

SPECIAL FEATURE

New Directions in Microbial Ecology¹

Microorganisms are the most diverse and abundant group of organisms on Earth. Yet, within the field of ecology, microbial studies have typically focused on the processes microorganisms carry out, rather than on the ecology of the organisms themselves. In contrast, studies of environmental microbiology have primarily characterized the diversity of microbial populations. A true integration of classical ecological thinking and organism-based microbiological studies is a surprisingly recent phenomenon.

Recent efforts to link microbial ecology and environmental microbiology are taking advantage of new methods and technologies. New molecular tools allow researchers to describe large-scale biogeographical patterns of microbial diversity and to compare such patterns to those of plant and animal taxa. Scientists can now describe microbial community composition and determine its stability across time and space. Additionally, molecular tools for describing community composition can be combined with ecosystem and biogeochemical measurements to identify environmental controls on microbial processes and the specific roles of microbes in biogeochemical cycles. From methane emissions to decomposition, microbes are the engines that cycle nutrients and control trace gas concentrations in the atmosphere.

New methods and the fusion of ideas from microbial ecology and environmental microbiology are allowing ecologists to tackle previously unanswerable questions. Some current examples include: What factors influence microbial diversity at small and large spatial scales? How stable are microbial communities in nature? What can microbial phylogenetics tell us about the functioning of microbial communities? How do ideas from physiological, population, and community ecology apply at the scale of microorganisms? The goal of this Special Feature is to address these and other questions, timed to highlight the formation of a new Microbial Ecology Section within the Ecological Society of America.

In the first paper in the feature, Horner-Devine and colleagues use 124 data sets to examine the patterns of co-occurrence of microbial communities and the “assembly rules” that govern those patterns. They evaluate nonrandom patterns of taxa co-occurrence, compare patterns for microorganisms with those for macroorganisms, and evaluate the influence of taxonomic group, habitat, and sampling method on the degree of taxon co-occurrence. Their results provide insight into the underlying processes that control the structure of microbial communities.

The second article in the feature by Fierer et al. also examines the structure of microbial communities at large spatial scales and how environmental factors affect that structure. Using an analysis of 71 soils from diverse habitats across North America, they examine which soil and environmental characteristics help predict the abundance of six bacterial phyla: Acidobacteria, Bacteroidetes, Firmicutes, Actinobacteria, α -Proteobacteria, and β -Proteobacteria. Their results suggest that bacterial phyla can be differentiated into copiotrophic and oligotrophic groups corresponding to the *r*- and *K*-selected categories commonly applied to plants and animals. Such a classification scheme may help researchers interpret the ever increasing amount of taxonomic information on soil bacterial communities from an ecological perspective.

In the third paper of the feature, Crump and colleagues continue the theme of discovering which environmental factors control microbial community composition. They compare bacterioplankton communities across a complex aquatic landscape of 24 connected and isolated lakes and streams at Toolik Lake, Alaska, USA, to determine which environmental factors predict the composition of those communities. Their results reveal large differences in lake-specific and stream-specific bacterioplankton composition over small spatial scales (<10 km), suggesting that geographic distance and connectivity strongly influence the distribution of bacterioplankton across a landscape.

¹ Reprints of this 52-page Special Feature are available for \$10.00 each, either as PDF files or as hard copy. Prepayment is required. Order reprints from the Ecological Society of America, Attention: Reprint Department, 1707 H Street, N.W., Suite 400, Washington, DC 20006 (esaHQ@esa.org).

Their research also highlights the importance of terrestrial and aquatic links in shaping patterns of microbial diversity.

The last two papers in the feature examine how changing environmental conditions affect the composition and functioning of microbial communities. Schmidt and colleagues describe how recent advances in molecular and isotope techniques are allowing researchers to study the dynamics of soil microbial communities and associated biogeochemical processes. They present recent research in the tundra and forests of Colorado linking carbon and nitrogen cycling with rapid shifts in the composition of microbial communities. In contrast to some of the earlier papers in the feature, this paper suggests that the composition of soil microbial communities changes on short time scales, making it important for researchers to assess the intra-annual variability in microbial diversity.

The final paper in the feature by Schimel et al. examines how microbial communities are shaped by environmental stress. Focusing on the effects of drought and freezing stress in particular, they argue that soil microbial ecology would benefit from the stress-physiology perspective that has driven advances in plant ecology in recent decades. They provide examples of these stresses and their effects on microbial communities in a number of ecosystems, including Arctic tundra and California grasslands. One of their recommendations provides a nice summary for the feature: that integrating microbial ecology into ecosystem studies will require aspects of physiological ecology, population biology, and process ecology, combined with the promise of molecular tools and technology.

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Key words: biogeochemistry; community assembly rules; environmental stress; microbial ecology; microorganisms; nutrient cycling; quantitative PCR (qPCR); soil bacteria and fungi.

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