

Preface

The rapid and ongoing process of functional and comparative genome analysis has revealed novel aspects of microbial biology and evolution, as well as of pathogenicity. In this book on 'Pathogenomics', we focus on the genomics aspects of pathogenic bacteria because of their importance and their unique host-adaptation strategies.

Genomes from each important human bacterial pathogen have now been sequenced. For many of them multiple sequences of different strains and of closely related species (non-pathogenic or animals pathogens) are available. Population genomics of pathogenic bacteria have metamorphosed epidemiology and provided astonishing information on the mechanisms related to bacterial persistence or host adaptation. In addition, 'Pathogenomics' has also shed new light on the forces that shape the evolutionary history of bacterial pathogenesis and virulence acquisition in some cases through co-evolution with the host. Even more spectacular, bacterial genome information was used successfully to retrace the ancient human population migrations, as is illustrated in this book by the gastric pathogen *Helicobacter pylori*.

More generally, multiple genomic sequences provide insights into the evolutionary processes that have shaped bacterial genomes and generated their diversity. Analysis of genome plasticity and the bacterial gene pools have led to new concepts such as the core genome (genes in common to all sequenced strains) and the pan-genome (the sum of the core and of dispensable genomes shared by all sequenced strains). The overwhelming quantity of information couldn't have resulted in answers to biologically relevant questions without a concomitant revolution in the development of bioinformatics approaches and high throughput experimental technologies (functional genomics).

This book intends to summarize these different aspects and novel trends in bacterial pathogenomics by presenting a unique collection of reviews written by leading

researchers in the field. The contributions were peer-reviewed by a panel of international experts.

The current technologies including computational tools and functional approaches for genome analysis are presented in illustrated chapters. This includes visualization tools for genome comparison, databases, *in silico* metabolic reconstructions and function prediction, as well as interactomics for the study of protein-protein interactions. Contributions dealing with pan-genomics and reverse vaccinology introduce the reader to the actual strategies used by genomics researchers to face the problems generated by bacterial diversity in the prevention and treatment of infectious diseases.

Taking individual bacterial pathogens as examples, the authors discuss the evolutionary forces that accompany human-pathogen interactions in the light of bacterial ecology. Most important frameworks of host-adaptation are illustrated by *Helicobacter pylori* and *Mycobacterium tuberculosis* that are human-specific and highly persistent.

Other chapters outline how bacterial pathogens have evolved through several mechanisms with one major role for horizontal gene transfer. Bacteria with different pathogenic strategies have been shaped. Some, like *Escherichia coli* have acquired the capacity to rapidly adapt to changing environments in order to enhance the spectrum of sites within the host that can be infected. For *Pseudomonas aeruginosa*, the strategies allow versatility for the occupation of a wide range of different environmental niches in addition to the human host. Others, like *Legionella* manipulate and subvert host mechanisms by synthesizing eukaryotic-like proteins that mimic specific cellular functions. Most fascinating are the signatures or possibility to deduce the life style of a bacterium as illustrated by a host-restricted organism such as *Bartonella* or by the versatile *Pseudomonas*. In the case of other pathogens such as *Helicobacter pylori* or *Campylobacter*, genome evolution through loss, gain and mutation of genes is also discussed.

In conclusion, the unique combination of topics dealing with technology, pathogenesis and evolution provides the reader with a global view of current and future trends in bacterial genomics. Teachers and lecturers will make use of the illustrative presentation to optimize knowledge transfer and learning strategies.

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