tons of coral are harvested annually, making Fiji one of the largest suppliers of live rock in the world.

The Fiji ICBG began a pilot arrangement that allowed the community to produce “cultured live rock,” an artificial coral, while they suspended any live rock collections. The scientific expertise of the ICBG team helped optimize culture conditions. An international company agreed to purchase this rock from the community in place of live rock. The newly opened Georgia Aquarium in Atlanta agreed to purchase the cultured material and use it in their displays, and the community was able to collect and sell several harvests of this product to the aquarium [33] and the company. Other communities have shown an interest in engaging in similar projects on their reefs, and the national government has discussed banning all sale of live rock in Fiji should this approach be successful and scalable. This local alternative enterprise is now being expanded, and new versions of the cultured rock are being explored for broader markets by the project with new cycles of funding.

In parallel, the discovery research of the Group has discovered new bioactivities from organisms collected on these community reefs [34–37], in part using ecologically guided techniques involving antifeedant behavior in fish. Based partly on results from experiments originally conducted elsewhere [38], the team worked with the community leaders to alter fish catching practices to optimize both increases in fish yield and enhanced coral conservation on their reefs. These methods have become part of a newly initiated and rapidly growing network of Fijian local marine management areas. The project established a small trust charity, Adopt a Reef (<http://adopt-a-reef-fiji.org/>), to attract charitable donations to support careful management and conservation at the community level, including the marine management areas.

Finally, in the conduct of the research, they have made significant investments in enhanced scientific infrastructure and training of local scientists to build the capability of the University of the South Pacific to conduct independent and collaborative natural products research.

This integrated strategy has produced new science, enhanced protection of the biodiversity on which both new discoveries and the livelihood of the local communities are based, and has laid the groundwork for future biodiscovery by Fijians in Fiji.

27.4 Conclusions and Recommendations

27.4.1 Commercial Drug – A Rarity!

With the signing of the treaty on the Convention on Biological Diversity, there was a surge of optimistic anticipation that the rich biodiversity located in many source countries, particularly in tropical and subtropical regions, would yield a host of new miracle drugs which would rapidly generate considerable wealth for many source (mainly developing) countries (so-called green gold). An oft-quoted estimate is that 1 in 10,000 biologically active leads will lead to the development of a commercial, conventional drug, but with natural products, this ignores the initial phase of isolating and identifying the active lead compound from the original active crude extract. Thus, unfortunately, the realities of natural product drug discovery and development are in direct contradiction to the “green gold” expectations.

In their chapter on natural products and the pharmaceutical industry, ten Kate and Laird [10] estimate that the primary screening of five million “compounds,” presumably crude extracts, will yield 1,000 “hits” (a “hit rate” of 1/5,000), which, after bioassay-guided fractionation and purification, dereplication, structural elucidation, and secondary screening, will yield ten bioactive novel leads. Subsequent optimization of the lead candidate, involving yield improvement, analog synthesis, formulation and bioavailability studies, and enhancement of the therapeutic index (the ratio of the activity versus toxicity ratio), narrows the field to five drug candidates which enter advanced preclinical development and, after approval by the regulatory authorities, enter clinical trials. After Phase III clinical trials, one of these candidates is finally approved for registration and marketing. Their numerical estimates probably apply best to the discovery of new antibiotics from microbial broths produced by the fermentation of many microbial cultures under multiple different fermentation conditions. Comparable probability estimates for collection-based natural products research range widely in both directions from those above, but the essential truth here is that the probability of discovering a novel commercial drug is extremely low.

Possibly a more relevant example is the NCI experience in the early years of its natural product drug discovery and development program. From 1960 to 1982, some 35,000 plant samples (representing about 12,000–13,000 species) were processed to yield 114,000 extracts. Despite the discovery of a significant number of interesting active chemotypes, only two pure compounds advanced to the stage of development into commercial products. These were Taxol[®] (e.g., paclitaxel and its analog, docetaxel) and camptothecin, which, though it proved to be too toxic in clinical trials to become a commercial drug, has yielded commercial analogs, such as topotecan (Hycamtine[®]) and irinotecan (Camptosar[®]). One other product, homoharringtonine, has advanced through clinical trials for the treatment of several refractory leukemias, though it is limited to investigational clinical use. Thus, 114,000 extracts derived from approximately 12,000 species, thus far, have given only two compounds currently yielding products of commercial value (further derivatives and analogs of Taxol and camptothecin are being developed which

will probably become commercial products), with homoharringtonine being another likely product. Another discovery from the early NCI program was maytansine which has been conjugated to suitable carrier molecules such as monoclonal antibodies that target specific tumors. These products are in various stages of clinical development, and it is possible that one or more may advance to commercial use. Thus, new developments aimed at the targeting of toxic products to tumors through conjugation to suitable carrier molecules, such as monoclonal antibodies, may well improve the success rate.

Irrespective of which scenario is used, the message is clear – the chances of discovering a product that will eventually become a commercial drug are extremely small! Having made this observation, it is also clear that exposure of the initial natural product extracts to as many screens as possible enhances the chances of discovering a useful commercial drug. Thus, host (source) countries can optimize the potential value of their resources through expanding their collaborations with suitable screening organizations, subject to the negotiation of agreements protecting the rights of all the parties. Projects such as the ICBGs in which samples from a given project are exposed to screens in multiple end use areas, including potentially three or four therapeutic targets as well as agricultural or energy targets, would logically enhance probabilities of success. However, to date, this younger program has yet to yield a commercial product, despite many successes in other areas.

27.4.2 Drug Development Costs and Time Frame

Numerous estimates of costs and times of drug development have been proposed. In 1991, the estimated cost of “bringing a new medicine to the market” was US\$231 million [39], and current estimates range from over US\$800 million to US\$1.7 billion [40] (although see Angell [41] on how these calculations are made). In considering costs, allowance must be made for the considerable costs of research and development devoted to the many potential leads and candidates which eventually fail to become commercial products, as well as the substantial costs of “borrowing money” to finance these very expensive enterprises.

The time frames for drug discovery and development also vary considerably. ten Kate and Laird [10] provide estimates ranging from 7 to 18 years. In the case of Taxol[®], 30 years elapsed from initial collection of the source plant material (1962) to final approval of paclitaxel (1992). Another valuable case study is that of the discovery and development of the cholesterol-lowering drug, lovastatin, where some 30 years elapsed between the discovery of HMG-CoA as the major rate-limiting step in cholesterol biosynthesis to the final approval of lovastatin as a drug [39]. With the discovery and development processes constantly being streamlined, the time frame for “bringing a new medicine to the market” should be greatly reduced; nevertheless, it remains an extremely costly and time-consuming operation.

The time frames for development of an agrochemical, herbal drug, or dietary supplement may be somewhat shorter than for conventional drugs, but there remain

considerable challenges involved in their development. Safety and toxicity studies are still necessary for these products, while there are substantial issues related to achieving acceptable quality control of herbal drugs and dietary supplements [10].

27.4.3 Recommended Collaborative Process

It is clear from the above discussions that the preclinical and clinical drug development processes are costly and lengthy undertakings which require considerable international and multidisciplinary collaboration. The same principle applies to the development of other bioactive entities, such as agrochemicals, which have to meet strict regulatory requirements, although the total costs are significantly less than those for drugs. The discovery and development processes must be carried out with prior informed consent and the necessary collection and export permits from the relevant source country government and stakeholders, and working in close collaboration with source country organizations. Appropriate agreements must be negotiated encompassing the terms of training and technology transfer, protection of the environment and sustainable development, and plans for benefit-sharing. Mechanisms for establishing such agreements have been discussed above, and based on the NCI and ICBG experience, a “two-phase approach” to the exploration of source country genetic resources as a source of potential novel drugs and other bioactive agents may often be the best approach.

A two-phase approach is favored, both to shorten the time required to negotiate an agreement where the probability of commercialization is low, and facilitate development decisions for nonblockbuster products since the terms of the second phase, the Phase II Commercial Development Agreement (CDA; Sect. 27.4.3.2), could vary considerably depending on the nature of the drug (or other agent) being advanced into preclinical and clinical development. If the drug has been selected for treatment of a rare disease with a small patient population, or for a tropical disease with no developed country market, the returns on commercialization and sales are likely to be far smaller than if the candidate is being developed for treatment of a common disease having a large patient population and potentially large sales. If a drug has the potential for large sales, and hence large revenues for the company involved in its development, the percentage of royalties or other possible benefits which could accrue to the source country could be substantially higher.

This approach has been widely embraced by the research and policy communities, including in the Nagoya Protocol on Access and Benefit-Sharing (<http://www.cbd.int/abs/>), a supplementary agreement to the Convention on Biological Diversity adopted by the Conference of the Parties to the CBD at its tenth meeting held on October 2010 in Nagoya, Japan.

27.4.3.1 Phase I. Basic Research Agreement

Phase I of the process can involve negotiation of a *Basic Research Agreement* between a research organization in a “developed” country and another research organization or relevant government department or agency in the source or host

country. The significant involvement of a suitably qualified local organization is an ethical standard today even where not legislated. It is also important to enable transparency of the project, to maximize understanding of the legal environment, to facilitate logistical feasibility, and to minimize the likelihood that follow-up of an exciting outcome is not blocked by regulatory bodies or political turmoil. The Basic Research Agreement should incorporate terms of collaboration covering exchange of data, joint publication, training, and technology transfer. In addition, there should be requirements for adequate protection of the environment and endangered species.

Obtaining the prior informed consent of relevant local stakeholders (e.g., indigenous peoples, local communities, and healers, where appropriate) ideally should be the responsibility of the local collaborating organization, or if an appropriate collaborator is not identified, the relevant local government agency can often assist in this process. If a pharmaceutical or other company is involved as a partner with the research organization in negotiating the agreement, the possibility of establishing a trust fund to support local source country stakeholders in small community projects may be considered. Most importantly, the Basic Research Agreement should clearly require the negotiation of separate agreements (Phase II agreements) covering any agents which are subsequently selected for preclinical or equivalent advanced development.

An important but less commonly articulated benefit that can accrue to host country organizations in low- and middle-income countries is the development of long-term collaborative relationships with international scientists. Such things are not generally included in agreements. However, these relationships are especially important to a host country after a project is completed, and are an important avenue for future collaborative support for research and training and for access to scientific literature and modern technological innovations. ICBGs often have career-changing effects for participating scientists from both countries and can be transformative for smaller developing country organizations. But maintaining those collaborations in some form after a project terminates is often more important for the developing country partners than for US or European scientists and merits some forethought.

Selection of an agent for advanced (e.g., preclinical) development will probably trigger submission of an application for patent coverage, but it is important to emphasize that issue of a patent is far removed from the possibility of commercialization. In fact, very few patented agents ever reach the stage of commercialization. Generally, from available data we estimate that less than 4% of patented pharmaceutical drug candidates actually become commercial drugs [42].

27.4.3.2 Phase II. Commercial Development Agreement (CDA)

Selection of a drug lead candidate for preclinical or equivalent development should trigger negotiations of a new Phase II Commercial Development Agreement (CDA) covering the specific issues related to the development and possible commercialization of the candidate. Local scientists and communities should be involved in these negotiations or at the least kept abreast of their nature, trajectory, and terms, depending on the terms of the Phase I agreement and the nature of the collaboration.

The CDA should address terms of collaboration in the large-scale procurement of supplies of raw material for production of sufficient quantities of the drug candidate for preclinical and possible clinical development in the case of pharmaceutical agents. Such terms should address environmental impact studies, the possibility of sustainable harvest, and the possible need for cultivation of the source organism. The CDA should also include terms of collaboration in the production of the development candidate (extraction, isolation, analysis, etc.) depending on the facilities and expertise available in the source country, and training and technology transfer where appropriate, as well as training in the preclinical development aspects of a drug candidate (e.g., formulation, pharmacology). In the above two points, it must be noted that conditions of current Good Manufacturing Practice (cGMP) (e.g., approved facilities) have to be met to satisfy the requirements of the US Food and Drug Administration (FDA) and equivalent regulatory bodies in other countries. These are extremely expensive conditions to fulfill, and generally, these processes will be best performed by the collaborating research organization.

Finally, terms should be included covering milestone payments when certain stages of development are achieved (e.g., FDA approval for entry into Phase I clinical trials, completion of Phase I trials), and payment of a percentage of royalties on the sales of the drug, should it become commercialized. An attractive alternative or complement to royalties that may be considered by a source country may be the provision of supplies of the drug free or at highly discounted cost for treatment of the local population, and/or provision of other drugs more useful to the source country, or the granting of a royalty-free license for production of the drug for use in the source country only.

Given the very low success rate in actually developing a product to the stage of commercial use, it is strongly recommended that agreements should focus on short-term and accessible benefits such as training, technology transfer, and milestone payments, rather than attempting to maximize royalty payments which, in all likelihood, will never materialize. There are decided advantages to maximizing short-term benefits in terms of improving the capacity of host country organizations and personnel to perform the drug discovery and early development steps in-country, thereby optimizing the value of their resources. In addition, discovery of promising drug leads entirely in-country creates the opportunity for source country organizations to gain complete control of their inventions through application for appropriate sole source country inventorship patent coverage (composition of matter patents in the case of novel chemical entities or use patents in the case of novel uses for known chemical entities).

27.5 Study Questions

1. What are the prime objectives of the UN Convention on Biological Diversity? When first introduced, the CBD led to some unrealistic expectations. What were these expectations, and how would you address these issues when negotiating an agreement for initiating a joint biodiscovery exploration program with host

- country stakeholders, including government officials, institutional collaborators, and local communities?
2. In exploring the possibility of initiating biodiscovery programs in biodiversity-rich nations, research groups have often encountered obstacles on issues, such as identifying the correct points of contact for obtaining the necessary approvals, permits, etc. Elaborate on how you think the recently published Nagoya Protocol (April 2011) has addressed some of these problems.
 3. “A ‘two-phase approach’ to the exploration of host/source country genetic resources as a source of potential novel drugs and other bioactive agents may often be the best approach to initiating a biodiscovery program.” Discuss this statement, and identify the possible advantages and disadvantages of such an approach.
 4. You wish to carry out a biodiscovery project in country X in collaboration with country X institution and a local community. On the basis of the information and experiences recorded in this chapter, discuss the factors you would consider in conducting negotiations for entering into an agreement with the authorities in country X for initiation of the project.
 5. During the course of studying sponges collected in country X coastal waters as a source of novel bioactive compounds, you discover that the likely sources of some of the bioactive compounds are microbial symbionts. Microbial sources were not included in your original agreements with country X government authorities, nor with the local collaborating institution. Discuss what measures you would take in negotiating amendments of the agreements to include microbes as sources of bioactive compounds.
 6. Discuss the impact of biodiscovery programs on the conservation and sustainable development of biological resources in host/source countries.

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Part 6

Marine Toxins: A Problem for Public Health and Seafood Resources

Patrizia Ciminiello, Martino Forino, and Carmela Dell'Aversano

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Abstract

Once believed to affect only scattered areas of the world, nowadays, harmful algal blooms (HAB) plague virtually any coastal area of the planet. Usually caused by a pool of microalgae, HAB-related outbreaks not only harm human health but wreak havoc on maritime economy. Over the past decades, following the steadily increase of human poisonings, an ever-growing number of countries have been forced to set appropriate measures in order to cope with the sanitary

P. Ciminiello (✉) • M. Forino • C. Dell'Aversano
Dipartimento di Chimica delle Sostanze Naturali, Università degli Studi di Napoli "Federico II",
Via D. Montesano, 49, Naples, Italy
e-mail: ciminiel@unina.it, forino@unina.it, dellaver@unina.it

and economic predicaments brought about by HABs. Out of the thousand microalgae reported this far, only a limited number of them have been proven to produce marine biotoxins. Such molecules, once assumed by seafood, easily find their way up to the table of unaware consumers. Moreover, particular phytoplankton blooms can directly affect humans through contaminated marine aerosol. Depending on the symptoms shown by patients, the major human illnesses caused by toxin-contaminated seafood are commonly referred to as paralytic, neurotoxic, amnesic, diarrhetic shellfish, and ciguatera fish poisonings (PSP, NSP, ASP, DSP, and CFP, respectively). In this chapter, a wide-ranging and multifaceted overview of the main marine biotoxin classes is presented.

28.1 Introduction

As healthy a food for humans as it may be, occasionally, fish and shellfish can cause serious harm to consumers by accumulating high levels of natural marine biotoxins produced by noxious algae. Every year, some 50,000–500,000 human intoxications following exposure to marine biotoxins are reported worldwide with an alarming mortality rate on a global basis [1]. Until a few decades ago, only scattered locations seemed to be plagued by harmful algal blooms (HABs), while nowadays, every coastal State is virtually exposed to toxic outbreaks, often induced by more than just one toxic algal species. Out of the thousands of microscopic algal species, only several dozens have been this far individuated as producers of potent marine biotoxins [2, 3], frequently occurring in seawater in such small amounts as to not pose any hazard to human health and environment as well. Nevertheless, when toxic algal species happen to proliferate abundantly in seawater, they can be accumulated by filter-feeding shellfish, zooplankton, fishes, crabs, and tunicates, among others [4–6]. As a result, algal toxins find their way up through the food chain, landing onto the table of unaware seafood consumers.

The major illnesses following assumption of toxin-contaminated shellfish are commonly referred to as paralytic, neurotoxic, amnesic, diarrhetic shellfish, and ciguatera fish poisonings (PSP, NSP, ASP, DSP, and CFP, respectively), according to the symptoms shown by patients [6, 7]. Beyond these well-known classic intoxications, also other toxin-related poisoning syndromes have been described after exposure to azaspiracid toxins, yessotoxins, cyclic imines toxins, and palytoxins [6, 7]. ASP aside – which are caused by diatoms – all of the other major intoxications are basically due to blooming in the phytoplankton of dinoflagellates – microscopic, often unicellular, flagellated algae.

The HAB impact on public health grows even more alarming if it is considered that particular phytoplankton blooms can directly affect humans either accidentally swimming in infested waters or breathing contaminated marine aerosol.

Even though HABs often take place as massive “red tides” or blooms capable of discoloring seawater, sometimes, high concentrations of noxious cells get noticed only because of the harm they provoke by means of their potent biotoxins, which

rank among the most potent toxic compounds in the world, with some of them lethal to humans even at doses in the range of few micrograms per kilogram [8].

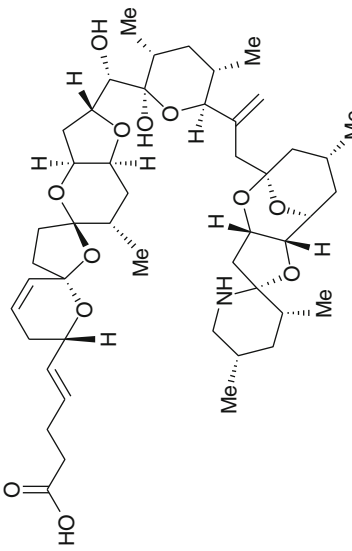
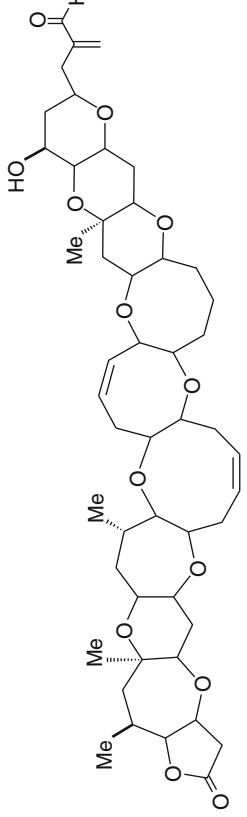
The role toxins play in the internal economy of their producers has not yet been totally understood. In this regard, toxins are likely used as tool for competing for space, for fighting predation, or even for warding off possible overgrowth of other organisms [9].

Unfortunately, toxin-contaminated seafood neither looks nor tastes any different from safe seafood, and no culinary treatment can guarantee inactivation of marine biotoxins. As a consequence, fish and shellfish farms have to run costly monitoring programs in order to check constantly the quality of their products before putting them on the market. At the moment, there are several chemical, functional, and biological methods able to check the occurrence of algal toxins in seafood, each with its own shortcomings. Considering that the only common feature of all of the known marine toxins is toxicity, it is little wonder that live-animal bioassay, such as the mouse bioassay, is still the most widely used detection method in any regulatory setting [10]. It is generally carried out by intraperitoneally injecting a given sample extract into a 20-g mouse kept under observation over a certain stretch of time, with the purpose of determining the onset of specific symptoms and eventually the time-to-death. Both symptoms and time-to-death are correlated to the kind as well as to the amount of a toxin possibly occurring in the injected extract. Toxicity is reported in terms of “mouse units,” which refer to the amount of toxin(s) capable of killing a mouse in a given stretch of time. Nonetheless, the mouse bioassay, even though suitable to the analysis of nearly every class of biotoxins, is quite controversial. In fact, it lacks specificity as it does not allow any differentiation between the various components within each class of toxins, and in addition, it requires both specialized animal facilities and proficiency without mentioning that many countries across the world have been dealing with both ethical and scientific issues regarding the employment of live-animal assay in their regulatory settings.

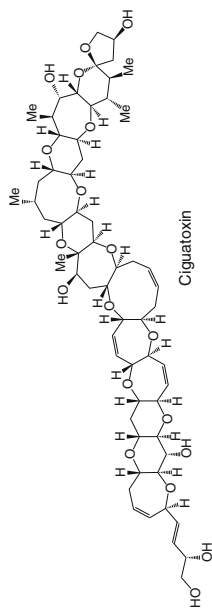
Besides their noxious impacts on human health, some marine toxins also induce severe ecological disruption through occasional widespread killing of fish, shellfish, marine mammals, seabirds, and any other living organism linked to the marine food web [4, 5]. Furthermore, the steady increase of HABs across the world has become a global concern also for the havoc they wreak on the economy. In fact, in coincidence with toxic algal proliferations, shellfish production areas as well as aquacultures are forced to stay closed for weeks, sometimes for months. From this predicament, fishery and tourism do not emerge unscathed either, since in the presence of HABs, governmental and competent institutions responsible for public safety have to shut down large stretches of coast to any fishing and/or recreational activity.

