

Cover Crop and Fertilizer Effects on Soil Bacterial Community Structure and Function in Organic Farming Systems

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Introduction

Cover cropping and the incorporation of biological fertilizers are crucial aspects of management of soil health and fertility in organic systems. This project uses 16S bacterial DNA sequencing to investigate the effects of organic amendments on soil bacterial community structure, and to examine the associations between bacterial community composition and biologically mediated soil nutrient cycling functions. This project will help growers and researchers go beyond generalizations about the benefits of organic matter additions to better understand and predict the specific effects of particular crops and fertilizers.

Table 1: Experimental Sites

Site	Farm	Coordinates
Lamberton, MN	Elwell Agroecology Farm (U of MN)	44.23, -95.31
Madison, MN	A-Frame Farm (Carmen Fernholz)	45.01, -96.15
Farmington, MN	Spruce Valley Organic Farm (Scott Johnson)	44.65, -93.04



Table 2: Amendment Treatments

Hairy vetch (<i>Vicia villosa</i>)	Planted August 2012 Incorporated May 2013
Winter rye (<i>Secale cereale</i>)	
Oilseed radish (<i>Raphanus sativus</i>)	
Buckwheat (<i>Fagopyrum esculentum</i>)	
Beef manure	Applied October 2012
Sustane 8-2-4	Incorporated immediately
Pelleted poultry manure (Chickety Doo-Doos)	
Control (no amendment)	

Methods

A field experiment was established in spring 2012 at three southern Minnesota locations (Table 1). Organic amendment treatments (Table 2) were applied to field plots in fall 2012 following barley. The study fields were planted to corn (*Zea mays*) in spring 2013. Field soil samples were collected before and after treatment, and rhizosphere soil samples were collected from the corn crop. Soil respiration was quantified in post-treatment soil samples by measuring headspace CO₂ accumulation over two days of incubation in Mason jars, and net N mineralization was measured using KCl extraction over a 28-day incubation. Enzyme activity potential of phosphatase, N-acetyl-β-D-glucosaminidase, and β-glucosidase were measured using fluorometric assays. Bacterial community structure was determined using Illumina sequencing of the V5-V6 hypervariable region of bacterial 16S rDNA. Sequence data was analyzed using mothur (Schloss et al., 2009). Due to dataset size, OTU clustering was performed within sites.

Datasets

- Corn rhizosphere bacterial community profiles (16S V5-V6 region)
- Soil enzyme activities: N-acetyl-β-D-glucosaminidase (NAGase), β-glucosidase, phosphatase
- Soil respiration
- Net N mineralization
- Soil test values
- Corn yields

