28. Sequence-Enabled Gene Discovery in Setaria viridis: A Model Panicoid Grass

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http://sviridis.org/
http://foxmillet.org/

Project Goals: "A Systems-Level Analysis of Drought and Density Response in the Model C4 Grass Setaria viridis". The specific aims of the proposal are to: 1) Identify QTL for the effect of drought and density on biomass and seed yield components of Setaria. 2) Conduct in–depth physiological profiles in roots and leaves of a subset of selected lines 3) Integrate datasets and develop metabolic and gene networks for Setaria 4) Develop transformation technologies for Setaria viridis 5) Functionally examine the role of candidate genes deduced by network models; and 6) Develop protocols and best practices for monitoring gene flow in transgenic Setaria. To achieve these aims we will produce one of the most extensive molecular characterizations of plant growth in the field to date, generating several million data points that will be collected from physiological and molecular genetic studies. We will develop novel informatics models and network tools that will guide future molecular characterization in S. viridis and guide breeding efforts in major feedstock targets.

To accelerate the adoption of Setaria viridis (S. viridis) as a model system, genetic resources and tools are being developed that exploit high throughput sequencing technologies. To create mutant populations for forward and reverse genetics, we have conducted an NMU-mutagenesis and, to date, have generated and characterized approximately 3000 NMU mutant families, from which a TILLING population is being developed. A total of 55 mutant individuals are being sequenced to ~30 x coverage by JGI-DOE to empirically determine mutation frequency. Initial characterizations of the families' shows the majority are transition mutations and the median number of non- synonymous disruptive mutations was 48 per individual. A panicle mutant has been crossed with S. viridis accessions to fine map the gene using Bulk Segregant Analysis (BSA) followed by deep sequencing. We have also initiated the construction of six recombinant inbred populations generated by crossing diverse S. viridis accessions with A10.1. We have assembled a diverse germplasm collection of 430 S. viridis accessions with contributions from many collaborators. A subset of accessions are being sequenced at JGI-DOE to establish a panel for population genetic analysis and genome wide association studies (GWAS). We demonstrate that phenotypes of interest can be mapped to fine resolution with a thorough characterization of the standing phenotypic variation in a subset of this panel. To date, 60 lines has been characterized for phenotypic traits and have been propagated for seed distribution at the USDA GRIN (http://www.ars-grin.gov/cgi-bin/npgs/html/taxon.pl?430573).