Preface

The pursuit of knowledge of the ocean has progressed in recent years due to the availability of new technologies and tools. Satellites are now equipped with sensors that can measure the optical densities of surface waters; profiling floats can collect physical and chemical data from around the world; and fluorescence detectors can provide information about the chlorophyll concentrations at depths beyond reach of satellite-based sensors. These technologies have stimulated a renewed interest in ocean exploration, and the vast quantities of physicochemical data collected have aided in the development of predictive models for some of the major ocean processes. By contrast, the integration of cell biology and genomics into oceanographic research is much less developed, even though biological (and especially microbiological) processes are fundamental for maintaining a functional global ecosystem. The study of aquatic organisms at the sub-molecular or molecular level spans from the smallest of viruses to the largest marine mammals. Issues addressed using molecular techniques are deeply rooted in questions posed by biological oceanographers: What species are present? How are they related to one another? How do they respond to alterations in the chemical and physical environment? What role do they play in biogeochemical cycling, food webs, and maintenance of global climate? Can we use specific organisms as indicators of environmental change? One of the major challenges in understanding ocean processes is the difficulty in four-dimensional sampling of a complex and dynamic habitat because of a lack of suitable microbial and biogeochemical sensors. The solution to this challenge is to develop new tools and methodologies for genomic-enabled oceanography.

The study of aquatic organisms at the molecular level is now widespread in ocean sciences. These techniques target molecular signatures (i.e., carbohydrates, lipids, proteins, and nucleic acid sequences), which provide a broad foundation for identifying specific organisms, revealing evolutionary relationships, inferring metabolic potential and function, and indicating stress due to environmental change. Subjects span from environments from all corners of the globe, including the shallowest of waters to the deep sea and cold seeps to hot vents. Target organisms range from viruses and phage to the largest marine mammals. Most recently, research on aquatic organisms has come to include genomics and associated technologies. The initial phase of the global ocean survey, an ambitious expedition to chart the ocean genome, generated an impressive number of open reading frames equivalent to half of the entire GenBank inventory of known genes. This study of marine bacteria highlighted the vast and previously unknown genetic information contained in extant marine microorganisms, from new protein families to novel metabolic processes. However, many of the open reading frames are unlike any known genes, which could encode metabolic processes that are yet to be discovered or be important in the regulation of cellular activity in the dynamic and variable marine environment. Metatranscriptomics and/or proteomics allowed us to elucidate metabolic activities under different conditions in the ocean in various organisms. The collection of large amounts of sequence information from these molecular studies paved the way for construction of DNA microarrays—high-density matrixes of DNA probes immobilized on a solid support. DNA array technology offers the possibility of detecting the presence and expression of many genes simultaneously in a single sample. They are able to identify functional groups, species, and ecotypes reliably

and rapidly. Protein arrays on the other hand, complement those based on nucleic acids by providing a basis for detecting specific gene products. Applications of DNA and protein arrays are projected to enable multivariant assessments of species diversity and function in relation to changes in the chemical and physical environment on scales not possible previously. Increasing reliance on cell-free analytical techniques like DNA and protein has also probably spur application of probes in the whole-cell format, to relate genetic content and expression to identifiable, intact cells and associations.

Although application of molecular techniques has become well established in ocean science, the vast majority of the work typically occurs in the laboratory after the return of a discrete set of samples, limiting opportunities to collect molecular data in near real time. While many molecular-based analyses are described as "high-throughput," those methods are generally restricted to laboratory use and require substantial effort to process and collect. Molecular techniques can form the basis for remote instrumentation sensing technologies for marine microbial diversity and ecological function. For example, molecular biological approaches may be deployed in the ocean sensor platforms to track microorganisms or processes of interest in real time. Most of the sensors used today utilize optical techniques to derive presence, abundance, and activity of organisms. New molecular analytical-based sensors are also emerging, such as ecogenomic sensors. Ecogenomic sensors provide measures or microbial presence and function at the molecular level. Included in the latter are the Autonomous Microbial Genosensor (AMG) and Environmental Sample Processor (ESP). The AMG is a microbiological sensing buoy developed by scientists from College of Marine Science at the University of South Florida. The AMG is the first microbiological detection buoy designed that uses nucleic acid-based amplification. Currently, the AMG is designed to transmit data through a WiFi connection and is battery powered for complete autonomous operation and can be connected to a cable network system for data transmission and power. The ESP was developed by Chris Scholin and his colleagues from Monteray Bay Aquarium Research Institute in Moss Landing, California. It is an electromechanical/fluidic device that collects water samples from the ocean subsurface and allows for the application of DNA probe arrays to detect target rRNAs present in crude homogenate using sandwich hybridization assay. Previous applications of the ESP have focused on detecting harmful algae and invertebrate larvae in situ.

The availability and the reliability of commercially available instruments, methods, and supplies have made it possible to dig into the molecular underpinnings of just about everything that is "environmental." These achievements, coupled with advances in ocean observatory technology and plans to extend those networks, have fueled the idea of applying molecular sensors in remote settings. The evolution and application of ecogenomic sensors seems as natural as instruments that have brought real-time chemical, physical, and bio-optical assessments of the ocean to our desks at a mere click of button. A key to autonomous observations of microbes in the ocean is the continuing development of sensing technologies in the laboratory, transitioning sensors from the bench to the field, and integrating sensor suites into observing platforms appropriate to spatial and temporal dimensions of specific process and phenomena. More exciting advances on molecular ocean sensing are still to come as more remotely operated autonomous undersea vehicles are incorporated into oceanographic research. There is no doubt that much work remains to define the assays that will be deployed in situ and the concomitant sample collection and processing requirements. Sustained investment in the development of in situ instrumentation is essential to bring to fruition the testing of ideas and models discussed in this book.

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