Optimizing Tradeoffs Implicit During Bioenergy Crop Improvement: Understanding the Effect of Altered Cell Wall and Sugar Content on Sorghum-Associated Pathogenic Bacteria

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Project Goals: The first project goal is to quantitatively model the disease triangle that describes sorghum, pathogenic bacteria, and the environment. Field and laboratory experiments are being combined to determine bacterial susceptibility of genetically diverse sorghum genotypes that differ in cell wall and sugar composition. Standard plant pathology techniques combined with powerful phenomics approaches are providing a holistic view of this pathosystem within variable environments. Further, transcriptomics is being employed to elucidate mechanisms used by bacterial pathogens to induce sorghum susceptibility. Microbial pathogens are known to manipulate the sugar and cell wall characteristics of their hosts. Consequently, these characteristics will be analyzed during pathogen invasion. This research will reveal the mechanisms underlying tolerance to pathogens that must be maintained during biofuel trait optimization.

Plant-derived production of renewable fuels and chemicals has the potential to enhance US farming and agricultural economic opportunities, increase domestic energy security, and reduce fossil fuel dependency and greenhouse gas emissions. Realizing the potential of these alternative energy sources necessitates the development of high-biomass-yielding crops. These specialized crop varieties may harbor modifications to cell walls, which are a major barrier to pathogen entry, and to the tissue distribution of sugars, which are the pathogen's food source; hence they are likely to present previously unseen challenges for disease resistance. Over the last several years, disease from the bacterial pathogen *Xanthomonas*, has caused significant yield losses in many crops where bacterial diseases had historically been rare, including corn and cotton. It is currently unclear why these diseases are emerging. *Xanthomonas* is a known pathogen of sorghum (*Sorghum bicolor* (L.) Moench), though similar to corn and cotton, the incidence and impact of the disease has historically been low. Taken together, these observations highlight a vulnerability in sorghum's resilience to pathogens that is likely to be magnified by alterations in cell wall and sugar content. In this project, we aim to establish the sorghum – *Xanthomonas* pathosystem as a model for deducing how latent microbial pathogens might exploit key biofuel crop traits.

We will report results to date including efforts to classify over one hundred sorghum varieties for resistance/susceptibility to *Xanthomonas* and an accompanying GWAS analysis, dual-RNAseq data that has revealed gene expression patterns in both host and pathogen during compatible and incompatible interactions, and characterization of cell wall and sugar profiles during pathogen attack.