Soil- and Root-associated Microbiomes Across Twelve Switchgrass Cultivars

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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:


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