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Long-term soil microbial community and enzyme activity responses to an integrated cropping-livestock system in a semi-arid region☆

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ABSTRACT

Water availability is a primary limiting factor facing agricultural systems in most semi-arid regions across the world. This study is part of a larger long-term project to develop and evaluate integrated crop and livestock systems in order to reduce dependence on underground water sources by optimizing cotton (*Gossypium hirsutum*) production in the Texas High Plains of U.S. Selected microbial, chemical and biochemical properties were studied (between 7 and 10 years) in a clay loam soil (fine, mixed, thermic Torrertic Paleustolls) under continuous cotton compared to an integrated cropping-livestock system that included cotton, forage, and Angus-cross-stocker beef steers (initial body weight 249 kg). For the integrated system, steers grazed in sequence a perennial warm-season grass 'WW-B. Dahl' old world bluestem (*Bothriochloa bladhii*) paddock, and then rye (*Secale cereale* L.) and wheat (*Triticum aestivum* L.) grown in two paddocks (stages) of a rotation with cotton. Our previous studies after 5 years showed greater microbial biomass C (MBC) in perennial pasture (193 mg kg^{-1} soil) and the rotation when sampled under rye or cotton (average of 237 mg kg^{-1} soil) compared to continuous cotton (124 mg kg^{-1} soil) at 0–5 cm. After 7 years, MBC became significantly higher in the rotation independent of the crop compared to continuous cotton in this study. At the end of 10 years, total C was higher in both the rotation and pasture of the integrated cropping-livestock system (average across grazing treatments: 17.3 g kg^{-1} soil) compared to continuous cotton (11.4 g C kg^{-1} soil). Soil MBC and several enzyme activities were higher under non-grazed areas compared to grazed areas within the integrated cropping-livestock system in some samplings. Microbial community structure of pasture soil showed higher FAME indicators for G− (i.e., *a*17:0 and cy19:0) and actinomycetes (i.e., 10Me17:0) under grazed areas compared to non-grazed areas. Microbial community structure of pasture soil showed higher fungal populations compared to continuous cotton. The rotation showed intermediate sum of bacterial FAME indicators among systems (continuous cotton > rotation > pasture) and a tendency for numerically slightly higher fungi:bacterial ratios compared to continuous cotton. This study demonstrated increases in microbial biomass and enzyme activities of C-, N-, P- and S-cycling within an integrated cropping-livestock system that may represent positive changes in soil functioning compared to continuous cotton.

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1. Introduction

Water availability is a significant factor limiting agricultural production in many semi-arid regions including the Texas High Plains region. Efforts to sustain cotton production in this region have focused on integrating small grain crop rotations with cotton and pasture for livestock production systems in order to reduce irrigation needs relative to typical continuous cotton monoculture (TAWC, 2007; Allen et al., 2005, 2008). The benefits for integrated livestock-crop production systems compared to specialized systems (i.e., monoculture crop production) has been shown to reduce water usage and fuel costs associated with irrigation, and to improve soil chemical, microbial and/or physical properties (Franzluebbers, 2007) with potential positive implications to soil quality (Acosta-Martínez et al., 2004).

To evaluate potential soil quality enhancements including soil nutrient cycling capabilities, soil C sequestration and other processes, the size, composition and activity of soil microbial communities must be considered. Soil microbial communities, as the primary source of soil enzymes, mediate critical nutrient cycling

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functions such as decomposition, nutrient mineralization, and soil organic matter transformation (Tabatabai, 1994; Sotomayor-Ramirez et al., 2009). Furthermore, the soil microbial component is sensitive to changes in soil due to land use or management before changes in other soil properties are detected (Gregorich et al., 2006; Acosta-Martínez et al., 2007). Ingram et al. (2008) stated that to better understand C- and N-cycling, it is important to gain understanding of microbial communities and related processes. Further, studying several enzyme activities involved in C, N, P and S cycling can provide information of soil metabolic or functional responses to changes in management practices (Powlson et al., 1987; Turco et al., 1994; Kandeler et al., 1999; Kennedy, 1999; Karlen et al., 2003).

In 1997, a long-term research site was established in the Texas High Plains in order to compare a monoculture cotton cropping system with an alternative system that integrated cotton and livestock production, in which cattle sequentially grazed a 2-paddock cotton and small grain crop rotation and a perennial pasture paddock throughout the year while maintaining cotton production during summer. This type of cattle grazing is a common practice in the livestock production industry sector, which views the rotation and pasture as a single integrated cropping-livestock system because of the interaction of the sequential cattle grazing between pasture and crop-rotation paddocks over time. Non-grazed zones were also established within each paddock area to evaluate long-term soil responses to the effects of grazing within the integrated cropping-livestock system.

