Utilizing *Setaria viridis* as a Model for Molecular Characterization of Jasmonate-Mediated Growth and Defense Responses

Christine Shyu*, Kimberly Maxson-Stein, Indrajit Kumar, Dustin Mayfield-Jones and **Thomas P. Brutnell**
Donald Danforth Plant Science Center, St. Louis, MO 63132

*Presenter. Contact e-mail: CShyu@danforthcenter.org

Project Goals: This project aims to utilize molecular, genetic, and genomic resources in *Setaria viridis* to dissect the jasmonate signaling network in panicoid grasses. Outcomes from this research provide opportunities to engineer bioenergy feedstocks for improved stress resistance without compromising growth.

The plant hormone jasmonate (JA) and its derivatives control many important agricultural traits from growth and development to defense against biotic and abiotic stresses. Though JA signaling components have been studied in the dicot model Arabidopsis, mechanisms underlying JA-mediated growth and defense in grasses have not been elucidated. *Setaria viridis* is a model panicoid grass with a rapid life cycle, short plant stature and rapidly developing genetic and molecular toolsets. It is closely related to bioenergy feedstocks such as sorghum, switchgrass, and Miscanthus, making it an ideal model for gene discovery and molecular studies. The core JA signaling pathway consists of JASMONATE ZIM-DOMAIN (JAZ) repressors that interact with COI in the presence of bioactive JA. Upon COI-JAZ interaction, JAZs are ubiquitinated and targeted for degradation, resulting in activation of downstream transcription factors (TFs) that regulate JA-responsive gene expression. In this study, *Setaria viridis* COI-JAZ interactions were examined and unique interaction partners were identified. Cas9-mediated genome editing of *SvCOI*s with different JAZ-interaction patterns were generated and preliminary phenotypes were observed. To identify downstream TF interaction partners of JAZ proteins, a wound treatment was applied to the *S. viridis* leaf and transcriptional responses measured over a developmental gradient. One hundred and eight RNA-seq libraries were generated from control and wounded leaf segments across time. Clustering analysis of the RNA-seq data coupled with co-expression analyses led to identification of novel basic helix-loop-helix TFs that are candidates for regulating JA signaling outputs. Outcomes from this research provide insight into the dynamics and complex regulation of JA responses in grass systems, and provide opportunities to engineer bioenergy crops for enhanced stress resistance without compromising growth.