# Systems Analysis of the Physiological and Molecular Mechanisms of Sorghum Nitrogen Use Efficiency, Water Use Efficiency and Interactions with the Soil Microbiome

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**Project Goals:**

**The *overall project goal*** is to establish a foundational, systems-level understanding of plant, microbial, and environmental interactions that will lead to strategies for enhancing growth and sustainability of sorghum through genetic and microbial adaptations to water and nitrogen limited environments.

**The *specific goals* are:**
1. Conduct deep surveys of root microbiomes concurrent with phenotypic characterizations of a diverse panel of sorghum genotypes to define the associated microbes and the most productive lines under drought and low nitrogen conditions.
2. Associate systems-level genotypic, microbial, and environmental effects with improved sorghum performance using robust statistical approaches.
3. Develop culture collections of sorghum root/leaf associated microbes.
4. Test hypotheses regarding Gsorghum x Gmicrobe x E interactions in controlled environments.
5. Validate physiological mechanisms, map genetic loci for stress tolerance, and determine the persistence of optimal microbial strains under greenhouse and field conditions.

To compete in the biofuel energy market, cellulosic feedstocks will need to be high yielding and carbon neutral or negative while requiring low inputs. To avoid competition with existing food production systems, these crops will also need to be grown on marginal lands. This will require the introduction of novel traits to increase abiotic stress tolerance associated with marginal soils. This project is using multiple interdisciplinary approaches in varied settings – including the laboratory, controlled environments, and the field – to identify plant genes and sorghum associated microbes that will enhance the sustainable production of sorghum as a biofuel feedstock.

In 2016 the team conducted large field experiments and two large controlled environment studies on 30 sorghum varieties with several aims including: finding the most water and nitrogen use efficient germplasm, studying how the genotype of sorghum alters the microbiome, how low nitrogen and water deficit alters the microbiome, how transcript and metabolite profiles are influenced by abiotic stress and genotype. The field data has been processed and will be presented. DNA from roots, rhizosphere and soil has been extracted and

is currently be analyzed at JGI using iTAGS.  Root and leaf material have been sent to the Danforth Center and Colorado State University for transcript and metabolite profiling.  This poster will contain a description of the field trials, the biomass and height data as well as stable isotope data and plant nitrogen content.