

Defining the Functional Genome Associated with Enhanced Water and Nitrogen Use Efficiency in Bioenergy Sorghum

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Project Goals:

- **Overall project objective: 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.**
- **Perform controlled environment, high-throughput phenotyping at multiple scales to investigate responses of diverse sorghum lines to low water and low nitrogen.**
- **Generate RNA-seq-based transcript profiles and genome-wide accessible chromatin maps for developing leaf and root tissues across genotypes in response to water and N stresses.**
- **Integrate transcriptional, epigenomic, and physiological signatures with existing genetics and genomics resources to prioritize genetic loci for functional validation.**

The overall goal of this work is to establish a functional genomics resource that can be leveraged for investigating effects of low water and nutrient inputs on growth and development of three diverse sorghum accessions; BTx623 (reference line, NAM parent, EMS population), Grassl (bioenergy, NAM parent, EMS population) and PI_510757 (high NUE, WUE and large biomass, NAM parent). These lines are representatives of three diverse races of sorghum (Kafir, Caudatum and Durra, respectively) and thus will serve as founders for deeper explorations of the genetic diversity present in sorghum. Here, we investigate morphological, physiological, and molecular responses of sorghum diversity to low water and low nitrogen (N) using controlled environment phenotyping. Transcriptome profiles analyzed across emerging leaf and root samples were aligned with respective chromatin accessibility generated using ATAC-seq. Together with the exhaustive imaging data collected, these genomics data are being integrated to identify physiological, transcriptional, and/or epigenetic signatures associated with enhanced water and N use efficiency. An integrated resource that utilizes the same founder lines (i.e. three diverse sorghum lines), tissues and developmental time series will **i**) improve resolution of our gene regulatory networks, **ii**) provide a foundation for a sorghum pan-genome ENCODE-like project to identify regulatory regions across sorghum races and **iii**) identify targets for engineering enhanced biomass, NUE and drought tolerance.