

Plan-Microbe Interfaces: Pleiotropic and Epistatic Network-Based Discovery of Plant Functions Involved in Microbial Interactions: Integrated SNP Correlation, Co-expression and Genome-Wide Association Networks for *Populus trichocarpa*

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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.

Biological organisms are complex systems that are composed of pleiotropic functional networks of interacting molecules and macro-molecules. Complex phenotypes are the result of orchestrated, hierarchal, heterogeneous collections of expressed genomic variants regulated by and related to biotic and abiotic signals. However, the effects of these variants are the result of historic selective pressure and current environmental as well as epigenetic interactions, and, as such, their co-occurrence can be seen as genome-wide associations in a number of different manners. In this context, a plant's association with its microbiome is a complex set of interactions involving many genes and metabolites. We are using data derived from the re-sequenced genomes from over 1000 alternate *Populus trichocarpa* genotypes in combination with transcriptomics, metabolomics and phenomics data across this population in order to better understand the molecular interactions involved in plant-microbe interfaces. The resulting Genome-Wide Association Study networks, integrated with SNP correlations and co-expression networks, are proving to be a powerful approach to determine the pleiotropic and epistatic relationships underlying cellular functions and, as such, some of the molecular underpinnings for plant-microbiome associations.

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