

Preface

This book is essentially the outcome of my intellectual cooperation with Werner Arber in the last couple of years. Our work toward the development of a previous journal I lead as *EiC* gave birth to discussions on different aspects of life, especially related to the microbial world, our mutual interest.

Through these enlightening discussions, I came to realize that one of the grand challenges in science nowadays is to understand how evolution continues to reshape life at a time when significant changes in biodiversity are happening all over the world. Moreover, the biggest current gap within this fundamental question is our limited understanding of the dynamics of microbial evolution in nature. If the past century and a half of studies has been mostly about the diversity and evolution of (macro) species (thanks to the landmark work of Darwin and the pioneer evolutionists), the twenty-first century will be mostly about the diversity and evolution of microbes (thanks to the next-generation sequencing technologies).

This gradual shift to a better understanding of the microbial world has also been driven by the fact that many of the ecological, environmental, and health challenges faced by our society are somehow linked to microbes. Although it is obvious for problems such as the rapid evolution of antibiotic resistance, it has, until recently, been less obvious for many other changes. The invasions of tree-boring insects devastating forests worldwide are not simple insect invasions. They are invasions by assemblages of species, including fungi and bacteria, of which insects are just the most visible members. On a different example, neuroscientists are convinced and supported by my many pieces of evidence that intestinal microbiota might influence brain development and behavior, which has caused a paradigm shift in neuroscience.

As such, it is possible to realize that one of the most profound paradigms that have transformed our understanding about life over the last decades was the acknowledgement that microorganisms play a central role in shaping the past and present environments on Earth and the nature of all life forms.

Stimulated by this paradigm shift, the field of microbial evolution is experiencing tremendous progress. Recent advances in DNA sequencing, high-throughput technologies, and genetic manipulation systems have enabled studies that directly characterize the molecular and genomic bases of evolution, producing data that are

making us change our view of the microbial world. The notion that mutations in the coding regions of genomes are, in combination with selective forces, the main contributors to biodiversity needs to be reexamined as evidence accumulates, indicating that many noncoding regions that contain regulatory signals show a high rate of variation even among closely related organisms. Comparative analyses of an increasing number of closely related microbial genomes have yielded exciting insight into the sources of microbial genome variability with respect to gene content, gene order, and evolution of genes with unknown functions. Furthermore, laboratory studies (i.e., experimental microbial evolution) are providing fundamental biological insight through direct observation of the evolution process. They not only enable testing evolutionary theory and principles, but also have applications to metabolic engineering and human health. Overall, these studies ranging from viruses to bacteria to microbial eukaryotes are illuminating the mechanisms of evolution at a resolution that Darwin, Delbruck, and Dobzhansky could barely have imagined.

As a natural consequence, by late 2015 I found myself discussing with Werner the interesting possibility of exploring these topics in more detail through a concise and reliable reference featuring the current knowledge on the molecular mechanisms of microbial evolution with a collection of chapters written by the leading experts in the field. Werner gave full support to the project and was willing to write a chapter summarizing his decades of work in the field. That was the driving force to launch this unique book within the Grand Challenges Series. I hope our readers share the same enthusiasm I felt when working in this project. This landmark work will certainly have a special place in my library.

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