

212. Plant-Microbe Interfaces: Genome re-sequencing reveals a species-specific whole-gene deletion associated with *Populus-Laccaria* mycorrhizal symbiosis

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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.

Mycorrhizal symbiosis between perennial plants and fungal associates has critical implications for diverse phenomena including global carbon, water and nutrient cycling, as well as agricultural and forestry productivity with limited inputs on marginal croplands. As such, characterizing the molecular genetics underlying such interactions holds tremendous potential in engineering biological systems for enhanced carbon sequestration and sustainable biomass production.

In the perennial bioenergy feedstock *Populus*, numerous studies have demonstrated the species-dependent colonization efficiency by the fungal symbiont *Laccaria bicolor*, with *P. trichocarpa* exhibiting high levels of mycorrhization compared to *P. deltoides*. This highly species-specific attribute of the interaction presents an opportune platform for the discovery of host genetic factors governing mycorrhizal interactions using inter-specific hybrids. To this end, we identified a major quantitative trait locus (QTL) contributing up to 60% of the phenotypic variance explained (PVE) in colonization of *P. trichocarpa* x *P. deltoides* F1 hybrids by *Laccaria*. Genome anchoring of this QTL using single nucleotide polymorphism (SNP) markers with known physical positions revealed its co-location with a region harboring tandemly repeated lectin-type receptor kinases. Alignment of the *P. trichocarpa* and *P. deltoides* re-sequenced parental genomes suggested major structural differences in this region including a whole-gene deletion event in *P. deltoides* involving a D-mannose lectin receptor kinase. Analysis of allelic effects of the indel revealed that individuals carrying a full copy of the gene exhibited 2X more colonization by the fungal symbiont compared with individuals missing segments of the same gene. Further, we screened pure *P. trichocarpa* and *P. deltoides* natural variants to assess penetrance of the indel in the species' natural habitats. We could not detect a full copy of the gene in any of the 60 *P. deltoides* genotypes collected from diverse geographical origins in eastern United States whereas the gene was highly conserved in 673 re-sequenced *P. trichocarpa* genomes evaluated. Since D-mannose receptor kinases have been implicated in innate immunity and self-incompatibility responses, which require highly specific recognition of cells and microorganisms, we hypothesize that this indel polymorphism contributes substantially to the

species-specificity observed in *Populus* interaction with *Laccaria*. Transgenic validation of putative effects of the receptor kinase on mycorrhization is currently underway and results of these analyses will be presented.

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