

Plant-Microbe Interfaces: Genetic mapping and genomic resequencing identify a lectin receptor-like kinase as a regulator of *Populus-Laccaria bicolor* interaction

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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.

Populus species, as keystone members of boreal and temperate ecosystems, interact with a wide variety of microbes. The *Populus-Laccaria bicolor* system has emerged as an excellent system of choice for studying plant-ectomycorrhizal interactions aided by the availability of both *Populus* and *Laccaria* reference genomes and genetic tools. Modes of action and molecular mechanisms underlying ectomycorrhizal interactions are poorly understood in this and all other plant-mycorrhizal systems though progress has been made in recent years. Active recruitment and acceptance of mycorrhization have been proposed to occur in a species-specific manner and *L. bicolor* has been found to preferentially colonize *P. trichocarpa* over *P. deltoides*. We therefore hypothesized the existence of distinct genetic loci that are present in *P. trichocarpa* but absent in *P. deltoides* and harbor high-fidelity recognition mechanisms for *L. bicolor*.

Using genetic mapping and re-sequencing, we identified a whole-gene deletion event in *Populus* that was associated with a decrease in colonization by the ectomycorrhizal fungus *L. bicolor*. This locus contains a gene encoding a lectin receptor-like kinase, designated as PtLecRLK1. The role of PtLecRLK1 mediating mycorrhization was validated via heterologous expression in a non-host species for *L. bicolor*, *Arabidopsis*, conveying the ability in the transgenic plants to accept interstitial hyphal growth and Hartig net-like structure formation by *L. bicolor*. Expression and metabolomics analyses indicated that plant defense-related genes and metabolites were down-regulated in *Arabidopsis* plants expressing *PtLecRLK1*. These results uncover an important molecular step in the establishment of symbiotic plant-fungal associations and provide a molecular target for rational design of mycorrhizal symbiosis in economically important crops to enhance water and nutrient acquisition in marginal lands.

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.