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

Meng Xie*[1] (xiem@ornl.gov), Sam Seaver[2], Daifeng Wang[3], Doreen Ware[4,5], Qun Liu[1], Timothy Paape[1], **Crysten E. Blaby-Haas[1]**

[1]Brookhaven National Laboratory, Upton, NY; [2]Argonne National Laboratory, Argonne, IL; [3]University of Wisconsin, Madison, WI; [4]Cold Spring Harbor Laboratory, Cold Spring Harbor, NY; [5]US Department of Agriculture, Agricultural Research Service, Ithaca, NY, USA

Project Goals: Bioenergy crops that thrive in marginal soils and maintain performance in diverse and fluctuating environments are an essential component of a sustainable energy and carbon portfolio. However, understanding and predicting productivity in these environments is challenging, in part, because of the general lack of sequence-to-function information in the plant lineage. The Quantitative Plant Science Initiative (QPSI) is a versatile and scalable 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 gene-, protein-, and molecular-level experimentation. In this way, we leverage the scalability of ‘omics data and bioinformatic approaches to capture system-level information for DOE-relevant crops, while generating experimentally determined sequence-specific understanding of gene and protein function. By incorporating molecular-level experimentation in our workflow, we can address the question of how a protein functions and establish mechanistic insight into how sequence variation impacts phenotype. This knowledge also 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.

The development of ‘omics technologies provides an unprecedented opportunity for the study of plants as complex biological systems. With these technologies and the associated genome-wide data, nearly any plant species, including DOE-relevant crops such as poplar and sorghum, can be fast-tracked to a level of understanding that was previously attainable for only a few “model organisms”. The challenge is shifting from acquiring genomic data, such as whole-genome sequences and transcriptomics datasets, to using that knowledge to enable predictive biology. Central to this challenge is the paucity of sequence-to-function understanding in the plant lineage, generally, and in bioenergy crops, specifically. While our aspiration is a large-scale capability that generates gene and protein functional understanding in bioenergy crops, our initial focus addresses the need for micronutrient stress resilience for sustainable bioenergy/bioproduction. Of the essential micronutrients, insufficient zinc and iron bioavailability causes widespread decreases in crop yield. We will broadly use resources developed in the DOE complex together with a multi-omics experimental strategy to discover adaptive responses to suboptimal zinc and iron availability in two DOE flagship bioenergy crops, poplar and sorghum. This data will be used for a computational simulation of cofactor availability in the chloroplast, the major metal sink and site of carbon fixation and energy generation. At the same time, we will deploy an interdisciplinary approach and use high-throughput methodologies to provide a layer of experimentally grounded sequence-specific understanding of molecular-level functions for major players involved in chloroplast metal trafficking. These studies will serve to improve our model of micronutrient dynamics in bioenergy crops and to provide a foundation for establishing how metal scarcity and excess affect the biomass yield of bioenergy crops.

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