Preface

During the past 25 years, a nearly exponential increase has occurred in nucleotide sequences available from databases. The first microbial genomes were published in 1995 (Fleischmann *et al.*, 1995; Fraser *et al.*, 1995; Himmelreich *et al.*, 1996); the NCBI database currently contains 534 complete bacterial chromosome sequences. The genomes have been determined not only from different species, but also from different strains of the same species. This has paved the way for comparative genomics and has allowed detailed analysis of genetic differences between strains (Wren, 2000; Dobrindt and Hacker, 2001; Edwards, Olsen, and Maloy, 2002; Raskin, Seshadri, Pukatzki, and Mekalanos, 2006). Since infectious diseases are a major health threat worldwide and range among the most frequent causes of death worldwide (WHO Health Statistics 2006), it is not surprising that the first two organisms to be sequenced were pathogenic bacteria.

During the past decade many attempts have been made to understand the molecular basis of microbial pathogenicity, and our knowledge has advanced quickly, in particular through the use of methods of cellular biology, genomics, and proteomics. Various events in the pathogenesis of microbial infections, such as adherence to and entry into human and animal host, invasion of host cells, toxin production, establishment and dissemination of bacterial populations in the host, and the role of the host immune system, have been studied in detail for many host-pathogen interactions. In most cases, the specific features that define microbial pathogenicity are encoded by mobile genetic elements such as bacteriophages, plasmids, and pathogenicity islands, and fast transferability is often facilitated by transposable elements (for reviews, see Finlay and Falkow, 1997; Low and Porter, 1978).

In particular, the sequencing of whole genomes and the development of more sophisticated bioinformatics tools have shown that the genomes of microorganisms in even a single species may vary enormously (for example, in *Staphylococcus aureus*; see Chapter 10). Improved methods for generation and analysis of sequence data, as well as application of techniques for molecular typing, such as multilocus sequence typing (MLST) and single-nucleotide polymorphism (SNP) analyses, have been used throughout the kingdoms of life and have shown that the sequence diversity between organisms, even between members of the same species, is greater than previously suspected. Microorganisms can be found in every ecological niche on earth, and this ecological speciation could occur only through the acquisition of new genetic traits.

Although horizontal gene transfer is much more elaborate in eukaryotic cells and can lead to changes in the progeny by meiosis and mitosis, recombination events also take place in bacteria following DNA uptake in many ways (Andersson, 2005; Ochman, Lawrence, and Groisman, 2000). Adaptation of bacteria to extreme environments is a consequence of changes in the genetic content and is stabilized by selective pressure. Genome changes may develop by gene loss, gene duplication, gene mutation, or acquisition of new genetic material by lateral gene transfer (LGT; Lawrence and Hendrickson, 2003; Ochman and Moran, 2001; Campbell, 2000). It has been hypothesized that between 1.6% and 32% of the genes of a given genome have been acquired by LGT (Ochman, Lawrence, and Groisman, 2000; Koonin, Makarova, and Aravind, 2001; Marri, Hao, and Golding, 2007).

The main mechanisms of DNA uptake in bacteria are conjugation, transduction, and transformation. These mechanisms must be followed by recombination events that allow the genetic traits to be inserted more or less stably into the chromosome. As Low and Porter summarized in 1978: "The term recombination can be used in a sense that it means a reassortment of series of nucleotides along nucleic acid molecules."

In this book, articles on the basics of lateral gene transfer are provided by authors who are leading scientists in the field.

In the first part, the chapters written by Jeffrey G. Lawrence and Heather Hendrickson (Chapter 1) and by Xavier Didelot and Daniel Falush (Chapter 2) provide an overview of the impact and the mechanisms of LGT as well as detailed insight into the mathematical approaches in evolutionary biology.

The second part of the book contains contributions to the role of distinct mobile genetic elements in bacterial evolution. This section contains comprehensive chapters on the role of bacteriophages as "accelerators" of bacterial evolution by Harald Brüssow (Chapter 3) and on the global

impact of bacteriophages (Chapter 4) from Roger W. Hendrix and Sherwood R. Casjens. Whereas the chapter by Hendrix and Casjens explains mechanisms of gene acquisition and moron acquisition of Gram-negative bacteria and their phages, Harald Brüssow points out the predator-prey relationship and gives a more evolutionary view of bacteriophages. A further important group of mobile genetic elements are genomic islands (GEI), in particular the subgroup of pathogenicity islands (PAI). In Chapter 5, Tobias Ölschläger and Jörg Hacker describe the structure and function of these elements and provide various examples for the impact of GEI and PAI in bacterial evolution.

The third part of the book includes a selection of paradigms for the evolution of important bacterial pathogens. Dawn L. Arnold and Robert W. Jackson provide a state-of-the art chapter on genomic islands in plant-pathogenic bacteria (Chapter 6); Sébastien Lemire, Nara Figueroa-Bossi, and Lionello Bossi focus on the contribution of prophages to virulence and diversity of *Salmonella enterica* serovars (Chapter 7). Elisabeth Carniel describes in Chapter 8 how pathogenicity and transmission in the genus *Yersinia* progressively evolved together with the gradual acquisition of foreign mobile genetic elements. Genomic and pathogenicity islands of *Streptococcus pneumoniae* are addressed in Chapter 9 by Barbara Albiger, Christel Blomberg, Jessica Dagerhamn, Staffan Normark, and Birgitta Henriques-Normark.

In Chapter 10, Richard P. Novick provides detailed information on the current knowledge on mobile genetic elements of *Staphylococcus aureus*. In the last part of this section, Wolfgang Witte sheds light on the influence of socioeconomic parameters on the dissemination of transferable elements (Chapter 11). The specific emphasis of this chapter is on the spread of antibiotic-resistant genes in bacteria.

In the last section, Jan O. Andersson gives insight into gene transfer events in eukaryotes (Chapter 12). Finally, in Chapter 13 Andrés Moya and Amparo Latorre describe the events that are involved in genome reduction of bacterial endosymbionts in the paradigmatic system of aphids and their endosymbionts *Buchneria* spp.

The information given in this book shows clearly that LTG is a driving force in the evolution of various groups of bacterial pathogens; however, LTG is not restricted to this kingdom. The tools of high-throughput sequencing and the development of more sophisticated bioinformatics and genome and proteome techniques facilitate the analysis of LGT and recombination and help us to understand the processes of diversification, reduction, and adaptation to different environments.

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