

## **Plant Microbe Interfaces: Emerging analytical techniques for controlling and monitoring architectural changes in developing multi-kingdom systems**

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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 serve as the experimental system for understanding how these events manifest themselves within the spatial, structural, and temporal complexity 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) studying model microbial systems to elucidate *Populus*-microbial interactions at the molecular level and dissect the signals and pathways responsible for initiating and maintaining microbial relationships and, 3) developing metabolic and genomic models of these interactions to aid in interpreting the molecular mechanisms that shape the *Populus*-microbial interface.**

The structure and development of natural systems depend on complex physical and chemical signal exchanges over space and time. The ephemeral nature of these signals and the dynamically changing host and community phenotypes associated with these events requires the use of complementary imaging, chemical, and genetic sampling strategies that can be used to capture and correlate these properties over time. In this work, we present a suite of techniques and emerging technologies to monitor and interpret the drivers of host development and colonization. A combination of microfluidic and 3D printed plant-microbe co-culture platforms enabled the characterization of root colonization patterns by plant-growth promoting bacteria isolated from *Populus*. These platforms have the potential to provide insights into how physical and chemical features of the host shape colonization, niche formation, and microbe-microbe interactions within the rhizosphere. Likewise, the influence of constructed communities on a dynamic host phenotype can be quantified. Ultimately, this suite of multi-modal sampling and measurement techniques will allow us to understand the influence of biochemical transport and exchange on the functional composition and structure of these dynamic plant-microbe systems in tractable model environments that capture critical features of their natural habitats.

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