

Using Molecular Genetics and Precision Phenotyping to Map Gene Function Contributing to Drought Resilience in Sorghum

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Project Goals:

- **Overall project objective: To define and functionally characterize genes and pathways related to drought stress tolerance in sorghum and the molecular mechanisms by which these factors drive phenotypic diversity.**
- **Establish a foundation for deep explorations of gene regulatory networks in sorghum through integrative genomics analyses.**
- **Enhance understanding of how genotype drives phenotype and environmental adaptation using high-resolution, field-based phenotyping of sorghum mutant collections.**
- **Map and characterize genes contributing to drought responsive phenotypes in sorghum.**
- **Experimentally validate predictions of gene function using molecular and genetic assays and targeted gene editing.**

Development of the next generation of bioenergy feedstocks will require strategies that utilize resource-limited agricultural lands, including the introduction of novel traits into crops to increase abiotic stress tolerance. This project investigates the innate drought resilience of sorghum (*Sorghum bicolor*), a bioenergy feedstock and cereal crop. Drought is a complex trait and identifying the genes underlying sorghum's innate drought tolerance and how they are regulated in the broader context of the whole plant and its environment requires advanced approaches in genetics, genomics, and phenotyping.

This project leverages a sequence-indexed population of EMS mutagenized sorghum and a field-based phenotyping infrastructure at Maricopa, AZ, which provides an exceptional capability for managed stress trials in a hot and arid environment through controlled irrigation. An automated field scanner system collects high-resolution phenotyping data using a variety of sensors throughout the growing season, from seedling establishment to harvest. 430 EMS families in the tx623 background were phenotyped under the field scanner to compare drought-stressed and well-watered plants. Each mutant's genome has been sequenced so that sequence variants can be linked with phenotypes. Being able to assess the genotype-to-phenotype link in response to drought over the life cycle of the plant will facilitate discovery of genes and their functions. To accelerate mapping of causal loci that underlie mutants of interest, we use bulked segregant analysis-seq. So far, we've identified candidate genes underlying defects in leaf senescence, plant architecture and male fertility. Regulatory maps generated from diverse sorghum lines in response to stress are being used to nominate gene candidates and place them in the larger context of a drought response network. This work will identify control points for enhancing the

productivity of bioenergy crops in marginal environments through precision breeding or engineering, and thus accelerate the development of improved varieties that are high-yielding with limited water resources.

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