Causes of the worldwide expansion of HABs are still a long way off from being completely ascertained, but explosive growth of toxic plankton seems to be strictly intertwined with continuous changes in weather conditions. Also, other factors, such as variations in upwelling, temperature, transparency, turbulence, or salinity of seawater alongside concentration of dissolved nutrients, wind, and surface illumination, are likely playing a crucial role [9].

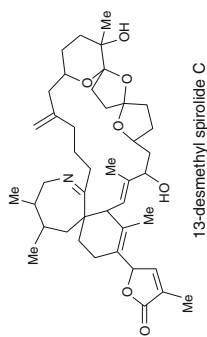
Table 28.1 Algal toxins: most common classes of marine biotoxins

Toxin class	Main algal sources	Toxicity	Structure of a representative
Azaspiracids	<i>Protoperidinium crassipes</i>	Neurotoxic	 <p style="text-align: center;">Azaspiracid</p>
Brevetoxins	<i>Karenia brevis</i>	Neurotoxic	 <p style="text-align: center;">Brevetoxin-1</p>

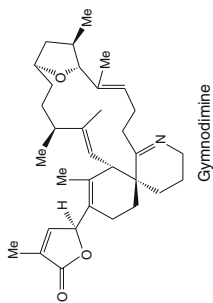
Ciguatoxins *Gambierdiscus toxicus* Ciguatera



Cyclic imines *Alexandrium ostenfeldii*
(spirolides)

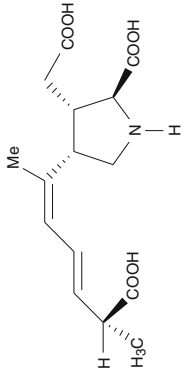
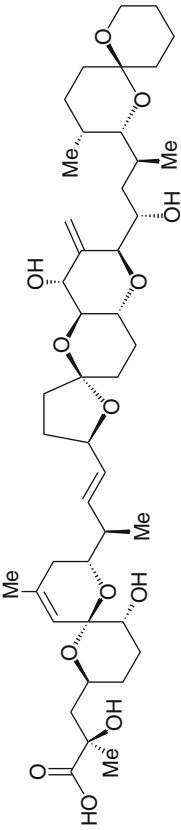


Karenia selliformis
(gymnodimines)

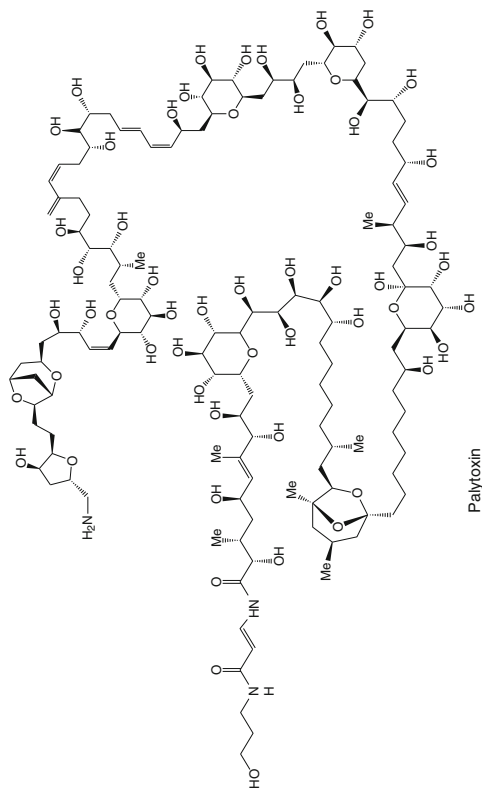


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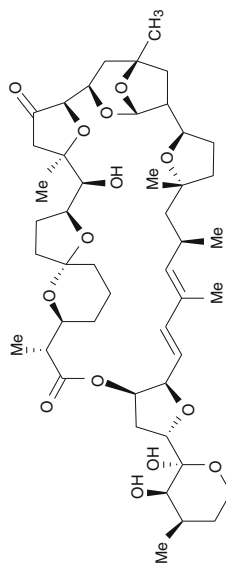
Toxin class	Main algal sources	Toxicity	Structure of a representative
Domoic acids	<i>Pseudo-nitzschia</i> species	Amnesic	 <p>Domoic acid</p>
Okadaic acids	<i>Dynophysis</i> species <i>Prorocentrum lima</i>	Diarrhetic tumor promoter	 <p>Okadaic acid</p>

Palytoxins *Ostreopsis* species Neurotoxic tumor promoter



Palytoxin

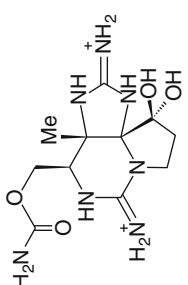
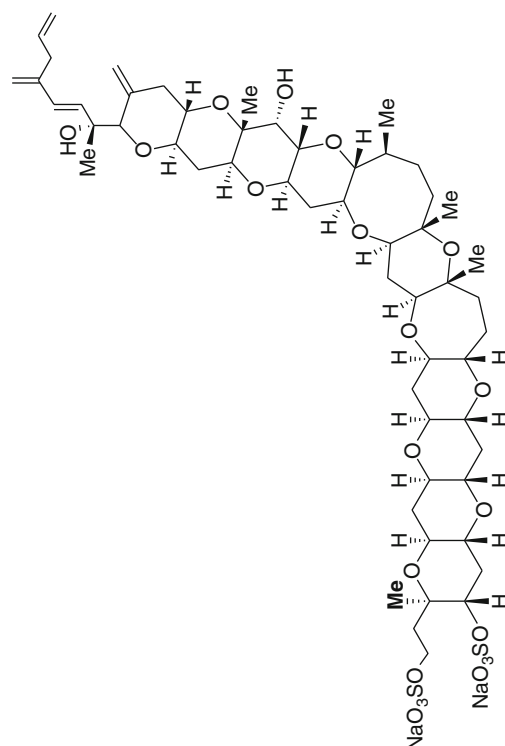
Pectenotoxins *Dynophysis* species Diarrhetic



Pectenotoxin-2

(continued)

Table 28.1 (continued)

Toxin class	Main algal sources	Toxicity	Structure of a representative
Saxitoxins	<i>Alexandrium</i> species	Paralytic	 <p>The structure of Saxitoxin is a complex pentacyclic molecule. It features a central five-membered ring with a nitrogen atom. This ring is fused to a six-membered ring containing a carbonyl group and a methyl group. Another six-membered ring is fused to the five-membered ring, containing a hydroxyl group and a methyl group. The fifth ring is a five-membered ring with a nitrogen atom, which is part of a guanidinium-like group. The overall structure is highly symmetrical and contains several nitrogen and oxygen atoms.</p> <p style="text-align: center;">Saxitoxin</p>
Yessotoxins	<i>Protoctercatium reticulatum</i>		 <p>The structure of Yessotoxin is a long, complex polyether chain. It consists of a series of interconnected rings, including several six-membered rings and one seven-membered ring. The chain is highly branched and contains numerous oxygen atoms, methyl groups, and a terminal vinyl group. The structure is highly symmetrical and is characteristic of the yessotoxin family.</p> <p style="text-align: center;">Yessotoxin</p>

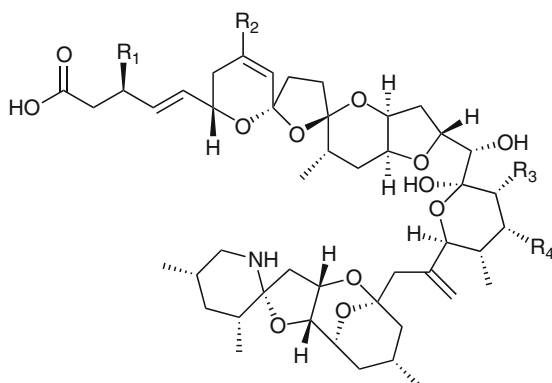
Chemically, marine toxins are often large molecules and only available in small quantities (Table 28.1). So, investigation of marine biotoxins structure usually requires employment of sensitive NMR- and mass spectrometry-based techniques along with HPLC analysis and sometimes combination of chemical degradation and partial or total synthesis as well.

Etiological studies are also a challenging goal since they call for in-depth knowledge in marine ecology and analytical chemistry alike. In this frame, once a candidate organism is thought to be the producer of a given toxin, it needs to be cultured with the purpose of confirming its toxigenicity. Still, some species are difficult or totally unable to be cultured, without mentioning that not all of the clones produce toxins in quantities sufficient for a chemical analysis.

28.2 Azaspiracids: A Recent Class of Toxins Targeting the Human Gastrointestinal Tract

The recently discovered azaspiracids (AZAs) are toxins structurally characterized by a polyether backbone and some unique structural features: a trispiro ring assembly, an azaspiro ring fused with a 2,9-dioxabicyclo[3.3.1]nonane, and a terminal carboxylic acid group (Fig. 28.1).

The first incident due to azaspiracids occurred in the Netherlands in 1995 following consumption of Irish mussels (*Mytilus edulis*) [11]. The symptoms of intoxication closely resembled those associated with DSP including vomiting,



	R ₁	R ₂	R ₃	R ₄
Azaspiracid-1 (AZA1)	H	H	Me	H
Azaspiracid-2 (AZA2)	H	Me	Me	H
Azaspiracid-3 (AZA3)	H	H	H	H
Azaspiracid-4 (AZA4)	OH	H	H	H
Azaspiracid-5 (AZA5)	H	H	H	OH

Fig. 28.1 Structures of principal azaspiracids (AZAs)

severe diarrhea, stomach cramps, and headache. AZA1 was identified as the causative toxin of the outbreak [12]. Later on, the methyl and desmethyl analogues of AZA1, namely AZA2 and AZA3, respectively, were identified in Irish mussels responsible for a second human intoxication [13]. Hydroxylated derivatives of azaspiracids have also been identified in shellfish and structurally determined [14, 15]. Up to now, approximately 20 analogues have been reported to occur naturally in shellfish [16]. However, only two of these, AZA1 and AZA2, have been reported to be produced by the previously unknown dinoflagellate *Azadinium spinosum* [17]. Following development of liquid chromatography–mass spectrometry (LC–MS) methods for determination of azaspiracids, a wide geographical distribution of such toxins across Europe was established, including Norway, the eastern coasts of England, Denmark, Northern France, and northwestern coasts of Spain [18].

Mice-based toxicological studies demonstrated that the major target of azaspiracids is the gastrointestinal tract, where an extensive necrotic atrophy of lamina propria of the villi was observed [19]. Multiple organ damages were also observed mainly in the liver (fatty changes and single cell necrosis) and in T and B lymphocytes in the thymus and spleen [20]. Repeated administrations of the toxins were shown to induce lung tumors [21]. However, the limited availability of pure azaspiracids limited the statistical value of the in vivo studies.

The mechanism of action of azaspiracids has been studied using in vitro systems. Roman et al. indicated the cytoskeleton as an important cellular target for AZA1 and that it does not induce apoptosis [22]. In addition, AZA1 did not alter membrane potential in excitable neuroblastoma cells, suggesting that it does not produce neurotoxic effects. In human lymphocytes, AZA1 increased cytosolic calcium and cAMP levels and did not affect cytosolic pH. The effect of AZA2 and AZA3 on intracellular cAMP, cytosolic calcium, and pH has also been evaluated, and the obtained results highlighted a structure–activity relationship (SAR) among the different azaspiracids on intracellular pH and calcium levels [23]. Risk assessment individuated a safe level of 0.16 mg/kg of azaspiracids in shellfish. This was adopted by the food safety authority of Ireland and proposed to the European Food Safety Authority and Codex Alimentarius.

28.3 Brevetoxins: Typical Aerosolized Red-Tide Neurotoxins

Brevetoxins are neurotoxic polyether toxins produced by *Karenia brevis* (formerly known as *Gymnodinium breve* and *Ptychodiscus brevis*). This toxic microalga has a long history of extensive blooms in the Gulf of Mexico that initiated offshore and subsequently carried inshore by wind and current conditions [24, 25]. These blooms have caused massive fish kills and respiratory irritation in humans [26]. It was later realized that the toxins in these blooms could also be passed on to humans via shellfish to cause a syndrome named neurotoxic shellfish poisoning (NSP). In the early 1990s, outbreaks of neurotoxic shellfish toxicity were also reported in New Zealand and Australia and resulted in the identification of additional *Gymnodinium* species producing NSP-like toxins [27]. This dinoflagellate species produces two

types of lipid-soluble toxins: hemolytic and neurotoxic compounds [28] causing massive fish kills, bird deaths, and marine mammal mortalities [29, 30].

Recently, neurotoxins have also been found in other fish-killing flagellate species, *Chatonella marina*, *C. antiqua*, *Fibrocapsa japonica* and *Heterosigma akashiwo* [31–33].

It was only in the 1960s, nearly two decades after the toxic episodes in Florida caused by *K. brevis*, that a toxic fraction causing a neurological poisoning was isolated from this dinoflagellate and contaminated shellfish [34]. Over the next years, substantial efforts were dedicated to purifying brevetoxins. However, it was not until 1979, with the introduction of high-pressure liquid chromatography, that the primary congeners of brevetoxins were isolated [35], and within the next 5 years, their long cyclic polyether structures were elucidated by X-ray crystallography and NMR [36, 37].

Like many of the known marine toxins, brevetoxins are tasteless, odorless, and heat (up to 300°C) and acid stable.

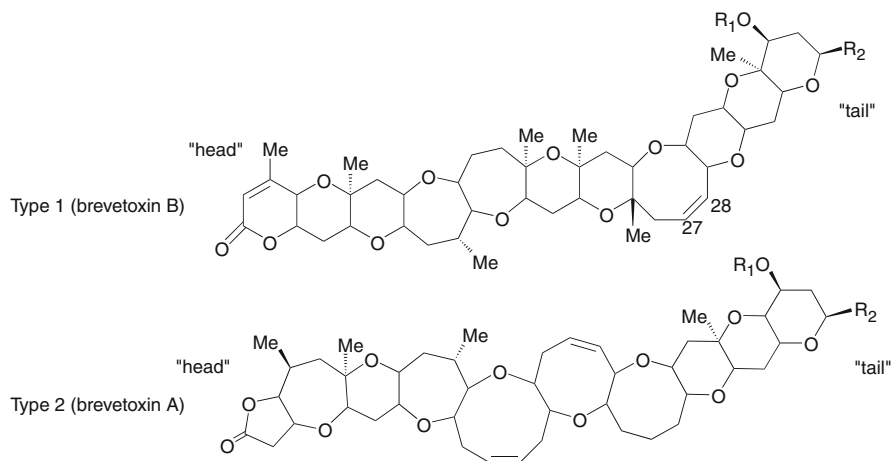
Structurally, brevetoxin congeners fall into two types based on their backbone structure (Fig. 28.2): brevetoxin B backbone (type 1) and brevetoxin A backbone (type 2) [38, 39]. The B-type backbone consists of 11 fused cyclic ether rings, while the A-type backbone is formed by ten fused cyclic ether rings, including a unique nine-membered ring in the E-position connecting the A-D and F-J moieties, thus inducing greater flexibility than that found in the B backbone. Type 1 and type 2 toxins share a lactone in the A ring (“head” of the molecule) and a conserved structure on the “tail” ring, comprising three six-membered fused cyclic ether rings with conserved R-ring substitutions. Both ends are required for the toxicity of brevetoxins. Proximal to the three six-membered rings, there is an eight-membered ring that gives the molecule flexibility to form a boat-chair or crown conformation.

Among brevetoxins, PbTx-2 T is the major brevetoxin produced by *K. brevis* [39]. This alga also produces shorter ring structures (Fig. 28.3) with only four-fused cyclic ether rings (7, 7, 6, 6), named hemibrevetoxins [40]. Two five-fused cyclic ether rings (6, 7, 6, 7, 7) have also been described and named brevenals [41, 42].

Brevetoxins are depolarizing substances that open voltage-gated sodium (Na^+) ion channels in cell walls interacting with neurotoxin binding site 5 on the α -subunit of the channel in a 1:1 stoichiometry [43]. This alters the membrane properties of excitable cell types in ways that enhance the inward flow of Na^+ into the cell, resulting in inappropriate opening of the channel under conditions in which it is normally closed, and it also inhibits channel inactivation. The increased membrane permeability to sodium initially determines excitatory cellular response (including release of neurotransmitters at some synapses), then followed by loss of cell excitability, leading to paralysis [44].

The mouse LD50 is 170 $\mu\text{g}/\text{kg}$ body weight (0.15–0.27) intraperitoneally, 94 $\mu\text{g}/\text{kg}$ body weight intravenously, and 520 $\mu\text{g}/\text{kg}$ body weight orally [45]. Pathogenic dose for humans is in the order of 42–72 mouse units.

In humans, the symptoms of NSP intoxication may occur after either inhaling aerosol containing the toxins or as a consequence of eating contaminated seafood. In the former case, symptoms include primarily respiratory distress, as well as eye and nasal membrane irritation, caused principally by exposure to sea-spray aerosols



Toxin	Type	R ₁	R ₂
PbTx-1	2	H	
PbTx-2	1	H	
PbTx-3	1	H	
PbTx-5	1	COCH ₃	
PbTx-6	1	H	27,28 epoxide
PbTx-7	2	H	
PbTx-8	1	H	
PbTx-9	1	H	
PbTx-10	2	H	

Fig. 28.2 Structure of brevetoxins (PbTxs)

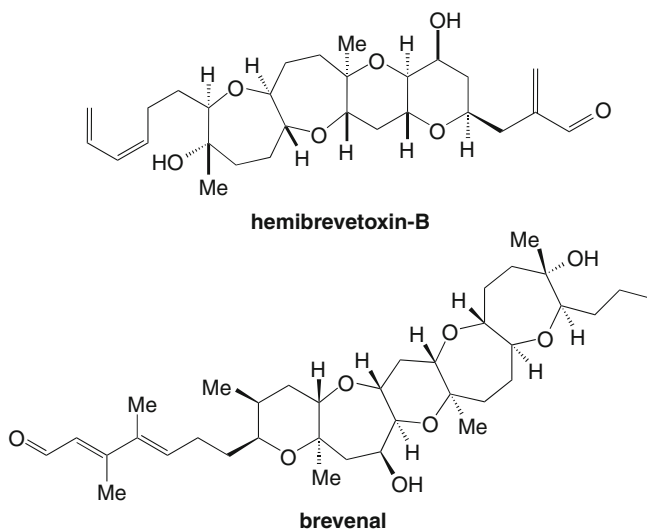


Fig. 28.3 Structure of hemibrevetoxin B and brevenal

and by direct contact with toxic blooms while swimming [46]. When intoxication is through contaminated shellfish, the symptoms are more severe than those found when contaminated aerosol is involved and include nausea, tingling and numbness of the perioral area, loss of motor control, and severe muscular pain [47]. There have been no reported fatalities from NSP, although the toxin kills test mammals when administered by various routes, including the oral one.

To date, brevetoxin-group toxins have not been reported in shellfish or fish from Europe. However, the discovery of new algae producing brevetoxins and the apparent trend toward expansion of algal bloom distribution suggest that this group of toxins could also emerge in Europe. Currently, there are no regulatory limits for these toxins in shellfish or fish in Europe.

28.4 Ciguatera: A Fitting Example of How Chemical Structure of Marine Biotoxins Is Investigated

In subtropical and tropical regions, consumption of contaminated coral reef fishes may cause a syndrome referred to as ciguatera, so called after the Caribbean word “cigua” indicating small marine snails whose ingestion had long induced human poisonings [48]. Every year, some 25,000 people are affected by ciguatera fish poisoning (CFP) that for such a reason has long been regarded as a world health problem [49]. The exogenous origin of the causative agent of ciguatera has been easily ascertained because fish toxicity entwined with this poisoning has all along fluctuated individually, seasonally, regionally, and even annually. In the late 1960s, a Hawaiian research group isolated from moray eels a toxin – named ciguatoxin (CTX) – that was proposed to be accumulated in fish by the food chain [50].

To the aim of tracking the real producer of CTX down through the food chain, Yasumoto et al. chose to investigate the guts of a small surgeonfish, *Ctenochaetus striatus*, on the basis of the following considerations: (1) the fish was clearly intertwined with many ciguatera outbreaks in Tahiti, (2) the fish grazes on a limited variety of microalgae and other microorganisms, and (3) it is a favorite prey for carnivores thus being a clear link with larger fishes in the food chain. The outcome of Yasumoto's studies was the identification in the guts of the analyzed fish of a lipophilic toxin chromatographically identical with CTX [48]. In the late 1970s, in the digestive contents from *C. striatus* was detected the occurrence of a dinoflagellate successively classified as *Gambierdiscus toxicus* that is now well known to be the producer of ciguatera toxins [51]. This confirmed the hypothesis that surgeon fishes obtain CTX from their diet and transfer it to carnivores through the food chain.

Ciguatoxins are a class of more than 20 heat-stable, lipid-soluble, cyclic polyether molecules whose chemical architecture is strictly reminiscent of that of brevetoxins [52–57] (Fig. 28.4). The planar structure of ciguatoxin was achieved by Yasumoto et al. who had to work on less than 1 mg of pure compound isolated from 124 kg of viscera deriving from 4 t of contaminated moray eels [52]. Despite the very small amount of pure compound, Yasumoto succeeded in elucidating the structure of CTX by extensive NMR analysis. Successive studies on both wild and cultured *G. toxicus* allowed the isolation and structure determination of further CTXs, such as gambierol [58], and a potent antifungal compound named gambieric acid [59]. Yasumoto could also establish the stereochemistry of the isolated CTXs by resorting to a combination of chiral fluorescent HPLC reagents or anisotropic NMR reagents with chemical degradation and synthesis of partial structures [60].

