

Linking Microbial Community Structure and Function for Sustainable Production of Bioenergy Crops

Alonso Favela,^{1,3} Sierra Raglin^{1,2}, Niuniu Ji¹, Sandra Simon¹, Rachel Waltermire¹, and **Angela Kent**^{1,2,3*} (akent@illinois.edu)

¹DOE Center for Advanced Bioenergy and Bioproducts Innovation; ²Department of Natural Resources and Environmental Sciences and ³Program in Ecology, Evolution, and Conservation Biology; University of Illinois at Urbana-Champaign, Urbana, IL

Project goals: Our overall objective is to identify the genomic and biochemical mechanisms by which plants influence their rhizosphere microbiome and its functions, enabling future germplasm improvement; and to determine the impact of altered rhizosphere nitrogen cycling functions on nutrient retention and sustainability in agroecosystems. Our interdisciplinary team employs a combination of metagenomics, measures of N cycling process rates, and plant breeding genetics to address these knowledge gaps.

The plant microbiome helps plants acquire scarce resources and is an essential target for improving agricultural sustainability, particularly for biofuel feedstocks where reduction of anthropogenic inputs is desirable. However, the ability of modern crops to recruit and structure their microbiome may be altered by domestication and breeding. Selection for crop plants based on aboveground traits in high nutrient environments may inadvertently lead to changes to belowground plant physiology and relationships with the soil microbiome. In doing so, we have likely altered microbiome functions that contribute to sustainability and environmental quality (e.g. nutrient acquisition, nutrient retention, and GHG production).

The first step to investigate this is to examine the structure and activity of the microbiome as a function of plant genotype, with a specific focus on N cycling functional groups. The functional capacity of the rhizosphere microbiome and the benefit to the host plant, as well as ecosystem services such as nutrient cycling and greenhouse gas emissions, vary with the composition and abundance of microbial assemblages. We hypothesized that plant genotypes differ in their ability to recruit microbial functional groups, and ultimately that the functional profile of the microbial community can be treated as a selectable plant phenotype and optimized through plant breeding. We used targeted functional metagenomic sequencing to survey the rhizosphere of diverse genotypes of several crops to compare their capability to recruit microbial nitrogen cycling functional groups, and examined rates of nitrogen transformations. Using maize as a model for bioenergy grasses, we observed significantly different N cycling microbial community structure among crop genotypes that represent the endpoints of directed evolution. In addition, differential abundance and composition of N cycling functional groups was associated with significant reduction in nitrification and denitrification in specific maize lineages. We are following up with examination of sorghum genotypes that strongly vary in nutrient use efficiency. Our results allow the linkage of host-associated microbial communities and ecosystem function and suggest that there is genetic capacity to optimize recruitment of N cycling functional groups, and improve

crop sustainability. Understanding the mechanistic underpinnings of this relationship will allow breeders and ecosystem scientists to select bioenergy crop cultivars that interact with the nitrogen cycle in ways that improve the efficiency and sustainability of agriculture, while protecting environmental quality.

Funding statement: This work was funded by the DOE Center for Advanced Bioenergy and Bioproducts Innovation (U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research under Award Number DE-SC0018420). Any opinions, findings, and conclusions or recommendations expressed in this publication are those of the authors and do not necessarily reflect the views of the U.S. Department of Energy.