

Microbial Functional Genomics

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Preface

The overarching aim of genomics is to provide a comprehensive, genome-level understanding of the molecular basis of the structure, functions, and evolution of biological systems using whole-genome sequence information and high-throughput genomic technologies. The goal of functional genomics is to obtain a system-level understanding of the functional aspects of biological systems, that is, gene functions and regulatory networks. This is a formidable task given that knowledge of the nucleotide blueprint of an organism is only the initial step toward understanding the dynamic nature of gene function and gene product interactions that enable a cell to grow, replicate, and adapt to changes in its environment. To address the avalanche of data generated from numerous genome sequencing projects, a variety of high-throughput, parallel genomic technologies and bioinformatic, data-mining tools have emerged that allow a comprehensive analysis of biological systems at different levels. These technologies, combined with traditional molecular approaches, are beginning to provide a physiological, evolutionary, and ecological context for genomic sequence information.

The main purpose of this book is to establish a systematic description and review of the principles, methodology, applications, and challenges in the emerging field of microbial functional genomics from the viewpoints of genetics, biochemistry, cell biology, physiology, and ecology. As the title suggests, this book emphasizes studies that focus on microorganisms; however, some studies related to higher organisms are included for comparative purposes. The book's purpose is to identify research gaps, challenges, and experimental directions in microbial functional genomics, as well as to point out the advantages and limitations of recently developed high-throughput genomic technologies, most notably DNA microarrays and proteomic tools. The impact of functional genomics on such established research areas as bacterial pathogenesis, antimicrobial drug discovery, and toxicology is also described. The intent of this book is not to present an exhaustive survey of the published literature on microbial functional genomics, but to provide the reader with representative examples illustrative of basic principles, approaches, and applications in the field, with an emphasis on genomic-scale studies using integrative multidisciplinary approaches. Clearly, there are many studies employing functional genomics that we have not been able to include or cover in sufficient detail because of space constraints. This book is intended as a guide and reference for senior undergraduate and graduate-level students, as

well as for professionals interested in microbial genomics and functional genomics in general.

This book begins with a chapter that attempts to codify and distinguish various aspects of functional genomics by defining the purpose and scope of genomics and functional genomics. Chapter 1 also provides a brief overview of the history of genomics and discusses the general approaches employed in functional genomics studies. Chapter 2 discusses the microbial diversity present in natural environments from biochemical and genetic perspectives and addresses the challenges associated with describing prokaryotic diversity. This chapter also reviews recent insights into microbial diversity that have emerged from whole-genome sequencing projects. Chapter 3 explores the strategies, approaches, and tools for annotating microbial genomic sequences by focusing on comparative analyses and different computational models. The potential problems associated with assigning gene functions based on sequence homology are also addressed in this chapter. Chapter 4 provides the latest insights into molecular evolution that have recently resulted from whole-genome sequence comparisons.

Chapters 5 through 10 address the various genomic technologies that are currently being used to elucidate gene function, regulatory networks, and protein interaction maps on a global scale. Chapter 5, for example, presents bioinformatic approaches to predicting gene function and discusses *in silico* methods for constructing metabolic pathways based on genome sequence information. Chapter 6 provides a detailed description of DNA microarray technology related to fabrication, hybridization, and detection, microarray experimental design, and general approaches to using microarrays for gene expression profiling. Chapter 7 is an overview of the current methods being used for microarray data mining and analysis. Chapter 8 discusses the principles behind and applications of three major strategies for genome-wide mutagenesis to the study of gene functions: gene disruption by allelic exchange, transposon mutagenesis, and expression inhibition using antisense RNA molecules. The advantages and disadvantages of each method are also presented. Chapter 9 describes proteomic tools for analyzing gene expression, with an emphasis on mass spectrometry for protein profile analysis on a genomic scale. Chapter 10 ends this section by discussing the tools for studying DNA–protein and protein–protein interactions. Two-hybrid systems and phage display for gene functional analysis and protein arrays are reviewed.