With regard to their biological activity, CTXs give rise to a wide array of symptoms remarkably varying depending on the geographic region that can be classified in four main categories: gastrointestinal, neurological, cardiovascular, and general symptoms [61]. If injected intraperitoneally into a mouse, ciguatoxin shows a DL_{50} of 0.45 $\mu\text{g}/\text{kg}$, while oral intake of 0.1 μg of toxin can cause illness in humans. As previously pointed out, CTXs chemically resemble brevetoxins, of which they exert also the same mechanism of action. In fact, CTXs activate the voltage-sensitive Na^+ channel at nM to pM concentrations thus being around 30-fold more affine than brevetoxins [62]. CTXs are particularly active on sodium channels located along peripheral nerves (nodes of Ranvier) thus inducing a massive influx of Na^+ with cell depolarization and the onset of spontaneous action potentials in excitable cells [63]. As a result, plasma membranes are no longer able to preserve the internal environment and the volume of cells with a consequent alteration of bioenergetic mechanisms. Concerning the cardiovascular impact of CTXs, it must be underlined that once these toxins make Na^+ move intracellularly, cells start extruding sodium and taking up calcium, which is a known intracellular trigger for muscle contraction. Indeed, an increased force of cardiac muscle contraction is a common symptom associated to CFP. Likewise, surge of calcium concentrations in intestinal epithelial cells induced by CTXs

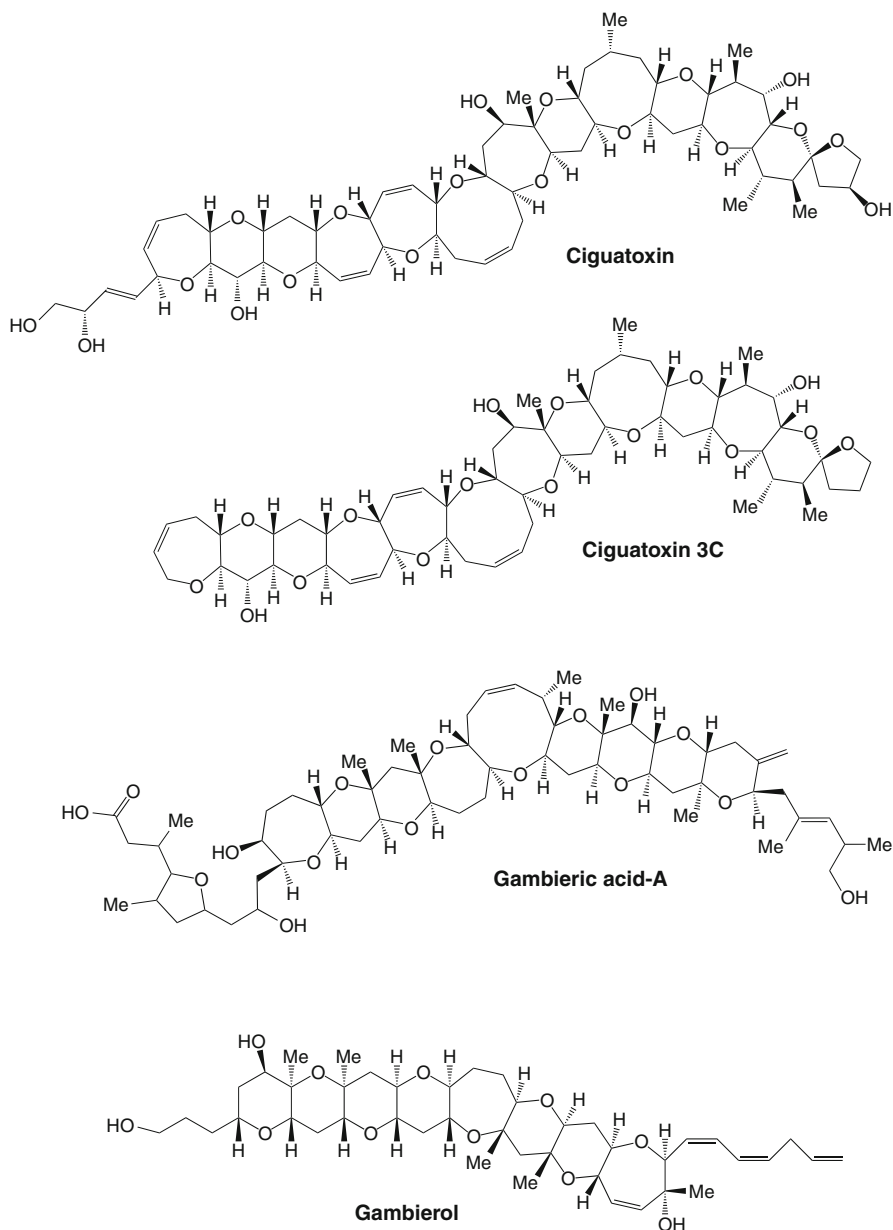


Fig. 28.4 Structure of principal ciguatera-related toxins

affects important cellular ion-exchange systems thus triggering fluid secretion and diarrhea [64].

Another important neurotoxin involved in CFP is maitotoxin (MTX, Fig. 28.5). So far, three further analogues of MTX have been identified from *G. toxicus* [65].

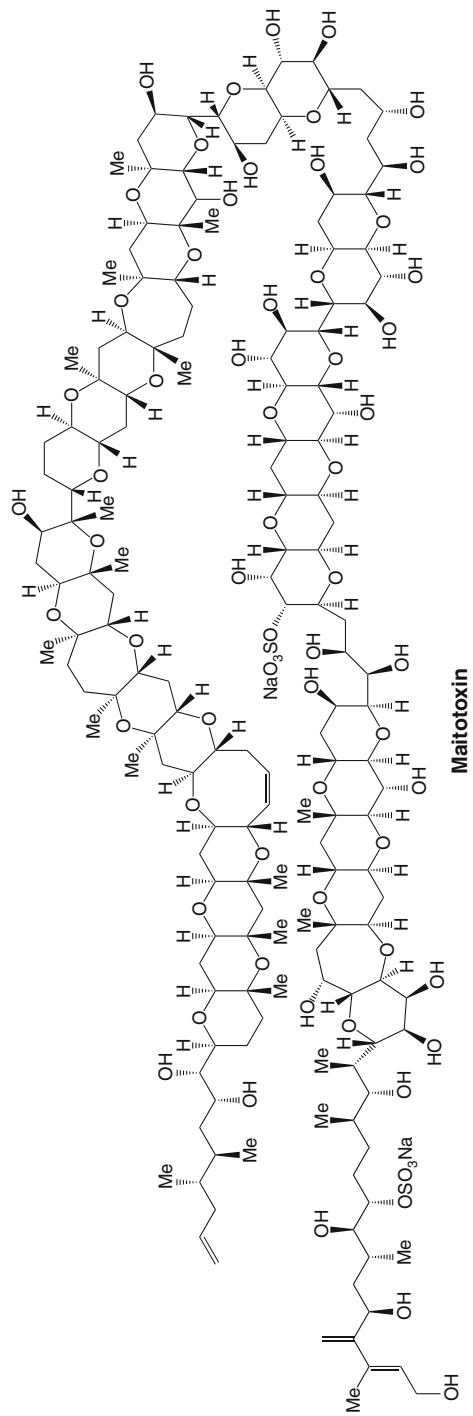


Fig. 28.5 Structure of maitotoxin

With a molecular weight of 3,422, maitotoxin is by far the largest nonpolymeric natural product of all, and apart from some proteic bacterial toxins, it is also one of the most toxic compounds. From a chemical point of view, MTX is a ladder-shaped polycyclic highly hydroxylated molecule. Pharmacological studies have proven MTX a potent activator of voltage-gated calcium channels [66]. At the moment, though, its primary target remains undefined and the molecular mechanism of action still presents many blind spots.

28.5 Cyclic Imine Toxins: A Category of Miscellaneous Emerging Toxic Compounds

Cyclic imine toxins constitute a heterogeneous class of marine biotoxins all featuring a macrocyclic structure with a typical imine moiety apparently being the bioactive pharmacophore. Quite a number of toxic compounds currently belong to this class of toxins:

- Gymnodimines [67]
- Pinnatoxins [68]
- Prorocentrolides [69]
- Pteriatoxins [70]
- Spirolides [71]
- Spiro-prorocentrimine [72]

In Fig. 28.6, representatives of each class of cyclic imines are reported. All of these compounds are referred to as a class of emerging toxins as in-depth knowledge about them is still lacking. First and foremost, it would be necessary assessing their real impact on human health. Cyclic imine toxins are indeed usually classified as fast-acting toxins since they induce death within minutes from their intraperitoneal injection into mice and show an acute threshold response in mammalian bioassays. Beyond this, though, the real toxicity of this class of toxins is still a long way off from being clearly elucidated. This is surely due to their relatively recent discovery – dated back to about two decades ago – with a concurrent lack of standards, reference, or purified material, which has so far hampered thorough toxicological evaluations. In addition, regulatory authorities have been all along reluctant to undertake studies on the effect of such a class of compounds in the absence of ascertained cyclic imine-related human intoxications. As a result, no regulatory limits have been set for any of the above cyclic imines, which are at the moment relegated to a category of compounds supposed safe for consumers until proven otherwise [73].

All of the cyclic imine toxins with the exception of spirolides – that have been detected worldwide – have been individuated only in scattered locations and in taxonomically restricted group of vectors. Nonetheless, their geographical distribution is reasonably bound to spread as monitoring programs increase and sensitivity in analytical methods improves.

Unlike pinnatoxins and pteriatoxins that have been detected exclusively in shellfish even though thought to represent a dietary incorporation in bivalves, all

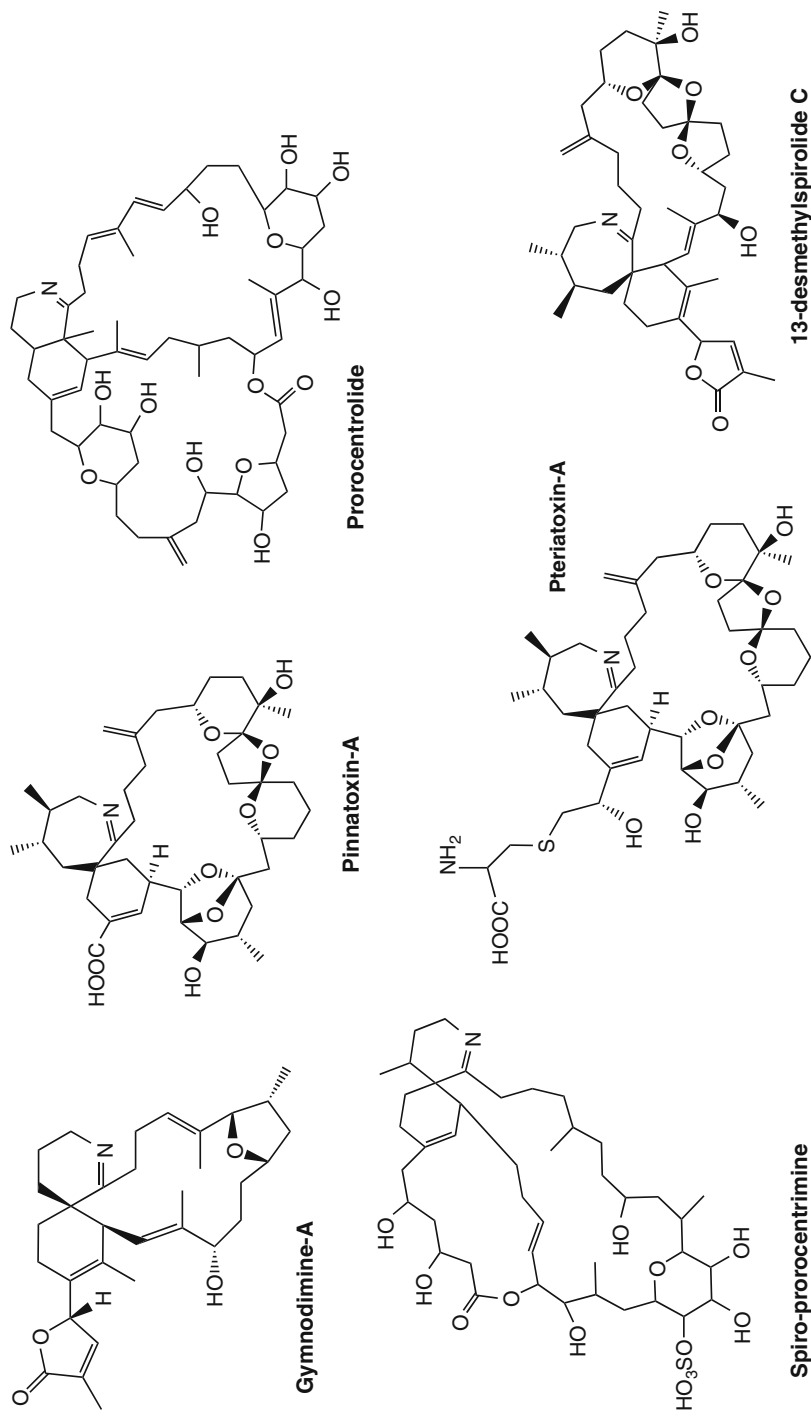


Fig. 28.6 Structure of representatives of cyclic imine toxins classes

of the other cyclic imines are strongly believed to be synthesized by either benthic or pelagic marine dinoflagellates on account of their chemical features apparently deriving from polyketide biosynthetic pathways common to other polyether biotoxins [74].

Gymnodinium sp. was first regarded as culprit species of gymnodimine toxicity [67], but successive taxonomic studies individuated the marine dinoflagellate *Karenia selliformis* as the most likely producer of this group of toxins [75].

Benthic or epiphytic *Prorocentrum* species are the microorganisms producing prorocentrolides [69] and spiro-prococentrimine [72], clearly termed after their producers.

Regarding the biological origin of spirolides, the marine dinoflagellate *Alexandrium ostenfeldii* has been described as their primary, if not exclusive, producer [76]. It is worthwhile highlighting that such a dinoflagellate is reported to produce different kinds of toxins depending on its geographical provenance. In fact, while Canadian [77] and Adriatic [78] strains of *A. ostenfeldii* were proven to produce high levels of a number of spirolides, New Zealand strains only produced PSP toxins [79]. Even more complex was the toxin profile of certain *A. ostenfeldii* populations from Scandinavia that were shown to produce both spirolides and PSP toxins [76].

As already described above, biological activity and mechanism of action of cyclic imine toxins are not comprehensively understood. What seems quite plain is that the intact imine group plays a crucial role in their toxicity as pointed out by a dramatic decrease in biological activity upon its hydrolysis. Indeed, spirolide E and F originating from keto amine hydrolysis are both basically inactive [80]. On account of the similar symptomatology shown by cyclic imine toxins, a common mode of action for all of them can be presumed. More in detail, spirolides seem to affect calcium ions [80], while gymnodimine activates sodium channels even in a far weaker way than other classic ion channel effectors, namely brevetoxins, tetrodotoxin, or even saxitoxin [67]. Moreover, both transcriptional and histological analyses of brain tissues revealed that muscarinic and nicotinic subreceptors were upregulated following exposure to spirolides. Consequently, such receptors could represent the spirolides' biological target [81].

Effort should be expended to extend the knowledge on cyclic imine toxins toxicology well beyond what is currently accessible, with the purpose of resolving their oral toxicity and assessing the real risks they pose to human health.

28.6 Domoic Acids: The Only Marine Biotoxins Produced by Diatoms

One morning in the summer of 1961, hundreds of crazed birds attacked the seaside town of Capitola, California. The birds “cried like babies” as they dove into streetlamps, crashed through glass windows, and attacked people on the ground. Most of the birds were sooty shearwaters, a normally nonaggressive species that feeds on small fish and comes ashore only to breed. The incident fascinated Alfred

Hitchcock, who was vacationing nearby and likely inspired one of his most famous movie, *The Birds*, which appeared in cinemas 2 years later.

In the winter of 1987, the agent that is now believed to be responsible for the Capitola incident struck on the opposite shore of the continent. This time, it struck higher on the food chain. Over a hundred people became extremely ill within hours after dining on cultured blue mussels in restaurants around Prince Edward Island in Canada [82]. It quickly became apparent that this was no ordinary outbreak of food poisoning. Vomiting, cramps, diarrhea, and incapacitating headaches were followed by confusion, loss of memory, disorientation, and (in severe cases) seizures and coma. A few exhibited emotional volatility, with uncontrolled crying or aggressiveness. Three elderly victims died in the hospital and one 3 months later [83].

The causative agent of this deadly syndrome, now known as amnesic shellfish poisoning (ASP), was identified as domoic acid [84, 85], a nonproteic amino acid with antihelminthic activity originally isolated in 1959 from a red marine macroalga, *Chondria armata* [86].

The chain-forming diatom *Pseudo-nitzschia multiseriis* (formerly known as *Nitzschia pungens*) was recognized as the causative agent of that toxic event [87, 88]. Several further species of *Pseudo-nitzschia* (*P. australis*, *P. pseudo-delicatissima*, *P. galaxiae*, *P. multistriata*, *P. pungens*, *P. seriata*, *P. turgidula*, *P. fraudulenta*, *P. delicatissima*, *P. calliantha*) have successively been found to produce domoic acid, although some species are not always toxic and there is a considerable variability in toxicity [89–91]. These diatom species are distributed worldwide. Consequently, accumulation of domoic acid in bivalves has also been reported from various parts of the world [92–94]. On the other hand, domoic acid is reported to accumulate in sea birds and marine mammals by a food-web transfer, which can result in mass mortality of these animals [95]. Scholin et al. [96] suggested that the origin of the domoic acid causing the deaths of sea lions on the California coast is *Pseudo-nitzschia australis*. Such findings show that domoic acid occurs widely in marine ecosystems. However, knowledge of the distribution of domoic acid in various organisms is limited to those in temperate waters. Little is known about accumulation of domoic acid in tropical marine organisms. It is worthwhile emphasizing that ASP is the only shellfish poisoning produced by a diatom.

Structurally, domoic acid (DA) is a water-soluble excitatory tricarboxylic amino acid (Fig. 28.7), belonging to the kainoid class of compounds, structurally resembling the excitatory neurotransmitter glutamic acid. Its molecular structure was determined in the late 1950s [86, 97–99] and then confirmed following total synthesis [100].

Several congeners of domoic acid have been identified so far, of which three geometrical isomers, isodomoic acids D, E, and F, and the C5'-diastereomer were found in small amounts in both the diatom and shellfish tissue (Fig. 28.7) [101, 102].

The biological mode of action of domoic acid results in neuronal depolarization; the resultant short-term memory loss is symptomatic of domoic acid poisoning

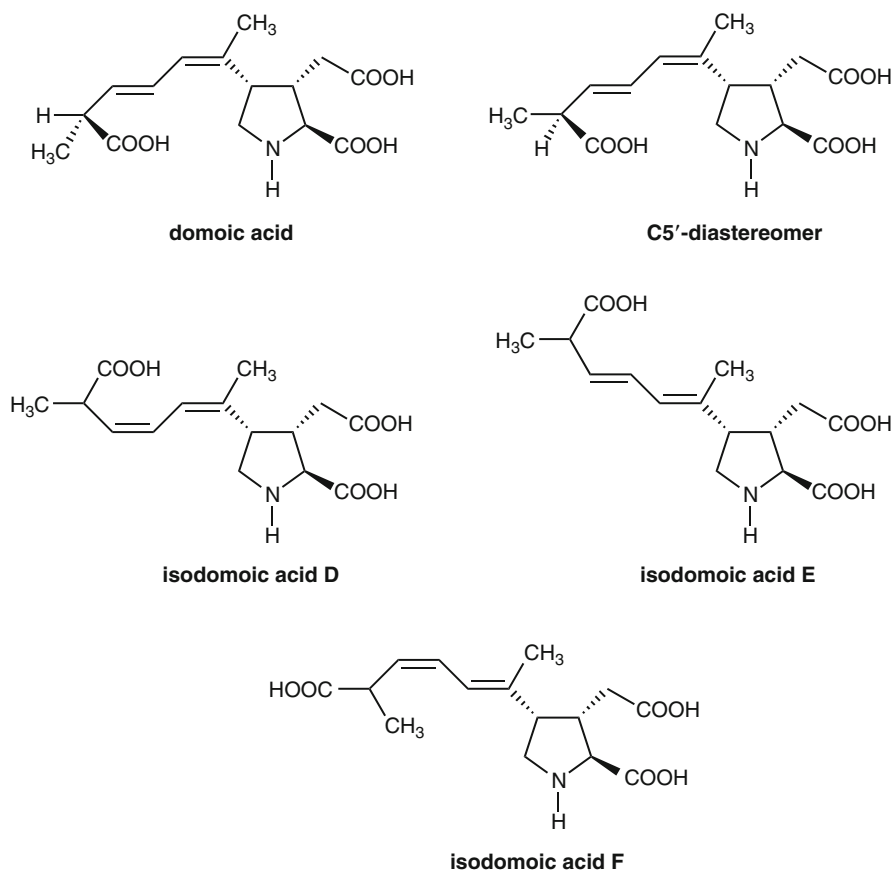


Fig. 28.7 Structure of principal domoic acids (DAs)

(reported by 25% of those affected by the Canadian amnesic shellfish poisoning outbreak). The mechanism of DA toxicity is explained by its structural similarity with the excitatory neurotransmitter glutamic acid but with a much stronger receptor affinity. Domoic acid binds predominantly to both kainate and AMPA subtypes of glutamate receptor [103], resulting in depolarization of neurons. Subsequently, the permeability to calcium ions increases [104]. This induces lesions in areas of the brain where glutaminergic pathways are heavily concentrated, particularly in the CA1 and CA3 regions of the hippocampus, areas responsible for learning and memory processing [105]. The loss of memory in patients intoxicated with mussel toxin appears to be similar to patient with Alzheimer's disease. However, the loss of memory in mussel-intoxicated patients was not affected by the age of patients, whereas symptoms of Alzheimer's disease intensify with aging and are generally noted in older people. Further, the findings that intellect and higher cortical functions are not influenced by DA intoxication distinguish the mussel-induced intoxication from Alzheimer's disease.

Other clinical symptoms of ASP include abdominal cramps, vomiting, diarrhea, incapacitating headaches, and disorientation. In the most severe case of poisoning, patients are victims of seizures, coma, profuse respiratory secretions, unstable blood pressure, and even death.

