

## **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 bacteria 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. Diversity analyses of rhizosphere samples collected early in the growing season show a significantly lower Shannon diversity compared to those collected later in the season. Investigation of taxonomic profiles from the early season rhizosphere samples reveal a dominance of bacteria from the genus *Pseudomonas*. In a second, larger scale field experiment in 2016, we sequenced ~ 4100 samples from all genotypes cultivated under the different N and water treatments. Additionally, we sampled three selected genotypes at four time points throughout the growing season to monitor changes in the

bacteria communities over time. Results from the analysis of the large genotype panel suggest a strong effect of sorghum genotype on bacterial community diversity in rhizosphere and root samples. We also observe a decrease in Shannon diversity in rhizosphere samples at one early time point, which again appears to be driven by a marked increase in the relative abundance of *Pseudomonas*. Most recently, we completed the sequencing of ~3200 samples collected from the 2017 field season. Consistent with the results from 2015 and 2016, initial analyses reveal a marked increase in the relative abundance of *Pseudomonas* bacteria in rhizosphere samples early in the growing season. Additionally, ordination analyses suggest water stress may drive differences in bacteria community composition in rhizosphere and root samples. Our ongoing work focuses on statistical confirmation of our current observations, quantification of experimental treatment effects, and integrating our findings with the metabolomic and phenotypic data being generated with project collaborators.

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