Patterns of diversity in the North American Populus mycobiome

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Project Goals: Despite apparently strong geographic patterns in the dominant form of mycorrhizal symbiosis and the associated ecosystem consequences, ecologists have a limited understanding of why these patterns emerge. Why and how do ectomycorrhizal host trees outcompete arbuscular mycorrhizal host trees in certain ecosystems? Does climate play a direct or indirect role in determining the success of ectomycorrhizal symbiosis? Given that ectomycorrhizal fungi are themselves highly diverse, do changes in the ectomycorrhizal community expand the range of climates a host tree can grow in? For this project we are using *Populus* as a model to determine the mechanisms by which mycorrhizal symbiosis influences the distribution of tree species across North America.

Populus species are important bioenergy feedstocks and prevalent throughout North American forests[1]. Identifying biotic communities that may promote their persistence under different environmental conditions is vital to the sustainability of feedstock programs and forest conservation and management into the future. Microbial communities are especially important to consider as they form symbioses with host plants and influence their overall performance, stress tolerance, and disease susceptibility[2,3]. However, we know relatively little about how the distribution of microbial symbionts varies among and within *Populus* species, and how this relates to the broad environmental gradients underlying host tree species ranges. We surveyed five *Populus* species from across the United States to understand how host-associated fungal communities vary across major soil and climate gradients.

We collected leaf, root, and soil samples across five widespread Populus species ranges in the US, measured ectomycorrhizal fungi root colonization, and performed fungal (ITS1) amplicon sequencing (Illumina MiSeq) to characterize fungal community diversity and composition[4]. We tested how fungal community diversity and composition varies among tree species and broad environmental gradients. We used soil measurements and climate data to predict the amount of community turnover across each Populus compartment (Leaf, Root, and Soil) with generalized dissimilarity models[5]. We used distance decay analysis to examine how community structure varies over geographic space. We also identified distinct ecological clusters of fungal taxa using semi-partial correlations and visualized their natural clustering using co-occurrence networks. Our analyses showed that there are significant differences in the composition of fungi across the leaf, root and soil compartments of the *Populus* mycobiome, and that composition of these respective communities are affected by different combinations of climate and environmental variables, resulting in highly unique regional microbiomes. Finally, we show that different *Populus* tree species vary in their ectomycorrhizal affinity, and that this correlates with predicted litter decomposition rates (k) in a manner consistent with global biogeographic patterns of mycorrhizal root associations[6].

Populus associate with diverse fungal communities across their leaf, root, and soil compartments, which are structured by different soil and climate gradients across the US. Identifying these environmental drivers of host-mycobiome relationships will aid in designing sustainable feedstock programs and managing forest systems into the future.

References

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