## 62. Key microbial decomposition pathways in soils from bioenergy agroecosystems.

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**Project Goals**: Because of the amazing diversity of soil, it has been identified as a "Grand Challenge" for exploring microbial diversity. Here we investigate the diverse metabolic potential of soil microbial communities involved in decomposition by identifying key functions and organisms involved in cellulose decomposition. Our goal is to develop effective strategies to analyze soil metagenomes allowing exploration of the biological basis for decomposition. This work is being done in soils cultivated for bioenergy feedstocks, where we aim to optimize plant-microbe- soil interactions for the development of sustainable biofuel production systems.

The Comparison of Biofuel Systems (COBS) research site in central Iowa, USA is a replicated field experiment managed to investigate the potential for alternative biomass production systems to produce fossil---fuel replacement and concurrently support biogeochemical benefits. Corn continues to be the most readily abundant and available crop for biofuel production in the United States1. However the current corn---soy management that dominates the Corn Belt is no longer sustainable in the context of climate feedbacks, demand for clean water, and the requirement for cellulosic biofuel. One promising solution is to incorporate diversified biofuel cropping systems that provide multiple ecological benefits coincident with provisioning harvestable cellulosic biomass. The potential benefits of diversified agroecosystems are derived from the known relationship between biodiversity and the productivity and sustainability of Earth's ecosystems2,3,4,5. Diversified biofuel cropping systems may augment microbial diversity and the associated biogeochemical benefits, including enhanced decomposition of plant detritus, increased soil aggregation and reduced loss of soil organic matter. Yet the biological basis for how plant and microbial diversity interact to influence soil carbon (C) storage remains an important frontier.

Identifying the microbial metabolic pathways that most strongly influence ecosystem C cycling requires a deeper understanding of the relationships between microbial community functions in a field context. However, characterizing these community--scale functions requires adoption of a scale relevant to microbial habitats in soil. Soil aggregate fractions can be used to enhance the ability to detect metabolic relationships, because aggregates approach the scale of ecological drivers that structure microbial communities. The present study addresses the composition and functional potential of C cycling microbial communities using soil aggregate fractions from diversified, reconstructed, fertilized prairies that are harvested for bioenergy feedstock. We posit that the most abundant sequences may not capture the central C cycling steps regulating decomposition and soil organic matter formation. Because C---cycling occurs in soil as the concerted action of multiple, interacting microbial groups, we developed a novel co---occurrence workflow that uses Bayesian hierarchical methods to identify community-scale relationships that may drive C---cycling. In addition to producing multivariate networks of co-occurring microbial taxa and functions, this methodology allows for greater consideration of uncertainty between co---occurrence relationships and provides a straightforward framework for testing our pathways, we concentrated this analysis on protein---coding genes identified with the Carbohydrate Active Enzyme (CAZy) database6. With a focus on glycoside hydrolases (GH's), we saw many families of unclassified enzymes positively co-occurring with families of well-known enzymes. For example, we detected a strong and positive co-occurrence between the abundance of the xyloglucanase family, GH12, and a poorly characterized β-xylosidase in family GH54, that may be important for breaking down complex, structural plant biomass. Co-occurrence between these functions illustrates complementary functions between multiple bacterial phyla and the fungal phylum, Ascomycota. Together these results suggest that the presence of keystone organisms or functions may be central to initiating decomposition in soils

and producing a diversity of C-rich substrates that can maintain diversity and coexistence across multiple domains of microbial life.

In addition to co-occurrence strength, position in the network can be used to generate hypotheses about metabolic dependencies. Our analysis suggests that genes in GH52 and GH2 may be pivotal to decomposition in our soils. A GH52 (xylosidase) present only in γ-Proteobacteria was central in the network, supporting a high dependency of other enzymes. Notably, a variety of proteins encoding for GH2, β---acting enzymes (galactosidase, mannosidase, glucoronidase, glucosaminidase) were strongly correlated with the γ-Proteobacteria associated xylosidase. While some functions like those involving GH52 were phylogenetically limited, many other co---occurring functions involved a larger diversity of microorganisms. These analyses have provided key phylogenetic and functional targets to monitor in both field and lab based studies of microbial decomposition in feedstock production systems.

References:

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