

Conservation Tillage Impacts Soil Microbial Community Structure and Function in a Long-Term Corn-Soybean Cropping System

Hussein Alserae¹, Virginia L. Jin², Humberto Blanco-Canqui¹, Marty R. Schmer², Rhae A. Drijber¹

¹Dept of Agronomy and Horticulture, University of Nebraska-Lincoln, Lincoln, NE.
²USDA-ARS, Lincoln, NE.



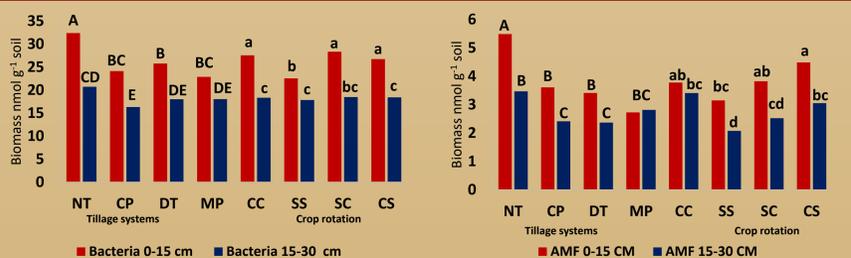
Justification

- Soil microbial response to disturbances caused by crop and soil management may lead to changes in the soil microbial community and their function.
- Soil enzymes play an important role in organic matter decomposition and nutrient cycling. Some enzymes facilitate the breakdown of organic matter (e.g., cellulase and glucosidase), while others result in nutrient mineralization (e.g., urease, phosphatase, and arylsulfatase).

Experimental Design

- This ongoing study at Rogers Memorial Farm was established in 1986, 10 km east of Lincoln, NE (40°5' N, 96°3' W) on Aksarben (fine, smectitic, mesic Typic Argiudoll) and Wymore (fine, smectitic, mesic Aquertic Argiudoll) silty clay loam soils.
- Long-term tillage experiment managed by USDA-ARS, Lincoln NE.
- Experimental design: RCBD 4*4*2 with 3 rep (since 1986):
 - 4 Tillage systems: No-tillage (NT), Chisel plow (CP), Disk tillage (DT), and Moldboard Plow (MP).
 - 4 Crop Rotations: Continuous Corn (CC), Continuous Soybean (SS), Soybean Corn (SC), and Corn Soybean (CS).
 - Fertilizer N was urea 168 kg N ha⁻¹ applied to corn via injection knives to a depth of 10 to 15 cm.
- Sampling date: 4/14/2015, prior to tillage and planting.
- 2 Depths: 0-15 cm and 15-30 cm.
- Microbial biomass and community structure determined on freshly sampled and frozen soil by Fatty Acid Methyl Ester (FAME) analysis.
- Extracellular enzyme activities (EEA) determined on air-dried soil using standard protocols.
- ANOVA and canonical discriminant analysis was conducted by running PROC GLIMMIX and PROC CANDISC in SAS version 9.4.

