

Functional Metagenomic Comparison of Soil Microbiomes Associated with Six Cellulosic Biofuel Feedstock Production Systems

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<https://www.glbrc.org/research/sustainability>

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<http://cme.msu.edu/tiedjelab/jtiedje.shtml>

Project Goals: The Sustainability Research Area of the Great Lakes Bioenergy Research Center (GLBRC) addresses the sustainability of producing liquid transportation fuels from cellulosic materials, with an emphasis on evaluating and enhancing novel cropping systems that can provide cellulosic feedstocks. A key component of this work has been the study of soil microbes to better understand how plant-microbe interactions shape microbial communities and enhance plant productivity, and how microbial communities influences biogeochemical cycling. Here, we focused on how a diverse array of potential cellulosic feedstock production systems, including traditional annual crops, perennial crops, and assemblages of native species, reshape the functional metagenomic profile of their associated soil microbial communities in the years following cropping system.

Among the most exciting aspects of a cellulosic bioenergy economy is the potential to commercialize agroecosystems that provide valuable environmental services but that have historically been overlooked in favor of more conventional agricultural production systems (1). These systems include perennial natives such as switchgrass (*Panicum virgatum*), highly productive exotics such as miscanthus (*Miscanthus x giganteus*), and even diverse assemblages of native prairie species. Much of our understanding of many of these systems derives from conservation projects, which may not accurately reflect the management conditions for cellulosic feedstock production. It is thus imperative to understand how agronomic management emphasizing feedstock production impacts the agroecological properties of these highly promising systems.

There is growing awareness of the critical role soil microbes play in determining the ecological functionality of agroecosystems (2). Previous work from the GLBRC has demonstrated the tremendous influence cropping systems and their management exert on soil microbial community compositions (3), as well as the potential for those differences in composition to impact key agroecosystem processes such as soil respiration and methanotrophy (4). Our present study expands on these earlier findings, leveraging both the experimental infrastructure of the GLBRC's Bioenergy Cropping Systems Experiment (BCSE) and the recent, rapid development in use of high-throughput sequencing to characterize the functional metagenomics of complex microbial communities.

We studied six experimental cellulosic feedstock production systems: continuous, no-till corn (*Zea mays*), monocultures of switchgrass, miscanthus, and hybrid poplar (*Populus nigra* x *P. maximowiczii*), a mixture of five native grass species, and a mixture of 18 native prairie species, established in 2008 and sampled annually from 2010 through 2012. We extracted environmental genomic DNA from the unseparated bulk and rhizosphere soils from these systems, which was subjected to shotgun metagenomic sequencing by the DOE Joint Genome Institute. Our dataset consists of 164 annotated, individually-assembled metagenomes, 1 to 2 Gbp in size. We used clusters of orthologous group (COG) annotation to define the functional genetic composition of these communities, relativizing by COG model length and abundance of a suite of single-copy housekeeping genes to derive relative abundances of individual COGs.

We observed considerable interannual variability within cropping systems, particularly in the continuous corn. There were significant differences among cropping systems in their overall functional gene content, but contrary to our expectations, the corn system did not function as an outlier relative to the perennial systems. Similarly, there were very few differences among systems in the relative abundances of key denitrification genes, despite considerable differences in the emissions of nitrous oxide observed during this time (5). Our findings suggest the overall functional genetic profile of soil microbial communities may display a less consistent response to differences among cropping systems than is observed in microbial biomass. Alternatively, it is possible that there are system-driven changes in the identity of the organisms possessing a particular function which may not translate to differences in the relative frequency with which that function occurs in the overall population.

References

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