

78. Soil Microbial Community Composition as an Indicator of Agroecosystem N₂O Emissions

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Project Goals: This project is part of a larger effort that aims to use high throughput molecular methods for microbial community characterization to understand the effects of different bioenergy cropping systems on the composition and function of soil microbial communities. The primary focus is on nitrogen cycling and linking microbial community composition to soil nitrous oxide emissions. This is a preliminary study exploring changes to the microbial community as measured by a variety of molecular methods during the establishment phase of a prairie restoration contrasted with continuous corn.

High throughput molecular methods for taxonomic and functional characterization have revolutionized microbial ecology. These changes have motivated several fields, including ecology and medicine, to consider microbial communities as sources of information about complex environments and systems. In the study of soils and soil-based processes, microbial communities are a particularly appealing source of information because of their capacity to integrate a broad range of environmental factors, while filtering these for biological relevance. At the same time, many key processes in soils, particularly those involving nutrient and carbon cycling, are directly mediated by microbes, so measurements of the community may indicate the biological potential of a system to respond to environmental stimuli. Among these processes, the nitrogen cycle, and particularly the emission of nitrous oxide (N₂O), has received considerable attention both because of its relative biochemical simplicity and conservation and because of its importance to global climate change.

Our project takes place within the context of the Great Lakes Bioenergy Research Center's (GLBRC) cropping systems experiment, located at Arlington, WI. Through this experiment, we have established eight managed agroecosystems whose biomass could serve as a feedstock for biofuel or bioenergy production. As part of GLBRC's mandate to evaluate and improve the sustainability of novel biofuels, the cropping systems experiment has included the collection of a variety of ecologically relevant environmental measures, including trace gas fluxes from soils and inorganic nitrogen pool sizes. In our project, we have collected soils from a range of the ecosystems under consideration, including continuous corn, miscanthus, switchgrass, and a mixture of prairie species. Our long term objective is to combine microbial community characterizations from these soils with the rich environmental dataset being generated to provide a robust estimation of the interactions among microbial community properties and environmental drivers in determining N₂O emissions.

Here, we present a preliminary component of that study, where we focused on the two most strongly contrasting cropping systems: continuous corn and restored native prairie. We sampled these systems in years 3-5 of establishment to capture their ongoing divergence from a common background state. We employed a variety of characterization techniques including phospholipid fatty acid (PLFA) analysis, targeted 16S ribosomal subunit and bacterial nitrous oxide reductase (*nosZ*) sequencing, and Illumina whole metagenome shotgun sequencing. Each of these techniques characterizes a different aspect of the microbial community. We analyze the extent to which each technique captures differences between the two cropping systems, as well as among years. In addition, we test the degree to which different sources of microbial community information can explain variation in aggregated annual N₂O fluxes within systems and within years.