

Data access, mining and visualization. Tools to accommodate an interdisciplinary project.

Philip Ozersky<sup>1\*</sup> ([pozersky@danforthcenter.org](mailto:pozersky@danforthcenter.org)), Jeff Berry<sup>1</sup>, Scott Lee<sup>1</sup>, Todd Mockler<sup>1</sup>, and Daniel Schachtman<sup>2</sup>

<sup>1</sup>Danforth Plant Science Center, St. Louis, MO; <sup>2</sup>University of Nebraska, Lincoln;

**Website for the project:** [www.sorghumsysbio.org](http://www.sorghumsysbio.org)

### **Overall Project Goals:**

- Establish a foundational, systems-level understanding of plant, microbial, and environmental interactions that will lead to translational strategies to enhance growth and sustainability of sorghum through improved genetic and microbial adaptations to water and nutrient-limited environments.

### **Project Objectives:**

- Conduct deep census surveys of root microbiomes concurrent with phenotypic characterizations of a diverse panel of sorghum genotypes across multiple years to define the microbes associated with the most productive lines under drought and low nitrogen conditions.
- Associate systems-level genotypic, microbial, and environmental effects with improved sorghum performance using robust statistical approaches.
- Develop culture collections of sorghum root/leaf associated microbes that recapitulate root-enriched sequences defined in the census.
- Perform controlled environment experiments for in-depth characterization and hypothesis testing of  $G_{\text{sorghum}} \times G_{\text{microbe}} \times E$  interactions.
- Validate physiological mechanisms, map genetic loci for stress tolerance, and determine the persistence of optimal microbial strains under greenhouse and field conditions.

Our project generates a wide variety of data from field crop measurements to indoor phenotyping systems and analytics of *Sorghum bicolor* samplings such as metabolites and stable isotopes. Additionally, sequences were produced for transcriptomic and metagenomic data. These datasets are disseminated through our project website and interface allowing all members of the project access to foster coordinated efforts and data sharing. Integration of tools like JBrowse and project produced Shiny apps allow project members to visualize, mine and parse project data. We are also leveraging pipelines to utilize *Sorghum bicolor* pan-genome data to help identify the most productive lines under drought and low nitrogen conditions. The poster will display our project website, database structure, interface utility, tools, and pipeline.

*This project is funded by the DOE BER Sustainable Bioenergy Research Program, Award DE-SC0014395, and was also supported by DOE JGI Community Science Program.*