

## **Plant-Microbe Interfaces: Plant-based Genome-Wide Association Viriome/Microbiome Analysis (GWAVA)**

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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.

Metagenomic or metatranscriptomic analyses can capture the diversity and functional potential of a microbiome, though viruses are often a neglected component. The microbiome (here defined as the combination of the bacteria, fungi, archaea and viruses found in plant tissue) not only interacts with the host, and thus may elicit or suppress a defense response, but there may be interactions among the constituents of the microbiome. This multi-directional influence can have a number of phenotypic responses, both pathogenic as well as mutualistic. To better understand these influences we have applied modified genome-wide association (GWAS) methods in order to associate host genotypic variation to the putative viral, bacterial, fungal and archaeal community composition. Metatranscriptome samples extracted from *Populus trichocarpa* xylem tissue were used to identify the different taxa present via several computational approaches. The resultant members of the microbiome then served as phenotypes in a GWAS analysis involving 444 genotypes of *Populus trichocarpa* (against over 8 million single-nucleotide polymorphisms). After correcting for multiple hypotheses testing, and viewing the results in a network context, we find shared associations between microbiome phenotypes and receptor kinases, signal transduction genes, transcription factors, xenobiotic stress, biotic stress, cell organization, biological control agents and other stress related genes among other functions. The resultant network provides a rich framework for biologically driven hypothesis generation. Thus the use of microbiome constituents as GWAS phenotypes is helping to elucidate the host mechanisms

responsible for host-microbiome interactions (and the regulation thereof) and provides indications of possible interactions among different members of the microbiome itself.

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