Figure 1: Relatedness of bacterial community samples

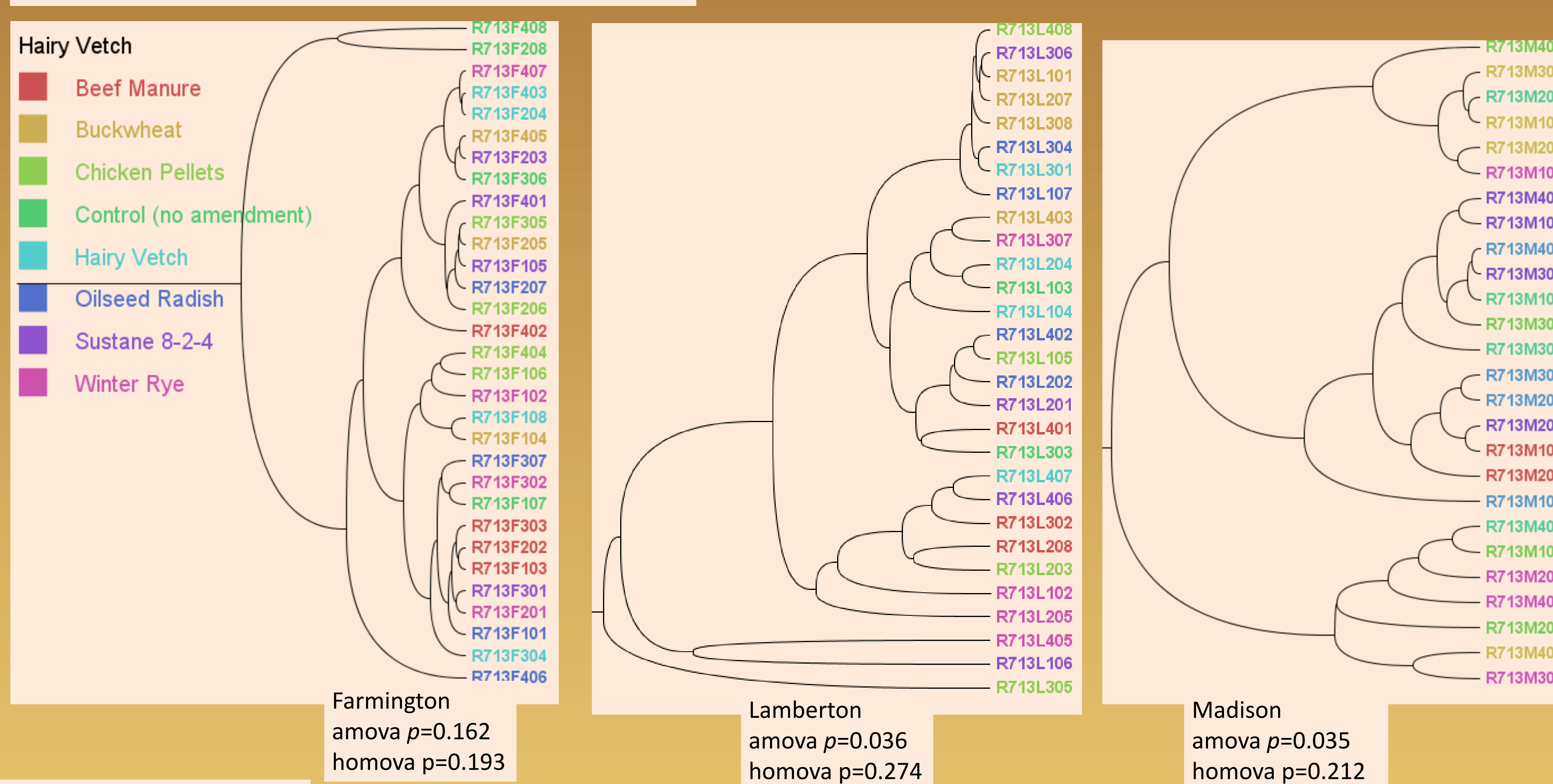


Figure 2: Activity of NAGase (nmol g⁻¹ hr⁻¹) by amendment treatment and location

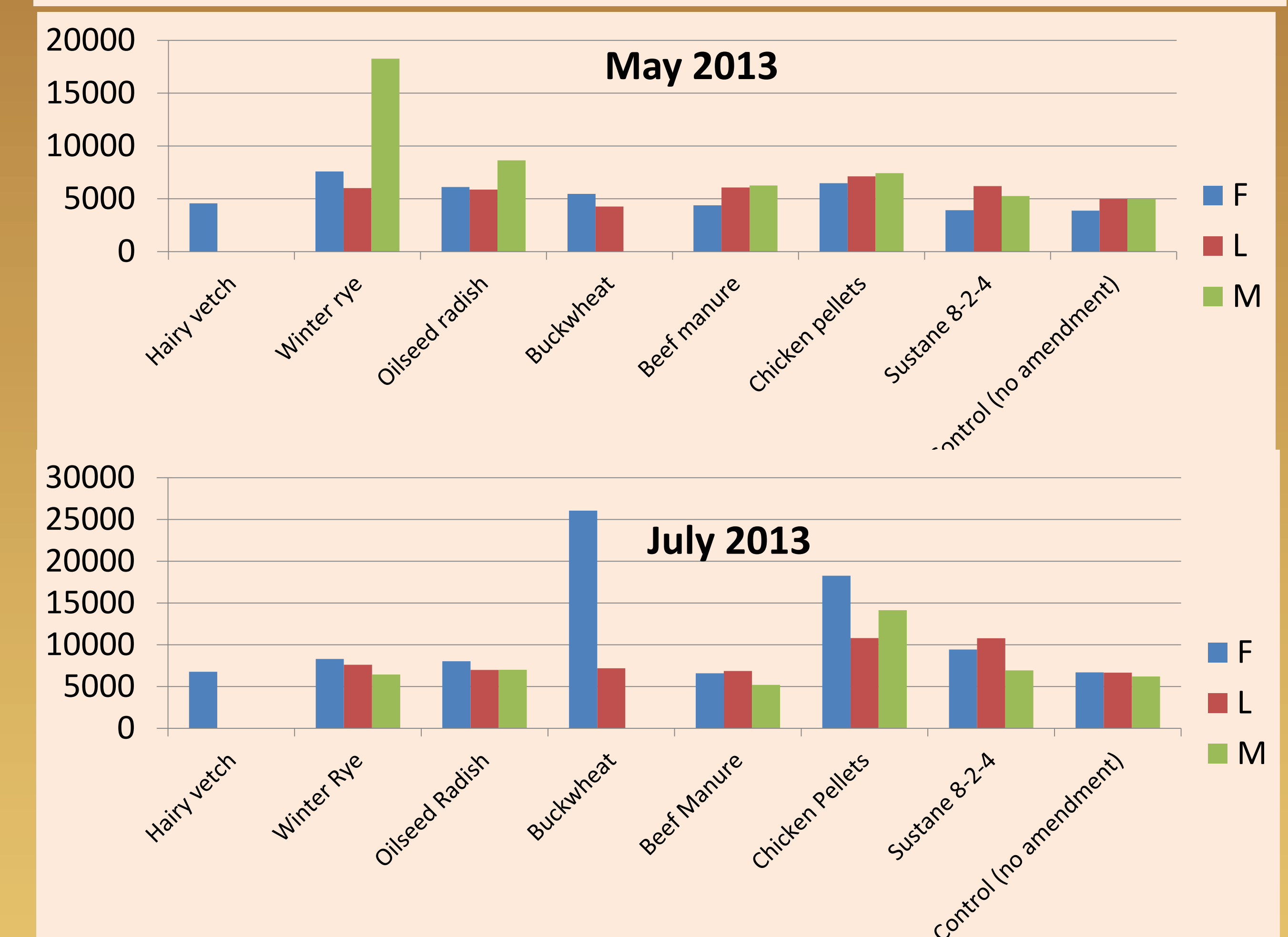
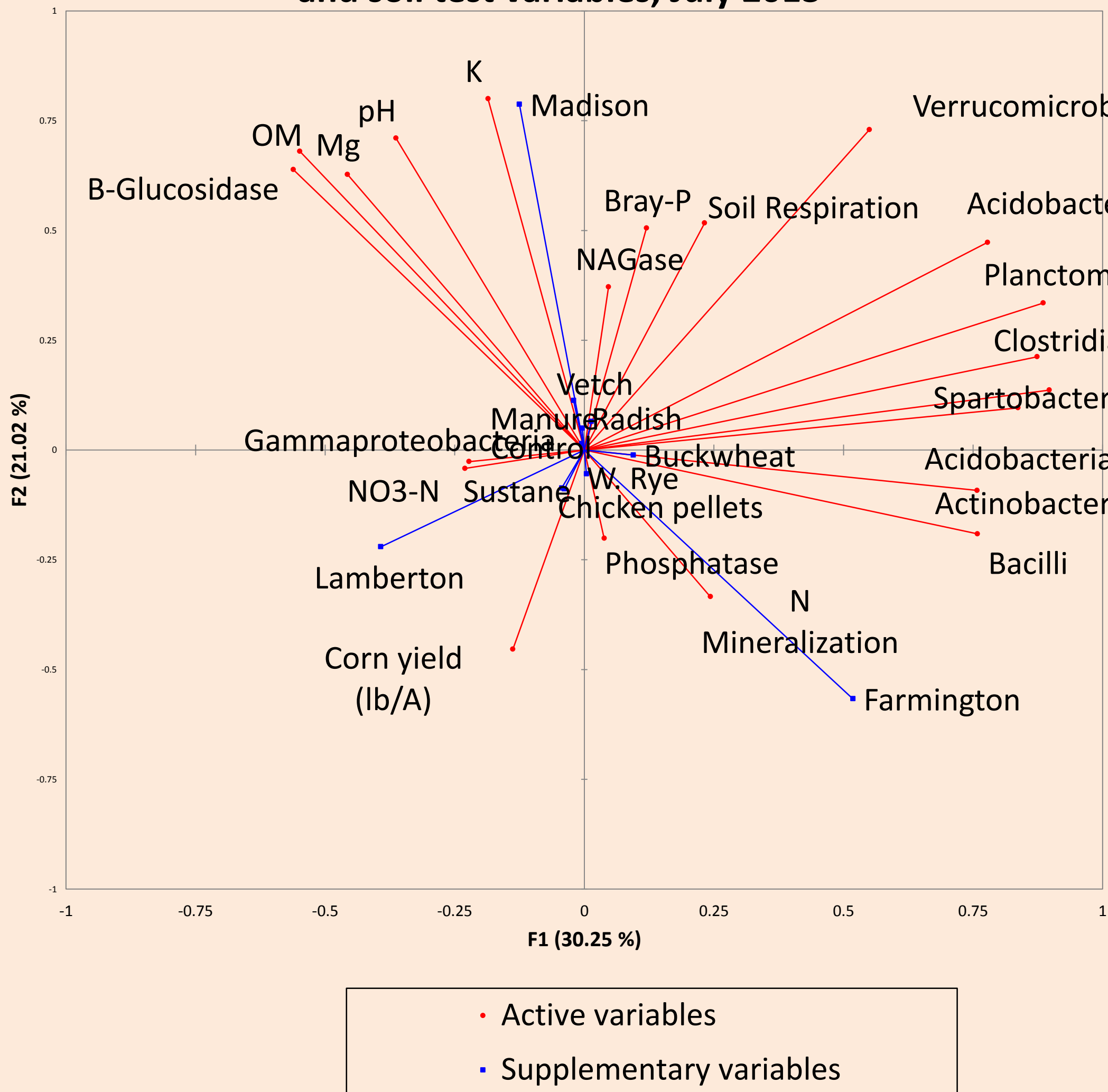


Figure 3: PCA of soil community structure and function and soil test variables, July 2013



Results

Figure 1: Amendment treatments affected microbial community membership at Madison and Lamberton, but did not affect community diversity.

Figure 3: Abundances of bacterial taxa at the class level were correlated with soil nutrient levels, OM, pH, respiration and net N mineralization. Associations of community structure and function measures with experimental sites were stronger than associations with amendment treatments.

Figure 2: Activity of NAGase, measured in May and July 2013 (Figure 2; missing bars represent cover crop treatment failure at that location), was affected by amendment treatment ($p \leq 0.05$). β-Glucosidase and phosphatase activity varied with location, but not with amendment. Effect of amendment on net N mineralization was not significant.

Conclusions

- Organic amendment treatments produced changes in soil function; however, community structure and function were much more strongly affected by site (soil type) than by amendment treatments.
- Amendment treatments affected corn rhizosphere community membership, but did not change community diversity.
- Individual bacterial classes showed differing associations with soil function, nutrient levels, OM, and pH.

Acknowledgments

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References
Schloss, P.D., et al., Introducing mothur: Open-source, platform-independent, community-supported software for describing and comparing microbial communities. Appl Environ Microbiol, 2009. 75(23):7537-41.