# Title: Genetic signatures influencing host-microbiome interactions in switchgrass (*Panicum virgatum*)

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## Project goals:

- Uncover the role of host genotype in the assembly of plant microbiota
- Use isolated bacteria to test predictions
- Manipulate microbiota to increase sustainability

## Abstract:

Plants make partnerships with soil bacteria via their roots, entering into relationships with microbiota ranging from detrimental to commensal to beneficial. While it is known that the composition of root-associated microbiota is driven by environmental factors and the genotype of the host plant (Singer et al. 2019; Edwards et al. 2018), the underlying genetic mechanisms used by the host to modulate bacterial members of the microbiota are unresolved. In this study, we use an expansive population of switchgrass natural variants (Lovell et al. 2021) planted across several common gardens across the United States to explore the genetic architecture of host-microbiome interactions. We find that genetic control of microbiota is a complex trait, i.e. many loci contribute to the abundance of different root-associated bacteria. We find a particular enrichment of significantly associated SNPs near genes involved with cell wall composition and defense response. We next used high-throughput bacterial culturing to isolate bacterial members of the switchgrass root microbiome and test for their effects on root growth when in mono-association. We find that some isolated members of the microbiome with significant associations to host genotype have large effects on root growth dynamics. Together, these efforts contribute important information to the host-microbe interaction field as well as provide interesting avenues for increased sustainability through manipulation of host genetics and microbial amendments.

## References:

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