

Unlocking the Molecular Basis of Plant-Pathogen Interactions to Create Resilient Bioenergy Crops

PI: Qun Liu, Brookhaven National Laboratory

Co-PI: Sean McSweeney, Brookhaven National Laboratory

Co-PI: Shinjae Yoo, Brookhaven National Laboratory

Co-PI: Ljiljana Paša-Tolić, Pacific Northwest National Laboratory/Environmental Molecular Sciences Laboratory

Co-PI: Mowei Zhou, Pacific Northwest National Laboratory/Environmental Molecular Sciences Laboratory

Co-PI: Yasuo Yoshikuni, Lawrence Berkeley National Laboratory/Joint Genome Institute

Co-PI: Christopher S. Henry, Argonne National Laboratory

Co-PI: Huimin Zhao, University of Illinois, Urbana-Champaign

Co-PI: Clint W. Magill, Texas A&M University

Co-PI: Jeffery Dangl, University of North Carolina, Chapel Hill

The development of resilient and sustainable bioenergy crops such as sorghum, poplar, and switchgrass is a focal point within the Department of Energy (DOE) Office of Biological and Environmental Research (BER). Bioenergy crops, like all crops, are susceptible to diseases that can vastly impact yield and quality. With the large-scale deployment of bioenergy crops, pathogen outbreaks will inevitably occur. With climate change and growth in marginal conditions without competition with food crops, bioenergy crops are facing biothreats and diseases. Plant pathogens (fungi, bacteria, and viruses) produce a stunning array of virulence effector proteins and other molecules that interact and hijack plant defense systems resulting in infection and disease. Conversely, all plants encode intracellular innate immune receptors called nucleotide-binding leucine-rich repeat proteins (NLRs) that recognize effectors to elicit successful immune responses. The coevolution of plants and pathogens drives cycles of infection and immunity. The team, therefore, proposes to integrate systems biology, biomolecular characterization, and synthetic biology with computation, artificial intelligence, and machine learning to provide foundational insights into the dynamic plant-pathogen interactions. The output of this proposal will contribute to the development of a resilient bioeconomy which includes the bioengineering and breeding of broad pathogen-resistant bioenergy crops and biocontrol of disease through mutualistic plant-bacteria interactions. The technologies and resources that are developed in this proposal may be rapidly deployable for combating emerging biotreats.

Sorghum is the second amongst US biofuel crops and is the primary source of biodiesel production worldwide. However, a devastating anthracnose disease, caused by a fungal pathogen *C. sublineola*, can lead to its yield losses of up to 67%. The co-evolution and genetic diversity of both sorghum and *C. sublineola* make this a highly relevant model system to study plant-pathogen interactions. The primary objective is to advance a fundamental understanding of plant-pathosystem interactions by investigating the molecular interactions between sorghum, its anthracnose-disease causative fungal pathogen *C. sublineola*, and antifungal biocontrol bacteria to create disease-resilient bioenergy crops.

This proposed project is organized into four linked aims: Aim 1: Identify molecular interactions underlying the pathogenicity of *C. sublineola* and its inhibition by bacteria; Aim 2: Characterize the molecular basis of key interactions determining *C. sublineola* pathogenicity, anthracnose resistance, and its susceptibility to biocontrol; Aim 3: Create synthetic pathogen infections to study pathogenicity,

resilience, and disease biocontrol; and Aim 4: Develop innovative computational resources to study plant-pathogen interactions across biological scales.