

## 211. Plant-Microbe Interfaces: Fungal-bacterial interactions within Populus rhizosphere

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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 molecular events leading to recognition and colonization of a host plant by beneficial microorganisms are poorly understood. Our ongoing research is aimed at identifying and isolating microbes associated with natural Populus ecosystems in order to determine molecular, genetic and cellular events involved in recognition and establishment of beneficial microbial interactions with Populus. Several research investigations to enhance our understanding of plant- microbe interactions focus on elucidating the genetic and molecular mechanisms of the interactions of the host plant and the bacterial network associated with fungal partners within the natural Populus ecosystems.

The mycorrhizal symbiosis is the most widespread plant-microbe association that supports forest growth and sustainability. In soil, roots and fungi are surrounded by diverse microbial communities, which modulate the mycorrhizal symbiosis. This community includes the so-called mycorrhiza helper bacteria (MHB), which are thought to assist mycorrhizal formation and symbiosis. Other bacteria are confined to living inside of fungal hyphal cells and cannot sustain life independently outside of their hosts. Because very little is known about the role of these helper and endosymbiotic bacteria in Populus-fungi interactions, this project is aimed at dissecting the signaling mechanisms underlying Populus–fungal–bacterial interactions. To this end, our experimental approach integrates transcriptomes, metabolomes, proteomes, and genomes. We have sequenced genomes of several endosymbionts and free-living helper bacteria, constructed mutant libraries and have begun mutant phenotype screening. We demonstrate that some helper bacterial strains influence Populus–*L. bicolor* colonization and some mutants are affected in their beneficial effect. In parallel we have characterized diverse endosymbiotic bacterial communities in several fungal *Mortierella elongata* strains, a fast-growing coenocytic fungus found in association with Populus. We then cleared bacterial endosymbionts from the strains and observed various effects on fungal host fitness in specific conditions. Hereby we provide new insights into the mechanism of multi-partite interaction between Populus and its complex microbial communities with clear synergistic effects on plant growth, stress tolerance, and fitness.

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