

## **Metabolome and transcriptome responses to a water deficit time course in the model C4 grass *Setaria Viridis***

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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.

As a first step in understanding the conserved gene networks underlying the metabolic response to drought in biofuel relevant C4 grass species, we used untargeted metabolomics and transcriptomics to profile *Setaria viridis* at multiple time points during drought stress. We quantified the levels of 7,486 metabolites using hydrophilic interaction chromatography (HILIC) and another 6,157 metabolites using reversed phase liquid chromatography (RPLC), along with 35,065 transcripts using 3' end labeled RNA seq. This will allow us to identify key pathways impacted by drought, and describes how their behavior shifts across time. We selected drought responsive metabolites and used principal component analysis (PCA) as well as partial least squares discriminant analysis (PLS-DA) to detect a peak in the drought response at day 6 across the metabolome and transcriptome. We are in the process of conducting the same analysis in *Sorghum bicolor*. Using *Setaria viridis* and *Sorghum bicolor* diversity panels we will conduct a dual species metabolomic GWAS of drought stress to explore the role of conserved genes regions in regulating the response to water deficit in both species.

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