

## **Plant-Microbe Interfaces: Investigating how interactions and local environments in the rhizosphere influence microbial responses and behavior**

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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.**

The rhizosphere is a dynamic and heterogeneous environment and the behavior of organisms within the rhizosphere depends on local environmental conditions and spatial organization. Developing methods to monitor community organization and map local chemical and physical environments and to correlate these data with microbial responses are necessary to understand, and ultimately predict, microbiome function. To this end, we have visualized the dynamics of plant-microbe interactions using engineered habitats and found that many plant-associated bacteria show reproducible root colonization patterns. We hypothesize that differing chemical profiles around the root contribute to the recruitment and growth of bacteria at these preferred sites. To better understand how the chemical environment around the root influences microbial responses and behavior, we examined proteome profiles of poplar-associated bacterial strains grown in the presence of a poplar cutting. For these studies, we examined the proteome profiles of individual bacterial strains grown in the presence of a plant compared to the proteome profiles when all ten strains were grown as a synthetic community in the presence of the plant. Common to all strains were significant changes in the proteome profiles involving proteins predicted to be involved in nutrient transport and metabolism, sensing, and motility. Current efforts are underway to test hypotheses derived from these proteomic experiments in *Pantoea* sp. YR343 using mutant strains, growth assays, and plant colonization experiments.

*Oak Ridge National Laboratory is managed by UT-Battelle, LLC for the U.S. Department of Energy under contract no. DE-AC05-00OR22725. 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 under FWP ERKP730.*