Sorghum root microbiome dynamics under nutrient-limited and drought conditions

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Project Goals:

We aim to establish a foundational, systems-level understanding of plant, microbial, and environmental interactions that will lead to translational strategies to enhance growth and sustainability of sorghum through improved genetic and microbial adaptations to water and nutrient limited environments. In working towards this goal, we are conducting deep census surveys of root microbiomes concurrent with phenotypic characterizations of a diverse panel of sorghum genotypes across multiple years to define the microbes associated with the most productive lines under drought and low nitrogen conditions.

Abstract:

Sorghum bicolor is a genetically diverse crop cultivated for a variety of agronomic uses, including grain, sugar, and energy production. However, cultivation of energy sorghum for biofuel production will require the use of marginal lands with potentially low nutrient availability and/or periods of water stress. All plants growing in soil harbor diverse communities of microbes that inhabit the areas in, on, and around their roots. Selected members of these microbial communities can provide benefits to their plant hosts, including direct growth promotion and conferring tolerances to abiotic and biotic stress. To examine the effects of nutrient and water stress on soil and root microbial communities and explore a possible microbial solution to increase the nutrient use efficiency and resilience to water stress in sorghum, we are utilizing 16S rRNA sequencing to survey the bacterial communities in replicate soil, rhizosphere, and root samples collected from ~30 different sorghum genotypes grown under different nitrogen (N; high/low) and water (watered/drought) treatments over multiple growing seasons at two sites in Nebraska.

In a small-scale pilot experiment in 2015, we collected ~200 soil, rhizosphere, and root samples from 10 different sorghum genotypes grown under high or low N conditions. We observed that early rhizosphere samples exhibit a significant reduction in overall diversity attributable to a dramatic increase in the bacterial genus *Pseudomonas* which occurred independent of host genotype in both high and low N fields, and was not observed in the surrounding soil or associated root endosphere samples. Nearly all the *Pseudomonas* reads in this dataset were assigned to a single OTU at 97% identity; however, ASV-level resolution demonstrated that this OTU comprises a large number of distinct *Pseudomonas* lineages. Furthermore, single-molecule long read

sequencing enabled high-resolution taxonomic profiling of the *Pseudomonas* lineages within the dataset. In additional field experiments in 2016 and 2017, we sampled three selected genotypes at four time points throughout the growing season to monitor changes in the bacterial communities over time and again observed decreases in Shannon diversity in rhizosphere samples early in the growth season concomitant with a marked increase in the relative abundance of *Pseudomonas*. Our ongoing work focuses on characterizing the genomic and metabolic features of these Pseudomonas populations and integrating our findings with the metabolomic and phenotypic data generated with project collaborators.

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