

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: The objective of this project is to discover the sorghum genes that recruit and sustain the root microbial community, especially the AMF community, that promotes high sorghum biomass yield under a known range of environmental conditions, and to build/test predictive models derived from these insights. These studies are designed to discover the interactions between genetic and environmental factors that cause the variable performance of mycorrhizal symbioses in field conditions, using a series of field and greenhouse experiments with genetically diverse sorghum lines in Georgia and Arizona. Through six integrated sub-projects, we will collect tens of thousands of phenotypic measurements, including root morphology, AMF morphology, AMF taxa abundance, other microbial abundances, plant root gene expression, AMF gene expression, plant mineral content and biomass yield. Promising candidate associations of these phenotypes with each other and with the sorghum genotype will be identified under a multiple testing scenario and then confirmed by independent experiments to find validated causal links (metadata) for increased biomass production.

Abstract: The roots of most plants form symbioses with arbuscular mycorrhizal fungi (AMF), which can enhance nutrient uptake, drought tolerance and disease resistance for host plants. Harnessing these symbioses could reduce irrigation and fertilizer inputs for more sustainable production of biofuel crops like sorghum. Despite decades of effort, successful use of AMF as bioinoculants has been elusive, largely because mycorrhizae are complex systems and their effects are context dependent. The positive contributions of AMF and other microbes to crop productivity have been broadly documented, but the same microbes can vary in their contributions, from highly beneficial to functionally parasitic, depending on the field environment. Though the contributions of some plant genes in plant-AMF interactions have been studied in controlled laboratory conditions, none of these interactions are well understood in field conditions, and it is likely that whole categories of interactions are completely unknown at this stage. The project teams' laboratories have recently identified plant genome segments that determine which AMF and other microbial taxa are abundant in the root/soil environment. This suggests that sorghum genetics can be a key to unravelling the plant-microbe-environment system and optimizing plant-microbe interactions for yield. These predictions will be more than just biomass yield associated with particular sorghum genotypes, AMF communities and input regimens, but also predictions of the other phenotypes that will be commensurate. These predictions will be tested both in small-scale controlled-environment experiments, and in analyses of agricultural field data produced during the project but not used in the initial model building. These data and metadata associations will be utilized to create systems models that predict in detail the performance of novel sorghum genotypes under a variety of environmental conditions. Mutagenized sorghum will also be employed to test the impact of specific sorghum genes on AMF type, abundance and functions. Confirmations of predicted associations will have tremendous value in uncovering the mechanisms that determine beneficial plant-AMF-environment interactions. Moreover, the iteratively improved models will not only have exceptional impact for inspiring and guiding future experimental design, but also for applied use by farmers to guarantee optimal sorghum biomass yield by using beneficial microbial associations that require only the appropriate sorghum genotype and agricultural inputs, not any artificial microbial inoculum.