Plant-Microbe Interfaces: Systems biology approaches to understanding a plant's adaptation to and regulation of the phytobiome

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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.

We have created Parakraken, a parallelized kmer profile-based taxa identification approach, which uses full kmer profiles from every publicly available genome sequence (including bacteria, archaea, fungi, viruses, nematodes, insects, protists, etc.) to allow detection of the cryptic phytobiome in the DNA or RNA sequence of any host tissue. We are using Parakraken to identify taxa in different host tissues across a genome wide association study (GWAS) population of *Populus trichocarpa*. We also have other independent layers of 'omics data across this population and over 28,000 temporal-climactic phenotypes (climatypes) measured across the original locations of the genotypes in the population. In addition, we have developed new methods for GWAS using the presence/absence of genes in the pan genome of this population. Furthermore, we have developed supercomputing and explainable-AI approaches to find complex epistatic architectures responsible for the host's ability to detect and modulate its microbiome and other phenotypes. The result is a comprehensive systems biology model of a plant and its microbiome, its adaptation to its climactic environment and the metabolic intermediaries involved therein. Thus, we combine the results of these approaches with many orthogonal layers of information in order to score each hypothesis supported by multiple lines of evidence to prioritize specific mechanisms for experimental validation.