28.7 Okadaic Acids: The Subtle Threat of Potent Tumor Promoters

The syndrome diarrhetic shellfish poisoning (DSP) was first discovered in the 1970s following the occurrence of a mussel intoxication in northeastern Japan [106]. Ever since, DSP has known a steady spreading across the globe. It is essentially associated with seafood consumption such as mussels, clams, and scallops, which can accumulate dinoflagellate toxins in their digestive glands by seawater filtering process. The major toxin responsible for most DSP in humans is okadaic acid (OA) alongside a number of analogues termed dinophysistoxin-1 (DTX1) and dinophysistoxin-2 (DTX2), among others (Fig. 28.8) [107]. A number of further congeners are also involved in DSP syndrome, but all of them are believed to be either precursors or shellfish-modified metabolites of the active toxins [108].

OA was primarily isolated from the marine sponges *Halichondria okadae* and *Halichondria melanodocia*, and subsequently proven to be produced by dinoflagellates belonging to the genera *Dinophysis* and *Prorocentrum* [109, 110]. With regard to this latter, the benthic species *Prorocentrum lima* is worth being mentioned [111, 112], while among the *Dinophysis* species, *D. acuta*, *D. fortii*, *D. acuminata*, *D. norvegica*, *D. mitra* and *D. caudata* must be listed [113].

Chemically, OA is a polyether compound characterized by a carboxylic acid group and three spiro-keto ring assemblies, one of which connects a five with a six-membered ring.

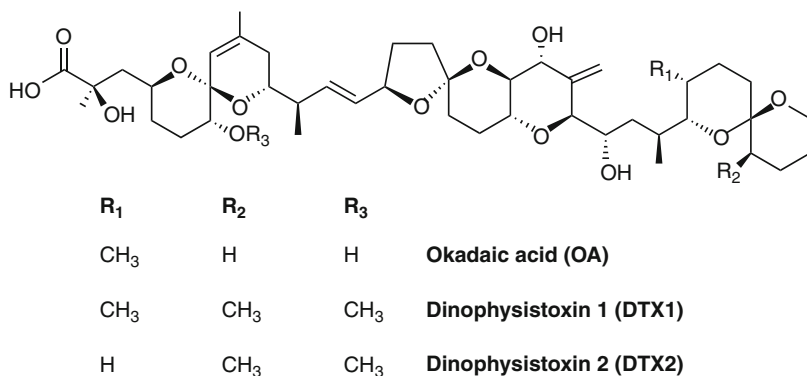


Fig. 28.8 Structure of principal okadaic acids (OAs)

Oral assumption of okadaic acid–contaminated seafood leads to the typical DSP symptoms usually within 30 min from ingestion. Symptoms shown by intoxicated patients are mainly gastrointestinal-like. Diarrhea, nausea, vomiting, and abdominal cramps are among the most common disturbances suffered by humans. No DSP-related casualty has been reported so far, but sometimes remarkable morbidity has required hospitalization. The treatment, if necessary, includes fluid replacement and electrolyte reintegration.

OA has long been known as a potent inhibitor of Ser/Thr protein phosphatases that represent an array of enzymes catalyzing dephosphorylation of phosphoserine or phosphothreonine residues in eukaryotes [114]. Ser/Thr protein phosphatases are involved in an extraordinary number of physiological processes in mammals ranging from glycogen metabolism to coordination of cell cycle and even gene expression. It follows that DSP toxins impact on Ser/Thr protein phosphatases can be devastating for living organisms. More in detail, of the four major groups of Ser/Thr protein phosphatases, OA inhibits PP2Ac at the lowest concentration ($IC_{50} = 0.2$ nM) and PP1c at the next lowest concentration ($IC_{50} = 20$ nM) as opposed to PP2B – which is slightly affected by the toxin – and to PP2C on which no effect is detectable [115]. Inhibition of Ser/Thr protein phosphatases by OA is known to provoke all of the gastrointestinal disorders in humans as soon as the toxin reaches the digestive tract.

Besides, there is another far more harmful threat posed by okadaic acids (OAs) to unaware contaminated seafood consumers: their potent tumor-promoting activity. Indeed, OA and DTX1 are classified as non-12-*O*-tetradecanoylphorbol-13-acetate (TPA)-type tumor promoters [116]. Unlike phorbol esters which activate protein kinase C, these two DSP toxins neither bind to phorbol ester receptors in cell membranes nor activate protein kinase C in *in vitro* studies [116]. OA and DTX1 have shown a potent tumor promotion activity on mouse skin. It appears that by inhibiting PP2A, OA causes a general decrease of cell adhesion and cytoskeletal reorganization resulting in an increased cell motility and invasiveness alike [114].

Considering the alarming harmfulness of OAs to consumers, it is apparent that a strict monitoring program needs to be run on seafood aimed at preventing possible human intoxications. With regard to this, it needs to be emphasized that the European Community has been recently forced to modify the official extraction procedure for analyzing seafood. In fact, by applying the old extraction method, yessotoxins – which in many toxic outbreaks have occurred together with DSP toxins – and OAs were recovered in the same organic layer [106]. Therefore, the mouse bioassay – the reference method in Europe to detect toxicity in seafood – could not lead to any confident assessment of the toxin(s) involved. So, as these two classes of toxins show a remarkably different toxicity on humans with, accordingly, very different official allowance levels in shellfish (16 μ g of OA and 100 μ g of yessotoxin in 100 g of mollusk, respectively), a new extraction method capable of separating yessotoxin in an aqueous layer and OAs in a lipophilic one was set up [117].

28.8 Palytoxins: Potent Tropical Toxins Now Rife Across the Mediterranean Basin

The lethal potency of palytoxin was well known to ancient Hawaiians who used to smear a moss containing such toxin on their spearpoints to make them fatal. According to an old legend, the lethal moss – known to native Hawaiians as limu-make-o-Hana – started lining the walls of a tide pool near the harbor of Hana after the ashes of an evil Shark God killed by some fishermen had been thrown into it [118]. In the early 1960s, thanks to some local informers, P. Helfrich and J. Shupe from the Hawaii Institute of Marine Biology succeeded in individuating the tide pool, from which they collected some samples of the toxic moss. Fascinated by the legend and propelled by his profound interest in marine toxins, Professor P. Scheuer from the University of Hawaii, a pioneer of the chemistry of marine metabolites, in collaboration with P. Helfrich and R. Moore, investigated the toxic samples collected from the legendary tide pool [119]. It was then assessed that the limu-make-o-Hana was not a seaweed but an animal belonging to the phylum Coelenterata – possibly a new species – assigned to the genus *Palythoa* [120] after which the molecule responsible for its high toxicity was named palytoxin. After its isolation in 1971 and the preliminary structural insights offered by Scheuer [119], it took nearly 11 years before the correct chemical structure of palytoxin (Fig. 28.8) was disclosed [121, 122]. It is a complex polyhydroxylated water-soluble compound, containing both lipophilic and hydrophilic part structures. In 1982, the complete stereochemistry of palytoxin – encompassing as many as 64 stereogenic centers in addition to eight double bonds – was disclosed [123], and a few years later confirmed by its total synthesis [124].

Following the first report on palytoxin in 1971, many research groups from across the world have undertaken scientific studies with the purpose of investigating this fascinating molecule. Efforts carried out by proficient chemists have significantly contributed to identify quite a number of palytoxin analogues (Fig. 28.9).

The real biological origin of this class of toxins remains controversial. In fact, even though several palytoxin-like compounds have been isolated from zoanthids belonging to the genus *Palythoa* – such as homopalytoxin, bishomopalytoxin, neopalytoxin, deoxypalytoxin [125], and 42-hydroxypalytoxin [126] – of late many have defended the assumption that palytoxins are indeed produced by microorganisms. In particular, dinoflagellates belonging to the genus *Ostreopsis* seem to be the most probable biogenetic originators of palytoxins [127, 128]. In 1995, in fact, Yasumoto isolated and structurally characterized some palytoxin analogues, named ostreocins, from extracts of the dinoflagellate *O. siamensis*. The major constituent of the isolated ostreocins, accounting for 70% of the total toxicity, resulted to be ostreocin D, whose chemical structure was assigned as 42-hydroxy-3,26-didemethyl-19,44-dideoxypalytoxin by detailed 2D NMR analyses of both the intact compound and its ozonolysis products [129, 130].

Successively, further palytoxin-like compounds, termed mascarenotoxins, were extracted from *O. mascarenensis* [131]. These toxins were confirmed as palytoxin analogues on the basis of their mass spectrum profile and fragmentation pattern obtained by nano-electrospray ionization quadrupole time-of-flight MS.

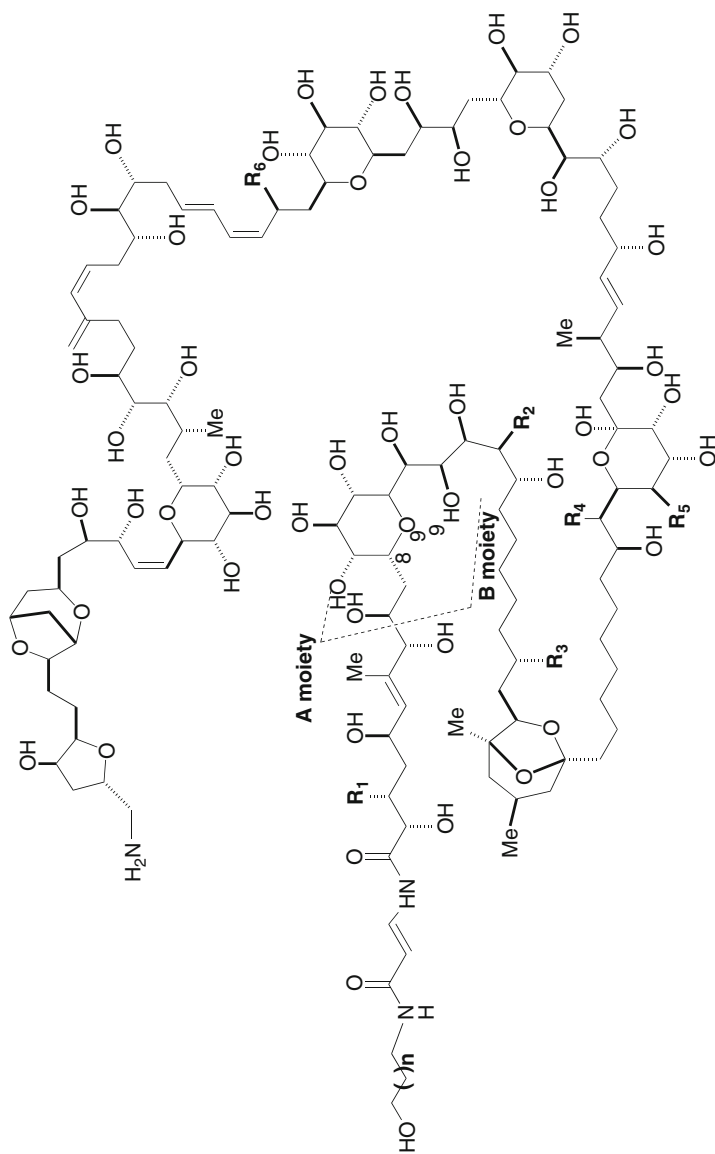


Fig. 28.9 (continued)

	n	R ₁	R ₂	R ₃	R ₄	R ₅	R ₆
Palytoxin	1	Me	OH	Me	H	OH	OH
Ostreocin-D	1	H	H	H	OH	H	OH
Homopalytoxin	2	Me	OH	Me	H	OH	OH
Bishomopalytoxin	3	Me	OH	Me	H	OH	OH
Neopalytoxin	1	-	OH	Me	H	OH	OH
Deoxypalytoxin	1	Me	OH	Me	H	OH	H
42-Hydroxy-palytoxin	1	Me	OH	Me	OH	OH	OH

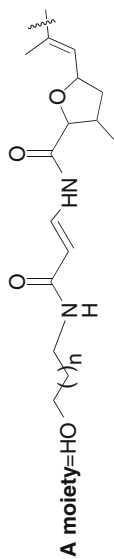


Fig. 28.9 Structure of palytoxin and some of its analogues

Recently, palytoxin and some of its analogues, named ovatoxins, have been detected in the Mediterranean *O. ovata* [132–134]. Ovatoxins have been identified by high-resolution LC–MS/MS and present molecular formulae similar to palytoxin's, with elemental composition differences residing either in the A or B moiety of palytoxin molecule [133, 134].

More in detail, by accurately interpreting complex HRMS/MS spectra, it was ascertained that (1) ovatoxin-a presents two oxygen atoms less than palytoxin and the same A moiety; (2) ovatoxin-b presents C_2H_4O more than ovatoxin-a, the structural difference between the two molecules residing in the A moiety whereas part structure B is identical; (3) ovatoxin-c presents the same A moiety as ovatoxin-b and an additional oxygen atom in the B moiety; and (4) ovatoxin-d and ovatoxin-e are isobaric compounds that present one oxygen atom more than ovatoxin-a, located either in the B moiety (ovatoxin-d) or in the A moiety (ovatoxin-e).

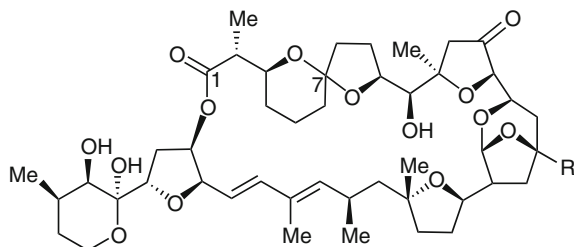
Palytoxins constitute a class of extremely potent nonproteic marine biotoxins, whose main biological target is the Na^+/K^+ -ATPase, membrane pumps maintaining ionic gradients critical to cell function [135]. The effect of palytoxins is basically a conversion of these ion-specific pumps into nonselective cationic pores, thus triggering several biological effects, some of which even life threatening.

Due to their high potency, palytoxins harm human health through diverse routes of exposure ranging from ingestion of contaminated seafood to dermal contacts, or inhalation of marine aerosol [136, 137]. Some fatal human poisonings attributed to palytoxin have been reported worldwide [138, 139]; the toxin has been suggested as the possible cause of clupeotoxism, a poorly understood syndrome caused by ingestion of edible fish [140]. Symptoms of intoxication include vasoconstriction, hemorrhage, ataxia, muscle weakness, ventricular fibrillation, pulmonary hypertension, ischemia, and death. Toxicity strongly depends on the route of administration. As way of example, palytoxin exhibits high toxicity in mammals when intravenously administered (LD50 ranging between 25 and 450 ng/kg) [141], while intragastric administration in rats shows a significantly lower toxicity (LD50 > 40 μ g/kg) [141, 142].

In the late 1980s, palytoxin was also identified as a skin tumor promoter [143, 144]. In contrast to TPA (12-O-tetradecanoylphorbol-13-acetate), palytoxin induces neither ornithine decarboxylase in mouse skin nor HL-60 cell adhesion. Furthermore, palytoxin neither binds to protein kinase C in vitro nor increases ornithine decarboxylase activity in mouse skin. On the basis of such evidence, palytoxin is classified as a non-TPA-type tumor promoter [145].

28.9 Pectenotoxins: Potent Cytotoxic Compounds with Still Unknown Potential Implications to Public Health in the Long Term

Pectenotoxins (PTXs) are lipophilic macrocyclic polyethers, whose chemical structures resemble okadaic acid in having cyclic ethers and a carboxyl group in the molecule. Unlike okadaic acid, in many PTXs, the carboxyl moiety is engaged in a macrocyclic lactone (Fig. 28.10). To date, 15 different PTXs have been isolated



R	C-7	C-7
CH ₂ OH	<i>R</i> Pectenotoxin 1 (PTX1)	<i>R</i> Pectenotoxin 2 seco acid (PTX2SA)
CH ₃	<i>R</i> Pectenotoxin 2 (PTX2)	<i>S</i> 7-epi-Pectenotoxin 2 seco acid (PTX2SA)
CHO	<i>R</i> Pectenotoxin 3 (PTX3)	
CH ₂ OH	<i>S</i> Pectenotoxin 4 (PTX4)	
COOH	<i>R</i> Pectenotoxin 6 (PTX6)	
COOH	<i>S</i> Pectenotoxin 7 (PTX7)	

Fig. 28.10 Structures of principal pectenotoxins (PTXs)

and characterized from a range of source organisms [146]. PTXs in filter-feeding organisms originate from dietary microalgae. Up to now, only the genus *Dinophysis* (e.g., *D. acuta*, *D. fortii*, *D. acuminata*, and *D. caudata*) has been implicated in contamination of shellfish with PTXs [146]. However, only PTX-2 and the seco acids of PTX-2 (PTX-2SA and epi-PTX-2SA) have been isolated from phytoplankton, while the other compounds have been detected only in shellfish samples. Therefore, it has been supposed that an oxidation occurs in the hepatopancreas of shellfish, and that many PTXs are products of shellfish metabolism after ingestion of PTX-producing microalgae [146, 147].

Pectenotoxins in shellfish are always accompanied by okadaic acids and/or yessotoxins and are co-extracted with them. So, initially, pectenotoxins have been grouped together with okadaic acids and yessotoxins in the DSP class. However, animal studies have indicated that pectenotoxins do not induce diarrhea and they are much less toxic than okadaic acid by oral administration [148]. In addition, unlike many DSPs which are potent phosphatase inhibitors, PTX-1 and PTX-6 are inactive against PP-1 and PP2A [149]. Thus, PTXs are currently considered as a separate group of toxins.

Since PTXs often co-occur with other phycotoxins in shellfish, no toxic episodes in humans can be unequivocally related to them, and therefore, there is no information about their toxicity to humans. It has been shown that PTXs are potentially cytotoxic [150] and cause necrosis to hepatocytes [151]. Nothing is known of the chronic toxicology of PTXs or the potential implications to public health in the long term.

28.10 Saxitoxins: The First News We Have About Seafood Toxin-Related Human Poisoning

One of the first recorded fatal cases of human poisoning after eating shellfish contaminated with dinoflagellate toxins happened in 1793, when Captain George Vancouver and his crew landed in British Columbia in an area now known as Poison Cove [152]. He noted that for local Indian tribes, it was taboo to eat shellfish when seawater became phosphorescent due to dinoflagellate blooms. However, the link between toxic shellfish and dinoflagellates was only ascertained right before World War II, when Sommer et al. studied toxic outbreaks that occurred in the San Francisco Bay between 1920 and 1937 [153, 154].

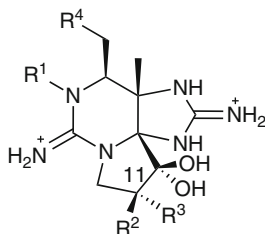
The causative toxins of these events are alkaloids, referred to as paralytic shellfish poisoning (PSP) toxins.

Historically, PSP incidents are associated with dinoflagellates, such as *Alexandrium* [155] – the first to be identified as PSP toxin producers – *Pyrodinium* and *Gymnodinium* species [156]. Besides, with developments in technology and research on marine algae, more species and classes of microorganism have been found to produce these toxins. Marine bacteria such as *Moraxella* [157] and *Alteromonas tetraodonis* [158] and freshwater cyanobacteria such as *Aphanizomenon flos-aquae*, *Anabaena circinalis*, *Lyngbya wollei*, *Cylindrospermopsis raciborskii* and *Protogonyaulax* [159] have all been found to produce or influence the production of these toxins in algae. Infection of *Ostreopsis lenticularis* by *Pseudomonas* species was also found to affect the production of toxins [160].

The parent compound of this class of toxins is saxitoxin (STX), of which over 29 congeners are currently known [161]. Chemically, they are tetrahydropurine derivatives whose structures vary by different combination of hydroxyl and sulfate substitutions at four sites on the molecule. Based on substitutions at R4, the saxitoxins can be subdivided into four groups: (1) the neurotoxic and highly potent carbamate toxins which include the nonsulfated saxitoxins (STX) and neosaxitoxin (NEO), and gonyautoxins (GTX1-GTX4) which are singly sulfated and more lethal than the nonsulfated carbamate toxins; (2) weakly toxic N-sulfocarbamoyl toxins (B1, B2, C1-C4) which are the least toxic to mammals of all the PSP toxins; (3) decarbamoyl (dc-) analogues which are thought to arise from the metabolism of dinoflagellate toxins within the shellfish; and (4) deoxydecarbamoyl (do-) toxins that have been detected until now only in Australian populations of *G. catenatum* [162] (Fig. 28.11).

Recently, the use of hydrophilic interaction liquid chromatography–mass spectrometry (HILIC–MS) followed by in-depth NMR investigation allowed to elucidate the structure of new analogues: 11 β -hydroxy-N-sulfocarbamoyl saxitoxin and the unusual 11,11-dihydroxy saxitoxin and 11,11-dihydroxy-N-sulfocarbamoyl saxitoxin [163, 164].

Saxitoxins are classified as fast-acting neurotoxins as PSP symptoms develop fairly rapidly, within 0.5–2 h after ingestion of contaminated shellfish, depending on the amount of toxin consumed [165]. In humans, the peripheral nervous system



STX = saxitoxin

NEO = neosaxitoxin

GTX = gonyautoxin

<u>R¹</u>	<u>R²</u>	<u>R³</u>	<u>R⁴</u>	Carbamate toxins	N-Sulfocarbamoyl toxins	Decarbamoyl toxins	Deoxydecarbamoyl toxins
				-O-C(=O)-NH_2	$\text{-O-C(=O)-NH-SO}_3^-$	-OH	-H
H	H	H		STX	GTX5, B1	dcSTX	doSTX
OH	H	H		NEO	GTX6, B2	dcNEO	
H	H	OSO ₃ ⁻		GTX2	C1	dcGTX2	doGTX2
H	OSO ₃ ⁻	H		GTX3	C2	dcGTX3	doGTX3
OH	H	OSO ₃ ⁻		GTX1	C3	dcGTX1	
OH	OSO ₃ ⁻	H		GTX4	C4	dcGTX4	
H	H	OH		11αOH-STX		11αOH-dcSTX	
H	OH	H		11βOH-STX		11βOH-dcSTX	
OH	H	OH		11αOH-NEO		11αOH-dcNEO	
OH	OH	H		11βOH-NEO		11βOH-dcNEO	

Fig. 28.11 Structures of principal paralytic shellfish poisoning (PSP) toxins

is affected, with symptoms ranging from tingling of the tongue and lips, followed by a numbness spreading toward the extremities, to vomiting, pain, diarrhea, loss of coordination, and breathing difficulty. In severe cases, ataxia, muscle weakness, and respiratory paralysis can occur. Symptoms can turn into coma or death, but recovery is generally complete, with no lasting side effects, when respiratory support is provided within 12 h of exposure. In unusual cases, because of the weak hypotensive action of the toxins, death may occur from cardiovascular collapse despite respiratory support.

