Plant-Microbe Interfaces: Metabolomics of non-host switchgrass plants expressing a poplar lectin receptor-like kinase in response to the mycorrhizal fungus *Laccaria bicolor*

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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.

A black cottonwood poplar (*Populus trichocarpa*) lectin receptor-like kinase (PtLecRLK1) was recently identified that mediates the symbiosis between *P. trichocarpa* and *Laccaria bicolor* (Labbé *et al*., 2019). When PtLecRLK1 was heterologously expressed in *Arabidopsis thaliana*, a non-host species for *L. bicolor*, the transgene induced the ability of *Arabidopsis* to display interstitial hyphal growth and Hartig net-like extracellular structures created by *L. bicolor*, and suppressed the host's defense responses upon exposure to *L. bicolor*, a key mechanism initiating colonization. Given that *Arabidopsis* is not known to harbor ectomycorrhizal relationships, a new study was initiated to determine if heterologously expressing PtLecRLK1 in a grass species that is a known host of ectomycorrhiza can result in establishing a symbiotic relationship that, otherwise, would not occur. Four transgenic switchgrass (*Panicum virgatum*) lines expressing PtLecRLK1 were generated and gas chromatography-mass spectrometry (GC-MS)-based metabolomics were conducted on roots of transgenic plants in contrast with wild-type plants growing in the presence of *L. bicolor*. The largest metabolomic responses of transgenesis were associated with accumulation of numerous nitrogenous metabolites, which are likely associated with the observed decline in plant growth. Given that there were declines in fatty acids and organic acids, which have been observed previously with symbiosis, the metabolomic results suggest that many of the early steps in successful colonization occurred, but that later-stage events were lacking.

References

1. Labbé, J., W. Muchero, O. Czarnecki, J. Wang, X. Wang, A.C. Bryan, K. Zheng, Y. Yang, S.S. Jawdy, L.E. Gunter, W. Schackwitz, J. Martin, F. Le Tacon, T. Li, Z. Zhang, P. Ranjan, X. Yang, D.A. Jacobson, T.J. Tschaplinski, J. Schmutz, J-G. Chen, and G.A. Tuskan. 2019. Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. Nature Plants 5:676-680.

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