

## **Plant-Microbe Interfaces: AI-GWAPA, explainable AI-based approaches to genome wide phytobiome association**

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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 molecular events manifest themselves within the spatially, structurally, and temporally complex scales 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) utilizing microbial model system studies to elucidate *Populus*-microbial interactions at the molecular level and dissecting the signals and pathways responsible for initiating and maintaining microbial relationships and 3) develop metabolic and genomic modeling of these interactions to aid in interpreting the molecular mechanisms shaping the *Populus*-microbial interface.**

The phytobiome consists of the plant, organismal communities, and their environment. The interactions between these have significant effects on observable measurable traits that have potential economic and sustainability implications. A better systems-level understanding of the beneficial and antagonistic relationships between these components will enhance our capacity to influence these systems to produce desirable and impactful traits.

In Artificial Intelligence – Genome Wide Association Phytobiome Analysis (AI-GWAPA), a project that utilizes machine learning, deep learning and general artificial intelligence (AI) techniques, the goal is to elucidate the interactions between microbial and viral constituents of the 1000 member *Populus Trichocarpa* population arrayed in common gardens in the Pacific Northwest. Metatranscriptome samples from leaf, xylem and root along with approximately 28 million SNPs called across the population allows us to associate host genetic variants to microbial/viral constituents. Sample-specific networks, which is a machine learning approach that allows us to model contributions that a genotype has to putative pathogenic-mutualistic relationships between taxa, is being used. Furthermore, we utilize an AI approach by training a deep learning neural network to estimate putative phytobiome-derived protein interactions

among the host proteome. Together these approaches allow us to improve our fundamental understanding of the relationships between the plant and its phytobiome.

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