
Preface

Microorganisms inhabited Earth long before any higher organisms. During the course of evolution they have occupied diverse environments such as soil and fresh and marine water, and different ecological niches including symbiotic relationships with plants, animals and humans. Until recently the main source of information we had about microorganisms in the environment arose from what we now refer to as 'conventional' or 'traditional' approaches. These approaches primarily relied on cultivation of selected microbes in broth or agar, whereby we could then identify them and study their properties in isolation or in defined communities. Now we live in an era where 'modern' tools can be utilized to study microorganisms in environmental samples without the necessity to cultivate them. The current molecular toolbox encompasses a range of molecular approaches. The majority of these are based on analyses of DNA, but new approaches for study of RNA and proteins extracted from environmental samples are rapidly becoming available. Currently, there is a major emphasis on the application of 'omics' approaches to directly study molecules extracted from samples of interest and to use these approaches to determine the identities and functions of the microbes inhabiting different environments.

This concept for this book originated from a series of workshops since the first meeting at Wageningen, the Netherlands in 2004 sponsored by The Scientific Committee on Problems of the Environment (SCOPE) and the International Council of Scientific Union Workshop

on Microbial Environmental Genomics (MicroEnGen), with participation from several leading, international microbial ecologists and molecular biologists, many of whom are authors of chapters in this book. In addition, several of the authors are involved in the newly launched TerraGenome initiative: the international consortium dedicated to sequencing the soil microbiome (<http://terragenome.org>) and other ongoing national and international collaborative projects. These initiatives highlight the need for collaboration between scientists and between countries for accomplishing ambitious goals that are currently too challenging for individual laboratories to pursue on their own. The collaborative nature that is now becoming more commonplace is illustrated by the shared authorship of many of these chapters by authors from more than one laboratory and country.

The first half of this book focuses on the microbial diversity and phylogeny of microorganisms on Earth and describes the molecular toolbox now in hand for the study of microbial diversity. Chapter 1 describes the use of the 16S rRNA gene as a phylogenetic marker for identification and classification of Bacteria and Archaea, and then compares this approach with recent advances in knowledge gleaned from sequenced microbial genomes. The subsequent chapters explain the basis of different molecular approaches, including metagenomics, metaproteomics, microarrays, and molecular fingerprinting approaches for the study of the composition and diversity of microbial communities and their functions.

The second half of this book describes how these approaches have been used to study microbes in different environments, such as soil, marine water, plants, humans and wastewater treatment plants. Each of these environments contains a specific type of microbial community that is responsible for key functions. The last chapter of the book describes the formation of microbial biofilms, the genetics behind this process and environmental implications.

What we have learned from application of these tools is that microbial diversity on Earth is enormous and much greater than originally thought. We also know that most of the microbes that we have identified to be present are unknown and their functions remain hidden. Therefore, there is a continuous need for better tools and more information as we continue to explore the microbial world. The importance of microbial functions for our health and environment has also gained increasing recognition. For example, their

roles in carbon and nutrient cycling and how these functions are impacted by climate change are key areas of interest. There has also been a shift away from a focus on pathogens, towards understanding the beneficial functions of microorganisms for plant growth and for human health that are discussed in the chapters devoted to those topics.

In conclusion, the field of environmental microbiology is continuously evolving and at such a rapid pace that it is difficult for even experts in the field to keep up with the latest methods and the increase in information that is obtained. This book lays the platform with respect to the current state-of-the-art in the field of Environmental Molecular Microbiology and our hope is that it can serve as an aid to students, research scientists, environmental agencies and to industries that can benefit from application of these tools or this knowledge.

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