Microbial Ecology in Genomics Era: Challenges and Opportunities

Jizhong Zhou

Institute for Environmental Genomics, University of Oklahoma, Norman, OK, USA
Earth and Environmental Sciences, Lawrence Berkeley National Laboratory
Berkeley, CA, USA
School of Environment, Tsinghua University, Beijing, China

Twenty-first century microbiology faces several grand challenges. First, microbial diversity is extremely high with most (>99%) as-yet uncultured. Characterizing such vast diversity and understanding the mechanisms shaping it presents numerous obstacles. Second, although microorganisms control, at least to some degree, various ecosystem processes, establishing the linkage between ecosystem functioning and microbial community structure is even more difficult. Third, human activities are causing multiple types of global environmental changes, including elevated atmospheric CO₂ concentration, climate warming, increased nitrogen deposition, land use change, and as a potential consequence of each of these, biodiversity loss. It is critical to understand the responses, adaptations and feedback mechanisms of biological communities to climate change. In addition, scaling the information from molecules to populations, to communities, and to ecosystems for understanding ecosystem behaviors and dynamics is a formidable task. With the recent advances of omics technologies, microbiologists have begun to tackle some of these challenges. In this talk, representative examples of metagenomics studies relevant to biogeochemistry and global climate change will be highlighted. I will first compare the differences and performances of various types of metagenomic technologies in analyzing microbial community structure, followed by description of using metagenomic technologies to study global diversity and biogeography of wastewater treatment plants (WWTPs). I will also describe the most recent advance in GeoChip development, and examples on how to use high throughput metagenomics technologies to address biological questions such as microbially mediated feedback mechanisms in response to climate warming in Arctic tundra ecosystems. Furthermore, I will describe several novel theoretical approaches to study the importance of stochastic processes in controlling microbial community diversity, and novel random matrix theory (RMT)-based frameworks for discerning the network interactions in microbial communities. Finally, I will present two examples on how to incorporate omics information into ecosystem models to improve predictions of grassland ecosystem’s responses to climate warming and elevated CO₂.