A hierarchy of ecological filters acts at a hierarchy of phylogenetic resolutions to shape arbuscular mycorrhizal fungi spatial distribution

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Abstract

Traditionally, species is the taxonomic unit used to quantify the importance of ecological factors shaping communities of arbuscular mycorrhizal (AM) fungi, but it may not provide the appropriate resolution. Using an Illumina amplicon dataset of large subunit (LSU) ribosomal DNA (rDNA) sequences from a chronosequence of soil agricultural recultivation, we tested whether the correlation between soil parameters and AM fungal community composition changes across phylogenetic resolution. We inferred amplicons sequence variants to resolve phylogenetic diversity at resolutions finer than provided by traditional sequence clustering methods, and we used a phylogenetic framework to cluster variants into operational taxonomic units at coarser resolution. Clustering variants up to a genetic distance of 0.03 substitutions per site increased the correlation between community composition and soil plant-available phosphorus (P) and nitrate (NO3-). Furthermore, P better correlated with community composition at a broader phylogenetic resolution compared to NO3-. Our study suggests that a hierarchy of ecological filters acts at a hierarchy of phylogenetic resolutions in shaping AM fungal communities. By informing on the ecological preferences of AM fungal clades at multiple phylogenetic levels, our approach can address the challenges of assessing functional complementarity and predicting the consequences of environmental changes on AM fungal diversity.

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