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Soil fungal distribution and functionality as affected by grazing and vegetation components of integrated crop–livestock agroecosystems

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ABSTRACT

Integrated crop and livestock (ICL) agroecosystems are characterized by a mixture of perennial or annual vegetation grazed by livestock and annual harvested crops. Compared to annual crops, ICLs hold the potential to enhance soil organic matter (OM) inputs, carbon sequestration, nutrient cycling, and water conservation. Soil fungi play an essential role in the transformation of OM and nutrients and soil structure stabilization; however their specific role in OM transformations in ICL agroecosystems has not been studied. This study evaluated mycorrhizal and saprophytic fungal populations (via fatty acid methyl ester profiles; FAME) and saprophytic fungal functionality (via FungiLog analysis) under two ICL agroecosystems and a continuous cotton (*Gossypium hirsutum* L.) system in the Southern High Plains of the U.S. The first ICL system included non-irrigated perennial native grasses, an annual cotton and foxtail millet (*Setaria italica*) rotation and deficit-irrigated 'WW-B. Dahl' old world bluestem (*Bothriochloa bladhii*; OWB). The second ICL agroecosystem consisted of deficit-irrigated OWB and bermudagrass (*Cynodon dactylon*). The effect of grazing by cattle was evaluated via grazing exclusion areas. Abundance of saprophytic fungal FAMEs (10–26% of total FAMEs) and mycorrhizal FAMEs (2–24% of total FAMEs) were higher under ICLs compared to the continuous-cotton system at 0–5 cm. Overall, vegetation impacted the distribution of the fungal FAME markers, whereas the fungal saprophytic functionality was more sensitive to grazing. Perennial vegetation of ICLs was associated with an increase in fungal markers (saprophytic and mycorrhizal) as well as increased soil OM content. Greater utilization of multiple C sources and increased saprophytic fungal functional indices were found under cotton, non-grazed perennial vegetation (with exception of bermudagrass) and the rotation under millet. Among the grazed perennial vegetation, bermudagrass showed the highest fungal FAMEs abundance and functional diversity values. These fungal improvements were also reflected in the highest OM content under this grass, potentially indicating improved sustainability under the OWB and bermudagrass agroecosystem.

1. Introduction

Integrating grazing livestock production into cropping systems is an alternative agronomic practice to monoculture cropping and has been successfully utilized in diverse ecoregions including the cold, subhumid region of northcentral USA and Canada and the semiarid Southern High Plains (SHP) USA (Allen et al., 2005, 2012; Franzluebbers, 2007; Russelle and Franzluebbers, 2007). In the SHP, these integrated crop–livestock agroecosystems (ICL) have been shown to reduce irrigation and energy needs in comparison to monoculture cropping while increasing nutrient supply and carbon (C) storage (Allen et al., 2005, 2012; Acosta-Martínez et al., 2010a). This has been especially beneficial in the SHP region that faces declining water supplies from the nonsustainable extraction of the Ogallala Aquifer. The dominant crop is irrigated monoculture cotton that returns less biomass than other major crops (Lal, 2004) and leaves more soil exposed to the strong winds of this region. In contrast, ICLs typically include perennial grass paddocks which protect the soil surface from erosion (Kort et al., 1998) and increases nutrient availability from the decomposition of diverse plant residues via aboveground litter inputs (Patra et al., 2005; Seastedt et al., 1988) and root exudates (Bardgett et al., 1996). Although ICLs have been shown to sustain multiple ecological, economic, and agronomic benefits, the vast combinations of crop, livestock, and soil management options warrant long-term evaluation of the systems components to best understand the mechanisms and drivers responsible for enhanced sustainability.

