

## **Plant-Microbe Interfaces: Integrated omics and phytobiome analysis of the adaptation of *Populus deltoides* to acute progressive drought and cyclic drought**

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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.**

Plant drought stress causes systematic changes to photosynthesis, metabolism, growth, and potentially the phytobiome. Additionally, drought affects plants in both a species-specific and water-deficit-driven manner, causing the response to drought to be dependent both on how drought is being experienced and on any adaptation to prior drought exposure. Thus, understanding the effect of drought on plants requires assessing drought response in multiple conditions, such as progressive acute drought and recurrent cyclic drought, and at different levels of severity. In this study, we have utilized RNA sequencing, GC-MS and LC-MS in order to identify changes to the plant transcriptome, metabolome, proteome and the phytobiome during both acute progressive drought and cyclic drought at multiple severities. Co-analysis of these omic layers with the phytobiome, allows for the identification of novel associations that would not be possible otherwise. We have identified that the drought response ranges from increased transcripts related to photosynthesis and metabolic activity in mild acute drought to decreased transcripts related to photosynthesis and metabolic impairment in severe drought. Moreover, while water deficit is a main driver of transcriptional responses in severe drought, there are increases in reactive oxygen species (ROS) metabolism and photosynthetic transcripts in cyclic severe drought compared to acute severe drought, independent of water deficit. The phytobiome exhibits alternate responses to drought when compared to the transcriptome. Specifically, the phytobiome is affected more by the cyclic or acute nature of the drought rather than the severity of the drought, with the phytobiome having an increase in taxa under cyclic drought that are often reported to have beneficial effects on the plants. Lastly, we have identified associations between taxa in the phytobiome with expression of disease response, ROS metabolism, and photosynthesis transcripts suggesting interplay between the host plant and its phytobiome in response to drought.

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