

**Title:** Leveraging multi-omics data and pan-genomic sequence variation in *Setaria viridis* and *Sorghum bicolor* for candidate gene discovery and nomination for crop improvement.

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**Project Goals:** This project aims to leverage *Setaria viridis* as a model system to develop novel technologies and methodologies to redesign the bioenergy feedstock *Sorghum bicolor* to enhance water use and photosynthetic efficiencies. Through the advancement of candidate gene discovery platforms and leveraging multi-omics datasets including analyses of pan-genomic sequence variation, we are identifying candidate genes for crop improvement efforts. These candidate genes are implicated in key traits of interest including water use and photosynthetic efficiencies and responses to drought stress.

**Abstract Text:** Bioenergy crop yields are likely to be limited by the availability of water during the growing season. Historically, efforts to improve water and photosynthetic use efficiencies and resilience to abiotic stresses such as drought have been limited by the challenge of efficiently identifying and harnessing genes that underly these traits. We have established a suite of genomic and transcriptomic datasets, tools, and approaches that enable elucidation of new insights into pathways and genes involved in water use and photosynthetic efficiencies and responses to drought stress. Integration of these datasets, tools, and approaches provides insights into associations between genotype, phenotype and environment that inform our efforts to improve bioenergy sorghum through breeding and engineering. We have leveraged whole-genome re-sequencing datasets, *de novo* reference grade genome assemblies, multi-omics profiling (e.g., transcriptomic, metabolomic, elemental, and isotopic ratios), pan-genomic sequence variation analyses, GWAS, and multi-model phenotyping datasets. We have combined these datasets and approaches to understand the genetic architecture of how plants respond to water deficit and to reveal and nominate new sets of candidate genes and loci as targets for engineering enhanced water use efficiency and drought response in C4 bioenergy crops.

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