

Microbial successions in switchgrass roots

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Project Goals: Short statement of goals.

Our project aimed at establishing a high-throughput pipeline for characterizing diversity and community composition of the switchgrass microbiome. The pipeline we aimed to establish includes the optimization of 1) sampling techniques of various plant tissue types, 2) sample processing protocols as well as 3) the streamlined analysis of large 16S rRNA and ITS amplicon sequence datasets. The results of this project contribute essential information for the exploration of plant-microbe-soil interactions across continental scale environmental gradients.

Part of the DOE's strategy to ensure American energy independence is to produce biofuels from dedicated biomass crops. Achieving DOE's ambitious goal of displacing 30% of 2004 gasoline demand with biofuels by 2030 will require major increases in plant productivity. In an effort to providing sustainable solutions for enhanced plant growth in marginal lands, plant microbiomes play a vital role. Especially root colonizing bacteria have a large impact on plant traits, including biomass yield and overall plant health, which has been demonstrated for a number of plants. Switchgrass (*Panicum virgatum*) has been championed as a promising bioenergy species, however, few switchgrass microbiome studies have been conducted to date. We here present 3 complementary studies, in which 16S rRNA gene and ITS amplicon surveys were used to obtain insights into root microbial community dynamics across 3 different field sites and over 3 years. We show that plant genotype/ecotype, site and seasonal changes impact microbiomes differentially across different plant compartments¹. Root endosphere showed most sensitivity towards plant genetic variance. Seasonality affected rhizosphere microbial communities more than site and showed a transition of dominant bacterial classes from *Gammaproteobacteria* and *Actinobacteria* in the spring to *Alphaproteobacteria* in phyllosphere and rhizosphere in the fall. We identified re-occurring microbial players *Streptomyces* and *Sphingobium* conserved across rhizosphere and root endosphere from various switchgrass genotypes and even across various *Panicum* species. These results of these studies have allowed unprecedented insight into switchgrass microbiomes and will direct future field microbiome studies QTL mapping and GWAS populations.

References

1. Singer, E., Bonnette, J., Kenaley, S., Woyke, T. & Juenger, T. E. Plant compartment and genetic variation drive microbiome composition in switchgrass roots. *Environmental Microbiology Reports* doi:10.1111/1758-2229.12727

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