

Plant-Microbe Interfaces: *Populus* genomics, genetics and molecular biology

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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) developing metabolic and genomic modeling of these interactions to aid in interpreting the molecular mechanisms shaping the *Populus*-microbial interface.

Previous and ongoing PMI SFA research has led to the development and application of a number of *Populus* genomic and genetic resource tools for realizing the project goals of the PMI SFA. These include ~1,000 *Populus trichocarpa* natural variants for Genome-Wide Association Studies (GWAS), ~400 *P. trichocarpa* × *P. deltoides* hybrids for Quantitative Trait Locus (QTL) mapping, *Populus* protoplast transient expression system and *Populus* hairy root transient expression system for molecular, cellular and biochemical validation, and a *Populus* transformation platform for generating stable transgenic lines over- or under-expressing the gene of interest. These resources and tools have enabled us to identify genetic loci regulating the interactions between *Populus* and microbes and to characterize these interactions at the molecular and biochemical levels. In particular, they have enabled us to effectively evaluate the host genotype influence on microbial community composition, diversity and function, and to pinpoint the action of these genetic regulators in the signaling events in *Populus*-microbial interactions. We have identified a lectin receptor-like kinase as a key regulator of *Populus*-*Laccaria bicolor* interactions. By using *Populus* transgenic lines and a bacterial lactonase, we will evaluate the role of quorum sensing in shaping the composition and structure of the *Populus* microbiome.

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