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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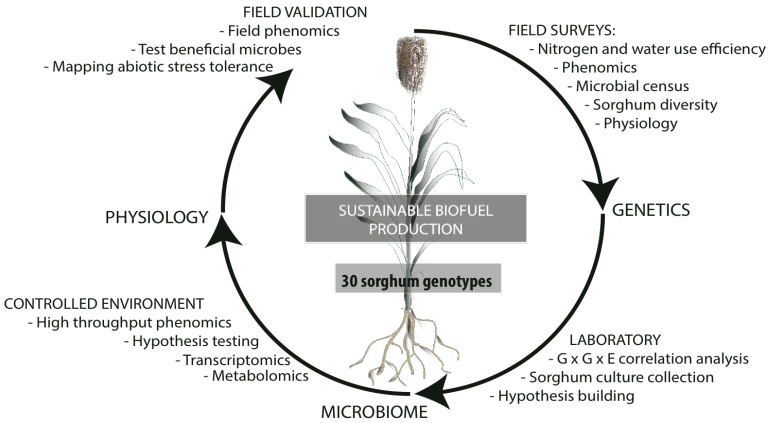
Project Goals:

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 will utilize 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. Basic knowledge about physiological and genetic mechanisms involved in nitrogen use efficiency (NUE) and water use efficiency (WUE) and potential mechanisms involved in microbe interactions will be generated. A range of methods will be used, including: classical whole plant physiology, stable isotope detection,



System-wide knowledge and tools to breed sorghum and identify microbes to enhance biomass, NUE and WUE

phenomics, transcript profiling, metabolic profiling, 16S amplicon sequencing, metagenomics, microbial genome sequencing, comparative genomics, microbiology, genetics, and a range of computational methods for data analysis, integration and storage. To conduct these comprehensive studies, we have assembled a multi-institutional, interdisciplinary team with a wide range of expertise in these areas.

This research will increase our knowledge about the genetic and physiological mechanisms involved in WUE and NUE, which will be used to create sustainable biofuel feedstock systems on marginal land. Identification of microbial community membership and testing of culturable microbes, as well as genetic dissection of sorghum genotype X microbe interactions, will result in new strategies for the development of microbial solutions to increase abiotic stress tolerance and sustainable sorghum systems. We will create a sorghum microbe collection which may be the first available for an agricultural crop and a multi-dimensional relational database to house and access the biological materials and data generated in this project.

The project began in October when funding was finalized. Preliminary results will be shared in the poster.

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