Preface

Escherichia coli (*E. coli*) was discovered by the German bacteriologist, Theodor Escherich, in 1885 and was initially called *Bacterium coli commune*. *E. coli* is part of the intestinal microflora of humans and other mammals and is a beneficial organism in the gut, producing vitamins K and B12 and preventing pathogenic bacteria from colonizing in the intestine. *E. coli* is one of the most thoroughly studied prokaryotic species and has served as a model microorganism in molecular genetics investigations, yielding considerable information on bacterial genome evolution. *E. coli* has also evolved pathogenic mechanisms through acquisition of virulence genes, and the diseases caused by different *E. coli* pathotypes depend on possession of specific virulence factors, including adhesins, invasins, and toxins. The goal of this book is to describe the *E. coli* pathotypes and how whole-genome and other DNA sequencing approaches, as well as genetic analyses are allowing fascinating new insights into the evolution of the bacterium, paving the way for the development of novel detection and therapeutic strategies.

The virulence characteristics of the different *E. coli* pathotypes are described in Chapter 1, and Chapter 4 focuses on the virulence mechanisms and types of diseases caused by extraintestinal pathogenic *E. coli*. The importance of horizontal transfer of virulence genes among different pathotypes, leading to the emergence of hybrid hypervirulent *E. coli* strains that may have resistance to multiple antibiotics is highlighted. Analysis of genome sequence data of diverse collections of *E. coli* has indeed revealed the great genetic diversity of *E. coli*, as well as evolution and emergence of *E. coli* lineages due in large part to the acquisition and deletion of DNA elements (Chapter 2 and Chapter 7). Whole-genome

sequencing of *E. coli* and other pathogens is transforming public-health surveillance and outbreak investigations, providing an unparalleled level of strain discrimination and the ability to more accurately identify and characterize the organism (Chapter 8). Various sequencing technologies and available bioinformatics tools for assembly, annotation, and analysis of whole-genome sequence data are presented in Chapter 9. Determination of the presence of specific phenotypic traits, such as toxin production, has been employed for detection of *E. coli* pathotypes; however, this can be laborious, time consuming, and costly. Thus, genetic-based methods such as the polymerase chain reaction targeting pathotype-specific markers, which are often virulence-related genes, are increasingly replacing phenotypic-based testing (Chapter 3). Major advances have been made in recent years in the development of rapid methods that allow faster, more sensitive, specific, and expedient detection and identification of pathogens compared to traditional culture-based methods. In Chapter 6, a comprehensive overview of rapid technologies that can potentially be used as portable real-time detection systems is provided. Major advances in nucleic-acid sequencing technologies have allowed the development of metagenomics approaches for analysis of microbial communities, including those in food products. Metagenomics technologies are being utilized as culture-independent methods for studying the impact of perturbations in microbial communites on the growth and survival of pathogens, including *E. coli,* and for detection and characterization of pathogens in food and other types of samples (Chapter 10). 'Omics' technologies, including genomics, proteomics, transcriptomics, and metabolomics are revolutionizing

approaches for pathogen detection and control and for treatment of infections. In Chapter 11, the authors describe the use of omics approaches to understand the responses of *E. coli,* particularly Shiga-toxin-producing *E. coli,* to stress conditions and how the information can be used to develop control strategies, such as the identification of novel inhibitors, to decrease survival in food. Omics data can be integrated in systems-level investigations to understand more completely the physiological changes that occur in *E. coli* under stress conditions and to identify potential new drug targets (Chapter 12). Resistance of *E. coli* and other pathogens to multiple antibiotics is occurring at an alarming rate, and thus, alternative strategies to treat infections are needed. In Chapter 5, the authors describe the use of bacteriophages to treat *E. coli* infections as one alternative strategy. The editors anticipate that this volume will be a valuable resource for individuals interested in *E. coli* pathogenesis and control, as well as in the evolutionary dynamics of this microorganism.

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