

Microbial Ecology

Current Advances from Genomics, Metagenomics and
Other Omics

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Preface

The development of ‘meta-omics’ methods such as metagenomics, metatranscriptomics, metaproteomics, metametabolomics and other related methods is greatly contributing to the understanding of the complexity of interactions among microorganisms and of the interaction of microorganisms with their environment and with other organisms.

As in any ecological framework, the concepts of pattern, process and mechanism are of primary importance in the microbial ecology context and there is a pressing need to investigate the processes and mechanisms that may explain the occurrence of detected patterns. Some operative definitions and considerations to help microbial ecology researchers to become acquainted with these ecological concepts are presented in Chapter 1. This chapter also provides an account of the contributions of ‘meta-omics’ methods to the identification and understanding of patterns, processes and mechanisms in microbial ecology. The ‘omics’ approaches are also advancing the field of microbial ecology by developing new molecular methods to study microbiomes. As contamination in microbiome sequencing studies is a well-known but difficult to address problem, Chapter 2 presents a simulation model to examine when contamination is likely to be problematic in microbiome samples. Chapter 3 provides an overview of the advances in molecular methods based on DNA sequencing that improve our understanding of the dynamics of microbial communities in soil systems, in particular the study of patterns of microbial succession in soils. Chapter 4 demonstrates, by the development of an insular microbiogeographical model, that the same mechanism that underlies macro-ecological scaling laws also applies to microbial communities. This finding is useful in understanding the diversity and dynamic exchange of genes. Chapter 5 explores the contribution of metagenomics in the understanding of complex sediment microbial communities, an issue that remains a challenge because of the remarkable diversity of these communities. Finally, Chapter 6 addresses, in a novel interdisciplinary way, how genomic approaches to microbial ecology can be combined with host biology, endocrinology and disease data to characterize the overall health of animals, habitats and ecosystems. This new avenue is interesting from a theoretical point of view but also as a potential method to improve conservation and disease surveillance strategies.

The book is aimed at scientific researchers, educators and advanced students interested in approaching the microbial ecology field by utilizing the most recent and advanced ‘omics’ methods. The book covers both the theoretical and the applied aspects of microbial ecology.

I would like to thank all of the authors for their contributions. I am also very grateful to Hugh Griffin and Caister Academic Press for giving me the opportunity of editing a volume on such an interesting and dynamic field.

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