

Plant-Microbe Interfaces: Microbial transformation of *Populus* secondary metabolites by microbiome isolates

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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.

Populus is a widely studied model woody plant species and a potential cellulosic feedstock for biofuels. These trees host a wide variety of microbial associations within their roots and rhizosphere and thus serve as a powerful model to study interactions between plants and microorganisms. One of the defining characteristics of *Populus* is the production of secondary metabolites known as higher-order salicylates (HOS), which are involved in host defense and signaling mechanisms. We are interested in determining how the presence and production of these HOS influence the host-microbiome composition and physiology. We have isolated and characterized a number of bacteria from genera (*Pseudomonas*, *Sphigobium*, *Rhizobium*, *Bacillus*, *Pantoea*, *Duganella*, *Burkholderia*, *Caulobacter*, *Streptomyces*, *Bradyrhizobium*, *Rahnella* and *Varivorax*) prevalent in the endosphere and rhizosphere compartments of *Populus* roots and obtained whole genome sequence data. Here we describe physiological characterization of these bacterial isolates with the goals of determining the ability of these strains to transform salicin and other HOS extracted from *Populus* tissues, and measuring the sensitivity and resistance of these bacterial strains to HOS compounds and their degradation products. We present proteomics, metabolomics and comparative genomics data from select strains that have led to identification of potential microbial mechanisms for transformation of the

HOS. We hypothesize that the complex nature of these HOS metabolites may lead to microbial cross feeding and this has been borne out in bacterial co-cultivation experiments. This analysis provides initial insight into the prevalence and diversity of *Populus* microbiota capable of transforming HOS, potential transformation mechanisms, and interactions between microbiome community members.

The Plant Microbe Interfaces Scientific Focus Area is sponsored by the Genomic Science Program, U.S Department of Energy, Office of Science, Biological and Environmental Research.