

## INTRODUCTION

Corn grown in rotation with soybeans is a major agroecosystem in the northern Great Plains of the United States. The impact of this rotation when compared to continuous corn and the effect of long-term nitrogen (N) application on the soil microbial biomass (SMB) has implications for nutrient cycling, soil till, crop growth promotion, and carbon (C) storage. Bacteria and fungi are subsets of the SMB and may not respond to inputs and management in the same way (Petersen et al, 2002, Rousk and Bååth, 2007).

Within the soil fungal community there are functional and metabolic differences between the saprophytic and arbuscular mycorrhizal (AMF) communities based on C source (van Groenigen et al, 2010). Saprophytic fungi obtain their C from the decomposition of organic matter in the soil or from plant root exudates. These fungi are especially important in reduced tillage management as they can grow up into surface residue layers and cycle nutrients down into the soil (Frey et al. 2003).

In contrast, AMF exist only in a symbiotic relationship with plant roots and obtain their C directly from root cells in exchange for water and soil derived nutrients such as P, N and Zn (Smith and Smith (2011)). Both maize (Grigera et al, 2007) and soybeans (Frey and Ellis, 1997) have important AMF associations.

## REFERENCES

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## MATERIALS AND METHODS

This study was conducted on a long-term irrigated, minimum-till site in eastern Nebraska (USA) on a Fillmore/Sharpsburg silty clay loam:

### 3 crop rotations:

- Continuous corn (CC)
- Corn following soybeans (CB)
- Soybeans following corn (BC).

### 5 N rates: (urea) 0,50,100,150,300 kg N ha<sup>-1</sup>

- N rates in place on these plots since 1997
- Soil disked after fertilizer application

**Soil Samples:** 10 cores, 2 cm wide x 20 cm deep, composited by plot

**FAME biomarkers:** (Bååth and Anderson, 2003 Drijber et al, 2000)

- AMF (C16:1c11)
- Saprophytic fungi (C18:2c9,12)

**Statistics:** Ward's cluster analysis performed on transformed data as percent difference from the mean in nmol g<sup>-1</sup>

Fig. 1. Total soil microbial biomass

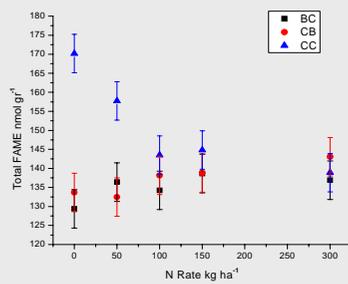


Fig. 2. Saprophytic fungal biomass

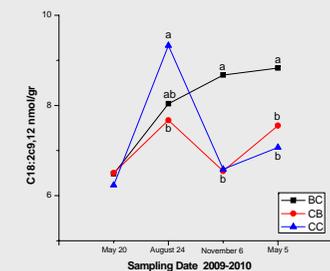
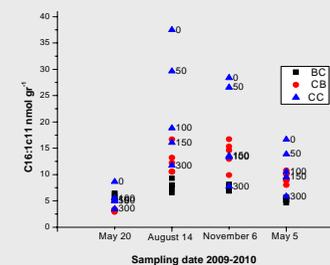


Fig. 3. Arbuscular mycorrhizal biomass



## RESULTS AND DISCUSSION

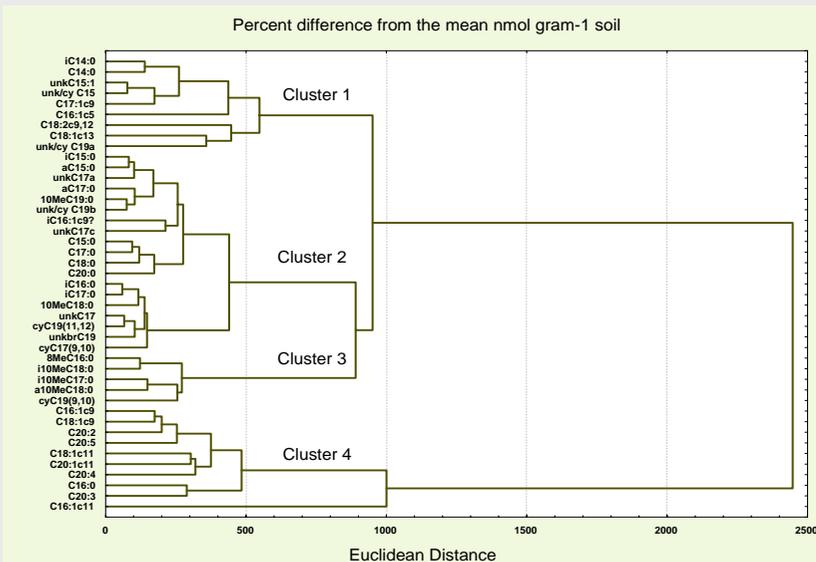
**Cluster 1** Eight bacterial FAMES and the saprophytic fungal marker C18:2c9,12. Most of these FAMES are higher during soybean growth and with the exception of C17:1c9 do not respond to N addition.

**Cluster 2** Bacterial or general FAMES most of which increase with increasing N rate and are higher under CC. All of the known FAMES in this cluster are saturated with many having methyl groups attached in either the iso or anteiso positions at the end of the C chain or in mid-chain. Two have cyclopropyl groups in mid-chain suggesting a bacterial membrane response to increasing soil acidity with increasing N rate.

**Cluster 3** FAMES containing a mid-chain methyl (actinomycete) or cyclopropyl group. These FAMES show no rotational differences. All of the FAMES increased with increasing N but for most the p values are closer to 0.1.

**Cluster 4** FAMES are highest under CC with the exception of C18:1c11 and all but C18:1c9 decline significantly with increasing N rate (C18:1c9 declines with increasing N only in CC). Cluster 4 is most distant from the other clusters and is composed mainly of FAMES with strong eukaryotic association (AMF, protozoa, collembola and saprophytic fungi). The exception with both bacterial and fungal contribution are C16:0, C16:1c9, C18:1c9, and C18:1c11.

Fig. 4. Ward's Cluster analysis of FAMES



## CONCLUSIONS

The fungal and bacterial portions of SMB respond differently to N rate and crop rotation (Fig 4.). Growth of bacteria is promoted by N in the form of increased saturated FAMES. Saprophytic fungi do not respond to N and are more abundant following soybeans due to a post-harvest flush of growth that persists into the next season (Fig 2.).

Extraradical AMF hyphae in soil decline dramatically with increasing N rate (Fig 3). The proliferation of AMF in the 0 and 50 kg N ha<sup>-1</sup> CC plots suggest that AMF may be playing a role in N uptake by the crop as well as P. Smith and Smith (2011) state that there is a mycorrhizal pathway for N from soil to plant but the amount of N supplied, mechanisms involved and the cost to the plant is not clear.

SMB is highest in CC where no N was applied due to large amounts of AMF biomass (Fig 1.). SMB declines after soybean growth and is replenished by the following corn crop.

Our work supports the conclusion of Russell et al. (2009) that management strategies that maintain high crop yields while reducing N fertilizer inputs would have environmental benefits. These benefits may be in the form of larger SMB with a greater proportion of fungi which play a larger role in no-till and minimum-till systems, and a promote a greater C sink in the form of AMF. The abundance of AMF in SMB at 0 or 50 kgNha<sup>-1</sup> encourage the inclusion of AMF in soil C models (Rillig, 2004).