

Plant-Microbe Interfaces: Dissecting the compatibility and diversity of the mycobiome of *Populus trichocarpa*

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Project Goals: The goal of the PMI SFA is to understand the genome-dependent molecular and cellular events involved in establishing and maintaining beneficial interactions between plants and microbes. *Populus* and its associated microbial community serves as the experimental system for understanding how these molecular events manifest themselves within the spatially, structurally, and temporally complex scales of natural systems. To achieve this goal, we focus on 1) characterizing host and environmental drivers for diversity and function in the *Populus* microbiome, 2) utilizing microbial model system studies to elucidate *Populus*-microbial interactions at the molecular level and dissecting the signals and pathways responsible for initiating and maintaining microbial relationships and 3) develop metabolic and genomic modeling of these interactions to aid in interpreting the molecular mechanisms shaping the *Populus*-microbial interface.

The *Populus* root microbiome harbors a diverse community of endophytic and ectomycorrhizal fungi that promote nutrient acquisition and plant health. In collaboration with the JGI, we have isolated and sequenced the genomes of over 50 ectomycorrhizal and endophytic fungi isolated from *Populus* roots. These genomes are being used to interrogate the metagenomics of North American soil fungal communities with other cottonwood species *P. nigra* collected from France in order to identify core groups of fungi associated with *Populus*. *Populus* genotypes often vary in their ability to form symbioses with different root-associated fungal taxa, and one aim of our studies is to identify the genetic determinants which underly host-specificity. A diverse collection of root associated fungi are being tested to evaluate their compatibility with different *Populus* genotypes representing different geographical ecotypes of *P. trichocarpa*. Selected species of *Populus*-associated EMF including *Lactarius*, *Hebeloma*, *Cenococcum*, *Laccaria* and *Paxillus* were inoculated on eight *P. trichocarpa* genotypes to address plant-fungal compatibility and function of the *Populus* mycobiome by in vitro synthesis of ectomycorrhiza and by using split-root systems with stable isotope tracing. The systems are under evaluation and will facilitate the understanding of *Populus*-fungal associations assessing the effects on the plant host using isotope methods, transcriptomics and assessment of plant health and fungal colonization. By using different split-root and in vitro systems in combination with genetic

tools and isotopic tracing methods, these studies will provide insight into *Populus*-fungal associations and their development in this model tree genetic system.

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