

Plant-Microbe Interfaces: Assembly and function of the ectomycorrhizome of *Populus trichocarpa*

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Project Goals: The goal of the Plant-Microbe Interfaces (PMI) SFA is to characterize and interpret the physical, molecular, and chemical interfaces between plants and microbes and determine their functional roles in biological and environmental systems. *Populus* and its associated microbial community serve as the experimental system for understanding the dynamic exchange of energy, information, and materials across this interface and its expression as functional properties at diverse spatial and temporal scales. To achieve this goal, we focus on 1) defining the bidirectional progression of molecular and cellular events involved in selecting and maintaining specific, mutualistic *Populus*-microbe interfaces, 2) defining the chemical environment and molecular signals that influence community structure and function, and 3) understanding the dynamic relationship and extrinsic stressors that shape microbiome composition and affect host performance.

The ectomycorrhizal fungi (EMF) are mutualistic associates of some of the most dominant and speciose trees on the planet, including pines, oaks, and eucalypts. Typically, an ectomycorrhizal plant species will play host to hundreds of different EMF species, however, there are cases where a restricted community of EMF can be found with specific host species. *Populus trichocarpa* is an unusual ectomycorrhizal host in that it harbors a root microbial community of diverse symbiotic guilds, including arbuscular mycorrhizae, EMF, rhizobia, and endophytic fungi. One aim of the PMI project is to characterize the fungal communities associated with *P. trichocarpa* to begin to assess the functional roles of different components in the root microbiome and how they impact plant health and resistance to pathogens. Field surveys of natural *P. trichocarpa* communities in the Pacific Northwest have yielded a specimen and culture collection of the EMF associates of *P. trichocarpa*. This EMF community is mostly restricted to a dozen or so core species including several that are host specific with *Populus*. Our objective is to sequence the genomes of this “core community” to test whether these core members are functionally partitioned through coevolution of their host or whether they are functionally redundant. Using established *in vitro* and *in planta* inoculation and mycorrhization systems, our goal is to reassemble the core EMF community to assess assembly and functional redundancy of core EMF communities.

The Plant Microbe Interfaces Scientific Focus Area is sponsored by the Genomic Science Program, U.S. Department of Energy, Office of Science, Biological and Environmental Research.