

Host Genetics Control the Composition of Root-associated Microbiota in Switchgrass (*Panicum virgatum*)

Joseph Edwards*¹(j_edwards@utexas.edu), Usha Saran¹, Jason Bonnette¹, Jane Grimwood², Felix Fritschi³, **Thomas Juenger**¹

¹University of Texas, Austin; ²Hudson Alpha Institute for Biotechnology, Huntsville, AL;

³University of Missouri, Columbia

- **Establish common gardens of clonally replicated switchgrass genotypes to study ecotype divergence, local adaptation, environmental gradients (e.g., precipitation, temperature, and soils).**
- **Identify genomic regions underlying adaptation and sustainability in switchgrass using genome-wide associations.**
- **Characterize the relative roles of switchgrass genotype and local environments in the assembly of the switchgrass bacterial and fungal microbiome communities in natural habitats.**

Plant root-associated microbiota mediate important below-ground processes such as nutrient availability, pathogen inhibition, and general growth promotion. Assembly of root microbiota is significantly impacted by the genotype of the host plant and the host's environment; however, specific loci in the host genome influencing the composition and relative abundance of root microbiota have not been identified. In this study, we use experimental populations of the bioenergy crop switchgrass (*Panicum virgatum*) planted across a latitudinal gradient to identify genomic loci affecting the composition of root-associated microbiota. We find many bacterial strains display heritable variation, and by using a QTL mapping approach, we identified genomic regions in the host plant associated with the abundance of specific bacterial taxa. A majority of the identified QTL showed consistent effects across locations, and only a few QTL displayed environmental deviations. Interestingly, many of the identified QTL coregulate multiple microbes, suggesting that either the same host signaling and response mechanisms govern the acquisition and maintenance of multiple bacterial strains, or that QTL may act on microbial keystone species, which in turn affect the abundance of other microbial taxa. Together, these results indicate that root-associated bacteria are under genetic control of the host and that altering the microbiome for greater yields or ecosystem sustainability may be possible through manipulation of host plant genetics.

This research was supported by the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research award number DE-SC0014156 to TEJ.