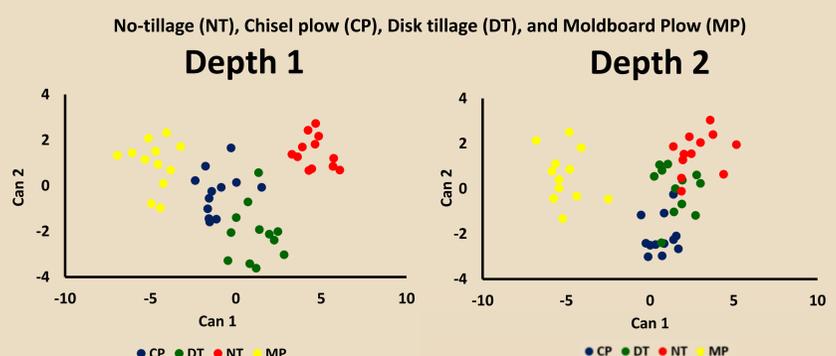
Results



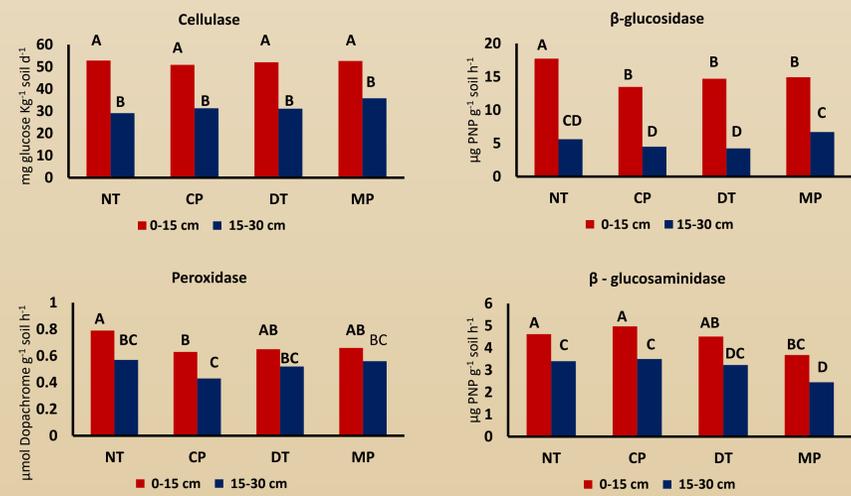
Effect	Total microbes		Actinomycetes		Saprophytic fungi		AMF	
	Pr > F	Pr > F	Pr > F	Pr > F	Pr > F	Pr > F	Pr > F	Pr > F
Block	<.0001	<.0001	0.0032	0.017	<.0001	<.0001	<.0001	<.0001
Tillage (T)	<.0001	<.0001	<.0001	0.029	<.0001	<.0001	NS	NS
Crop Rotation (CR)	0.0006	0.0046	0.0002	NS	NS	<.0001	<.0001	NS
Depth (D)	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
T*CR	NS	NS	NS	NS	NS	NS	NS	NS
T*D	0.0002	0.0061	<.0001	0.0342	<.0001	<.0001	<.0001	<.0001
CR*D	0.0331	0.0338	0.0179	NS	NS	NS	NS	NS
T*CR*D	NS	NS	NS	NS	NS	NS	NS	NS

Soil Microbial Community Structure and Enzyme Activities

TILLAGE

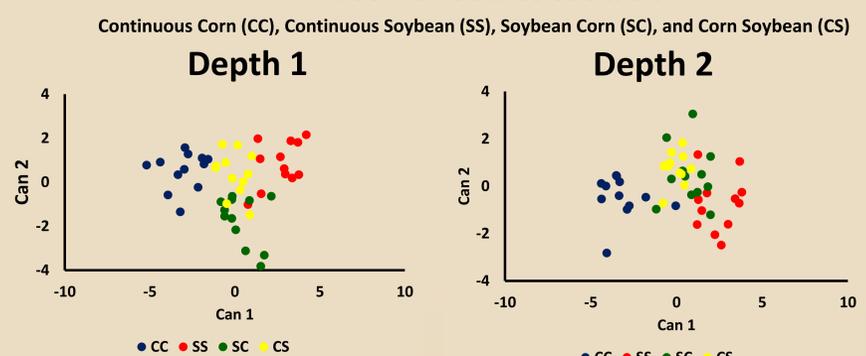


- Canonical discriminant analysis separated the impact of NT and MP on soil microbial communities.
- Separation of tillage systems CP and DT were less pronounced.

