

Plant-Microbe Interfaces: Temporal Variation in Plant-Microbe Interactions

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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.

It is increasingly recognized that microorganisms living inside or in close association with plant tissues are integral for plant health and survival. Our previous work has shown that *Populus* harbors distinct microbiomes among its different tissues¹; however, the temporal stability of these microbial communities is unclear as measurements across time have so far been limited. Here, we present work from two subprojects that aim to characterize the initial assembly as well as the intra- and inter-annual stability of the *Populus* microbiome. To assess the initial assembly of the *Populus* microbiome, we initiated a common garden study consisting of 10 *Populus* genotypes from two *Populus* species, *Populus deltoides* and *Populus trichocarpa*. Overall, we found that archaeal, bacterial, and fungal community assembly of the *Populus* microbiome is consistent among genotypes. The rhizosphere soils provide a significant proportions of taxa in the leaf and root endosphere. Additionally, using a null modeling approach, we estimate that the underlying assembly processes are at first stochastic but become more deterministic with time. We have continued to sample this common garden four times per year, and we are now in the fourth year of this experiment. These additional years will give us insights to the intra- and inter-annual variation of the *Populus* microbiome upon the first few years of planting.

To assess the inter-annual variation of *Populus* across longer times scales (*i.e.*, decades), we are taking advantage of a time-for-space substitution approach in multiple aspen (*P. tremuloides*) clones, including what is largely considered to be Earth's most massive organism: Pando. We have so far identified a gradient of ramet ages in four aspen clones, and this summer we plan to sample leaves, xylem, fine roots, and rhizospheres for microbiome analysis.

Taken together, these projects will begin to elucidate the stability of the microbiome at both large scales and fine resolution in a long-lived plant over the lifetime of the host. Such information on

the temporal dynamics of the microbiome may be useful in identifying circumstances where microbiome interventions would be most successful.

References

1. Cregger MA, Veach AM, Yang ZK, Crouch MJ, Vilgalys R, Tuskan GA, et al. The Populus holobiont: dissecting the effects of plant niches and genotype on the microbiome. *Microbiome* 2018; **6**.

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