Plant-Microbe Interfaces: Transcriptional co-regulation of *MYB46* and *WRKY33* by ANGUSTIFOLIA modulates *Arabidopsis* resistance towards biotrophic and necrotrophic pathogens

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Project Goals: The goal of the Plant-Microbe Interfaces (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.

ANGUSTIFOLIA (AN) is involved in the development of numerous plant organs. The primary role of the animal homolog of AN, C-TERMINAL BINDING PROTEIN (CtBP), is the transcriptional co-repression of tumor suppressor and pro-apoptotic genes (1,2). However, the nuclear function of AN remains unstudied in plants. Here, we found that AN can accumulate in the nucleus and functions as a transcriptional repressor. By interacting with another nuclear protein TYROSYL-DNA PHOSPHODIESTERASE1 (TDP1), AN imposes transcriptional repression on *MYB46* which encodes a key transcription factor regulating the phenylpropanoid biosynthesis pathway (3), while releasing the TDP1-imposed transcriptional repression on *WRKY33* which encodes a critical transcription factor regulating the ethylene/jasmonic acid (ET/JA) signaling pathway (4,5). Consistent with these molecular results, genetic analyses on transgenic *Arabidopsis* plants showed that AN is capable of regulating the expressions of *WRKY33*, *MYB46*, as well as their downstream genes involved in salicylic acid (SA) and ET/JA signaling pathways. Meanwhile, plant defense capability against biotrophic and necrotrophic

pathogen infection was altered by AN. Collectively, these findings indicate that the transcriptional co-regulation of *MYB46* and *WRKY33* by AN may play an important role in the integration of SA and ET/JA signaling, as well as defenses against biotrophic and necrotrophic pathogens.

References

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