Saxitoxins are potent, reversible blockers of voltage-activated sodium channels on excitable cells [166], but, due to the differences in charge state and substitution groups to the basic STX structure, they bind with different affinities to site 1 of sodium channels, resulting in different toxicities [167]. Thus, health risks can be reliably assessed just if the level of each toxin is individually determined.

28.11 Yessotoxins: Potent Toxic Compounds with Controversial Impact on Public Health

Yessotoxins (YTXs) represent a class of lipophilic polyether compounds, including a number of analogues that have been detected in shellfish and/or phytoplankton.

The parent compound of this class of toxins is yessotoxin (YTX), isolated for the first time in 1986 from the scallops *Patinopecten yessoensis* that were implicated in a diarrhetic shellfish poisoning episode in Japan [168]. The first unicellular organism identified as a producer of YTX was the dinoflagellate *Protoceratium reticulatum* (Claparède and Lachmann) Bütschli 1885 [169]. Subsequently, YTX has been found in cells of *P. reticulatum* from different places in Japan [170–172]; in the Adriatic Sea in Italy [173]; in Nova Scotia, Canada [174]; in Norway [175]; and in Spain [176, 177]. Other confirmed producers of YTXs are the dinoflagellates *Lingulodinium polyedrum* (Stein) Dodge [177, 178], and *Gonyaulax spinifera* Dodge [179]. Some authors suggested that the real producers of YTXs are bacteria associated with the dinoflagellates; however, to our knowledge, there is no solid evidence for this [180].

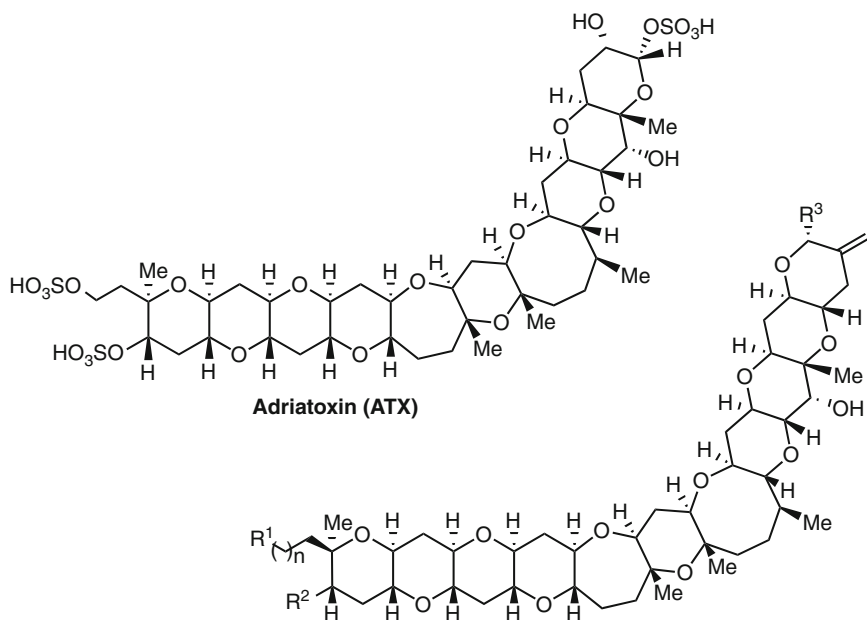
YTX production within and among dinoflagellate species tested to date is highly variable. As for the YTXs profile in the producing organisms, the data on the relative amounts are not so numerous, and all refer to cultures of *P. reticulatum*. The data reported in the literature concur that YTX is by far the major toxin produced by *P. reticulatum*. HomoYTX and a great number of other YTX analogues were sometimes shown to be present in the cultures, but in much lesser quantities [181]. There are, however, two reports in which the major toxin of *P. reticulatum* cultures is homoYTX [182, 183]. About the other two microalgae which were reported to produce YTXs, cultures of *Lingulodinium polyedrum* were shown to contain YTX [177], while *Gonyaulax spinifera* cultures were reported to produce unspecified YTXs identified by ELISA analyses [179].

Going to the contaminated shellfish, the YTX profile dramatically changes. YTX (or homoYTX) is no more the dominant toxin, but other analogues, such as hydroxylated and carboxylated derivatives, originating from metabolic oxidation within the mollusk, take the scene [181].

Chemically, yessotoxins are polycyclic ether compounds, structurally closely related to brevetoxins and ciguatoxins (Fig. 28.12).

The structure of YTX was established first [168, 184] and gave the basic framework to elucidate the structures of the other YTXs. It is a disulfated polyether, with a characteristic ladder shape formed by 11 adjacent ether rings of different sizes and a terminal acyclic unsaturated side chain consisting of nine carbons and two sulfate esters.

Since the initial discovery of YTX from Japanese scallops, a significant number of analogues, including the homoyessotoxins (homoYTXs), have been identified in toxic shellfish and/or algal cultures from different countries, suggesting the spread of this toxin worldwide [181]. Although the structure of some of them are still unknown [185], for many of them, full structure determination was carried out by NMR and/or liquid chromatography coupled with mass spectrometry (LC–MS).



	R ¹	R ²	R ³	n
Yessotoxin (YTX)	OSO ₃ H	OSO ₃ H		1
45-Hydroxyyessotoxin (45-hydroxyYTX)	OSO ₃ H	OSO ₃ H		1
45,46,47-Trinoryessotoxin (NorYTX)	OSO ₃ H	OSO ₃ H		1
Homoyessotoxin (homoYTX)	OSO ₃ H	OSO ₃ H		2
45-Hydroxyhomoyessotoxin (45-OHhomoYTX)	OSO ₃ H	OSO ₃ H		2
1-Desulfoyessotoxin (1-dsYTX)	OH	OSO ₃ H		1
Carboxyessotoxin (carboxyYTX)	OSO ₃ H	OSO ₃ H		1
Carboxyhomoyessotoxin(carboxyhomoYTX)	OSO ₃ H	OSO ₃ H		2

Fig. 28.12 (continued)

Noroxohomoyessotoxin (NoroxohomoYTX)	OSO ₃ H	OSO ₃ H		2
Noroxoyessotoxin (NoroxoYTX)	OSO ₃ H	OSO ₃ H		2
44,55-Dihydroxyessotoxin	OSO ₃ H	OSO ₃ H		1
1-Desulfocarboxyhomoyessotoxin	OH	OSO ₃ H		2
4-Desulfocarboxyhomoyessotoxin	OSO ₃ H	OH		2
45-Hydroxycarboxyessotoxin	OSO ₃ H	OSO ₃ H		1

Fig. 28.12 Structures of principal yessotoxins (YTXs)

There is evidence that some YTX analogues identified, such as hydroxylated and carboxylated derivatives, largely result from metabolism of yessotoxin in the shellfish after ingestion [186].

Yessotoxin and its analogues were at beginning included within the diarrhetic shellfish poisoning (DSP) group mainly because, following the standard procedure of mouse bioassay, they are extracted together with the DSP toxins okadaic acid (OA) and dinophysistoxins (DTXs), when they co-occur in contaminated shellfish. However, their toxic activities are significantly different; in fact, YTX and its analogues do not induce diarrhea and, compared to OA, show a much lower (four orders of magnitude) potency for the inhibition of protein phosphatase 2A [187]. On the contrary, their cardiotoxic effects have been demonstrated in mice after intraperitoneal (i.p.) and oral exposure of very high doses of YTX [188]. For these reasons, YTXs are not anymore included in the list of DSP toxins.

The toxicological studies carried out on YTX revealed that it is more toxic than any DSP toxin, when intraperitoneally injected, since the dose inducing 50% of mice lethality is very low (100 µg/kg) [188]; on the contrary, its oral toxicity is weaker, as deduced by considering that the oral dose of 1 mg/kg – which is ten times the lethal dose by intraperitoneal injection – does not kill the mice [187, 189]. Thus, on account of their diverse relative harmfulness, the European Food Safety Authorities have established an allowance level for yessotoxin in shellfish which is almost tenfold as high as that set for DSP toxins (16 µg of okadaic acid and 100 µg of yessotoxin in 100 g of mollusk, respectively) [117]. Accordingly, the EU set up a new protocol of extraction capable of separating OAs and YTXs in lipophilic and hydrophilic layer, respectively [117], as already described in the okadaic acids section of this chapter. Nevertheless, the recent finding of desulfocarboxy-homoYTXs in Adriatic mussels [190] raises some additional concerns, due to the fact that these two new desulfoyessotoxins are unexpectedly recovered together

with OAs in the lipophilic layer, so that the purpose of the European new protocol fails. Hence, a further overhaul of the EU control procedure would be urgently needed.

The chemical structure of YTX resembles that of brevetoxins, which are known to interfere with the voltage-sensitive sodium channel [191]; this finding suggested a possible interaction between YTX and cellular ion channels. Recently, however, it has been observed that YTX does not interact with sodium channels nor induces any competitive displacement of brevetoxins from site 5 of sodium channels [192]. It has been proposed that YTX may interact with calcium channels inducing an uptake of calcium in human lymphocytes [193, 194].

Another molecular effect elicited by YTX is the disruption of the E-cadherin system in epithelial cells [195, 196]. Finally, studies on immune cells point to phosphodiesterases as an intracellular target for YTX [197].

Although no human intoxication is known to have been caused by consumption of shellfish contaminated by YTXs, the widespread occurrence of these compounds in shellfish, sometimes at high levels, arouses an increasing interest in studying YTX toxicity. Unfortunately, data on the toxicity by oral ingestion for most YTX analogues are lacking; this appears particularly critical for some compounds, such as desulfoYTXs, where the lack of a sulfate group decreases their hydrophilicity in comparison to YTXs. So the biomembranes permeability and, consequently, the toxicity level by oral ingestion could be greatly affected. An additional issue related to the presence of desulfoYTXs in contaminated shellfish comes from two toxicological studies. In 1990, Terao et al. [187] found that totally desulfated YTX, differently from YTX, did not affect the heart but caused severe fatty degeneration and intracellular necrosis in the liver and pancreas. Finally, a recent report [198] provided evidence that desulfated YTX interacts with transmembrane helix domains.

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Abstract

Many marine animals produce protein toxins that are used for both predation and protection from predators. It is known that venomous stings by specific fish and jellyfish are sometimes fatal. For many years, detailed characterization of the causative toxins has been hampered by their instability. In recent years, various protein toxins have been successfully isolated and characterized from marine venomous animals. These studies have revealed that marine protein toxins exhibit unique structures and biological activities. A novel protein toxin family from the box jellyfish, the membrane-attack complex/perforin (MACPF) protein toxins isolated from the sea anemone, DNase II toxins from the starfish, and

H. Nagai

Department of Ocean Science, Tokyo University of Marine Science and Technology, 4-5-7

Konan, Minato-ku, Tokyo, Japan

e-mail: nagai@kaiyodai.ac.jp

a dermatopontin family toxin from fire coral are representatives of some of these unique toxins. In this chapter, the most current studies on protein toxins isolated from marine venomous animals are discussed.

29.1 Introduction

Numerous marine animals produce protein toxins that are used for both predation and protection from predators. Toxic proteins that cause severe illness or injury to humans by accidental contact are produced by marine venomous animals. Many species of fish, sea urchins, starfish, sea anemones, and jellyfish are often categorized as venomous marine animals. For example, the stonefish, Portuguese man-of-war, and *Chironex* jellyfish are famous for their painful stinging ability that may even result in human fatality.

Protein toxins produced by venomous marine animals have been extensively investigated for over 100 years. For example, Richet first examined the proteinaceous venom produced by the sea anemone *Anemonia sulcata*. In this study, dogs were intravenously injected with a small amount of venom before receiving a second dose 2–3 weeks later. The dogs immediately developed intense vomiting, pruritus, respiration difficulties, foaming at the mouth, bloody diarrhea, and died within a few hours. This hypersensitivity phenomenon was termed anaphylaxis [1]. Richet was later awarded a Nobel Prize for his investigations into anaphylaxis and its symptoms. Many studies of the protein toxins produced by jellyfish and sea anemones have subsequently been conducted. However, the precise characterization of these protein toxins remains incomplete. Interestingly, the vast majority of proteinaceous toxins synthesized by marine venomous animals are quite unstable, and thus, the isolation of these toxins in their active forms is often very difficult. In fact, this instability is the major reason why most proteinaceous marine toxins have not been precisely characterized to date.

Peptides and proteins are often categorized together as polypeptides. However, in this chapter, we have divided the overall polypeptide group into a peptide group that includes small polypeptides with a molecular weight (MW) of less than 10,000 and a protein group comprised of large polypeptides with a MW of greater than 10,000. Peptide toxins produced by venomous marine animals have been investigated since the 1970s. These smaller peptide toxins are generally more stable than protein toxins to purification, thus making them more accessible than protein toxins. Given this increased stability, a number of peptide toxins synthesized by sea anemones and cone shells have been isolated and characterized with high precision. For the interested reader, several published reviews provide a more detailed description of the peptide toxins of marine venomous animals [2, 3].

Recently, several protein toxins have been successfully isolated and characterized from venomous marine animals. These studies have revealed that protein toxins exhibit a unique structure and mode of action. In this chapter, some of the most current studies on protein toxins isolated from venomous marine animals will be discussed.

29.2 Protein Toxins of Fish

A number of fish species including stonefish, scorpion fish, striped eel catfish, weever fish, rabbitfish, and the stingray are known to generate proteinaceous toxins. All of these fish species use their protein toxins as defensive tools against predators. The venom apparatus of venomous fishes are generally located along either their spines or fins. Among the venomous fish described to date, stonefish are commonly regarded as the most dangerous fish worldwide. Stonefish are distributed throughout the tropical and subtropical oceans of the world. A sting from the spine of a stonefish causes excruciating pain, massive local edema, and necrosis of affected tissues. Such a sting is often fatal to humans [4]. The stonefish toxin was isolated and characterized by a research group in Singapore in 1996 [5]. However, from the initial report on the stonefish toxin in 1965 [6], three decades passed before it was fully characterized. The toxin, stonustoxin (SNTX, 148 kDa), was isolated from the stonefish species *Synanceia horrida* and is comprised of two subunits termed α (71 kDa, 702 amino acid residues) and β (79 kDa, 699 amino acid residues) (Fig. 29.1) [5]. The cDNA clone encoding SNTX was isolated and sequenced from a venom gland cDNA library and was shown to contain a B30.2 domain in the molecule. The B30.2 domain is thought to function as a protein–protein interacting module [7]. Thus, the molecular target of SNTX may be a specific protein encoded by a victim stung by *S. horrida*. The amino acid sequences of the α -subunit and β -subunit of SNTX revealed 50% homology with each other. SNTX is lethal to mice ($LD_{50} = 17 \mu\text{g}/\text{kg}$) when injected intravenously. SNTX also possesses edema-inducing, vascular permeability-increasing, hemolytic, and hypotensive activity. Many of the symptoms experienced by those injected with the venom of *S. horrida* are in accordance with SNTX activity, and therefore, SNTX most likely represents the major active toxin in *S. horrida* venom. Using cDNA cloning experiments, a French research group subsequently elucidated the complete amino acid sequence of the β -subunit (79 kDa, 708 amino acid residues) of verrucotoxin (VTX) isolated from the venom of *Synanceia verrucosa* originating from Kenya (Fig. 29.1) [8]. The amino acid sequence of the VTX β -subunit demonstrated 86% identity with the SNTX β -subunit. Information regarding the amino acid sequence of the α -subunit of VTX has not been reported to date. VTX is known to comprise the major component of the venom released by *S. verrucosa*. It has also been reported that VTX exhibits similar activity to SNTX [9].

Neoverrucotoxin (neoVTX) has also been isolated and was subsequently characterized from the venom of *S. verrucosa* (Fig. 29.2) originating from Okinawa, Japan [10]. NeoVTX was lethal to mice (LD_{50} of $47 \mu\text{g}/\text{kg}$) and demonstrated potent hemolytic activity. NeoVTX was found to be a dimeric 166-kDa protein composed of an α -subunit (702 amino acid residues) and β -subunit (699 amino acid residues) (Fig. 29.1). Alignment of the amino acid sequences revealed that the neoVTX α - and β -subunits shared 87% and 95% identity with the SNTX α - and β -subunits, respectively. In addition, the sequence of the neoVTX β -subunit revealed 90% identity with the VTX β -subunit. Thus, it appears that the major toxins isolated from stonefish (*S. horrida*, Kenyan *S. verrucosa*, and Japanese *S. verrucosa*) form a new family of

SNTX-alpha	SSD-LVMPALGRPFTIGMLYDARREKLI	189
neoVTX-alpha	SSD-LVMPALGRPFTIGMLYDTRREKLI	189
SNTX-beta	PSDILVVAALGRPFTIGMLYDARNDKLI	190
neoVTX-beta	PSDILVVAALGRPFTIGMLYDARNDKLI	190
VTX-beta	PSDILVVAALGRPFTIGMLYDARNDKLI	190
SNTX-alpha	YLNNTKKYQNSRVTLKYKATVYKQFTA	179
neoVTX-alpha	YLNNTKKYQNSRVTLKYKATVYKQFTA	179
SNTX-beta	YLNNTKQFKNSRVTLQYKATTFKQLM	180
neoVTX-beta	YLNNTKQFKNSRVTLQYKATTFKQLM	180
VTX-beta	YLNNTKQFKNSRVTLQYKATTFKQLM	180
SNTX-alpha	ISIEGASVQLTDEEKSILASNLCKF	269
neoVTX-alpha	ISIEGASVQLTDEEKSILASNLCKF	269
SNTX-beta	VEISGKASVQLTGEETDITNSFCE	268
neoVTX-beta	VEISGKASVQLTGEETDITNSFCE	268
VTX-beta	VEISGKASVQLTGEETDITNSFCE	268
SNTX-alpha	RIHTLLELHKLRANEAMDKLVQRI	359
neoVTX-alpha	RIHTLLELHKLRANEAMDKLVQRI	359
SNTX-beta	KVRNTLEAIVQVMRCNDALDDPTN	358
neoVTX-beta	KVRNTLEAIVQVMRCNDALDDPTN	358
VTX-beta	KVRNTLEAIVQVMRCNDALDDPTN	358
SNTX-alpha	LDAVEREIAVLKSCAGWEGTQAKFV	449
neoVTX-alpha	LDAVEREIAVLKSCAGWEGTQAKFV	449
SNTX-beta	MEFEEREINVLKSCMDILTKAKPKV	447
neoVTX-beta	MEFEEREINVLKSCMDILTKAKPKV	447
VTX-beta	MEFEEREINVLKSCMDILTKAKPKV	447

Fig. 29.1 (continued)



Fig. 29.2 The stonefish *Synanceia verrucosa* from Okinawa

highly bioactive proteins. It has been reported that neoVTX was soluble only in buffers with high ionic strength and that this unique property permitted purification of unstable neoVTX from *S. verrucosa* venom using a simple procedure [10]. It was hypothesized that this purification method may also be applicable to the isolation of the major protein toxins from other stonefish species.

Among the stonefish toxins isolated to date, SNTX is the only toxin that has been subjected to pharmacological investigations. These studies demonstrated that the primary lethal action of SNTX was due to its potent hypotensive effects. It was shown in studies using rat aortic strips that SNTX mediated its vasorelaxant activity via the L-arginine-nitric oxide (NO) synthase pathway [11]. It was also shown that hydrogen sulfide (H_2S) and NO acted synergistically in mediating SNTX-induced vasorelaxation [12]. Furthermore, it was revealed that SNTX occupied substance P receptors located on endothelial cells or induced substance P activity. This cascade of events subsequently results in the activation of potassium channels and leads to vasorelaxation in rat aortic rings [13]. In experiments using monoclonal antibodies directed against SNTX, it was suggested that different domains are responsible for the lethal and hemolytic activities [14]. Nevertheless, these studies on SNTX [5] represent the first reports of the characterization of an unstable protein toxin synthesized by a venomous marine animal.

Weever fish are the most famous venomous fish located in Europe. Dracotoxin (105 kDa) was isolated as the major proteinaceous toxin obtained from the venom of the greater weever fish species *Trachinus draco*. Dracotoxin was found to cause hemolysis of rabbit erythrocytes with an EC_{50} of 3 ng/mL. However, a precise characterization of dracotoxin has not yet been reported [15].

It has been reported that the major toxin produced by stingrays is also a proteinaceous toxin [16, 17]. However, no protein toxins have been characterized from this source to date. A 10-kDa vasoconstrictor peptide was isolated and subsequently characterized from the venom of the Brazilian stingray *Potamotrygon*

gr. *orbignyi* [18]. Envenomation caused by the stingray results in immediate, local, and intense pain and edema. Necrosis was also demonstrated in the skin of a number of victims. Given these symptoms, it is uncertain if the vasoconstrictor peptide is responsible for the major effects of stingray envenomation. Numerous other protein toxins have also been purified from venomous fish species, including the lesser weever fish *Trachinus vipera* [19], Indian catfish *Plotosus canius* [20], scorpion fish *Scorpaena guttata* [21], *Notesthes robusta* [22], and *Thalassophryne nattereri* [23]. However, among the protein toxins of fish, only the three toxins from the scorpion fish (*S. horrida*, Kenyan *S. verrucosa*, Japanese *S. verrucosa*) described above have been formerly characterized to date.

