

**Title:** Systems analysis of the beneficial associations of sorghum with arbuscular mycorrhizal fungi studied with genetics, genomics, imaging and microbiomics

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**Project Goals:** Arbuscular mycorrhizal fungi (AMF) are obligate symbionts/biotrophs that can enhance the disease resistance, nutrient access and/or drought tolerance of their plant host through their interactions with roots, but may also serve as negative contributors to plant yield depending on the agricultural environment. The primary goals of this project are to identify the plant genes that attract specific AMF interactions, to determine the possible benefits or costs of this interaction to the biofuel crop sorghum under varied field conditions, and to generate a systems analysis to assist plant breeders and agronomists to use endogenous AMF to improve sorghum productivity.

**Abstract Text:** In the first year of this project to determine the nature of AMF interactions and contributions to sorghum biomass production, we have developed the field and laboratory assays necessary for the full completion of this five-year project. Identical fields were planted in Georgia and Arizona that contained a small subset of the Genome Wide Association Study (GWAS) sorghum biomass panel that will be comprehensively analyzed in subsequent years. The root system microbiomes were analyzed over a time course to find the best (*i.e.*, least variable) time(s) to sample for robust results in subsequent seasons. These plants were also assayed for mineral content and aboveground biomass yield, and scored for disease incidence and plant developmental stage. Dramatic differences between the fields in Georgia and Arizona were noted, with very high levels of insects, weeds and pathogenic fungi in Georgia. Initial investigation of some of the observed diseases by our collaborator, Dr. Bochra Bahri at the University of Georgia, uncovered the organisms responsible for these diseases, including some that had not been reported previously as causing disease on sorghum in Georgia or, in some cases, anywhere in the world. DNA analyses of the root microbiome are ongoing, with precise values now established for the time, cost and personnel required for this science at this scale. High throughput imaging of AMF in these roots has also been advanced tremendously and is described in another poster from our project in this conference. Additional projects are underway to, first, define the best methods for RNA purification and analysis and, second, to test the effects of seed and foliage fungicide treatments on the root microbiome that is investigated in this project. Efforts to isolate and genome sequence specific AMF ecotypes are underway as well, in order to provide richer AMF sequence datasets to scan for homology to the RNA and DNA sequences we will find in the studied microbiomes. A linear model has been developed and fitted successfully to a subset of 79 BAP lines in the initial GWAS study as a first step in developing a structural equation model for the entire GWAS study.

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