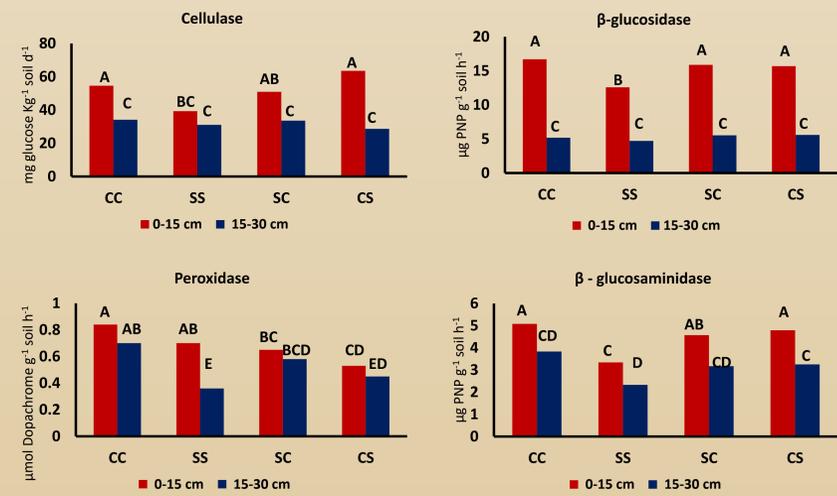


- EEA decreased with soil depth regardless of tillage system.
- Intensive tillage such as MP reduced EEA compared to NT.
- Urease and cellulase were nonresponsive to tillage.

CROP ROTATION



- Canonical discriminant analysis separated the impact of CC and SS on soil microbial communities.
- Separation of the crop rotations (SC and CS) were less distinct.



- Crop type and rotation significantly influenced all EEA's with the exception of urease.
- The lowest activity of C-cycling enzymes, cellulase, β-glucosidase, and β-glucosaminidase, was found under continuous soybean.

Effect	Arylsulfatase	β-glucosidase	β-glucosaminidase	Acid phosphatase	Alkaline phosphatase	Phenol oxidase	Peroxidase	Cellulase	Urease
	Pr > F	Pr > F	Pr > F	Pr > F	Pr > F	Pr > F	Pr > F	Pr > F	Pr > F
Block	NS	NS	<.0001	0.0164	0.0014	NS	NS	NS	<.0001
Tillage (T)	<.0001	<.0001	<.0001	NS	0.0260	0.0235	0.0008	NS	NS
Crop Rotation (CR)	<.0001	<.0001	<.0001	<.0001	0.0003	0.0362	<.0001	0.0018	NS
Depth (D)	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	0.0002
T*CR	NS	0.0266	NS	NS	NS	NS	<.0001	<.0001	NS
T*D	0.0004	<.0001	NS	NS	<.0001	NS	NS	NS	NS
CR*D	0.0466	0.0002	NS	NS	0.0015	NS	0.0005	0.0002	NS
T*CR*D	NS	0.0381	NS	NS	NS	NS	0.0038	NS	NS

Discussion

- Bacterial biomass, as measured by FAMES, was reduced under tillage compared to no-till suggesting loss of microbial habitat (e.g. stable aggregates) or less favorable environmental conditions.
- Although saprophytic fungi was only marginally affected by tillage, AMF sharply declined with any form of tillage indicating differential sensitivity to tillage among hyphal organisms.
- A fairly consistent effect of crop rotation was higher microbial biomass and C-cycling enzyme activities in continuous corn (CC) compared to continuous soybean (SS). This effect is likely due to the high inputs of plant biomass in continuous corn supporting a larger microbial biomass and greater potential for enzyme production.

Conclusion

- Tillage had a consistent and negative impact on soil microbial biomass and enzyme activities, especially in the 0-15 cm depth.
- High plant inputs resulted in increased soil microbial biomass and activities and vice-versa.
- Soil microbial biomass and function decreased with increasing depth irrespective of tillage systems or crop rotations.

Acknowledgements

I'd like to thank Dr. Rhae Drijber, Dr. Elizabeth Jeske, Dr. Virginia Jin, and Salvador Ramirez II for their assistance in this project.