Although microorganisms (archaea, bacteria), micro-eukaryotes (fungi), and macro- and mesofauna represent major components of the environment, we are far from appreciating their identity, diversity, functions, the interactions established between them, and lastly their relative impact on the ecosystem functioning [1, 2]. In both terrestrial and aquatic ecosystems, they represent a considerable fraction of the living biomass [3] and several studies have now highlighted their key role in processes such as nitrogen and methane cycles, organic matter degradation, soil quality, and plant health and nutrition [4]. Most of the current knowledge was generated using monospecific or reductionist approaches, balancing between cultivation-dependent (sampling of organisms, morpho/phenotyping, physiological and biochemical characterization) and -independent approaches mostly based on low-throughput sequencing technologies (e.g., fingerprinting or cloning/sequencing). Such approaches were, and remain, very important as they enroot the current physiological and biochemical knowledge of the microorganisms, macro- and mesofauna, and give the relevance to the content of gene or protein sequences of the international databases. However, the recent revolution in sequencing technologies with the advent of the high-throughput methods (454 pyrosequencing, Illumina, Ion Torrent, PacBio, etc.), associated with a real decrease in the sequencing cost, is now opening the way to really appreciate the tremendous distribution and diversity of our micro- and macroorganisms neighbors [5]. Aside from the sequence-based approach, more and more analysis based on high-throughput chemical screening of environmental libraries (genomic DNA and cDNA cloned in expression vectors) are developed, revealing the common effort of the biologists to decipher the diversity and function of these organisms, especially the nonculturable and rare ones. At last, statistical analysis, modeling, and bioinformatics are rapidly becoming more accessible to single investigator laboratories [6]. All these aspects have really revolutionized microbial ecology giving emergence to a new research field entitled “Microbial Environmental Genomics.” Microbial environmental genomics seeks to understand how organisms and gene functions are influenced by environmental (biotic and abiotic) cues while accounting for variation that takes place within and among environmental populations and communities. By combining multiscale and multidisciplinary methods, we are now able to depict the complex assembly of organisms of the environment and to decipher their functional role (Fig. 1). Such developments should permit to improve our ability to develop predictive models to better integrate the relative role of these organisms in the biogeochemical cycles and the ecosystem functioning [7].

In this context, this book presents a series of 17 chapters to guide research into the identification of still unknown organisms, of novel functional genes, and how environmental conditions drive gene responses and the fitness of the complex guilds of organisms inhabiting our environment. Methods to analyze the diversity of different organism types are presented in Chapters 1–8, covering the archaea, bacteria, fungi, protists, and soil fauna. Chapter 9 presents a method to decipher the interactions between fungi and trees using RNA stable isotope probing (RNA-SIP). Notably, methods to identify and characterize functions and functional diversity of both pro- and eukaryotes are presented in Chapters 10–16. Those include protocols for gene hybridization (gene capture, geochips), DNA stable isotope probing, construction and screening of metagenomic and metatranscriptomic libraries,
and for bioinformatics analyses (MG-RAST). Chapter 17 presents a method to analyze both taxonomic and functional diversity using ancient DNA. We envision that this book will serve as a primary research reference for researchers and research managers in environmental microbiology working in the expanding field of molecular ecology and environmental genomics. The level of presentation is technically advanced with a strong emphasis on describing cutting-edge protocols in light of the possible future directions for research.

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References

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