

**Genomic divergence in pattern recognition receptors and its implications on endophytic microbial associations in the genus *Salix***

Carly Shanks<sup>1</sup>, Timothy B. Yates<sup>1</sup>, Jing Hou<sup>1</sup>, Sara Jawdy<sup>1</sup>, Lee Gunter<sup>1</sup>, Steven Lebreux<sup>1</sup>, Jin Zhang<sup>1</sup>, Kate Stuart<sup>1</sup>, Stephen P. DiFazio<sup>2</sup>, Lawrence Smart<sup>3</sup>, **Wellington Muchero<sup>1</sup>**  
([mucherow@ornl.gov](mailto:mucherow@ornl.gov))

<sup>1</sup> Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN; <sup>2</sup> Department of Biology, West Virginia University, Morgantown, WV; <sup>3</sup> Horticulture department, Cornell University, Geneva, NY

**Project Goals: Identify and characterize species-divergence of immune-suppressing pattern recognition receptors in *Salix* spp.**

Recruitment of microbial symbionts by long-lived perennial plants is a key evolutionary strategy to deal with constantly changing environmental conditions as well as cope with limitations in nutrient availability over decades of life time. In these plants, some G-type pattern recognition receptors (PRRs) mediate the highly specific recognition of microbial symbionts to facilitate colonization by triggering suppression of the host defense machinery. Despite evidence to show strong species-specificity in symbiotic interactions, divergence of these PRRs across closely related host species remains poorly understood. In this study, we sampled root endospheres from ten *Salix* genotypes representing seven species, *S. purpurea*, *S. viminalis*, *S. udensis*, *S. integra*, *S. koriyanagi*, *S. alberti*, and *S. suchowensis*, in a fully replicated field site in Geneva, NY. Of these, six were also sampled across multiple replicates in Morgantown West Virginia. Microbial community profiling was performed using 16S rDNA community profiling to establish species-divergence in endospheric microbial communities within the same environment as well across the two sampling sites. To complement this study, divergence in genomic composition of PRRs is being characterized using targeted genotyping of whole-gene deletion events involving PRRs, de novo transcriptomes of the same root samples used in 16S profiling and long-read Nanopore sequencing and assembling of the ten *Salix* genomes. Patterns of genomic divergence in PRR composition and differences in endospheric microbial communities will be presented.

*Acknowledgement: This work was funded by the Department of Energy Office of Science under the Early Career Research Program.*