Elucidating the Molecular Mechanisms Underlying 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.**
- **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 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. Last summer, a sorghum mutant population was 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. State-of-the-art phenotyping data analytics pipelines have been developed as part of this project and DOE-funded initiatives (*see poster by Cosi et al.*) and will be extended to define stress-related phenotypes at multiple scales. Advanced genomics methods are being used to construct network maps that will provide a framework for predicting and investigating gene functions and interrogating differences in the gene regulatory architectures of diverse sorghum genotypes. For example, natural variation in a prioritized candidate gene from a drought-responsive gene regulatory network showed associations with whole-plant water use efficiency in controlled environment (Parvathaneni et al., 2021) and field conditions.

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.

Publications

Parvathaneni RK, Kumar I, Braud M, Ozersky P, Mockler TC, Eveland AL (2021) Regulatory signatures of drought response in stress resilient *Sorghum bicolor*. *bioRxiv*. **doi:** https://doi.org/10.1101/2020.08.07.240580

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