To evaluate the sustainability of the integrated cropping-livestock system agriculture practices, many different research activities were conducted at this Texas High Plains long-term research site. Research during the first 5 years (1997–2002) only assessed soil responses to the integrated cropping-livestock system in the non-grazed areas, and demonstrated that a tilled monoculture cotton system required more irrigation, was more susceptible to wind-induced soil erosion, and showed lower soil organic matter and microbial biomass than in the integrated cropping-livestock system (Acosta-Martínez et al., 2004; Allen et al., 2005, 2008). Furthermore, soil (0–5 cm) under the perennial grass pasture demonstrated higher soil organic C, aggregate stability, microbial biomass C, enzyme activities, and protozoan and fungal abundances when compared to continuous monoculture cotton; however, this trend for the two-paddock rotation within the integrated cropping-livestock system was crop dependent when compared to continuous cotton during the first 5 years of the study (Acosta-Martínez et al., 2004). Thus, it is important to evaluate beyond 5 years the responses of soil microbial communities to this rotation compared to continuous cotton. In addition, it is important to evaluate the grazing effects on the soil microbial communities and functionality within the integrated cropping-livestock system which have not been addressed. Relatively little is known about the long-term impacts of grazing on soil microbial communities and metabolic functioning. Research in grazed systems have shown contradictory responses of the soil microbial communities as many factors likely contribute to grazing effects on soil, including inherent soil properties, soil interactions with vegetation, environmental factors, and intensity of grazing (Schuman et al., 1999; Parton et al., 2001; Ganjegunte et al., 2005).

This study intends to evaluate the long-term (10 years) sustainability of integrated cropping-livestock practices at this Texas High Plains research site. Our first objective is to elucidate the soil microbial community size (microbial biomass C and N), structure (microbial functional groups abundances using fatty acid methyl ester profiling) and function (enzyme activities of C, N, P and S cycling) as indicators of potential soil quality changes between these contrasting management practices between 7 and 10 years. The second objective is to evaluate the long-term grazing effects (grazed vs. non-grazed areas) on the microbial community size, structure and functionality within the integrated cropping-livestock system. Therefore, this 10-year study will allow for a more complete and realistic assessment of the integration of livestock and cotton production impacts, and it will include grazing effects which were not investigated in first 5 years of this study. We hypothesize that a lag time greater than 5 years occurs before differences in soil microbial responses between integrated cropping-livestock system when compared to continuous cotton. Thus, this study intends to resolve if the continuation of an integrated livestock-cotton system beyond 5 years can cause a shift in microbial dynamics in the crop rotation compared to continuous cotton. This finding would suggest that an integrated cropping-livestock system as a whole is a viable option to maintain the sustainability of cotton-farming practices in semi-arid regions of the Texas High Plains by promoting soil quality and ecosystem health. We contend that soil microbial community structural and functional components between differing long-term cropping management practices (monoculture vs. integrated livestock-cotton system) will not be similar. We hypothesize that soil microbial biomass will maintain the highest levels in the pasture and lowest in the continuous cotton, with intermediate levels in the two-paddock crop rotation areas. Furthermore, very different microbial functional group abundances and enzyme activity levels in the soils should be apparent among these cropping management practices.

2. Materials and methods

2.1. Experimental design and soil management

The research site was initiated in 1997 at the Texas Tech University field laboratory located in northeast Lubbock County in the Texas High Plains (101°47′ west longitude; 33°45′ north latitude; 993 m elevation). This area has a dry steppe climate with mild winters. Mean annual precipitation is 465 mm (with most of the precipitation occurring from April through October). The soil was Pullman clay (Fine, mixed, thermic Torrertic Paleustolls) with an average pH of 7.4, 38% clay, 28% silt and 34% sand. A more detailed description of this research site can be found in Allen et al. (2005) and Acosta-Martínez et al. (2004) where soil microbial properties at year 5 were previously published. In brief, the research site was established to compare a continuous cotton system and an integrated cropping-livestock system, which were replicated three times in a randomized block design for a total of 12.75 ha in the experimental area (Fig. 1). Generally, both systems were irrigated with an underground drip irrigation system with tapes located on 1-m centers and buried about 0.36 m deep. The cotton varieties for both systems were Paymaster 2326RR (1998–2002), 'Fibermax 989 BR03-04 (2003–2004), Fibermax 960BR05 (2005) and Fibermax 9058F (2007).

Each replication of the continuous cotton system was comprised of a single 0.25-ha plot. Cattle were not a part of this system. Nitrogen was applied through the irrigation tape during the growing season (mean N application rate was 150 kg ha^{-1}). Phosphorus, K, and S were the only other supplemental nutrients applied as recommended by post-planting soil nutrient analysis. In addition, chemicals, herbicides, and plant growth regulators were applied as recommended by integrated pest management specialists.

Each replicate of the integrated cropping-livestock system comprised 4 ha divided into three- paddocks. Approximately 53.6% (2.14 ha) of the area consisted of a perennial warm-season grass 'WW-B.-Dahl' old world bluestem [*Bothriochloa bladhii* (Retz) S.T. Blake] paddock. The remaining 46.4% of the system was divided equally into 2-paddocks for two stages of a small grain forage–cotton rotation (0.93 ha each). Livestock production was