

Preface

Over the last 10 years, the field of microbiology has been transformed by the ability to conduct whole genome sequencing with The Institute for Genomic Research (TIGR) located in Rockville, Maryland playing a central role. TIGR scientists published the first three complete microbial genome sequences—*Haemophilus influenzae*, *Mycoplasma genitalium*, and *Methanococcus jannaschii*—and have subsequently contributed more than 40 of the more than 150 complete and published genomes that are available as of January 2004. It was therefore an exciting opportunity when Humana Press proposed a book that surveyed the current state of the field. In choosing authors for the chapters, we turned in many cases to the expertise of our colleagues at TIGR. The external contributors represent a diverse range of experience spread over the globe.

The field of microbial genomics is vast. In selecting themes for chapters, however, we quickly realized that we could either opt for broad coverage at a relatively introductory level or instead focus in depth on topics we considered of critical importance. We chose the former approach. We hope *Microbial Genomes* will convey the great expanse of the subject and that it will be of interest both to readers new to the field, as well as to those with specialized knowledge. As Editors, it was interesting to find that despite very disparate titles, certain recurring themes—horizontal gene transfer, the importance of comparative genomic analysis, and microarray-based gene expression analysis—were threaded throughout the volume.

Microbial Genomes is divided into six major parts. Believing it was important to have a section devoted to the history of microbial genomics so as to allow readers to understand how the field developed, the editors commissioned Hamilton Smith to prepare the Introduction. Bioinformatics As a Tool in Genomics describes some of the most common computational tools for genomics and their application. Core Functions deals with metabolism, transporters and cell cycle processes that are found in every microbial genome. The Evolution of Microbial Genomes is a series of chapters that aim to show how genomics can be used to reconstruct the history and dynamism of the microbial world. In A Survey of Microbial Genomes we have organized a series of chapters that deal with selected groups of organisms. Although not every microbial genome is covered (and several are described in multiple chapters), the aim is to provide an indication of the biological information that can be extracted by genomic studies. Finally, Applications of Genomic Data describes how the genome sequences are being used to tackle the most important issues in microbiology. It should also be noted that many genomes listed as unfinished when the chapters were written in late 2002/early 2003 have now been completed. Interested readers should consult a website such as the TIGR microbial database (www.tigr.org/tdb/mdb/mdbcomplete.html) for the latest details.

The successful publication of this book would not have been possible without the help of Trina Eacho. Trina devoted many weekends to the organization of chapters and to the formatting of manuscripts. The editors gratefully recognize her significant contribution.

We realize of course, that this book has some omissions—not every important story could be covered. We hope readers will find inspiration from the diverse chapters and authors that have been assembled. In its truest sense, microbial genomics, consisting of evolutionary and population biology, gene expression analysis, proteomics and all the other studies that begin from the knowledge of DNA sequence, encompasses the very breadth and scope of the science of microbiology itself.

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