29.3 Protein Toxins of Jellyfish

A vast number of jellyfish stings to humans occur in all of the world's oceans, especially in nearshore environments. Given the severe stinging ability of some species of jellyfish, a number have been categorized as venomous animals. Jellyfish are classified into the cnidarians, a group that consists of almost 10,000 species of related animals including jellyfish, sea anemones, hydra, and soft and hard corals. All cnidarians are armed with nematocysts, explosive capsule organs used for stinging (Fig. 29.3). The nematocysts vary from 5 to 100 μm in size and consist of an inverted compactly coiled tubule (needle) and venom surrounded by a strong outer wall. The role of the nematocyst is to capture prey and to guard against predation. Thus, all cnidarians generate venom to some extent.

Perhaps the best known venomous jellyfish is *Chironex fleckeri* (one of the box jellyfish) which has caused a large number of fatalities along the Australian coast. The Portuguese man-of-war *Physalia physalis* is also notorious given its severe sting that may occasionally result in death. Because of their importance to public health, jellyfish toxins have been extensively examined and were revealed to be mostly comprised of proteinaceous toxins. However, the precise chemical nature of jellyfish toxins has not been successfully determined, as the chemical instability of these toxins has hampered further studies [24, 25]. Among the many jellyfish species that have been identified as venomous, the box jellyfish (Cubozoan jellyfish) is recognized as an especially hazardous marine animal. *C. fleckeri*, *Chiropsalmus quadrigatus* (Fig. 29.4, recently renamed *Chironex yamaguchii* [26]), *Carukia barnesi*, and *Carybdea* spp. [27, 28] are genera and species generally known as venomous box jellyfish.

The box jellyfish *Carybdea rastoni* (Fig. 29.5) is one of the most hazardous marine organisms for swimmers and bathers along the Japanese seashore. A sting from *C. rastoni* may cause cutaneous pain and inflammation in humans. Given the frequency of stings by this jellyfish, and the symptoms that these stings cause, *C. rastoni* was chosen as the first target of investigation in our laboratory. During our studies on *C. rastoni*, we found that the toxicity of the proteinaceous toxins was markedly decreased during the process of purification, storage, and sample concentration. Thus, determining the optimal conditions for the purification and storage

Fig. 29.3 (a) The isolated intact nematocysts of the jellyfish *Chiropsalmus quadrigatus*. (b) The discharge nematocyst of *C. quadrigatus*



Fig. 29.4 The box jellyfish *Chiropsalmus quadrigatus*

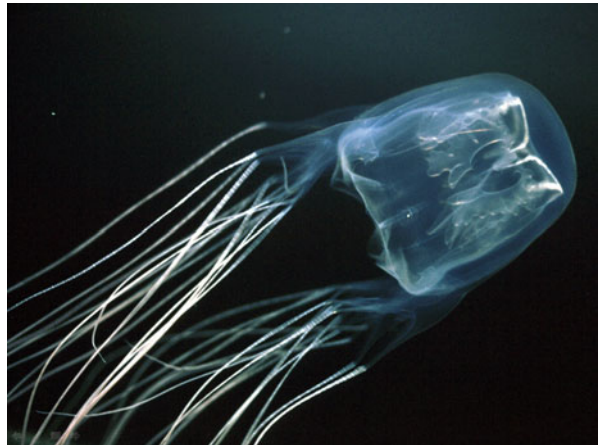
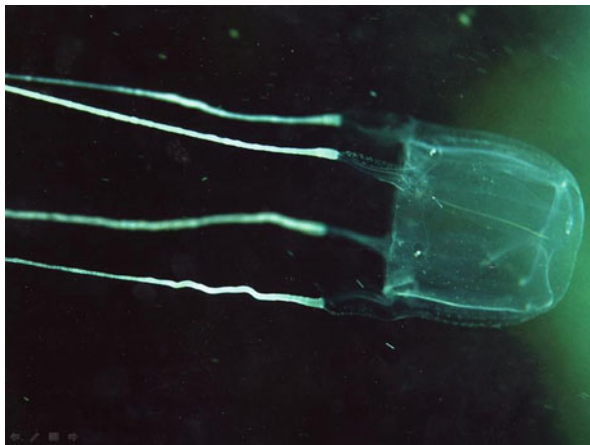


Fig. 29.5 The box jellyfish
Carybdea rastoni



of these toxins was a key step in their characterization. We demonstrated that ion-exchange chromatography rather than ultrafiltration was suitable for concentration of the toxins. We also found that storage of the purified samples in a high-salt-concentration solution was required and that the samples should not be frozen or freeze-dried. Thus, purified toxins were stored in a high-salt solution such as 0.8 M sodium chloride containing 10 mM phosphate buffer (pH 6.0) at 4°C. Under these conditions, 90% of the hemolytic activity of the *C. rastoni* toxin could be retained for more than 6 months of storage [29].

Using these methods, we were able to isolate the active forms of two proteinaceous toxins, *Carybdea rastoni* toxins A and B (CrTX-A, 43 kDa and CrTX-B, 46 kDa), from the tentacles of the box jellyfish species *C. rastoni*. We also determined the full-length cDNA (1600 bp) that encoded both CrTX-A and CrTX-B (Fig. 29.6) [29]. Histopathologic studies showed that CrTX-A (0.1 µg/injection) caused inflammation of the affected area, an effect that was comparable to the symptoms observed in humans after a *C. rastoni* sting. CrTX-A was found to be the main toxin housed in the nematocyst. Thus, the results of the pathologic study revealed that CrTX-A was responsible for the cutaneous inflammation observed in humans following a *C. rastoni* sting. CrTX-A was the first toxin isolated and shown to be the causative agent of cutaneous inflammation following jellyfish stings [29].

The sea wasp species *Carybdea alata*, also in the box jellyfish family, is another type of stinging jellyfish. A *C. alata* sting results in cutaneous pain and inflammation in humans, symptoms that are similar to those caused by *C. rastoni*. *C. alata* is widely distributed in the tropical zones of the Atlantic, Pacific, and Indian Oceans. On the southern shores of Oahu, Hawaii (Waikiki Beach), massive invasion by this species occurs every 9th or 10th day following a full moon [30]. The *Carybdea alata* toxins A and B (CaTX-A, 43 kDa and CaTX-B, 45 kDa) were successfully isolated using the toxin isolation procedure developed for *C. rastoni* [31]. Interestingly, it was found that CaTX-A, but not CaTX-B, was present in *C. alata*

nematocysts. The full-length cDNA (2000 bp) that encoded a 463-amino acid protein (CaTX-A) was also determined (Fig. 29.6).

The Okinawan sea wasp *Chiropsalmus quadrigatus* (synonym *Chironex yamaguchii*) is widely distributed in the tropical Indo-Pacific region. A sting from *C. quadrigatus* is sometimes so severe that it proves fatal to humans. In Okinawa, a tropical region of Japan, three fatal stings from *C. quadrigatus* have been officially reported to date. Death was caused by cardiac arrest in systole or respiratory failure with acute pulmonary edema. Children are particularly susceptible to stings from *C. quadrigatus*. *Chiropsalmus quadrigatus* toxin A (CqTX-A, 44 kDa) was isolated using the isolation procedure developed for the characterization of the *C. rastoni* toxin. However, the procedure for CqTX-A was modified in that cleanly isolated nematocysts were used as the starting material. Using these methods, a full-length cDNA (1938 bp) was defined that encoded a 462-amino acid proteinaceous toxin (CqTX-A) (Fig. 29.6) [32]. Alignment of the amino acid sequences for CrTX-A and CrTX-B, CaTX-A, and CqTX-A revealed 20–45% identity between the toxins [31, 32], suggesting that these box jellyfish toxins form another novel family of protein toxins.

The LD₅₀ values for the injection of CqTX-A, CrTX-A, and CaTX-A into crayfish (*Procambarus clarkii*) were 80, 5, and 5–25 µg/kg, respectively [29, 31, 32]. CqTX-A, CrTX-A, and CaTX-A were also found to result in 50% hemolysis in 0.8% sheep red blood cells at a concentration of 160, 2, and 70 ng/ml, respectively [29, 31, 32]. These findings generally indicated that CqTX-A was less toxic than CrTX-A and CaTX-A. The number of tentacles present on *C. quadrigatus* is known to be several times greater than that of *C. alata* and *C. rastoni*. Furthermore, the overall length of the tentacles of *C. quadrigatus* is at least three times that of *C. alata* and *C. rastoni*. Therefore, for human stings, the total amount of toxin injected into the victim from *C. quadrigatus* is likely much greater than the total amount injected by *C. alata* or *C. rastoni*. This is one reason why *C. quadrigatus* is considered more dangerous than *C. rastoni* or *C. alata*. Indeed, massive regional stings were observed at autopsy after fatal *C. quadrigatus* incidents. CqTX-A was the major toxin located in the nematocysts, and thus, CqTX-A is most likely the causative toxin in fatal *C. quadrigatus* sting cases.

Australian research groups have subsequently isolated two of the most abundant proteins in their non-active form from the nematocysts of the most deadly box jellyfish species, *Chironex fleckeri*. These proteins have been termed *C. fleckeri* toxin-1 (CfTX-1, 43 kDa) and toxin-2 (CfTX-2, 45 kDa). The amino acid sequences of the mature CfTX-1 and CfTX-2 have been shown to share homology with the CrTXs, CaTX-A, and CqTX-A (Fig. 29.6). Secondary structural analysis of these toxins predicted the presence of amphiphilic α -helices in the *N*-terminus region. It has been suggested that amphiphilic structures present in some cytolytic protein toxins promote the formation of pores in cell membranes [33, 34]. This activity of the amphiphilic structures present in the box jellyfish toxins may explain some aspects of their potent hemolytic activity. Indeed, further studies on the mode of action of these toxins may aid in the development of effective and specific treatments for box jellyfish stings.

A protein toxin termed CARTOX (102–107 kDa) has also been isolated in its active form from the nematocysts of *Carybdea marsupialis* that reside in the

CrTxS	MILKH-LPM-LFTVL--AITS-AKHG--KRSDVNSLLTKVETALKE-AS-GSNEAAL-EALEGLKGEIQTKP-DRVQQAATKILGVSYSAL	79
CaTX-A	MSRGSYSLHLVFLVLSLTAFFPSQARLSRYRRSAAADVSTDIDGIIGQNDLGFDTKRLKEALQGVQFAVKKEPATTIAKVSTIVGSVGGSL	90
CqTX-A	-----WANMLYFSLALLFMTGIA-SEGTISSGLASLAKAKIDAK-RPSGKQLFDKVVANMQQIIEKFSNDDERAKVMGAI-GSLSTAV	80
CfTX-1	-----MYKMLFFAFLPILLFMTGIA-AESTISSGLNSLTKIDAK-MPSGKQLFDKVVEMQKQIDAKFSNDDERAKVMGAI-GSLSTAV	80
CfTX-2	-----MILVSLPILLFMTGIA-SESTISSGLASLAKAKIDIK-KPTGKQLFDKVKVSMQALENKFSDDDERAKVMGAI-GSLGTAI	77
 * * * * * * * *	
CrTxS	GKLN SGDATKIIISGCLDIVAGIATFFGGFVGMGIGAVASVFSILSLFTGSSAKNSVAVIDRALSKHRDEAIQRHAAGAKRDFAESSAF	169
CaTX-A	SKEKSGDFDVASGCLDIIASVATFFGGFYGIAIGAVASLIISSILSLFSGNSMGSAIKQVIDDAFKYRDQLELDNVKGAKRRTFNAVITF	180
CqTX-A	GKFGSGDPAKIASGCLDIIIVGISSVLKD-FA-KFSPIFSIILSMVVGFLSGTKAEESYGSVVKVQEQSDQELQELQALYGVKREYAVSKAF	168
CfTX-1	GKFGSGDPAKIASGCLDIIIVGISSVLKD-FA-KFSPIFSIILSVWGLFSGTKAEESYGSVVKKAVQEQSDQELQELQALYGVKREYAVSKAF	168
CfTX-2	GKFGSGDPAIASGCLDIIIVGISSVLKD-FA-KFSPVFSIILSVWGLFSGTKAEESYSVVTKAIQEQSDQELQELQALYGVKREFAVSKAF	165
	***** ***** ***** ***** ***** ***** ***** *****	
CrTxS	-IQVMKQOSNLTDSDLSIIAANVPVYKFSNFICQLESRSIQGAATSLSDAKRAVDFILLYQLVVMRETLVLDLAILYRK-GNA-EHVA	256
CaTX-A	-VNSVSKTENLTEVHLDVSRDAVRVDAFTNMLGVLESRINRGSVSTDNNEAMRTINFIFLYLQLSYMRETLTQVILLIKRAGGAYDELA	269
CqTX-A	LDGVRNETSDLSPTSEVSALGANVPYQGVRFIAMVWQRIKNRKPRTESEI-KRVLSMLELFTDLCSLRDLILLDLYQLVATPFGHSPNIAS	257
CfTX-1	LDGVRNETSDLSPTSEVSALAANVPIYQGVRFIAMVWQRIKYIKPKTESEI-KRMLTMLELFTDLCSLRDLILLDLYQLVATPFGHSPNIAS	257
CfTX-2	LDGVRNEESDLRPTSEVSALAANI PVYQGVRFIAMVWQRIKYIKPKTESEI-KRMLTMLELFTDLCSLRDLILLDLYQLVATPFGHSPNIAS	254
	***** ***** ***** ***** ***** ***** ***** *****	
CrTxS	SAVENANRVNKELAADTLDFLHKLIPEQALI GAVYHPISASETSKALINITYKFGVPDVPR-PIGNRRYKFTN-SYWNITYSICSEAYMGN	344
CaTX-A	LSLSLTSQNKKEATRETVFLHQMETKYSLCGSYYPIDHSKAAIGILKLTFFFGVDPARYTFDGLIYRQW-RAWNRYSI CKESYAGN	358
CqTX-A	GIREVSNLGREEYKVFEDLLKTKNDKETYLFLSYLYPRENPEQSKIFKFFDLMKVKYDDRLKQDLTGIQVFSLSLHWPNYFLC---SSKD	344
CfTX-1	GIREVSNLGREEYKVFEDLLKNDDKETYLFLSYLYPREKNEQSRKIFNFDFDLMKVKYDDRLKQDLTGVKIFSNVHWPNYFMC---SSND	344
CfTX-2	GIREVTSLGREEYQRFVFDLLKTKDDEETFLFLSYLYPREKNEQSRKIFKFFDIEVKYDDRFKLDLSSGQALSTLQWPNYYLC---PHND	341
	***** ***** ***** ***** ***** ***** ***** *****	

Fig. 29.6 (continued)

Northern Adriatic Sea [35]. CARTOX was shown to possess potent hemolytic activity; however, the precise features of CARTOX giving rise to this activity have not been reported to date. A proteinaceous neurotoxin was also isolated from a Caribbean *C. marsupialis*, and the existence of some cytolysin was demonstrated [36]. However, once again, a precise characterization of Caribbean *C. marsupialis* toxin has not been reported to date. While CfTX-1 and CfTX-2 were suggested to be the main proteinaceous toxins of the box jellyfish *Chironex fleckeri* [37], the existence of two additional hemolytic protein toxins (39 and 41 kDa) in the nematocyst of *C. fleckeri* have been reported [38]. These toxin profiles were shown to differ from those of CfTX-1 and CfTX-2 by immunoblotting using rabbit polyclonal antibodies raised against CfTX-1 and CfTX-2 [38]. Nevertheless, a precise characterization of these new toxins has not yet been established. The existence of plural protein toxins was reported by Burnett's group [39] and indicated that numerous box jellyfish species contain both major and minor protein toxins. Thus, the severe symptoms resulting from a box jellyfish sting may be the result of multiple effects caused by different protein toxin types.

Scyphozoa jellyfish are of typical shape and size and include the moon jellyfish species *Aurelia aurita*. Another scyphozoan, *Chrysaora quinquecirrha*, is present in the Chesapeake Bay and is commonly known as the "sea nettle." Comprehensive studies on the venom of *C. quinquecirrha* have been conducted by Burnett's group [40, 41] who reported the presence of various protein toxins. From the scyphozoan *Rhizostoma pulmo* residing in the Bay of Naples, rhizolysin (260 kDa) was obtained and shown to function as a hemolytic protein [42]. However, rhizolysin did not exhibit any phospholipase A₂ activity. A protein toxin termed T-Ar (182 kDa) was isolated from the scyphozoan *Acromitus rabanchatu* located in the Bay of Bengal [43]. Pharmacological studies on T-Ar suggested that this toxin possessed a direct paralyzing effect on muscle membranes [43].

With the exception of the toxin isolated from the Mediterranean scyphozoan *Rhopilema nomadica*, none of the scyphozoan jellyfish protein toxins mentioned above have been precisely characterized to date. The polypeptide toxin (17 kDa) isolated in its active form from the tentacles of *R. nomadica* was found to be lethal to fish [44]. The N-terminal amino acid sequence of the *R. nomadica* toxin revealed homology with phospholipase A₂ toxins isolated from the lizard [45] and honeybee [46].

The Portuguese man-of-war *Physalia physalis* is one of the most famous venomous jellyfish and belongs to the hydrozoan jellyfish. While a hemolytic protein (240 kDa) that is lethal to mice has been isolated from the nematocyst of *P. physalis* [47], this toxin has also not been fully characterized.

29.4 Protein Toxins of Sea Anemones

Sea anemone toxins have been extensively studied, especially in regards to peptide toxins that have a molecular weight of less than 10 kDa. The most extensively studied group of these peptide toxins have been mainly categorized as either sodium

channel toxins or potassium channel toxins [2]. A number of these toxins have been used as valuable tools for the study of the structure and function of ion channels. Here, we describe protein toxins (molecular weight of more than 10 kDa) isolated from the sea anemone.

Among the protein toxins synthesized by sea anemones, only the actinoporin family of toxins has been subjected to extensive research (Fig. 29.7). Actinoporins are 20-kDa pore-forming cytolysins [48] and, as a family, are considerably more stable than other marine protein toxins investigated to date. Actinoporins create 2-nm pores in eukaryotic lipid membranes via the self-association of four monomers [49]. Sphingomyelin located in the outer leaflet of the plasma membrane has been shown to be the binding target of actinoporins [50]. The actinoporin family has been mainly isolated and characterized from Actiniidae and Stichodactylidae sea anemones [48], with more than ten actinoporin protein toxins isolated and characterized so far. The crystal structures of equinatoxin II isolated from *Actinia equina* and sticholysin II isolated from *Stichodactyla helianthus* revealed a tightly folded sandwich of ten β -strands that were embedded with two α -helices [51, 52].

It has also been shown that echotoxin 2 from the salivary gland of the marine gastropod *Monoplex echo* belongs to the actinoporin family [53]. Echotoxin 2 represents the first example of an actinoporin that was not isolated from a sea anemone. The cytolytic and lethal activity of echotoxins 1, 2, and 3 are known to be specifically inhibited by gangliosides [54]. When compared to this inhibition by gangliosides, sphingomyelin was shown to be almost 100 times weaker [54]. Thus, the mode of echotoxin action may differ from the usual actinoporins. The existence of an actinoporin-like protein (Dr1) was also found in the zebrafish *Danio rerio* genomic database [55]. This report represented the first characterization of an actinoporin in a vertebrate species. Dr1 has been subsequently cloned and expressed in *Escherichia coli*. The expressed Dr1 protein displayed membrane-binding behavior, but did not exhibit any permeabilizing activity or sphingomyelin specificity, two properties that are typical of actinoporins [55].

