

Species-specific evolution of membrane-bound receptors mediating host-symbiont specificity in the genus *Salix*

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Project Goals: The goal of this project is to identify and characterize species-specific Pattern Recognition Receptors (PRRs) that are involved in host immune suppression to allow successful colonization by microbial symbionts. Using *Salix*, a dominant species in the warming arctic region and a widely used biofuels feedstocks, we leverage strong species-specific colonization by endophytic microbes to create hybrid populations segregating for colonization efficiency. Complementary characterization of endosphere microbial communities, mapping genomic structural polymorphisms involving PRRs across segregating hybrid *Salix* populations and correlations of these features will enable assignment of species-specific PRRs to their microbial targets. Output from this project will inform efforts to rationally engineer plant-microbe interactions between previous un-associated host plants and microbial partners.

Abstract: Innate host defense poses a fundamental challenge in the utilization of beneficial microbes for improving plant productivity and carbon sequestration for applications in biofuels feedstock production and global warming mitigation. As an evolutionary adaptive mechanism to recruit symbiotic microbes, plants evolved membrane-bound Pattern Recognition Receptors (PRRs) that, upon recognition of microbe-associated molecular patterns (MAMPs) of beneficial microbes, will trigger molecular signals to suppress activation of the host defense machinery. In this study, we sought to establish species divergence in genomic composition of these PRRs as well as root endophytic microbial communities in two *Salix* species, *S. purpurea* and *S. suchowensis*. To assess putative species-level divergence, we sampled two genotypes to represent each species, P63 and P295 (*S. suchowensis*) and 94006 and 94001 (*S. purpurea*) from a replicated field trial in Morgantown, West Virginia. Differentiation in genomic PRR composition and their expression under field conditions was assessed using long-read genomic DNA and transcriptome sequencing. Microbial community divergence was established using 16S phylotyping. Results of host-species divergence in these two characteristics will be presented.

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