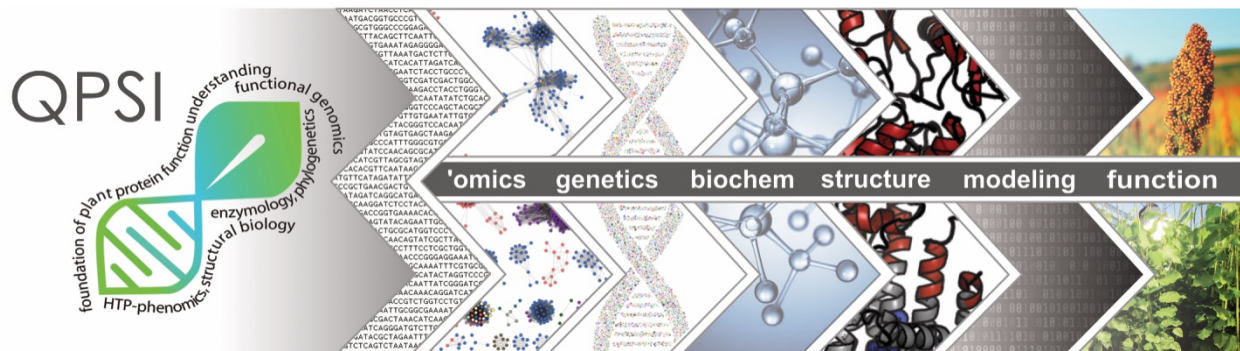


Understanding poplar and sorghum micronutrient stress by integrating functional genomics with molecular-level experimentation

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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.



Trace metal nutrients are of growing importance in maximizing bioenergy/bioproduction crop yield in marginal soil. Bioavailability in the soil is dynamic and variable, and yield-impacting deficiency can suddenly appear. Because these elements are essential for the proper assimilation and metabolism of macronutrients such as nitrogen, poor macronutrient availability can be exacerbated by metal deficiency. To support the development of bioenergy crops with improved micronutrient stress resilience, our goal is to develop a genome-based, molecular-level and system-level understanding for the two most abundant trace metal nutrients in plants: zinc and iron. Focusing on the bioenergy crops poplar and sorghum, we have completed a large-scale, hydroponics-based, transcriptomics timecourse to understand how these plants respond to and acclimate to different concentrations of metals in their environment. This data will be used to

construct gene-regulatory networks and a computational simulation of cofactor availability in the chloroplast, the major metal sink and site of carbon fixation and energy generation. We are also employing an interdisciplinary approach to provide a layer of experimentally grounded sequence-specific understanding of molecular-level functions for major players involved in metal homeostasis. Comparative genomics provides an in-silico platform to generate protein function hypotheses. Hypotheses are tested with reverse genetics in model organisms and biochemical assays of protein family members. Structure-function studies supply mechanistic insight into how sequence space translates into molecular function. These studies will improve our model of micronutrient dynamics in bioenergy crops and provide a sequence-based foundation for establishing how metal scarcity and excess affect plant health and biomass.

This research was supported by the DOE Office of Science, Office of Biological and Environmental Research (BER).