

Preface

Snyder and Champness-Molecular Genetics of Bacteria is a new edition of a classic text updated to address the massive advances in the field of bacterial molecular genetics. We renamed the book as a tribute to the original authors, Larry Snyder and Wendy Champness, who welcomed us as coauthors for the 4th edition and trusted us to continue to build on the strong foundation of their multiple editions in carrying this important text forward. As with the previous editions, we have endeavored to keep the page length approximately the same. This meant making many hard choices of what to remove to make room for exciting new and important material. We are very happy that every illustration is now in full color, which offered us the opportunity to rethink each drawing and clarify and standardize features, which we believe will improve their use by instructors in classroom lectures.

Perhaps the most significant force in molecular genetics research since the last edition has been the plummeting cost of DNA sequencing. This factor has created an explosion of new sequence information of both independent genomes and microbial communities in the form of metagenomics, where DNA is extracted directly from all of the organisms in an environment. This information has vastly expanded our picture of the tree of life and the massive contribution of uncultured species. The broader availability of DNA sequencing at a reasonable price has also left its mark on genomic techniques. These new techniques and new information have had a considerable impact in every chapter and provided the impetus for a new chapter, "Genomes and Genomic Analysis" (chapter 13).

We expanded chapter 1, on DNA structure, DNA replication, and chromosome segregation, to include many advances in our understanding of how chromosomes are managed and the molecular machines that carry out these processes. Our understanding of the nature of FtsK and related DNA-pumping enzymes, the evolving role of SeqA, the mechanism of chromosome partitioning, and the domain structure of the chromosomes also benefited from multiple technological innovations. Chapter 2 focuses on mechanisms of gene expression, from transcription through mRNA turnover, translation, and post-translational effects, including protein targeting, which was moved into this chapter. We reduced the historical aspects of chapter 3, retaining key landmarks such as the important role of the F plasmid discovered by Esther Lederberg, so the chapter now focuses more on practical aspects of genetic analysis.

Newer molecular techniques that have replaced some of the classic approaches (e.g., for generation of targeted chromosomal mutations) are now discussed in the new chapter 13.

Chapter 4 presents a concise understanding of bacterial plasmids as important contributors to the genomic content in bacteria as well as essential tools in molecular biology. Significant additions to the chapter include an expanded discussion of the two major mechanisms of segregation and the ever-broadening view of toxin-antitoxin systems. Toxin-antitoxin systems were first discovered for their role in plasmid stabilization, but while the diversity of molecular mechanisms has expanded, important questions remain concerning the real function of these systems when situated in bacterial chromosomes. Chapter 5, which focuses on conjugation, continues to set its roots in the original conjugal plasmid, the fertility plasmid. We included considerable new information that relates to our recognition that conjugal systems appear to be as common in the form of integrating conjugative elements (ICEs) as they are in stand-alone plasmids. The diversity of ICEs is remarkable, and this chapter strives to provide a foundation for these dynamic elements, which are responsible for the largest known genomic islands transmitted between bacteria.

In chapter 6, we expanded the discussion of natural transformation and its regulation to include additional comparative information about how these systems vary in different groups of organisms. We consolidated the discussion of lytic and lysogenic bacteriophages and their roles in transduction of bacterial DNA as chapter 7. We organized the information on phage biology based on the different functions required for phage infection and replication, and followed this with a discussion of phage genetics, their use in bacterial genetic transfer, and their roles as tools for molecular biology.

We streamlined chapter 8, "Transposition, Site-Specific Recombination, and Families of Recombinases," to make room for additional families of elements including the exciting and still somewhat enigmatic HUH transposons, as well as group II mobile introns, and an advanced appreciation of the interrelationship between mobile elements and host DNA replication. Transposons continue to provide an important tool in genomics, and mobile genetic elements in general provide the most significant mechanisms for the transfer of antibiotic resistance. As the spread of antibiotic resistance is slowly nullifying the effectiveness of antibiotics worldwide, understanding the mechanisms of this spread is more important than ever. Chapter 9, "Molecular Mechanisms of Homologous Recombination," continues to be grounded in the central role that homologous recombination plays in the repair of DNA double-strand breaks. We expanded the chapter to include a better appreciation of the multiple pathways used to load the RecA recombinase onto different types of DNA substrates.

We broadly updated chapter 10, "DNA Repair and Mutagenesis," to reflect our increased mechanistic understanding across many DNA repair systems, as well as information on how mechanisms established in bacterial systems continue to contribute to our understanding of disease in humans. We extensively updated chapter 11, which focuses on mechanisms of gene regulation of individual genes and operons, to include new information as the field continues to advance. In chapter 12, we then applied the principles learned in chapter 11 to global regulatory systems that regulate multiple sets of genes and operons, often in response to multiple regulatory inputs. *Bacillus subtilis* sporulation, a complex developmental system, is presented in depth as a final example that integrates many of the different mechanisms that are introduced in chapters 11 and 12.

Chapter 13, "Genomes and Genomic Analysis," is a new chapter that consolidates relevant topics previously found elsewhere in the book and provides considerable new information on this topic. We provide background on the multiple mechanisms used for DNA sequencing, including the newest generations of high-throughput sequencing strategies. Having hundreds of thousands of bacterial genomes has allowed us to gain a better understanding of how genomes are organized as well as the relationship between core genes and genes acquired by horizontal gene transfer. The chapter also provides basic information on genome annotation and comparative genomics. Chapter 13 further presents an expanded picture of numerous systems that bacteria use to guard against horizontal gene transfer. Although horizontal gene transfer is by far the most important mechanism for evolution in bacteria and archaea, it also provides the greatest vulnerability, with the relentless onslaught of bacteriophages and mobile elements that can sap cellular resources or inactivate important or essential host genes. Significantly, host defense systems also provide the most important tools ever developed for molecular biology. The new chapter provides expanded background on diverse restriction endonucleases and the important roles they play in molecular biology. We cover the variety of tools that are available for cloning and gene assembly, as well as the advantages and disadvantages of these techniques to help guide the investigator. These techniques allow never-imagined possibilities for quickly and accurately constructing synthetic DNA fragments for testing ideas or allowing advances in engineering, including assembling entire bacterial genomes. We greatly expanded the section on CRISPR/Cas systems and chose the Cas9 system, important in many applications in a multitude of model systems and human genome engineering, to illustrate on the book's cover. CRISPR/Cas systems are very diverse, falling into six distinct types and tens of subtypes. We provide the reader with the background needed to understand how these fascinating systems evolved, the role they play in the natural environment, and the massive promise they hold in genome engineering.