

Time-series analysis of phenotypic and transcriptomic responses to nutrient stress in two bioenergy crops

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Project Goals: The Quantitative Plant Science Initiative (QPSI) is a capability that aims to bridge the knowledge gap between genes and their functions. A central aspect of our strategy is combining genome-wide experimentation and comparative genomics with molecular-level experimentation. In this way, we leverage the scalability of ‘omics data and bioinformatic approaches to capture system-level information, while generating sequence-specific understanding of gene and protein function. By incorporating molecular-level experimentation in our workflow, we are addressing the question of how a protein functions and establishing mechanistic insight into how sequence variation impacts phenotype. This knowledge serves as a touchstone for accurate genome-based computational propagation across sequenced genomes and forms the foundation for robust predictive modeling of plant productivity in diverse environments.

Abstract

Iron (Fe) and zinc (Zn) are indispensable cofactors for critical aspects of plant growth including numerous metabolic pathways, post-translational modifications, cell-wall biosynthesis, and carbon/nitrogen assimilation. Regulation of function makes a significant contribution to the phenotypic variation observed among different plant species and genotypes. Identification of co-expressed gene modules can provide functional inferences for proteins contained within a defined module, while conserved function of a protein between two or more species can be supported by conserved regulation. We developed hydroponic growth chambers at Brookhaven National Laboratory for time course Fe and Zn deficiency and excess experiments using the *Populus trichocarpa* Nisqually-1 and *Sorghum bicolor* cv. BTx623 genotypes. In both species, we found root and leaf level accumulation of Fe or Zn reflected the excess or deficiency treatments compared with controls. We also used fluorometer and reflectance spectroscopy to estimate leaf responses to Fe or Zn deficiency and found chlorophyll, photosynthesis, and nitrogen estimates were significantly affected by Fe and Zn stress. Time-series analysis of transcriptional responses (using RNA-seq) induced by Fe and Zn stress allowed us to examine both short-term and long-term differential gene expression over a three-week period (7 time points). We are conducting co-expression analysis to characterize the temporal dynamics of gene regulatory networks (GRN's) and we will quantify the extent to which the GRN's are conserved between these two physiologically divergent bioenergy crop species. These large-scale transcriptome datasets will provide a valuable resource for functional genomics studies to identify the roles of proteins involved in resilience to marginal soils and increased biomass production.

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