

Title: Genetic dissection of AM symbiosis to improve the sustainability of feedstock production

Maria J. Harrison* (mjh78@cornell.edu) and Zhangjun Fei
Boyce Thompson Institute for Plant Research, Tower Road, Ithaca, NY 14850

Project Goals:

Fertilizers comprise a significant proportion of biofeedstock production costs and large-scale fertilizer use has many negative environmental consequences. If biofeedstock production is to be economically viable and environmentally sustainable, increasing the efficiency of mineral nutrient acquisition is an important priority. One approach to this is to harness the soil microbiota, in particular, arbuscular mycorrhizal fungi, with which plants form stable mutualistic symbioses. Currently, the genetic basis of arbuscular mycorrhizal symbioses in feedstock species is largely unexplored. The overall goals of the proposed research are to determine which genes control development and functioning of AM symbiosis in feedstocks through studies of a feedstock model species, *Brachypodium distachyon*, as well as sorghum, a feedstock species.

Using *B. distachyon*, we aim to identify genes that are critical for development and functioning of AM symbiosis. This will be achieved through analysis of *B. distachyon* T-DNA insertion mutants and/or transgenic lines in which gene function has been down-regulated by RNAi or disrupted by genome editing using the CRISP/Cas9 system. *B. distachyon* T-DNA insertion mutants will be obtained from the DOE-funded insertion mutagenesis project, <http://brachypodium.pw.usda.gov/TDNA/>. Candidate genes have been selected based on previous transcriptional analyses of *B. distachyon* during AM symbiosis with three AM fungi, *Glomus versiforme*, *Glomus intraradices* (now *Rhizophagus irregularis*) and *Gigaspora gigantea*.

With support from the DOE Feedstock Genomics Program, Dr. Stephen Kresovich and colleagues are developing nested association mapping (NAM) populations for diverse sweet and cellulosic (bioenergy) sorghums. These NAM populations may also provide an opportunity to investigate variation in responsiveness to AM symbiosis in biofeedstock sorghum genotypes. Relative to other crops, sorghum shows high nutrient use efficiency; however, in most production environments, fertilizers are still used and therefore improving nutrient capture would be economically and environmentally beneficial. As a first step, we will evaluate the parents of the NAM populations for responses to AM symbiosis including development of symbiosis, symbiotic mineral nutrient acquisition and increases in shoot biomass. For a selection of genotypes, root and shoot transcriptional responses to symbiosis will be analyzed by RNA-seq. The profiles will provide insights into AM symbiosis and the effects of plant genotype on symbiotic gene expression.

This research is supported by the DOE Office of Science, Office of Biological and Environmental Research (BER), grant no. DE-SC0014260.