

Plant-Microbe Interfaces: Effects of variation in host secondary chemistry across *Populus* genotypes on the composition of the rhizosphere microbiome

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Project Goals: The goal of the Plant-Microbe Interfaces (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.

Abstract

Plants have developed defense strategies for phytopathogen and herbivore protection via coordinated metabolic mechanisms. Low-molecular weight metabolites produced within plant tissues, such as salicylic acid, represent one such mechanism which likely mediates plant – microbe interactions above and below ground. Salicylic acid is a ubiquitous phytohormone at low levels in most plants, yet are concentrated defense compounds in *Populus*, likely acting as a selective filter for rhizosphere microbiomes. We propagated twelve *Populus trichocarpa* genotypes which varied an order of magnitude in salicylic acid (SA)-related secondary metabolites, in contrasting soils from two different origins. After four months of growth, plant properties (leaf growth, chlorophyll content, and net photosynthetic rate) and plant root metabolomics specifically targeting SA metabolites were measured via GC-MS. In addition, rhizosphere microbiome composition was measured via Illumina MiSeq sequencing of 16S and ITS2 rRNA-genes.

Soil origin was the primary filter causing divergence in archaeal/bacterial and fungal communities with plant genotype secondarily influential. Both archaeal/bacterial and fungal evenness varied between soil origin and with at least one SA metabolite (archaea/bacteria: populin; fungi: salicin and salicylic ACID). The production of individual salicylic acid derivatives - tremuloidin, populin, salicortin - that varied by host genotype, resulted in compositional differences for archaea/bacteria within a soil origin. Contrastingly, overall salicylic acid levels and its major derivative, salicortin, were associated with shifts in fungal

community composition, but to a lesser degree. Using regression-based analyses, it was revealed that changes in several dominant bacterial operational taxonomic units (OTUs) were drivers of these metabolite-community relationships; and most of these bacterial OTUs exhibited positive correlations with SA derivatives. No fungal OTUs were detected which significantly varied with metabolites regardless of overall compositional differences.

These results indicate microbial communities diverge most among soil origin. However, within a soil origin, bacterial communities are responsive to plant SA production, particularly populin, within greenhouse-based rhizosphere microbiomes. Fungal microbiomes are impacted by root SA-metabolites, but to a lesser degree within this experimental context. These results suggest plant defense strategies, such as SA and its secondary metabolites, may partially drive both archaeal/bacterial and fungal taxa-specific colonization and assembly.

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