

Plant-Microbe Interfaces: Understanding the *Populus* microbiome structure in response to host stress

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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.

Adverse conditions can affect plants, leading to decreased plant growth, productivity, and survival, and resulting in failure or poor yields of crops and biofeedstocks. In some cases, the microbial community associated with plants has been shown to alleviate plant stress and increase plant growth under suboptimal growing conditions. A systematic understanding of how the microbial community changes under these conditions is required to understand the function of the phytobiome system and the contribution of the microbiome to water utilization, nutrient uptake, and ultimately yield. Using a microbiome replacement strategy, we studied how the microbiome of *Populus deltoides* changes in response to diverse environmental conditions of water limitation, light limitation (shading), and metal toxicity. While plant responses to treatments in growth, photosynthesis, gene expression and metabolite profiles were varied, we identified a core set of bacterial genera that change in abundance in response to host stress. The results of this study indicate substantial structure in the plant microbiome community and identify potential drivers of the phytobiome response to stress. We further investigated the hypothesis that different plant stresses would affect the complements of secondary metabolites produced by microbial communities associated with the roots. We extracted methanol-soluble compounds from the soil samples at the conclusion of the stress experiment, analyzed the

extracts using liquid chromatography-tandem mass spectrometry (LC-MS-MS), and examined the data as a function of applied stress. Many similar MS-MS spectra were obtained across all treatments, but subsets characteristic of each abiotic stress could also be identified.

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