

Protein Function Discovery and Sequence-Function Understanding of Stress Tolerance in the Green Lineage

Ian K. Blaby¹, Agnidipta Ghosh², Kevin Keck¹, Kyoungsoon Kim¹, Gerry Guo^{1,4}, Miriam Pasquini¹, Shinjae Yoo³, Steven C. Almo², Sean McSweeney^{1,4}, Qun Liu^{1,4}, and **Crysten E. Blaby-Haas***¹ (cblaby@bnl.gov)

¹Biology Department, Brookhaven National Laboratory, Upton, NY

²Department of Biochemistry, Albert Einstein College of Medicine, Bronx, NY

³Computational Science Center, Brookhaven National Laboratory, Upton, NY

⁴National Synchrotron Light Source II, Brookhaven National Laboratory, Upton, NY

Project Goals: The Quantitative Plant Science Initiative (QPSI) seeks to provide fundamental understanding of genomics-based protein function to accelerate improvement of present and future bioenergy/bioproduct crops. The primary goals of this interdisciplinary capability are: i) to achieve a systems-level understanding of how plants across the green lineage have evolved to acclimate to suboptimal environmental conditions and ii) to provide the sequence-to-function-to-phenotype knowledge required to translate experimentally validated functions across species for enabling the design and redesign of target plant processes.

There are multiple challenges to implementing an economically viable and sustainable bioeconomy. In particular, hurdles still exist for plant crops as renewable resources of bioenergy and bioproducts, such as development of crops that can thrive in marginal soils and maintain performance in diverse and fluctuating environments. Post-genomic resources have accelerated our ability to achieve systems-wide information of how plants respond and adapt to biotic and abiotic stresses. Capitalizing on this torrent of genome-based data, the QPSI capability is developing approaches that combine the scalability of functional genomics with protein function characterization to generate the foundational knowledge needed for the design and redesign of stress tolerance. Trans-systems functional genomics analyses that utilize 'omic-derived data, cross-kingdom comparative genomics, and protein family evolution are being used to discover novel niche-specific and lineage-wide processes as potential targets for crop improvement. Protein function predictions are being used to guide characterization via genetic, biochemical and structural biology techniques. We are also developing approaches that combine target-specific experimentation with computational platforms for the accurate propagation of experimentally grounded functional characterization across sequence space.

This work is supported by the Office of Biological and Environmental Research in the DOE Office of Science