Plant-Microbe Interfaces: Characterization of IAA7.1 in *Populus* and its role in plant-microbe interactions

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Project Goal: 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 serves as an initial 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 will focus on 1) characterizing the natural variation in *Populus* microbial communities within complex environments, 2) elucidating *Populus*-microbial interactions at the molecular level and dissecting the signals and pathways responsible for initiating and maintaining microbial relationships, and 3) performing metabolic and genomic modeling of these interactions to aid in interpreting the molecular mechanisms shaping the *Populus*-microbial interface.

Auxins are a class of plant hormones regulating many physiological and developmental processes. Auxin signaling involve a group of transcription repressor proteins known as AUX/IAA (Auxin/IAA induced), and another family of transcription factors that induce auxin induced gene expression called ARFs (Auxin Response Factor). Both AUX/IAAs and ARFs have conserved protein family domains. Many studies in Arabidopsis have explored the individual roles of AUX/IAAs and ARFs. Our comparative bioinformatics analysis of the gene families in *Populus* and Arabidopsis shows that *Populus* typically has multiple orthologs (co-orthologs) for a given *Arabidopsis* gene. It is intriguing to understand whether the co-orthologs differ functionally in a more complex plant system such as *Populus*, with respect to the auxin signaling pathway and/or in establishing beneficial plant-microbe relationships. The present study examines the effect of knocking down two *Populus* co-orthologs (PtrIAA7.1 and PtrIAA7.2) of the *Arabidopsis* gene, IAA7- PtrIAA7.1 has a unique protein family domain that has thus far not been reported in any other member of the gene family, in any species. The domain is a tandem duplication of domain II, which is known to cause protein instability in other plant species. Physiological comparisons show that RNAi lines of PtrIAA7.1 have more severe phenotypes than those of PtrIAA7.2. PtrIAA7.1 mutants display reduced plant height, increased lateral branching, and reduced of apical dominance. Additionally, co-culture with *Piriformospora indica*, *Laccaria bicolor* strain S238N, and *Pseudomonas spp* strain GM30, resulted in decreased responses in the PtrIAA7.1 mutant compared to control plants, including reduced sensitivity to microbe induced changes in shoot and root growth and fresh weights. Protein profiling of shoot and root samples of PtrIAA7.1 revealed that shoots of PtrIAA7.1 lack a predicted importin protein belonging to a class of proteins involved in import of substrates into the nucleus. Additionally, PtrIAA7.1 mutant has lower abundance of ADP Ribosylation Factor proteins. Further experiments are underway to investigate the potential role of these differential expressed proteins in the auxin signaling pathway and their regulation during plant-microbe interactions.

The Plant Microbe Interfaces Scientific Focus Area is sponsored by the Genomic Science Program, U.S. Department of Energy, Office of Science, Biological and Environmental Research