40. Composition and Distribution of Core Carbohydrate-Active Microbial Genes in Biofuel Soils

K. Hofmockel[1]* (khof@iastate.edu), A. Howe,[2,3] R. Williams,[1] F. Yang,[1] E. Bach,[1] F. Meyer[2 1] Iowa State University, Ames, Iowa; [2] Mathematics and Computer Science Division and Institute for Genomics and Systems Biology, Argonne National Laboratory; Michigan State University, East Lansing, MI.

Project Goals: To identify the key organisms and functions involved in the metabolism of cellulose within soil communities and determine if the active carbon cycling microbial communities differ among soil aggregate fractions and bioenergy cropping systems.

Understanding how plant communities and management systems influence the composition and function of soil microbial communities is paramount for reducing environmental impacts associated with bioenergy agriculture. Because soil microbial communities are important drivers of carbon and nitrogen cycling, the integration of microbial metabolism into biogeochemical models is an important next step for accurate prediction of ecosystem responses to land use change and climate feedbacks. A key challenge for integrating microbial ecology into models is that soil contains highly complex and diverse microbial communities in a spatially heterogeneous structure. Soil fractionation techniques provide an opportunity to examine intact microbial communities in a context that is relevant to both microbial community metabolism and ecosystem processes. The dynamic hierarchy of aggregates of different sizes creates intra-aggregate pore spaces that are the habitats in which microbes live. By considering soil aggregates as the fundamental units of microbial assemblages, soil heterogeneity can be reduced, and microbial communities investigated in systems that reflect natural communities and at scales consistent with micron-scale processes. Our research aims to use soil aggregates to develop laboratory and field approaches that target metabolically active microorganisms and functions that drive carbon cycling in soils from bioenergy cropping systems.

As a first step we have identified core carbohydrate-active genes in multiple localized samples (n=4) of a fertilized prairie used for biomass feedstock production. The core metagenome from whole soil samples were compared to soil aggregate fractions (n=20) from the same site, as well as in soils from adjacent plots of both unfertilized prairie and corn. Among a total of 226,998 genes with similarity to known carbohydrate genes, 911 genes were common to all samples, encompassing our defined fertilized prairie carbohydrate-active core metagenome.

Within the carbohydrate-active core, the distribution of enzyme classes and their taxonomic origin were characterized. Abundant glycosyltransferases were found in Proteobacteria, Bacterioidetes, and Firmicutes; glycoside hydrolases were found in Fungi and Proteobacteria; and carbohydrate esterases in Proteobacteria, Chloroflexi, and Fungi. The core genes were present in the metagenome at a broad range of abundances, estimated from 1 to 6 copies of a carbohydrate gene per 100 cells. Many core fertilized prairie genes were also found to be present in multiple other agricultural and grassland metagenomes, with decreasing presence in forest, desert, and tundra metagenomes. Comparing core carbohydrate-actives with a database of known genomes from sequenced soil isolates revealed that current references lack information on several core phyla, especially Chlorobi, Spirochaetes, and Korachaeota. In soil ecosystems, where high diversity remains to be a key challenge for metagenomic investigations, these core genes represent a subset of critical functions necessary for carbohydrate metabolism, which can be targeted to compare and model carbon fluxes of varying soils.

This research was supported by the Genomic Science Program, U.S. Department of Energy, Office of Science, Biological and Environmental Research under Contract No. DESC0010775 and by the Carbon Cycling Science Program, USDA-NASA grant 20116700330364.