

Conference Abstract

Microbes matter: integrating microbial sequence information for biodiversity

Kelly S Ramirez ‡

‡ Netherlands Institute of Ecology, Wageningen, Netherlands

Corresponding author: Kelly S Ramirez (k.ramirez@nioo.knaw.nl)

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Abstract

The large efforts to document and map aboveground biodiversity have helped to elucidate ecological and evolutionary mechanisms and processes, predict responses to global change, and identify potential management options in response to those changes. Yet these concepts have mostly been applied to aboveground plant and animal communities, while microbial diversity remains difficult to incorporate. The ability to integrate microbial sequence data into an accessible global infrastructure has previously been limited by a few key factors: First, most of microbial diversity remains undescribed and unknown; there is just an enormous amount of biodiversity. Second, there is a lack of congruence between the many disparate microbial datasets (e.g. taxonomy, phylogeny, and methodological biases), which limits the ability to monitor and quantify global patterns of the terrestrial microbiome. Finally, there is a lack of coordination and networking between scientists studying microbes. In this presentation I will discuss two case studies that highlight how we can begin to link microbial data to the already well-established macro-knowledge and other environmental databases (like global carbon maps)

Study 1 – a megameta analysis: The emergence of high-throughput DNA sequencing methods provides unprecedented opportunities to further unravel microbial ecology and its worldwide role from human health to ecosystem functioning. However, in spite of the abundance of sequencing studies, combining data from multiple individual studies to address macroecological questions of bacterial diversity remains methodically challenging and plagued with biases. While previous meta-analysis efforts have focused on diversity

measures or abundances of major taxa, in a recent study⁽¹⁾ we show that disparate amplicon sequence data can be combined at the taxonomy-based level to assess bacterial community structure. Using a machine learning approach, we found that rarer taxa are more important for structuring soil communities than abundant taxa. We concluded that combining data from independent studies can be used to explore novel patterns in bacterial communities, identify potential 'indicator' taxa with an important role in structuring communities, and propose new hypotheses on the factors that shape microbial biogeography previously overlooked.

Study 2 – a global soil biodiversity database: Greater access to microbial data is an important next step for biodiversity research and conservation, and for understanding the ecology and evolution of microbial communities. In collaboration with the Global Soil Biodiversity Initiative and the German Biodiversity Synthesis Centre (sDIV) we outlined steps that must be taken to ensure microbial sequence data can be included in global measures and maps of biodiversity⁽²⁾. Here I will discuss how the plant associated microbiome is an optimal starting point to synthesize microbial sequence data on an open and global platform. The plant-microbiome is an optimal model system that goes across scales and time, can act as a bridge between microorganisms and macroorganisms, and as an opportunity to more thoroughly explore the synthesis of global microbial sequence data (for a global soil biodiversity database). Beyond expanding primary research, the patterns discovered in a synthesis of plant-microbiome can be used to explore and guide ecosystem restoration and sustainability. Overall, a better understanding of microbial biodiversity will help to predict consequences of (human-induced) global changes and facilitate conservation and adaptation responses.

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Presenting author

Kelly S Ramirez