In the subtropical and tropical coasts, venomous sea anemones such as *Phyllo-discus semoni* (Fig. 29.8) and *Actinaria villosa* (Fig. 29.9) (both Aliciidae) are widely distributed. Envenomation by these species results in a painful fulminant dermatitis. The protein toxins comprising the venom of these sea anemones have been studied from the Japanese Okinawan coast. It was shown that *Phyllo-discus semoni* toxins 60A and 60B (PsTX-60A and PsTX-60B) [56, 57] and *Actinaria villosa* toxin 60A (AvTX-60A) [58] were the major protein toxins present in the nematocyst venom of these anemones, respectively. Each of these toxins possessed a molecular weight of 60 kDa, and the cDNA of the three protein toxins was cloned and sequenced (Fig. 29.10) [56–58]. The results of protein domain analysis by Pfam [59] and SMART [60] revealed that PsTX-60A, PsTX-60B, and AvTX-60A were novel members of the membrane-attack complex/perforin (MACPF) domain family (Fig. 29.10). The MACPF domain consists of approximately 200 amino acid residues, and the MACPF family of proteins was originally described as pore-forming factors used in the mammalian host defense immune system [61, 62]. These sea anemone toxins represented the first MACPF proteins isolated from

EqtII	-----SADVAGAVIDGASLSFDIILKTVLEALGNVYRKRKIAVGVD--NESGKTW--TAL--NTYFRSGTSDIVLPHKV--PHGKALLYNGQKD	78
St-II	-----ALAGTI IAGASLTFQVLVDKLEELGKVSARKIAGID--NESGGTW--TAL--NAYFRSGTSDIVLPEFV--PNTRKALLYSGRKD	76
Echotoxin 2	AGGTIIATLSKIPLSTLASALNTALETGASVASAAAAATSSDYSVTCVIEVENWTKHLMKYVWVQFANSGLLTVAKNVLPAEIQSFAMR	90
Avt-I	-----SAAVAGAVIAGGELAKIILTKILDEIGKIDRKAITGVD--NESGLKW--TAL--NTYKSGASDVTLPEYV--ENSKALLYTARKS	78
PstX-20A	-----SAAVAGAVIAGGELAKIILTKILDEIGKIDRKAITGVD--NESGLKW--TAL--NTYKSGASDVTLPEYV--ENSKALLYTARKS	78
Dr1	-----MTESAEVAANV--SSRRHATVEITNLTNNY--CFLN--PK--V--YLENGETSNPPQP--TVRPL--KTEVCTFSKSAAHA	68
*.....*	
EqtII	RGPVATGA--VGLVLAAYLMSDGNLTLAVLFSVPYDYNWYSNWNV--RI--YKGRRADQRMEEELYNLSPFRGDNGWHTNRNLGY--GLKSRGF	163
St-II	TGPVATGA--VAAFAYMSSGNTLGMVSPFDYNNWYNNWV--KI--YSGKRRADQGMEDLYYG--NPYRGGNGWHEKNLGY--GLRMMKGI	160
Echotoxin 2	KAWGANGVGTVSWVLGQTNRRVIVMSPYDFYSNLAVGMSRPLAVPSSRSTWFDLMMYGNADISFVRGEYHSDVPIYFKNS	180
Avt-I	KGPVARGA--VGLVLAAYKMSGNTLAVMFSVPFDYNYLWV--KI--YDGEKKADEMYNELNWNV--PK--PSTWEKRDLDGDKLGRF	163
PstX-20A	KGPVARGA--VGLVLAAYKMSGNTLAVMFSVPFDYNYLWV--KI--YDGEKKADEMYNELNWNV--PK--PSTWEKRDLDGDKLGRF	163
Dr1	TGSVGLTYDLFERRRRNDYETLAIMFSPWYDNLKMWFAVGIIY--PK--GKECDQ--ALYKEMMY--QKNQH--GFVREE--ANGSG--INFEGK	151
*.....*.....*	
EqtII	MNSSGHAILEIHVSKA-----	179
St-II	MTSAGFAKMQIKISR-----	175
Echotoxin 2	EWETEGSMNIIHKARVRATVKPIKTMDLASSILTKLEALAGANGKRAIQQELARRAEFEKQKRKALDEMLK	252
Avt-I	MTSNGDAKLIVHIEKS-----	179
PstX-20A	MTSNGDAKLIVHIEKS-----	179
Dr1	NLDTRATMCPMGRRAIVKEVWD--K--L--L--SP--MAQMDC-----	184
*	

Fig. 29.7 Sequence comparison of the actinoporins. The alignment of equinatoxin II (EqII: GenBank, nucleotide, U41661), sticholysin II (St-II: GenBank, protein, P07845), echotoxin 2 (GenBank, nucleotide, AB110013), Dr1 (GenBank, nucleotide, CN510193), PstX-20A (GenBank, nucleotide, AB063314), and Avt-I (GenBank, nucleotide, AB175824) is shown by the single-letter amino acid code. Identical residues are marked by asterisks. Conserved residues are marked by dots

Fig. 29.8 The sea anemone
Phyllo-discus semoni



Fig. 29.9 The sea anemone
Actin-eria villosa



nonmammalian species as actual proteins. Furthermore, these reports were the first studies to describe the use of MACPF proteins as a venom in animals. These new sea anemone toxins also showed potent hemolytic activity. Thus, the mode of action of these MACPF toxins may be explained by their pore-forming activity, in a manner similar to the way in which MACPF proteins function in the mammalian immune system. Actinoporins PsTX-20A [63] and Avt-I [64] have also been isolated as minor toxic components from the nematocyst venom of *P. semoni* and *A. villosa*, respectively. On rare occasions, a sting by *P. semoni* may cause acute renal failure in humans [65]. A 115-kDa protein toxin called PsTX-115 was subsequently isolated as the nephrotoxic component of the venom. Crude venom isolated from the nematocysts of *P. semoni* as well as purified PsTX-115 was found to be highly nephrotoxic. These toxic effects were due to the induction of complement activation [66]. These findings suggest that the MACPF domain toxins may

PstX-60A	DKETEHIISAKPFSGIRGALGQGFETHREDLLSKQFEATEGKIFEDLPMDECTVTTLGTIERDDSFYNSTESLYQSVASSTKISGSLK	90
PstX-60B	-EDTEKVEVKAKEKTSRGAIGQGFELHKIDLLSKELQGTGAQVFEELPVECTTDNKLGIQKDDTFYNTESLYNSVASNSKIETPSLK	89
AvTX-60A	DKETEHIISAKPFSGIRGALGQGFETHREDLLSKQFEATEGKIFEDLPMDECTVTTLGTIERDDSFYNSTESLYQSVASSTKISGSLK	90
*	
PstX-60A	GAYTLGVSAAVTNNIASSEEVQGLSLNLKAYSMSIILKNCVNTKPLSKDLVSDFEALDSEITKPKWLSSWKYKVLLEKYGSRIVKE	180
PstX-60B	GPFLTGSVAVTNNIYSEKSEIQGLSLNLKAYSMIHALKQDCINPKPLAKDLVSDFEALDREVKKPWLKFSWRKVKVFLKFKGFHIVRE	179
AvTX-60A	GAYTLGVSAAVTNNIASSEEVQGLSLNLKAYSMSIILKNCVNTKPLSKDLVSDFEALDSEITKPKWLSSWKYKVLLEKYGSHIVKE	180
*	
PstX-60A	SISGSSIIQYVFAKSKQFNHRSFTRKACVSLAGPTKVGKLSFGGTGVSQOIEIQSSSQSMIKKILVVRGKGTETRASLIGELDPDQINK	270
PstX-60B	TMSGSSIIQYVFAKSSSEFKQRDFKIKACLSLGGPTQVKGKLSIACSDDVKKDVESSGREMVKLVVRGKSDTFVLDLIGELSKNQINK	269
AvTX-60A	SISGSSIIQYVFAKSNQFNHRSFTRKACVSLAGPNASKVGFAGGTGVSQOIEIQSSSQSMIKKILVVRGKGTETRASLIGELDPDQINK	270
*	
PstX-60A	FLIEAETDPSPIQYKFEPIWTLILKTRYVGTETHFAKAVNLEQFYKGFHLHFGCSYLHHTSAENKVAEMQKDFAKTSDPDAPTYVCKVGPGE	360
PstX-60B	FLKEATDPSPIQYTFYVWTLIKARYIGKEHYKATNLEQFYKGLNFDCAI-E-KS-EKGLELQKFEAEDSDPDAPTYVCKLGPGE	355
AvTX-60A	FLIEAETDPSPIQYKFEPIWTLILKTRYVGTETHFAKAVNLEQFYKGFHLHFGCSFLHHTSNADNADVEIQKDFAKTSDPDAPTYVCKVGPGE	360
*	
PstX-60A	CQHEDCHYRAAFWCECGGPDARTCFRHKFKLKS-GLTKKECPNK-ESGFAMHGCRLHGLTWCSPAHRNWEESWGSGE-DTNNALN	447
PstX-60B	CHSDDDCESDLLIYCACC--D--SCIRYNNVLLSTGDTKKAIFINDVDDEFRHDGCGRGLCKCKEENKWKQSWSGSDSDADAALR	440
AvTX-60A	CQHEDCHYRAAFWCECGGPDARTCLIRYKTEKLS-GSTKRECPNK-ESGFAMHGCQLHGLSCWCSAPKNWEETWSGE-DTNNALN	447
*	
PstX-60A	DVHQVLMKRRDQAQQY-----	466
PstX-60B	DINAMLDQNRDQAKRHHVKKGKSLH	467
AvTX-60A	DVHQVLMKRRDQAK-----	463
*	

Fig. 29.10 Sequence comparison of the membrane-attack complex/perforin (MACPF)-type sea anemone toxins. The alignment of PsTX-60A (GenBank, nucleotide, AB063315), PsTX-60B (GenBank, nucleotide, AB201429), and AvTX-60A (GenBank, nucleotide, AB107916) is shown by the single-letter amino acid code. Identical residues are marked by asterisks. Conserved residues are marked by dots. The boxed area indicates the MACPF domain

also be involved in acute renal failure due to their complement-like activity. However, a precise characterization of PsTX-115 has not yet been reported.

An 80-kDa cytolytic protein—designated metridiolysin has also been purified from the tissues of *Metridium senile* residing in the North Atlantic Ocean. Metridiolysin has an isoelectric point at a pH of approximately 5.0 and is composed of two unequal sized subunits. The hemolytic activity of metridiolysin was specifically inhibited by cholesterol [67]. The amino acid sequence of metridiolysin has not yet been determined. Thus, to date, only the protein toxins belonging to the actinoporins and MACPF-type toxins have been chemically characterized from the sea anemone.

29.5 Protein Toxins of Fire Coral

While the vast majority of hermatypic corals belong to the class Anthozoa, fire corals are members of the class Hydrozoa. Fire corals consist of only one genus known as *Millepora*. Branching and blade fire corals are most commonly encountered on coral reefs. Direct contact with fire coral causes a severe burning sensation but is usually not life threatening. Envenomation is caused by nematocysts, similar to other cnidarians such as jellyfish and sea anemones. Recent studies have revealed difficulties associated with the taxonomy and distinction among various *Millepora* species [68].

In the early 1970s, the venom of *Millepora alcicornis* from Florida and *Millepora tenera* (initially termed *M. dichotoma*) and *Millepora dichotoma* from the Marshall Islands were extensively studied [69–71]. In these investigations, it was shown that branching *Millepora* spp. produce unstable hemolytic and lethal protein toxins. In the late 1980s, an attempt was made to isolate the protein toxins from the venom of the branching fire coral *M. dichotoma* and the blade fire coral *Millepora platyphylla* from Okinawa [72]. While the protein from *M. dichotoma* was too unstable to isolate, a 31.5-kDa protein was isolated from *M. platyphylla*. At least one additional toxic component was located in the venom of *M. platyphylla* and subsequently reported [72]. In 2004, it was shown that a hemolytic protein—designated milleporin-1 (ca. 32 kDa) could be isolated from *M. platyphylla* collected from the Red Sea. Milleporin-1 was also shown to exhibit phospholipase A₂ activity [73]; however, no further information regarding the chemical structure of this protein has been published.

An 18-kDa protein toxin has subsequently been isolated and characterized from Okinawan *M. dichotoma* var. *tenera* (Fig. 29.11) [74]. This toxin was designated as *Millepora* cytotoxin 1 (MCTx-1) and was found to be unstable during purification. MCTx-1 was potently cytotoxic (EC₅₀ = 79 ng/mL) towards L1210 mouse leukemia cells, was able to hemagglutinate a 0.8% suspension of sheep erythrocytes (0.2 µg protein/mL), and was lethal to crayfish (LD₅₀, 106 µg/kg). The MCTx-1 toxin did not show any hemolytic or phospholipase A₂ activity. Therefore, it was suggested that MCTx-1 represented a different protein toxin to the formerly reported protein toxins isolated from *Millepora* spp. According to the BLAST database, MCTx-1 belongs to the dermatopontin family of proteins (Fig. 29.12).

Fig. 29.11 The fire coral *Millepora dichotoma* var. *tenera*



Dermatopontin was initially isolated from bovine dermal extracts as an extracellular matrix protein [75]. Thereafter, dermatopontins were isolated from human, pig, rat, and mouse as extracellular matrix proteins [76–78] and from invertebrates including the horseshoe crab, sponge, and snail [79–81]. However, MCT_x-1 was the first toxic dermatopontin to be discovered. MCT_x-1 exhibited highest homology (36%) with the hemagglutinin/amebocyte aggregation factor from the horseshoe crab *Limulus polyphemus* [79]. Of the reported dermatopontins, only MCT_x-1 and the *Limulus* aggregation factor have demonstrated hemagglutination activity. Bovine dermatopontin does not have hemagglutinating activity [82], whereas *Limulus* aggregation factor has phospholipase A₂ activity [83] and MCT_x-1 does not. Various proteins originating from snake and spider venom have also been shown to have hemagglutinating activity [84–86]. Galactoside-specific lectin (BJcuL) isolated from the venom of the snake *Bothrops jararacussu* [87] also has hemagglutinating activity and significant cytotoxicity [88]. Injection of BJcuL into the paws of mice results in a dose-dependent edema and vascular permeability [89]. Thus, BJcuL has been shown to participate in edema formation induced by snake bite. MCT_x-1 also exhibits hemagglutination activity and potent cytotoxicity similar to BJcuL. Thus, MCT_x-1 may be at least partially responsible for the edema associated with *Millepora* stings.

29.6 Protein Toxins of Hydra

Hydra are freshwater animals that belong to the phylum Cnidaria, and thus, they also synthesize proteinaceous toxins. A limited number of studies have investigated their toxic components. We have chosen to review the toxins synthesized by Hydra, even though these toxins do not originate from a marine animal, because of their relationships to other marine life forms.

It has been reported previously that two protein toxins exist in the isolated nematocysts of *Hydra attenuata* [90]. One of these toxins demonstrated hemolytic

MCTx-1	MVTLYLHVPILLLVVITARAAPKPDTHNPFDELSVA-EKQDLHYGDRSRKDPFIIAQNDVG-N-NFRDGTQENLTKVRSKVNQYDQFFTF	87
Limulus	M-NSPAIVII-FSTLTF-SEAWV---NDWDGALNFQCQLKDSIKTLSSIHSHHEDRRWNFGCERTLRD-PS-CYFTNYVNDWDKLLHF	82
Snail	M-SQSLYLAI-LMTVA--SAAYV---NDWDQPFNFRCPDGVVSYVSSVHDNRDRRWFELC-RARQTHS-CTDSGYVNDFDGPIVY	81
Sponge	MRMFEVNAVGLFVILVIALHAVAAFOYQNDYDKPLHVECPDKQALYYVQS IHSNRHEDRRFRFNCKHAANKWSHCFTWTGHLNNYDGLVNY	90
	* . * * * * * * *	
MCTx-1	KCPLETIKSIGSIHDNHYEDRQWDIDCKPAGYTMGIS TWSPYANDYDGS MNFECNEGSVVTGMSSI HDNYYEDRRYQLMCSYLNWKRK	177
Limulus	TCKSGEALAGFNSYHDNRDRRWKIYC---C-KDKNKCTDY-RTCAWT-GYVNSWDGDLHYTPKDYVLTGVI SEHDNHREDRRWKFO	165
Snail	TCFNGKVMGVHSYHNNRDRRFGFYC---C--DVQGSTP--RDCYTT-DYVNDWDGKLT LAVPEGRAVKAAFSHHNNRDRRWQFO	162
Sponge	QCFPNLMTGVKSEHSNHEDRRWSFKC---C-KANGYHT---KSCIMT-GYINSYDNPMPHAAHYNHFFAGAYSVHSNHEDRILWKMY	171
	* . . * * * * * * * * * *	
MCTx-1	SCAWTSYTTYDASFVELTPTGKFLVGMKSOHNNYEDRKFKMLYC	222
Limulus	HCLR-KNC-----	172
Snail	ICAL-----	166
Sponge	ECKYSKIYT-E-SLT-----	184
	*	

Fig. 29.12 Sequence comparison of invertebrate dermatopontin homologs and MCTx-1. The alignment of MCTx-1 from the fire coral (GenBank, nucleotide, AB299385), dermatopontin homologs from the horseshoe crab *Limulus polyphemus* (GenBank, protein, Q01528), from the snail *Biomphalaria glabrata* (GenBank, protein, Q3YJU8), and from the sponge *Suberites domuncula* (GenBank, protein, Q966Y2) is shown by the single-letter amino acid code. Identical residues are marked by asterisks. Conserved residues are marked by dots

activity and caused initial spasmodic contractions in larval and adult *Drosophila*. The second protein toxin caused long-lasting paralysis that caused death in the tested *Drosophila*. However, both toxins failed to exhibit any phospholipase activity. While the toxin molecular weights remain unclear, the hemolytic toxin was clearly larger than the lethal toxin when assessed by gel permeation chromatography [90].

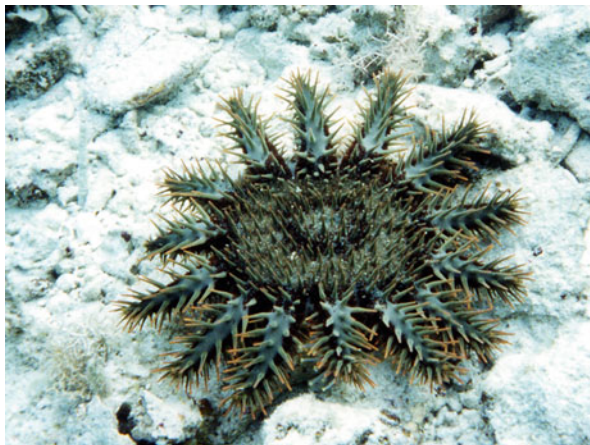
An Israeli research group also isolated a paralytic and cytolytic 27-kDa protein, termed hydralysin, from the body of the green hydra *Chlorohydra viridissima* [91]. The cDNA of hydralysin was subsequently cloned and sequenced. The deduced amino acid sequence of hydralysin revealed homology with pore-forming protein toxins isolated from bacteria and fungi [91]. Recombinant hydralysin also demonstrated dose-dependent cytotoxic effects on insect sf9 cells. It is also noteworthy that hydralysin is located within the hydra body, but not the nematocyst. Thus, the function of hydralysin in *C. viridissima* was speculated as follows [91]. Firstly, hydralysin may function as a defensive allomone that acts in combination with stinging cells to deter possible predators. The second possibility is that hydralysin acts as an allomone by prolonging the paralysis of the prey following ingestion. The same research group also reported the presence of hydralysin isoforms in *C. viridissima* [92]. Functional characterization of the hydralysin isoforms revealed that the soluble monomers were rich in β -structure, as shown by far UV circular dichroism and computational analysis [92]. A large-scale expressed sequence tag (EST) database for *Hydra magnipapillata* has recently been accumulated. Search within this database revealed that *H. magnipapillata* expressed orthologs of phospholipase A₂ as well as cytolytins belonging to the actinoporin family [93].

29.7 Protein Toxins of Starfish

Starfish are echinoderms that belong to the class Asterozoa. Among the approximately 2,000 starfish species, it is only the crown-of-thorns starfish *Acanthaster planci* (Fig. 29.13) that is known to produce a venomous sting within their spines. *A. planci* is covered with spines which each secrete a venom. This starfish is widely distributed throughout tropical and subtropical coral reef areas. Feeding almost exclusively on living coral polyps, *A. planci* prefers preys such as branching and plate corals. Indeed, massive proliferation of *A. planci* populations can be fatal to coral reefs. Thus, volunteer divers are currently attempting to collect and control the numbers of *A. planci* from coral reefs around Okinawa. During these collections, divers are often accidentally stung by *A. planci*. Envenomation by *A. planci* results in severe local pain associated with immediate and intense swelling, redness, and numbness at the site of envenomation. Severe sting cases may also cause necrosis at the sting site.

Protein toxins have been isolated from the spines of *A. planci* and were termed plancitoxins I and II for the major and minor toxins, respectively [94]. Both toxins demonstrated an LD₅₀ value of 140 μ g/kg when intravenously injected into mice. Injection of a sublethal dose of plancitoxin I or II into mice also significantly elevated serum levels of glutamic oxaloacetic transaminase and glutamic pyruvic

Fig. 29.13 The crown-of-thorns starfish *Acanthaster planci*



transaminase. This finding demonstrated that both toxins were potently hepatotoxic. SDS-PAGE analysis revealed that both of the plancitoxins were composed of two subunits termed the α -subunit (10 kDa) and the β -subunit (27 kDa) that were bridged by a disulfide bond. Based on the determined N-terminal amino acid sequences of the α - and β -subunits, the full-length cDNA (1,820 bp) encoding plancitoxin I was cloned. The α -subunit (92 amino acid residues) and β -subunit (240 residues) were coded in this order by the same cDNA. Interestingly, the deduced amino acid sequence of plancitoxin I revealed 40–42% homology with mammalian deoxyribonuclease II (DNase II) (Fig. 29.14). In addition, plancitoxin I exhibited DNA-degrading activity at a pH of 7.2. Plancitoxin I represents the first example of a toxic DNase II whose structure has been elucidated [94], and is the first DNase II to be reported from a marine invertebrate species. Intriguingly, plancitoxin I induced apoptosis in rat liver cells, an event that was found to be independent of the caspase-3 cascade, the signaling complex that is generally accepted to regulate apoptotic processes [95].

