

Preface

Microbial world is considered to be the largest unexplored reservoir of biodiversity on earth. Microbial systematics and phylogeny are the foundations and guiding light to understand different aspects of microbiology. Owing to the practical significance of identification, diversity, and species designation of microorganisms, microbial genomics offer novel insights for intraspecies variation and development of a potential tool for microbial diversity studies. In this regard, microbial genomes are considered to be highly dynamic and diverse due to the occurrence of horizontal gene transfer (HGT) which adds complexity in terms of understanding the bacterial genome as well as their evolution. Genomics has completely revolutionized every aspects of microbiology. The pioneer work of Carl Woese et al. of comparative analysis of small subunit of rRNA revolutionized the understanding of the species diversity and evolutionary relatedness. However, a uniform gold standard methodology for species designation and study of microbial phylogeny is still lacking.

Over the years, microbiologists have witnessed a paradigm shift in microbial diversity research owing to the development of genetic analyses and genomics studies of microorganisms. The data generated by application of genomics to microbiology should be dealt with multidisciplinary approaches by integrating microbiology with bioinformatics, statistics and mathematical approaches. Advancements in genomic research has led to the discovery of novel diagnostics, discovery of new bioactive compounds, application in bioremediation of toxic elements, and many other discoveries. However, with the increasing knowledge, we realize that we are just scrabbling the surface of the microbial world. Enhanced genetic information is challenging our existing knowledge of bacterial species designation, typing systems as well as the microbial taxonomy.

First, bacterial genome was sequenced in 1995 in *Haemophilus influenza*. Afterward, significant advancements have been taken place in the field of genomics and sequencing technologies for the assessment of microbial taxonomy and phylogeny. The technological progress has led the advanced techniques to completely dominate the conventional techniques for microbial diversity analysis. Thus, the aim of this book is to discuss about where we stand in the genomics era with respect to the microbial diversity, species designation, and typing. There are many techniques used to determine the genetic relatedness of microorganisms, and this book aims to discuss the techniques used for microbial taxonomy and phylogeny with their applications and respective pros and cons. Though much advanced techniques are available in genomics era for the identification of any unknown bacterium, still a lot of undiscovered microorganisms exist in the world. Thus, the assessment of microbial taxonomy and biosystematic techniques discovered and practiced in the current genomics era with suitable recommendations is the prime focus of this book.

The chapters of this book have been written by the authors with vast research and academic experience in the field of microbial diversity, molecular biology, genomics, and evolution. The whole book has been divided into six sections. Section I introduces the microbial diversity and describes various principles to study diversity in different ecosystems. Section II describes various molecular tools employed to study microbial diversity such as multiplex PCR, omics approach, next generation sequencing, and polyphasic taxonomy. Extremophiles play an important role in maintaining the biogeochemical cycles in the environment and are a huge source for biotechnological applications. Section III describes different genomic tools to study the extremophilic microbial diversity and exploitation of psychrophiles, thermophiles, acidophilic, and alkaliphilic microbes. Huge diversity of microbes imparts varied functions in the environment, and Section IV of the book describes the functional microbial diversity and their study using advanced genomics tools. Section V describes various genomics tools and techniques to study the diversity of microbes associated with infectious diseases and to deduce various preventive measures to promote significant medical and public health. Finally, the limitations and opportunities of the currently available genomics techniques and future directions for microbial diversity studies have been discussed in Section VI.

We have tried with our best possible efforts to accommodate the currently available knowledge, content, research advancements in the field of microbial diversity to an extent suitable for the students, budding and seasoned researchers, medical professionals, policy makers, and practitioners in the field of environmental and medical microbiology. Hope, this book will serve as a key point of reference to various stakeholders involved in microbial diversity study and research.

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