

**Title: Adaptive GWAS using MINE for discovery of structural equations in the AMF-Sorghum Project**

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**Project Goals:** Arbuscular Mycorrhizal Fungi or AMF are obligate root symbionts, associating with at least 80% of terrestrial plant families. The overarching project goal is to understand the AMF symbiosis in sorghum with a systems biology approach. Our particular components of the project are to identify a systems diagram for the network of AMF-sorghum interactions and imaging of AMF structures in the roots.

**Abstract Text:** Arbuscular Mycorrhizal Fungi (AMF) are obligate root symbionts, associating with at least 80% of terrestrial plant families and about which little is known. In return for plant assimilated carbon, these fungi provide nutrients, such as nitrogen and phosphorus, to their host plants. A systems biology approach is being used to understand this symbiosis in sorghum. To identify sorghum genotypes and genes that influence AMF abundance and plant biomass performance, a multi-year Genome Wide Association Study (GWAS) of AMF in sorghum on Wellbrook Farm in Watkinsville, GA is underway. Year 1 of the GWAS involves 79 accessions from the Bioenergy Accession Panel (BAP). The field was planted in early June, 2021 in 3 blocks with 79 rows and 9 seedlings of the same accession per row for a total of 2200 seedlings. 3 plants were harvested per row before and after flowering at three time points and measured for dry canopy weight and fresh and dry root weight. A high-throughput protocol for imaging symbiotic structures was developed using ink and vinegar staining. A total of 576 images of root intersections are being captured per plant for a total of 800 plants (88+288+424). Machine learning methods are being used to segment and classify AM fungal structures from the images for GWAS mapping to the sorghum genetic map. The results from GWAS, host biomass, microbiome, morphological, microscopic and transcriptome studies will feed into systems models, including structural equation models to predict sorghum genotypes that will maximize production (*i.e.*, plant health) knowing indigenous AMF in the field under different field conditions.

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