It is well established that phospholipase A_2 enzymes hydrolyze glycerophospholipids at the *sn*-2 position of the glycerol backbone to release lysophospholipids and fatty acids. Phospholipase A_2 occurs ubiquitously in nature in both intracellular and extracellular forms. Mammalian phospholipase A_2 enzymes generally play a nontoxic and important role in their host. In contrast, snake venom phospholipase A_2 demonstrates a variety of pharmacological effects such as hemorrhage induction and myonecrotic and neurotoxic activities [96]. Among marine animals, the first phospholipase A_2 -type toxin reported was isolated from the scyphozoan jellyfish *Rhopilema nomadica* [44]. Subsequently, two toxic phospholipase A_2 proteins termed AP-PLA $_2$ -I and AP-PLA $_2$ -II were isolated from the spines of *A. planci* [97]. AP-PLA $_2$ -I and AP-PLA $_2$ -II exhibited hemorrhagic and capillary permeability-increasing activity. The full-length cDNAs encoding AP-PLA $_2$ -I and -II were then individually cloned. In common with both of the

Plancitoxin I	MPSSVIMFTFLALTVLTAVMVGTSEAVSCMDKNKVPDWFIVYKLPQDSASSKPVIREGYQMYDMYNNQALKFSSTSLKDDDDHAIAYTV	90
Human DNaseII	M--I-PL--L-LAAL--LCV-PAGALTICYGDSQPQDFWVYVYKLP-ALRSGSAAQGRGQYKYLDESSGGWRDGRALIIINSEPGAVGRSL	79
Porcine DNaseII	MATLSPL--L-LAAL--LWV-FVGTLLTCYGDSQPQDFWVYVYKLP-AHSSPGDVAQSLRYKYLDESSGGWRDGCAGSINSSGTALGRSL	82
Murine DNaseII	MATLRSI--L-LAAL--LWV-PAEALSCYGDSQPQDFWVYVYKLP-A-HSGSRDTPKGLTYKYMDQNSDGMQDQGVGVINSSEGAVGGRSL	81
	* * * * * . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . *	
Plancitoxin I	DDIYKNHGKGNLAHVMYNDQPP-AGEEIQSLVGHGHTKGVLAFDGTSGFVWVHVSVPKPLP-ASKSYNWPDNAKRNGQTLLCITFKYDQFE	178
Human DNaseII	QPLYRSN-TSQLAFLLYNDQPPQPSKAQDSSMRGHTKGVLLLDHDDGGFWLHVSVPNPPAPASAAYSWPHSACTYGGTLLCVSFPFFAQFS	168
Porcine DNaseII	LPLXR-N-TSQIAFLLYNDQPPKYRGSQHSNRGHTKGVLLLDQEGGFVLIHVSVPNPPSSAAYSWPHSACTYGGTLLCVSFPFLTQFL	170
Murine DNaseII	QPLYRKN-SSQIAFLLYNDQPPKSSSRDSTGHGHTKGVLLLDQEGGFVLIHVSVPNPPAPASGAYTWPNAQTFGGTLLCVSPLFTQFA	170
	..* * * * * * * * * * *	
Plancitoxin I	KIGQQLKYNPEGVYDSLPLSKLVGKTPSIVLIVKNVHTSPNWRQLNLQSKSGQTFVFNKASKWGEDLYKKNWLAHFKSGLYCETWQN	268
Human DNaseII	KMGKQLTYEPWVYNYQLEGIFAQEFPPLENVKGVHVSQEPWNSSITLTSQAGAVTQSFPAKFSKFGDDLYSGWLAALGTLNLQVQFWHK	258
Porcine DNaseII	NISRQLTYTPMWYDYKLEGGDFARKFPLYEEVVKGHVLIQEPWNSSVTLTTSKAGASVQSFACNFGDDLYSGWLAALGTLNLQVQFWQR	260
Murine DNaseII	RIGKQLTYTYPLVYDVKLEGGFFAQKLPDLETVIKNQHVLIHHPWNSSVILTTSQAGATQSFPAKFGKFGDDLYSGWLAALGTLNLQVQFWQN	260
	..* * * * * * * * * *	
Plancitoxin I	GGRNLNSCEAGLNVYKVSLSG--GSDFKGTKDHSKMAVTTKSLKWTCTIGGINRQTSQMYRGGGAVLENNVHKAFYDSVAEYEP	356
Human DNaseII	TVGILPNSCSDIWQLNVNQIAFPGAPGSFNSTEDHSKWCV--SPKGPWTCVGMNRRNGEQRGGTLCQQLPALWKAQPLVKNYQP	346
Porcine DNaseII	SAGILPNSCSGVQVHLVDTQIAFPGAPGNFATEDHSKWCV--APERPWTCVGMNRRNREHRGGTLCQAQLPALWKAQPLVKAWEP	348
Murine DNaseII	SPGILPNSCSGAYQVLDVTQGTGFPGRSLTFSATEDHSKWCV--APOQPMACVGMNRRNKAETHRGGTVCQLPSPFWKAFQSLVKDWKP	348
	..* * * * * * * * * *	
Plancitoxin I	CT-----	358
Human DNaseII	CNGMARK-PSR-AYKI	360
Porcine DNaseII	CEKENRPFSPRPAKD	364
Murine DNaseII	CIEGS-----	353
	*	

Fig. 29.14 Sequence comparison of plancitoxin I and mammalian deoxyribonuclease II (DNase II). The alignment of plancitoxin I (GenBank, nucleotide, AB121229), human DNase II (GenBank, nucleotide, AB004574), porcine DNase II (GenBank, nucleotide, AJ001387), and murine DNase II (GenBank, nucleotide, AK145192) is shown by the single-letter amino acid code. Identical residues are marked by asterisks. Conserved residues are marked by dots

AP-PLA₂ forms, the precursor protein was composed of a signal peptide, a propeptide, and a mature protein (136 and 135 residues for AP-PLA₂-I and -II, respectively) [98]. These two proteins were the first specifically characterized toxic phospholipase A₂ enzymes to be described from a marine animal.

29.8 Protein Toxins of Sea Urchin

Sea urchins belong to the phylum Echinodermata, and several species such as *Diadema setosum*, *Toxopneustes pileolus*, *Tripneustes gratilla*, and *Asthenosoma ijimai* are known to be venomous. Envenomation has been shown to be caused by stings from either the pedicellariae or spines. It has been reported that the main toxins produced by sea urchins are proteinaceous [99, 100]. Only three isolated lectins, contractin A (18 kDa), SUL-I (32 kDa), and SUL-II (23 kDa), from the pedicellariae of *T. pileolus* have been partially characterized to date [101, 102]. Contractin A was shown to cause contraction of the tracheal smooth muscle [101]. Interestingly, the N-terminal amino acid sequences of contractin A and SUL-II showed similarities with secretory phospholipase A₂ [102]. However, the N-terminal amino acid sequence of SUL-I did not show homology with any known proteins. It has also been reported that SUL-I induces dendritic cell maturation from human monocytes in vitro [103]. However, the involvement of these lectins in envenomation remains vague.

29.9 Protein Toxin of Cephalopods

Cephalopods include cuttlefish, squid, and octopus. Cephalopods are largely predatory and carnivorous animals that feed on Crustacea, bivalves, and, on occasion, fish. It is well established that cephalopods utilize venom excreted from the salivary gland for hunting and capturing prey. Their venomous bites either prevent prey movement or kill the prey directly. However, deadly envenomation in humans has only been reported for the blue-ringed octopus *Hapalochlaena maculosa*. Tetrodotoxin, also known as puffer fish toxin, is the toxic compound present in the venom of *H. maculosa* [104]. Tetrodotoxin is a small-molecular-weight alkaloid with potent neurotoxic properties. With the exception of the *H. maculosa* toxin, it has been reported that proteinaceous toxins form the major toxic component of cephalopod venom.

Cephalotoxin is the cephalopod protein toxin that causes paralysis and eventual death in crabs. It is synthesized by the posterior salivary gland of the cuttlefish *Sepia officinalis* and the octopus species *Octopus vulgaris* and *O. macropus* [105, 106]. A cephalotoxin has also been purified from the octopus *Eledone cirrhosa* [107] and the salivary gland of *Octopus dofleini* [108]. Two additional paralysis-inducing proteins termed α -cephalotoxin (91 kDa) and β -cephalotoxin (34 kDa) have been isolated from the salivary gland of *O. vulgaris* [109]. However, detailed descriptions of the properties and primary structures of these cephalotoxins have not yet been reported.

The first detailed characterization of a cephalotoxin was conducted on SE-cephalotoxin isolated from the salivary gland of the cuttlefish *Sepia esculenta* [110]. SE-cephalotoxin was shown to be a 100-kDa monomeric glycoprotein with an LD₅₀ of 2 µg/kg (towards crabs). A full-length cDNA (3,402 bp) encoding SE-cephalotoxin was subsequently cloned and the deduced amino acid sequence of the mature SE-cephalotoxin (1,023 amino acid residues) determined. SE-cephalotoxin did not share homology with any proteins in the database search. The mode of SE-cephalotoxin action remains to be solved.

29.10 Concluding Remarks

This chapter describes the studies published to date on protein toxins isolated from venomous marine animals. For many years, detailed characterization of these toxins has been hampered by their instability and the difficulty in obtaining sufficient quantities of animal samples. Only recently has the precise characterization of a few of these protein toxins been reported. However, with the exception of the actinoporin family, the number of characterized toxins remains small. It has been revealed that protein toxins synthesized by marine venomous animals are quite unique in both their structure and biological activities. MACPF protein toxins isolated from the sea anemone, a novel protein toxin family from the box jellyfish, DNase II toxins from the starfish, and a dermatopontin family toxin from fire coral are representatives of some of these unique toxins.

At present, sting cases caused by venomous marine animals are only treated symptomatically. If the precise structure and mode of action of the proteinaceous toxins produced by venomous marine animals were better characterized, specific and effective remedies to treat these cases could be developed. Furthermore, protein toxins that exhibit unique bioactivities may be utilized as molecular pharmacological probes in the medical and biochemical fields. The study of protein toxins produced by venomous marine animals has the potential to generate many interesting discoveries in the future.

29.11 Study Questions

1. Which is the most dangerous one among venomous marine animals that utilize protein toxins?
2. Do cnidarians generally recognized as nonvenomous, for example, a moon jelly, also have the toxin?
3. From the marine animals, many famous nonpolypeptide toxins such as tetrodotoxin, palytoxin, and ciguatoxin have been reported. Why do most of the marine venomous animals use the protein (polypeptide) toxins instead of the nonpolypeptide toxins?
4. Why are most of protein toxins from marine venomous animals so unstable?
5. How do the marine venomous animals protect themselves from their own venom?

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Abstract

This chapter provides a general conclusion to this textbook on marine natural products science by discussing a few outstanding achievements in the field, and then identifies several areas for future investigation that may be fertile. New technological advances will allow researchers to investigate issues of the production, utility, and function of marine natural products in highly insightful ways. Prospects for the field of marine natural products appear very bright because the field has embraced the involvement of many disciplines and technologies, thus ensuring high levels of innovation and vitality.

30.1 Summary Perceptions on the Utility of Marine Natural Products

This volume, intended as a textbook for students as well as a handbook for practitioners of the marine natural products sciences, has broadly surveyed a majority of the disciplines which make up this field. From overview chapters on

W.H. Gerwick

Scripps Institution of Oceanography, Skaggs School of Pharmacy and Pharmaceutical Sciences,
University of California, San Diego, CA, USA

e-mail: wgerwick@ucsd.edu

the distribution and chemical trends associated with different life forms to the methods used to study the intricate structures of their unique compounds, from the biosynthetic origin in the producing species to the chemical ecology, toxicology, and pharmacology, it is this complement of subjects from which the field derives such vitality and widespread interest. The confluence of multidisciplinary research, as experienced in marine natural products, is inherently rich in opportunities for innovation and creativity.

However, another factor helps to explain the passion of those learning and studying this area – curiosity! It is nearly universal for people to wonder how it is that sea creatures adapt to their underwater world, from their unusual shapes, colors, and sizes, to here an exploration of their adaptations at a chemical, biochemical, and genetic level. How do soft-bodied creatures avoid being eaten in shallow-water tropical ecosystems? How do creatures constantly bathed in microorganism-laden seawater resist microbial and viral infections? How do various shrimp, worms, and bacteria cope with the intense pressure and temperature of deep-sea vents or the sub-0°C temperatures under meters of continuous arctic sea ice? While in some cases, the answers or partial answers to these questions are known, many marine phenomena and habitats remain incompletely examined for their unique inhabitants and interesting life histories, even now in the early twenty-first century.

The field of marine natural products research has made important and widely recognized contributions in several arenas. Perhaps most notably visible have been the spectacular discoveries of marine natural products with utility to the biomedical disciplines. As chronicled in various chapters of this volume, new antineoplastic agents have been discovered from various marine life forms, and several are now approved to treat specific human cancers, including Halaven and Trabectedin [1]. Other useful agents have been developed from marine organisms to treat chronic pain (Prialt), whereas still others have commercially useful anti-inflammatory properties (pseudopterosin A) [2, 3]. Various unique protein-based adaptations of marine life have been studied and yielded such important products as Taq polymerase for amplifying DNA and green fluorescent protein for visualizing cellular and physiological events [4, 5]. And many promising agents in diverse therapeutic areas lie nearby on the development horizon!

However, on the converse side of useful biomedical products from the sea has been the characterization of numerous poisons and toxins created by marine life which negatively impact human health. Some of these are experienced as venoms from contacting these life forms directly, such as scorpion fish, sea snakes, or fish-hunting mollusks. Others enter our food chain through their accumulation in fish, shellfish, and other edible creatures from their ultimate microbial or microalgal sources, and characterization of their chemistry and pharmacology is a critical step in the process of detecting, avoiding, and treating such encounters. Ultimately, these toxins are potent agents that have the capacity to teach us new vistas of receptor and ion-channel pharmacology and, in a few cases, to offer leads toward drug development [6].

In this latter regard, biotechnological approaches are rapidly emerging as effective and ultimately affordable methods by which to develop some of these medical leads from the sea. Already, the protein products described above are produced by (and in some cases enable!) industrial-scale biotechnological manufacture. On the other hand, new genetic and biochemical understanding of the biosynthetic processes used to produce small molecules is being employed to create novel analog structures that allow structure-activity relationships to be examined, even in extraordinarily complex molecular classes. This is complemented by tremendous advances in synthetic organic chemistry that permit the industrial scale chemical synthesis of such elaborate and complicated structures as erubulin and discodermolide [7, 8]. These are indeed outstanding human achievements of the early twenty-first century!

In 1960, Professor David Keeling at the Scripps Institution of Oceanography published the now-iconic graph which recorded the yearly increase and seasonal variation in atmospheric carbon dioxide at Mauna Loa, Hawaii [9]. This marked the beginning of the current era of appreciation that human impacts on the earth can occur on a global scale. Consequences of this increased input of fossil fuel-derived CO₂ on various oceanic and atmospheric processes are under broad examination, and one of the most alarming is the measurable increase of ocean acidity resulting from CO₂ absorption into seawater and the resulting production of carbonic acid [10]. Various pH-dependent physiological processes, such as the aggregation of CaCO₃ to form the shells of mollusks and exoskeletons of corals, are impacted and place these marine life forms under increased stress. This global change in ocean pH will certainly hasten the extinction of many species as well as potentially lead to physical changes in the nearshore environment (e.g., coral reefs). In one sense, it is a race against time to more thoroughly understand and appreciate the capacity of marine organisms to produce small molecules of biomedical utility before they disappear! In this regard, the extraordinary developments in genome sequencing speed and capacity may at least allow a “genetic record” to be preserved of some of those species greatest at risk.

Remarkably, one group of ocean organisms, the microalgae, may hold a solution to our broad need for a sustainable source of liquid fuel [11]. Microalgae have many desirable characteristics, including their capacity to grow quickly, produce an abundance of oil that can be used as biodiesel, and use salt or brackish waters with nutrients derived from wastewater. Additionally, their culture does not compete with food-producing land (e.g., desert land may be ideal for microalgal pond cultures). It is important to recognize that burning of algal oil for energy production is carbon neutral in that it derives from the fixation of atmospheric CO₂ (as versus fossil fuels which add more carbon to the planetary biosphere). Moreover, the non-oil constituents and nutrients of algae can be recycled in an algal production facility or be used in other product streams such as a rich protein source for animal feed or pigments with diverse biotechnological applications. However, there are numerous technological, engineering, and scientific challenges before this vision might be realized, and this will require the passion, ingenuity, and persistent efforts of many talented people in the future.

30.2 A Futurist View on Marine Natural Products Research

From a futurist perspective, what can we look forward to in the development of the marine natural products sciences? As detailed throughout the chapters of this volume, there are many exciting frontiers in the field of marine natural products chemistry. While some of the basics are now in place, such as which organisms elaborate which types of natural products, and most recent estimates indicate some 22,000 different molecules have been isolated and chemically defined from marine life, these discoveries actually catalyze the emergence of even more questions for the future. This area of science, as so many are, has been strongly driven by technological capability, and the thoughts below are largely based on predictions of how technological advances will change the nature of the questions we will likely be asking in the future.

Inherent to the finding that a given molecule has an interesting biological activity is the question of biological target. With which specific protein or other macromolecule does this new substance interact? What is the nature of the interaction at a molecular level and at an atomic level? It is when understanding develops to this very specific level that true understanding of mechanism and rational drug design can take place. Related to this, a frontier not well developed in marine natural products chemistry is the use of modern structural biology coupled with computational science to understand the specific interactions between proteins and small molecules. A rich interface exists between drug action, structural biology, and computational chemistry; however, to date, there has been relatively little integration of computational chemistry into the field of natural products, and this will certainly change as these fields “discover one another.”

In a sense related to the foregoing discussion, there is an enormous opportunity to refine and extend the field of chemical ecology to a molecular level of understanding. With a desire to deepen understanding of the evolution of defensive secondary metabolites, it becomes of interest to again know the specific target of the defensive compound and the nature of the interaction. Clearly, to appreciate coevolution of these chemical and biochemical systems, it is critical to know of them and to know the nature of the interactions at a very specific and precise level.

Several chapters have specifically dealt with biosynthesis of marine natural products, and others have alluded to the pathways leading to assembly of their exotic and oftentimes complicated molecular structures. Some of the biosynthetic principals have been defined in a few groups of marine organisms, but for the most part, this is an area ripe for more exploration and innovation. One ultimate vision is that by study of the biosynthetic pathways at the genetic, protein, and mechanistic biochemical level, we will enable the capture and harness of these capacities so as to have efficient production systems of natural products and their analogs. However, the field of marine biosynthesis needs to demonstrate its relevance to biomedical research, the major funder of this type of research, through the creation of actual molecular entities that can be evaluated in biological systems. Unfortunately, this goal and vision has been difficult to realize largely because the pathways are

exceedingly complex and a number of spatial and geometrical constraints appear to govern their catalytic efficiency. For those pathways involving modular polyketide synthases (PKSs) and nonribosomal peptide synthetases (NRPSs), such as the curacin A pathway from the marine cyanobacterium *Lyngbya majuscula* [12], the construction of the molecular scaffold occurs as a result of numerous consecutive passages of product from one enzyme to become substrate of the next. In effect, it is like running a relay race with passage of the baton between 40 participants as they traverse a complex maze! But there have been a few successes in these regards, such as production of cryptophycin analogs by provision of advanced precursors to unique catalytic machinery captured from the biosynthetic pathway [13], or the formation of unique salinosporamide analogs through production of blocked mutants followed by provision of alternate substrates [14]. Other successes from developing knowledge of biosynthetic pathways include the prediction, functional expression, and biological evaluation of the products of so-called cryptic gene clusters (gene clusters for which the encoded metabolite has not yet been found or described) [15]. With so many developments in other aspects of genetic engineering and molecular biology, this general area remains a prime opportunity for creative and innovative research.

As detailed in several of the chapters of this textbook, marine microorganisms are increasingly being revealed as responsible for the production of diverse marine natural products. Of importance to this observation, which will certainly become better defined with further study, is the increasingly deep knowledge of the evolutionary relationships of marine microorganisms to one another. The last few years have seen a welcome shift to the broad use of the 16S rRNA gene by which to define microorganisms under study. This will continue to evolve as technological advances enable ever-increasing speed and efficiency of DNA sequencing, predicted to be just \$1 per megabase in a few years' time. With such ready access to genomic information, we will analyze relationships of microorganisms at the whole genome level; our current efforts using one or a few genes to define relationships will be viewed in a few years as primitive and lacking in power.

In the area of structural analysis, technologies are already emerging wherein we can directly see organic molecules by atomic force microscopy [16], and this will certainly improve to the point where this approach to structure determination will be commonplace. Gone will be indirect methods of structural analysis, such as NMR spectroscopy or X-ray crystallography, at least so within a laboratory environment. Rather, high-field benchtop NMR spectrometers and handheld mass spectrometers may soon be available and will allow for the direct analysis of plant and microbial samples in the field. Similarly, methods for genetic analysis will become miniaturized and perhaps provide real-time phylogenetic information in the field through wireless connection with gene databases. Possession of such powerful chemical and genetic information will allow the focused collection of organisms for further study. By coupling this detailed knowledge of structure to complete metabolomic, proteomic, transcriptomic, and genomic analyses, we will understand the relationships of genetics, epigenetics, and splice variations to individual differences and their responses to the environment.

Marine-derived macromolecules already constitute an important class of useful material, including such substances as microorganism-derived fluorescent proteins and temperature-stable DNA polymerases to algal polysaccharides with useful emulsifying or gelling properties. The many and highly diverse small-molecule natural products of marine life are the result of an even greater diversity of biosynthetic enzymes with unique reactivities and substrate specificities. At present, these enzymes largely represent a “conceptual toolbox” of useful catalysts; in the future, we will see their application to the production of novel substances with pharmaceutical or biotechnological utility. The biosynthesis of polysaccharides and other macromolecular classes will become even better understood, and it can be envisioned that we will be able to control their molecular assembly to produce polymeric materials with specifically desired properties.

The problem of “supply” has long plagued natural products drug development [17], and with smaller and smaller sample sizes succumbing to structure elucidation, this will only intensify (indeed, the theoretical lower limit is the single molecule, a limit already reached by atomic force microscopy!). However, one of the goals of chemical biology and biosynthetic investigations is to learn how to harness this genetic and biochemical machinery to produce compounds of interest and in the quantities necessary for meaningful biological evaluation. Such clever technological developments will also enable methods to express and study the products of “cryptic” gene clusters wherein the encoded product is not yet known due to either low or nil expression under normal culture conditions. While the quantities of a natural product needed for 1534-well plate assays are relatively easily achieved, to translate “screening hits” into meaningful lead compounds requires multiple milligrams for mechanism of action and *in vivo* evaluations. This need will continue to be a strong driver of chemical biology and innovative microbiological research well into the future.

Drug screening of natural product mixtures is certain to advance in ways that make the process more efficient and effective. This may involve innovative preselection of molecular classes for “desirable” pharmaceutical properties. Alternatively, transcriptomic and proteomic profiling to first assess mechanisms or pathways being modulated in advance of disease-specific biological assays may be a powerful new approach. Informatics analysis of data from screening of agents to a panel of targets or disease-causing organisms can also be efficient in identifying new agents that work by novel mechanisms of action. Clearly, much creativity and innovation is possible in the biological screening arena, and equally apparent, much is needed so as to have this process identify better drug candidates ever more efficiently.

The above thoughts represent a sampling of predictions that can be made at the present time, mainly through envisioning of specific technological advances, such as increased analytical power, DNA sequencing capability, or heterologous expression systems. What is not predicted, however, are the game-changing advances, the paradigm shifters, and the new technologies which will allow completely new approaches to be used and questions to be investigated. In composite, marine natural products science continues to be a vital and frontier field of investigation largely because it has embraced new technological advances and multidisciplinary approaches, and the future looks equally exciting!

30.3 Study Questions

1. Describe a technological advance other than those suggested above that will impact the field of marine natural products science.
2. Can you think of a paradigm-shifting advance in the field of marine natural products science? What knowledge or technological advances would be needed to realize your vision?

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