

Soil- and Root-associated Microbiomes Across Twelve Switchgrass Cultivars

Tayler Chicoine (chicoi1@msu.edu),^{1,2*} Sarah S. Roley^{3,4}, G. Philip Robertson^{1,4,5}, Sarah Evans^{1,2}

¹W.K. Kellogg Biological Station, Michigan State University (MSU), Hickory Corners, MI

²Department of Integrative Biology, MSU, East Lansing, MI

³School of the Environment, Washington State University, Richland, WA

⁴Great Lakes Bioenergy Research Center MSU, East Lansing, MI

⁵Department of Plant, Soil and Microbial Sciences, MSU, East Lansing, MI

*corresponding author

Project Goals: Short statement of goals. (Limit to 1000 characters)

Switchgrass (*Panicum virgatum*), a C₄ perennial grass, is known to associate with beneficial microbial communities that may enhance its potential as a low-input bioenergy crop. Genetically distinct cultivars adapted to southern and northern regions of the United States differ in their tolerance to marginal, low-input production systems, but the extent to which microbial communities influence this variation is unknown. We hypothesized that different microbial communities, and specifically more abundant free-living Nitrogen(N)-fixers bolster the ability of some cultivars to tolerate N-limited soils.^{1,2} Further, we hypothesized that cultivars' specific root length (total root length/total dry weight), previously shown to correlate with switchgrass root-derived carbon, may contribute to differences in the cultivars' microbial communities.^{3,4} Here, we measured N-fixing potential, root traits, and fungal and bacterial communities (16S, ITS, *nifH* abundance) in soils and roots of 12 switchgrass cultivars (including upland and lowland ecotypes) at the Great Lakes Bioenergy Research Center at Kellogg Biological Station in southwest Michigan. Preliminary findings suggest that bacterial and fungal community compositions do not differ among the cultivars or by ecotype. We will also present results on the relationships between N-fixation potential, N-fixer abundance, and root morphology among the cultivars. This study will inform our understanding of how plant-microbial interactions can support sustainable switchgrass bioenergy production.

References:

1. Bahulikar, R. A., Torres-Jerez, I., Worley, E., Craven, K., & Udvardi, M. K. (2014). Diversity of nitrogen-fixing bacteria associated with switchgrass in the native tallgrass prairie of Northern Oklahoma. *Applied and Environmental Microbiology*, 80(18), 5636–5643. <https://doi.org/10.1128/AEM.02091-14>
2. Rodrigues, R. R., Moon, J., Zhao, B., Williams, M. A., Biology, C., Tech, V., & Tech, V. (2016). Microbial Communities and Diazotrophic Activity Differ in the Root-Zone of Alamo and Dacotah Switchgrass Feedstocks. <https://doi.org/10.1111/gcbb.12396>

3. Graaff, M. A. de, Six, J., Jastrow, J. D., Schadt, C. W., & Wullschleger, S. D. (2013). Variation in root architecture among switchgrass cultivars impacts root decomposition rates. *Soil Biology and Biochemistry*, 58(MARCH), 198–206. <https://doi.org/10.1016/j.soilbio.2012.11.015>
4. Adkins, J., Jastrow, J. D., Morris, G. P., Six, J., & de Graaff, M. A. (2016). Effects of switchgrass cultivars and intraspecific differences in root structure on soil carbon inputs and accumulation. *Geoderma*, 262, 147–154. <https://doi.org/10.1016/j.geoderma.2015.08.019>

Support for this research is provided by the Great Lakes Bioenergy Research Center (US DOE Office of Science: DE-FCO2-07ER64494 and Office of Energy Efficiency and Renewable Energy: E-ACO5-76RL01830) and Department of Energy BER Genomics Program grant (DE-SC0014108).