



Global-scale biogeography of soil microbes in the light of molecular data

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Bacteria and fungi are fundamentally important for soil nutrient cycles by functioning as key decomposers of organic matter and as important pathogenic and mutualistic symbionts in most ecosystems. These microbes are difficult to identify by conventional methods due to their great diversity as well as uncultivability. Recent advances in molecular methods have greatly facilitated the identification of microbes and advanced community ecology studies of microbes. In particular, high-throughput sequencing (HTS) techniques now enable us to determine millions of genes and identify thousands of microbial taxa from a single sample. Such information provides useful insight to disentangle the effects of environmental filtering and biotic interactions in structuring microbial communities. We have used these methods to understand various aspects of the biogeography of microbes. In my talk, I will discuss our recent findings on the global distribution of soil microbes, including the followings: i) there is a global latitudinal gradient in topsoil with the highest bacterial gene and phylogenetic diversity found in temperate zones across all major biome types; ii) topsoil bacterial and fungal taxonomic composition and gene functional potential are driven by soil and climatic factors more so than dispersal on a global scale; iii) bacteria and fungi in topsoil dominate complementary sites across the latitudinal gradient, reflecting niche differentiation and antagonism; and iv) fungal-bacterial antagonism is reflected in the distribution of antibiotic resistance genes in soil, consistent with a role of fungally produced antibiotics in microbial competition.