

## **Title: Resistance to Stalk Pathogens for Bioenergy Sorghum**

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**Project Goals: This research is focused on discovering molecular and metabolic networks that drive sorghum resistance or tolerance to stalk rot pathogens. We will use advanced molecular tools to identify key factors associated with resistance and tolerance to stalk pathogens in sorghum lines optimized for key bioenergy traits (modified phenylpropanoid metabolism), with enhanced drought tolerance (nonsenescent) or with increased tolerance to stalk pathogens. Some lignin altered lines and drought tolerant lines already have demonstrated increased tolerance to these pathogens but the mechanisms that mitigate pathogenic growth have yet to be identified. Our goal is to develop sorghum lines that can withstand increased pathogen loads under reduced water conditions based on knowledge gained through this research.**

Sorghum is a promising bioenergy crop with high yield potentials and significant tolerance to both drought and heat. However, sorghum is prone to stalk rots, which can significantly limit sorghum biomass production through yield reductions and lodging. Stalk rot-causing fungi normally grow endophytically within sorghum plants. When sorghum plants experience water stress, host changes often trigger a developmental switch causing the fungi to become pathogenic. The underlying plant molecular circuits that can limit or exacerbate this fungal transition from endophytic to pathogenic growth are not known and are the focus of this proposal. Several publicly available lines have previously demonstrated resistance or tolerance to sorghum stalk pathogens, including lines with postflowering drought tolerance (nonsenscence), which appears to suppress pathogenic growth. In addition, we have developed several near-isogenic sorghum *brown-midrib (bmr) 6* and *12* lines with altered lignin content and composition, which were previously demonstrated to have increased resistance or tolerance to sorghum stalk rot pathogens. Lignin, a component of plant cell walls, has been a focus for development of bioenergy sorghums because its presence increases recalcitrance of biomass to cellulosic conversion, but its presence also increases total energy content of biomass, which is important for thermal conversion technologies. To increase energy content, we have engineered sorghum plants overexpressing a Myb transcription factor that induces lignin synthesis, and a gene encoding caffeoyl-CoA *O*-methyltransferase, a monolignol pathway enzyme. Both the transgenic and *bmr* plants accumulate phenolic intermediates from lignin synthesis that inhibit stalk pathogens *in vitro*. We recently have developed the ability to apply water-stress in a controlled environment, which reliably induces the developmental switch from endophytic to pathogenic growth of sorghum stalk rot fungi. Using this unique collection of plant lines described above, in combination with genomics and metabolomics tools, the following hypothesis will be directly evaluated: “based on collected metabolite and transcriptome data, we will identify metabolic networks that will lead to host resistance.” To address this goal, we will

inoculate sorghum with fungi that are the most common causes of stalk disease in the U. S. (*Macrophomina phaseolina* that causes charcoal rot and *Fusarium thapsinum* that causes Fusarium stalk rot) using our newly-developed greenhouse drought bioassay under well-watered and water-deficient conditions. The specific objectives of this proposal are: 1) to determine pathogenic and endophytic growth of stalk pathogens in sorghum lines under water deficit conditions; 2) to identify host metabolites and metabolic pathways involved in resistance or tolerance to fungal stalk rot pathogens under water deficit conditions in lignin modified, nonsenescent and stalk rot resistant/tolerant lines; 3) to identify host genes from the phenylpropanoid and defense-related pathways with altered expression levels during pathogenic or endophytic growth of fungal stalk pathogens under water deficit conditions; and 4) to identify genes, gene networks, and metabolic pathways whose expression is altered in stalk rot tolerant sorghum lines under water sufficient *versus* deficit conditions. Our aim is to discover host metabolic and signaling pathways that enhance endophytic growth of stalk fungi and inhibit the developmental switch to pathogenic growth that frequently occurs under periods of prolonged abiotic stress. From this valuable research, we will identify biomolecular markers for resistance that will significantly enhance efforts to develop superior bioenergy sorghum with resistance to increasing disease and environmental stresses.

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