Chapters 11 and 12 focus on studies related to the functional analysis of genomic sequences of individual microorganisms. Chapter 11, for example, assesses some of the important contributions being made by functional genomics studies to further our knowledge of the well-studied model organisms *Escherichia coli*, *Bacillus subtilis*, and *Saccharomyces cerevisiae*. Chapter 12 discusses the functional genomic analysis of selected bacterial pathogens and several environmentally important microorganisms. More specifically, this chapter describes the contribution of genome sequence and *in silico* bioinformatic analyses to virulence gene identification, the impact of comparative genomics on revealing genetic diversity and evolutionary trends among pathogenic bacteria, and genomic and proteomic approaches to elucidating bacterial gene function and host–pathogen interactions.

Chapters 13 and 14 are concerned with the more applied aspects of microbial functional genomics or associated genomic technologies. Chapter 13 discusses the impact of genomics on antimicrobial drug discovery and toxicology. This chapter presents a brief historical overview of antimicrobial drug discovery, followed by a discussion of the challenges of new drug discovery, the impact of microbial genome sequencing on target identification, and the application of genomic-scale experimental technologies to target validation and drug candidate screening. The chapter concludes by discussing the newly emerged subdiscipline

of toxicogenomics. Chapter 14 reviews the basic principles and most recent advances in applying microarray technology to the analysis of genetic mutations and detection of microorganisms in natural environments. It explores various methods for the analysis of mutations using microarrays and the various types of microarrays specifically developed for analyzing microbial community structure within the context of environmental samples.

As the last chapter of the book, Chapter 15 discusses future directions in microbial genomic research and the likelihood that current understanding will guide future initiatives in productive directions. The two major areas are suggested to be further reductionistic work in the “omics” to provide a more comprehensive understanding of the cell’s coordinated function, and secondly, the use of genomics information to provide a more holistic view of the microbial community and its function. Eventually genomics-based microbial science may merge with ecology so that the functioning of ecosystems can be understood and perhaps even managed from the information and molecular catalyst perspective.

Foreword

Parallel with the genomic revolution, and a part of it, was the extraordinary expansion in information technology, yielding vast amounts of data from many sources that could be rendered interoperable and rapidly processed. Systematic understanding of the full complexity of the microbial environment then became possible. Development of analytic models of microbial ecosystems arising out of the information technology explosion moved microbial ecology out of a “black box” in the early ecological models to today’s “wiring diagrams” that have multiple pathways and incorporate entire sets of environmental parameters. The earlier, relatively primitive, hypotheses for water, air, and soil ecosystems gave way to the more complete analysis of the complex interactions comprising an ecosystem. From all these advances, the science of biocomplexity gained momentum and evolved into the interdisciplinary teamwork of scientists and engineers from many disciplines, mathematicians, chemists, physicists, atmospheric scientists, space scientists, geoscientists, clinicians, and social scientists, working together to provide a more profound knowledge of global ecological systems.

Into this mix has now come the capacity to determine the full genomic sequence of microorganisms and more than 100 such sequences have been published to date, with hundreds more in progress, all promising to deliver powerful information about the structure, function, and evolution of biological systems at a global level. Genomics may prove to be the most powerful tool to date. It opens up microbial diversity to inspection at details heretofore unimagined. Microbial genomes analyzed through whole genome sequencing reveal the enormity of diversity in the microbial world—a diversity that, with whole genome sequencing of total microbial populations, has been proven. A single gram of soil, a milliliter of seawater, or a cubic foot of air are now known to be the source of extraordinary diversity, suspected, but now revealed.

This book, then, provides valuable, highly technical information on the methodology of microbial genomics and offers great insight into specific aspects of microbial genomic ecology, using computational genome annotation, viewing microbial evolution from a genomic perspective, and providing details of DNA microarrays. It touches on the extraordinary capability to observe gene expression in real time and gives an entirely new perspective for microbial ecology. Functional genomics and metabolomics will certainly expand applications, as well as our understanding of microbial ecology in coming years. But, with this book, we have been given a passport to the new world of microbial ecology. . . exciting, fascinating, and rich with promise.

Rita R. Colwell
University of Maryland

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