

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

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Project Goals:

- **Establish controlled environment conditions for repeatable testing of low water and low nitrogen regimes on diverse sorghum accessions.**
- **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 nitrogen stresses.**
- **Integrate transcriptional and epigenomic signatures with existing genetics and genomics resources to prioritize genetic loci for functional validation.**

The overall goal of this work is to establish a baseline functional genomics resource that can be leveraged for investigating effects of low water and nitrogen 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. A series of chamber-based, controlled environment experiments are being carried out to interrogate gene regulation in these three genotypes at various stages of development; from seedling establishment to the floral transition.

Transcriptome profiles analyzed across emerging leaf and root samples were aligned with respective chromatin accessibility maps for these tissues generated using ATAC-seq. These datasets will be integrated to identify transcriptional signatures that are associated with enhanced growth under low water and N conditions. 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.