

Mathematical modeling strategies to study the impact of drought on plant growth and metabolism in *Setaria* and sorghum.

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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.

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Mathematical modeling is useful to determine how components function in a system to produce different phenotypes. We apply two different modeling strategies at two scales of plant growth in *Setaria* and sorghum. In the first modeling strategy, we abstract the process of the above ground *Setaria* plant tissue growth to develop a top-down trait based dynamical model. This model describes events that occur within the growth and development of above-ground tissue. The model is applied to a diversity panel of over 250 *Setaria* lines in drought and well-watered conditions. The parameters in our model are intended to describe growth and developmental decisions of the plant. The heritability of the parameter estimates were calculated for both wet and dry conditions. Heritable parameters will be used to identify loci that control processes critical to drought response.

In the second modeling strategy, we present a computational framework of multiscale metabolic modeling to investigate how plants allocate metabolic resources for biomass production in response to drought. The framework is centered on a cell type-specific genome-scale metabolic network model of *Sorghum bicolor*, generated from a generic sorghum model constrained by cell type-specific RNA-seq data. A C4 photosynthesis biochemical model was then integrated with the cell type-specific model to simulate dynamic environments by controlling carbon and energy sources of the metabolic network model. We collected a variety of physiological and omics data to inform the multiscale model, such as photosynthetic rates, metabolomic data, and RNA-seq data for sorghum under well-watered and drought conditions at multiple time points. Using the computational framework, we predicted that high light could alleviate biomass production induced by drought stress, which was validated by experimental testing. Moreover, a list of candidate genes were identified as potential targets to engineer for a higher biomass production. The trait based dynamical method provides a novel way to identify plant phenotypic traits for identifying new genes that control dynamic processes. This novel framework will be used in the future to understand if phenotypic variability may be emergent

from the interaction between environmental space searching strategies, biomass allocation strategies, and genotype. The multiscale metabolic model provides a novel platform for the analysis of inter-cellular metabolism with a dynamic constraint of carbon and energy exchange.

Funding Statement: *This research was supported by the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomic Science Program grant noDE-SC0018277.*