Plant-Microbe Interfaces: Quantification of *Populus* transcriptomic response to colonization by select bacterial symbionts.

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Project Goals: The goal of the PMI SFA is to characterize and interpret the physical, molecular, and chemical interfaces between plants and microbes and determine their functional roles in biological and environmental systems. *Populus* and its associated microbial community serve as the experimental system for understanding the dynamic exchange of energy, information, and materials across this interface and its expression as functional properties at diverse spatial and temporal scales. To achieve this goal, we focus on 1) defining the bidirectional progression of molecular and cellular events involved in selecting and maintaining specific, mutualistic *Populus*-microbe interfaces, 2) defining the chemical environment and molecular signals that influence community structure and function, and 3) understanding the dynamic relationship and extrinsic stressors that shape microbiome composition and affect host performance.

Poplar species (*Populus* spp.) associate with a diverse array of bacteria that are selected from the environment. However, the molecular mechanisms by which poplars recognize and establish symbioses with these microbes are largely unknown. To determine how these plants respond to colonization with bacteria, we inoculated germ-free *P. trichocarpa* root tissue with select bacterial strains isolated from field-collected roots and quantified plant gene expression using RNAseq. Colony forming units (CFU) were quantified for each bacterial strain and ranged over three orders of magnitude, demonstrating wide variation in the ability to colonize *Populus* root tissues. The number of differentially expressed poplar genes also varied among treatments but did not correlate with CFU count. Plant transcriptomic responses were largely strain-specific with no single gene induced or repressed among all treatments. Across all genes that showed differential expression relative to control tissues, those induced were enriched for biological processes including cell wall biosynthesis, vesicle trafficking, and root development while those repressed were enriched for processes including stress response and carbon metabolism. Comparisons between plants inoculated with pathogenic (*Pseudomonas syringae* isolate NP28-5) and non-pathogenic strains (including *Pseudomonas fluorescens* isolate GM79) revealed potential mechanisms by which poplar defends against pathogens, including the induction of genes coding for anti-microbial peptides and pathogen-associated microbial pattern (PAMP) receptors. Inoculation with *P. fluorescens* isolate GM79 compared to a knock-out strain missing the microbial gene pipA, involved in bacterial recognition of a plant-derived effector molecule, elicited the induction of ten poplar genes largely involved in transmembrane transport and signal transduction. Together, these data provide insight into the molecular mechanisms involved in the establishment of symbiosis between *Populus* and its microbiome. Future directions include qPCR validation of candidate loci

and leveraging metabolomic, proteomic, and network-based approaches to further interrogate poplar response to select bacteria.

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