

The Metabolome of Early Season Sorghum Plant Tissue is Predictive of End of Season Biomass

Sheflin, Amy¹; Prenni, Jessica E.^{1*} (jprenni@colostate.edu); Kresovich, Stephen²; Dweikat, Ismail³; Marsh, Ellen³; and **Schachtman, Daniel**³

¹Colorado State University, Fort Collins, CO; ²Clemson University, Clemson, SC; ³University of Nebraska – Lincoln, Lincoln, NE

<https://sorghumsysbio.org/>

Project Goals:

The overall goal of this project is to 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. Specific objectives that apply to this poster include: (1) Phenotypic characterizations of a diverse panel of sorghum genotypes across multiple years to define the most productive lines under drought and low nitrogen conditions. (2) Associate systems-level metabolomic and environmental effects with improved sorghum performance using robust statistical approaches.

Abstract:

To compete in the biofuel energy market, cellulosic feedstocks will need to be high yielding and carbon neutral or negative while requiring low inputs. To avoid competition with existing food production systems, these crops will also need to be grown on marginal lands. This will require the introduction of novel traits to increase abiotic stresses tolerance associated with marginal soils. Thus, efforts to maximize biomass production requires an understanding of both the genetic and environmental influences on plant growth. Metabolomics is an analytical approach that enables comprehensive profiling of plant metabolism at a given point in time, providing valuable information about how genetic diversity combines with the environment to affect phenotypic variation in plants. While often removed from the visible phenotype, metabolomics allows for a more functional interpretation of plant response to the environment at the molecular level, facilitating investigation of variation within the species, how metabolism affects the phenotype and discovery of new metabolic pathways that influence yield traits. This information is particularly useful when interpreting complex phenotypes such as adaptations to nutrient stress and can be used to select for phenotypes with the metabolic adaptations that maximize yield in marginal environments.

Importantly, the chemical variation in plant tissue can be associated with yield and other traits to create a *chemical profile predictive of phenotypic outcomes*. Furthermore, in the context of breeding efforts, metabolomics can provide valuable data about the adjustment of metabolism in hybrids in comparison to inbreds and has been suggested to contain mechanistic insights about how hybrids boost performance. While predictive modeling for yield phenotypes based on genomic resources has proven highly successful in multiple species, the models are less effective when environmental stresses are a factor. Metabolomics can capture the plant phenotype resulting from the genotype-environment interaction and has emerged as an effective molecular platform for predicting agronomic traits in multiple crops species.

Here, we present the generation of highly accurate predictive models for end of season biomass in field grown sorghum based on metabolite profiles of early season (29 days after planting) root and leaf tissue. Predictive models trained with data from plants grown under abiotic stress (nitrogen deprivation or drought) were more accurate for predicting biomass in plants grown under stress than models trained with data from controls. This result demonstrates the advantage of metabolomics to capture the unique phenotypes resulting from the environmental interaction. Furthermore, depending on the type of abiotic stress, the metabolome data from different tissues (e.g. roots or leaves) was most effective for training the predictive model of the given environment. For example, for plants grown under nitrogen stress, the most accurate models were trained on metabolite data from leaf tissue acquired using a gas chromatography mass spectrometry platform (GC-MS). Evaluation of the metabolites driving this model revealed biologically relevant molecules such as asparagine, aspartic acid, fructose, and maltose. Importantly, these compounds are not readily detectable by reverse phase liquid chromatography (LC-MS) approaches, highlighting the additional key consideration of analytical platform(s) in generating the most appropriate metabolome data for each stress condition. Finally, we also present the potential of the predictive models across fields (controls only). Ultimately, the results presented here demonstrate the effectiveness of metabolite profiles trained on young plants to accurately predict end of season sorghum biomass. In the future, larger scale studies could employ multiple genotypes and inbreds to evaluate the predictive capacity of the metabolome for biomass yield under environmental stress enabling enhanced and accelerated breeding for maximal biomass accumulation in low nutrient environments.

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