Plant-Microbe Interfaces: Modulation of microbial community dynamics by contrasting regulation of salicylic acid and jasmomic acid-ethylene signaling pathways.

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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.

Interactions between salicylic acid (SA) and jasmonic acid-ethylene (JA/ET) signaling pathways have been found to be important to activate the correct defense responses to biotrophic and necrotrophic pathogens. The understanding of the molecular regulation of SA and ET/JA signaling interactions is essential to rationally improve plant responses against different pathogens or in recruitment of beneficial microbes. Molecular studies focusing on the crosstalk between SA and ET/JA signaling have demonstrated the critical regulatory role of transcriptional mechanisms, however the exact mechanism remains poorly understood. Using *Arabidopsis* knockout and overexpression mutants, we showed that one nuclear protein TYROSYL-DNA PHOSPHODIESTERASE 1 (TDP1) physically interacts with ANGUSTIFOLIA C-terminus Binding Protein (AN) and enhances the nuclear accumulation of AN. In addition, AN was found to directly target and repress the transcription of *MYB46*, which encodes a master regulator of the phenylpropanoid pathway. Moreover, AN displayed the capability of releasing transcriptional repression on *WRKY33* by altering chromatin association of TDP1, which negatively affects *WRKY33* expression. The transcriptional effects of AN on the expression of *MYB46*, *WRKY33*, and their downstream genes were validated in *an* knockout mutant and *AN* overexpression plants. The antagonistic transcriptional regulation of *MYB46* and *WRKY33* by AN suggests a transcriptional co-regulation mechanism of SA and ET/JA signaling. Consistent with this notion, the alteration of *AN* expression in transgenic plants was shown to oppositely affect defenses against the biotrophic pathogen *Pseudomonas syringae* and the necrotrophic pathogen *Botrytis cinerea*. Our results demonstrate a transcriptional co-regulatory mechanism of the crosstalk of SA and ET/JA signaling and suggest that it may play a key role in the coordination of defense responses towards biotrophic and necrotrophic pathogens. Importantly, changes observed in defense responses also affected biomass accumulation suggesting a trait-tradeoff between defense and

growth. Work has now been initiated to establish the implication of these genetic modifications on microbial community dynamics.

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