Plant-Microbe Interfaces: Mining genomic signatures of species-specific microbe interactions in *Populus* using high density SNP arrays and whole genome resequencing

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Project Goal: 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 an initial 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 will focus on 1) characterizing the natural variation in *Populus* microbial communities within complex environments, 2) elucidating *Populus*-microbial interactions at the molecular level and dissecting the signals and pathways responsible for initiating and maintaining microbial relationships, and 3) performing metabolic and genomic modeling of these interactions to aid in interpreting the molecular mechanisms shaping the *Populus*-microbial interface.

Highly specialized plant-microbe interactions such as mycorrhizal symbiosis exhibit remarkable species specificity in economically important plants such as *Populus*. As such, molecular genomic signatures of these specialized interactions are expected to closely mirror the molecular genomic signatures of species differentiation, offering a manageable entry point in efforts to identify and characterize genetic elements essential for establishment of such interactions. In this study, we characterized genome divergence on Chromosome 1 of the *Populus* genome known to harbor major genetic determinants of *Populus-Laccaria* symbiosis as a test case for identifying candidate genes based on species-level genome divergence. We used a high-density single nucleotide polymorphism (SNP) array with a genome-wide coverage based on 34,130 probes to genotype three *Populus* species. Out of 3,716 SNPs on chromosome 1, we identified 229 SNPs that were not transferable between *P. trichocarpa* and *P. deltoides or P. fremontii*. These non-transferrable SNPs were over-represented in three regions on chromosome 1 representing putative zones of genome divergence during *Populu*s speciation. In these regions, 25 genes with putative functions in plant-microbe interaction were identified. These included a phosphate transporter-related gene previously implicated in symbiotic phosphate transportation in arbuscular mycorrhizae, as well as a Vapyrin gene that was reported to be an essential factor in intracellular progression of arbuscular mycorrhizal symbiosis. Resequencing data for these genes will be used to characterize differences in gene structure between *P. trichocarpa* and *P.deltoides* that could potentially explain species-related *Populus-Laccaria* interactions.

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