Metagenomic Analysis of Soil Bacterial Communities under Long-Term Organic Management

Soil-dwelling microbes carry out a wide range of functions essential to plant health and productivity (Rodriguez and Fraga 1999, Garbeva et al. 2004, Glick 1995). Organic farmers recognize soil biology as a key to crop productivity and a high-priority research issue in their cropping systems (Moynihan 2010), but until recently it has been difficult to study in detail the impact of organic production practices on soil microbial communities. Previous research with non-sequencing-based methods has indicated that organic soils harbor greater microbial diversity than conventional soils (Maeder et al. 2002); however, taxonomic diversity is not consistently related to functional effectiveness (Nannipieri et al. 2003). New sequencing-based approaches allow a more detailed examination of soil bacterial community structure and function based on analysis of DNA extracted from environmental samples (Huse et al. 2008).

This project consists of two experiments. The first experiment will determine the impact of cropping system by using metagenomic 16S rDNA sequencing to compare the bacterial communities at five sites where long-term organic and conventional management have been practiced side by side on the same underlying soil type. Sites are the Variable Input Crop Management Systems Trial at the Southwest Research and Outreach Station (SWROC) in Lamberton, MN; the Wisconsin Integrated Cropping Systems Trial in Arlington, WI; the Rodale Institute Farming Systems Trial in Kutztown, PA; Carmen Fernholz’s A-Frame Farm in Madison, MN; and Tony Thompson’s Willow Creek Farm in Windom, MN.

The second is a replicated field trial that uses both sequencing and bioassays to investigate the impact of organic amendments on soil bacterial community structure and function in longstanding and transitional organic systems. Treatments in this study are four cover crops: hairy vetch (Vicia villosa), rye (Secale cereale), oilseed radish (Raphanus sativus), and buckwheat (Fagopyrum esculentum); and three organic fertilizers: beef manure, poultry compost, and Sustane bagged commercial organic fertilizer; applied at recommended rates for corn production. This experiment will take place at four Minnesota sites: Carmen Fernholz’s A-Frame Farm in Madison, Mike Jorgenson’s Big Stone Farm in Clinton, Scott Johnson’s Spruce Valley Organics in Farmington, and the SWROC’s Elwell Farm in Lamberton. Soil bacterial community composition will be analyzed using 16S rDNA sequencing. Soil samples will be assayed for functions including denitrification, phosphate-solubilizing enzyme activity, and siderophore activity.

16S sequences will be analyzed using the software platform mothur (Schloss et al. 2009) to yield an inventory of bacterial taxa, which can be used to compare the composition and diversity of both the overall bacterial community and particular functional subgroups known to be involved in N cycling, P and micronutrient solubilization, carbon sequestration, and plant disease. In the second experiment, we will also assess the correlation of functional assay values with taxonomic features including diversity, composition at the phylum level or below, and abundance of individual Operational Taxonomic Units (OTUs).
Our findings will elucidate the differences between soil microbial communities under organic and conventional management. The use of multiple sites and treatments will allow us to distinguish the effects of soil type and preceding crop, which previous studies have shown to be the primary drivers of community composition in the short term (Garbeva et al. 2004; Bever et al. 2010), from those of long-term management system. Our results will demonstrate which organic amendments promote diversity in soil microbial communities to address specific functions important to organic production, thus enabling us to advise producers regarding the impacts of management practices. Results of this project will be communicated to growers and researchers through conferences, publications, and field days.

References:


