

Plant-Microbe Interfaces: Phytobiome and transcriptional 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 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.

Plant drought stress causes systematic changes to photosynthesis, metabolism, and its 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 much drought is being experienced and on any adaptation to prior drought exposure. As such, to understand 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 to identify changes to the plant transcriptome and the phytobiome during both acute progressive drought and cyclic drought at multiple severities. 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 species metabolism and photosynthetic transcripts in cyclic severe drought compared to acute severe drought, independent of water deficit. Lastly, the phytobiome is more separated by the cyclic or

acute nature of the drought rather than the severity of the drought, with drought-resistance and plant growth promoting organisms at higher abundances in cyclic drought.

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