

Population genetics investigates the spatial and temporal patterns of genetic variation among individuals and populations of organisms, including the mechanisms for such patterns. This field has a rich history, started with Charles Darwin in 1859 with his seminal publication *On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life*. His revolutionary idea of Evolution by Natural Selection revealed the fundamental issues of population genetics: the existence of heritable variations among individuals, the contributions of these variations to the differential survival and reproduction among individuals, the accumulation of advantageous variants in a population over time, and the divergence among populations due to the accumulation of different variants. For most of the 19th and the early 20th century, there was very little agreement within the scientific community about the genetic basis of phenotypic variation among individuals in natural populations. However, this period laid some of the most important foundations of biology, including population genetics. The early pioneers in genetics and specifically population genetics include Francis Galton, Karl Pearson, Gregor Mendel, Thomas Morgan, Herman Nilsson-Ehle, Udny Yule, Ronald Fisher, J.B.S. Haldane, Sewall Wright, Sergei Chetverikov, and Theodore Dobzhansky.

Most early population geneticists used mathematical models to examine the factors that might help explain phenotypic differences among individuals and populations. When the principles

of inheritance, the Mendelian laws, were re-discovered at the beginning of the 20th century, rapid advancements in population genetics soon followed, leading to the formulation of the New Synthesis of the theory of evolution. However, for the first half of the 20th century, most evolutionary biologists and population geneticists studied plants and animals. Few studies examined microbial populations.

The era of molecular population genetics began in 1966 when Lewontin and Hubby, and Harris, introduced the technique of protein electrophoresis to population genetics. Surprisingly abundant genetic variations were found in virtually all organisms examined, including some microorganisms. However, many of these variants had little phenotypic effect on the survival and reproduction of organisms. These findings have led to the emergence of the neutral theory of molecular evolution. The application of DNA sequencing technology into population genetics since the early 1980s further expanded our understanding of the extent of genetic variation among individuals and within and between populations. While most molecular population genetic studies from the 1960s to the early 1990s were still focused on macroorganisms such as plants and animals, the next phase of technical innovation, the development and application of high-throughput DNA sequencing and microarray technologies in the mid-1990s, were led by studies of microorganisms. These and other developments are now allowing unprecedented access to genetic materials from populations and communities

of micro- and macro-organisms in their natural habitats. Indeed, comparative genomics, phylogenomics, phylodynamics, evolutionary genomics, population genomics, metagenomics, and systems biology are now burgeoning fields of scientific investigations.

The objective of this book is to bring up-to-date research advances in broad areas of microbial population genetics and genomics. It reviews the application of various molecular tools in our understanding of the patterns and the potential mechanisms for genetic variation of microorganisms at a broad range of scales, from those within micro-niches to among populations from different continents. The book introduces both fundamental concepts and recent molecular population genetic tools and data from SNP surveys, whole-genome DNA sequences, and microarray hybridizations etc. It covers broad groups of microorganisms including viruses, bacteria, archaea, fungi, protozoa, and algae.

The 12 chapters in this book contain a wide range of topics. Chapter 1 introduces recent advances in microbial systematics, with a special focus on the unique utility of insertions/deletions in helping to resolve the phylogenetic relationships among bacterial and archaeal phyla and orders. Chapter 2 reviews comparative microbial genomics and the impact of whole genome sequences in helping us understand the large-scale population and evolutionary issues. Chapter 3 summarizes our current understanding of horizontal gene transfer in bacteria, including the patterns, rates, and fate of horizontally transferred genes. Chapter 4 describes the molecular diversity of a deadly group of human bacterial pathogens and discussed how such information could be

used for source tracking and rapid identification of human pathogenic microbes in general. Chapters 5 to 10 review the population genetics of large representative groups of microorganisms that include the nitrogen-fixing bacteria (Chapter 5), the photosynthetic cyanobacteria (Chapter 6), the eukaryotic microalgae (Chapter 7), the fungal mutualists (Chapter 8), the human fungal pathogens (Chapter 9), the human malaria parasites (Chapter 10), and human pathogenic viruses (Chapter 11). Chapter 12 presents an overview of the broad field of metagenomics and its wide-ranging impact on our understanding of microbial diversity, function, inter-relationships, and population genetics, from organisms ranging from viruses to bacteria, archaea, and eukaryotic microbes.

Microbial population genetics is a rapidly advancing field of investigation with relevance to many other theoretical and applied areas of scientific investigations. The theoretical issues that many of the chapters touched upon include the origins and evolution of species, of sex and recombination, and of life (Chapters 1, 2, 3, 11, and 12). On the applied side, population genetics lays the foundations for tracking the origin and evolution of antibiotic resistance and deadly infectious pathogens (Chapters 3, 4, 7, 9, 10, and 11). Population genetics is also an essential factor for devising strategies for the conservation and better utilization of beneficial microbes (Chapters 5, 6, 7, 8, and 12).

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