

Plant-Microbe Interfaces: Formation and characterization of emergent microbial communities

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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.

Microbial communities colonize throughout plant tissues and contribute to host function. How these communities form and how individual members contribute to shaping the community structure are not well understood. Synthetic microbial communities composed of well-studied individual isolates can be valuable model systems for elucidating the organizational principles of communities. Using genome-defined strains, systematic analysis by computational modeling can lead to mechanistic insights and metabolic interactions among species. In this study, 10 bacterial strains isolated from the *Populus deltoides* rhizosphere were co-cultured and passaged in two different media environments to form stable microbial communities. The membership and relative abundances of the individual strains in the resultant community stabilized after around 5 passages and resulted in only a few dominant strains that depended on the medium. To unravel the underlying metabolic interactions within the community, flux balance analysis was used to model microbial growth and predict metabolic interaction involved in organizing the microbial communities. These analyses were complemented by measuring growth curves of the individual strains, performing metaproteomics of the community and carrying out pairwise interaction screens between species. A fast growth rate can be advantageous for maintaining survival in the microbial community, and the final presence of a member also depends on selective antagonistic relationships and metabolic exchanges within the community. Revealing the mechanisms of interaction among plant-associated microorganisms provides insights into strategies for engineering microbial communities that can potentially increase plant growth and disease

resistance. Deciphering the membership and metabolic potentials of microbial communities will also enable the design of synthetic consortia with desired biological functions.

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