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At the core of many ecological services supporting long-term sustainability are the processes performed by soil microorganisms. Soil fungi constitute a major proportion of the soil microbial biomass and support ecological sustainability in all ecosystems due to their key roles in nutrient cycling (Suberkropp and Weyers, 1996), formation of stable soil aggregates (Schutter and Dick, 2000), crop disease introduction and suppression (Fravel et al., 2003; Janvier et al., 2007) and C storage (Adu and Oades, 1978; Suberkropp and Weyers, 1996). In semiarid environments, fungi are particularly important to help aggregate soil particles to protect against erosion and increase water and nutrient uptake via extension of rooting surfaces from mycorrhizal associations (Rillig, 2004). Furthermore, fungi are sensitive to environmental (Sobek and Zak, 2003) and agronomic disturbances (Drijber et al., 2000; Frey et al., 1999; Wang and Qiu, 2006), which ultimately impact ecosystem functionality and thus, monitoring soil fungal dynamics may serve as an excellent indicator group to assess the impacts from agronomic practices on ecosystem functioning. Our knowledge of the structure of soil fungal communities as affected by land management has been expanded by using specific fatty acid methyl ester (FAME) biomarkers to distinguish between arbuscular mycorrhizal fungi (Graham et al., 1995; Olsson, 1999) and saprophytic fungi (Frostegård and Bååth, 1996; Zelles et al., 1991). Saprophytic fungal activity can be assessed using the FungiLog method (Dobranic and Zak, 1999), which provides information about the catabolic profile of soil fungi and ecosystem stability, productivity and resilience (Bell et al., 2008, 2009; Sobek and Zak, 2003).

The ICL agroecosystems can influence soil microbial communities and overall ecosystem functioning but the extent and direction of the impact depends on a variety of management choices such as tillage, vegetation type(s) and grazing management. Although higher concentrations of fungal markers have been reported in agricultural systems associated with no-till systems with increased vegetative and litter cover (Acosta-Martínez et al., 2010a; Schutter et al., 2001), the relative abundance of fungi over bacteria is not consistently higher under no-till practices compared to more intensive tillage (Helgason et al., 2009). The composition and function of the heterotrophic microbial communities can also be influenced by changes in resource availability when plant community composition is changed due to shifts in plant biochemical composition (Zak et al., 2003). Compared to monoculture production, crop rotation systems result in increased organic C and N content, microbial biomass and microbial activity (Miller and Dick, 1995; Moore et al., 2000; Acosta-Martínez et al., 2004). Furthermore, higher soil microbial diversity, enzyme activities involved in nutrient cycling and greater fungal:bacterial ratios were found in a 5-year old ICL composed of perennial grass and a wheat-fallow–rye–cotton rotation compared to cotton monoculture in the SHP (Acosta-Martínez et al., 2004). These shifts in microbial composition and enhanced functionality in the ICL however, were dependent on the crop at time of sampling. In addition to the direct effects of vegetation type on soil microbial dynamics, grazing animals potentially impact microbial communities and functions through their interactive alteration to the chemistry, growth and composition of plant communities (Bardgett et al., 1998). Although grazing can negatively impact soil microorganisms (Bethlenfalvay and Dakessian, 1984), many other studies have reported beneficial impacts (Patra et al., 2005) including enhanced N cycling via inputs from animal excreta (McNaughton et al., 1997) and altered microbial community composition (Bardgett et al., 2001). Type of animal, grazing intensity, grazing history, and inherent soil properties likely account for much of the variation between reported results and highlight the need for more studies evaluating long-term impacts of grazing on ecosystem functioning (Bardgett et al., 1998).

The complexity of ICL agroecosystems requires a systems-level approach that evaluates vegetative and grazing components over the long-term. Therefore, the present study assessed the relative abundance of saprophytic and mycorrhizal FAME fungal markers and the C utilization patterns of fungi as impacted by vegetative components of two ICL agroecosystems compared to continuous cotton (*Gossypium hirsutum* L.), as well as the effect of grazing within the ICL systems in the SHP region.

2. Materials and methods

2.1. Site description

The three agroecosystems were located in the Southern High Plains at the Texas Tech Experimental Farm (TTEF) in New Deal, TX (33°44′6.7″N latitude; 101°44′20″W longitude; 93 m elevation). The area is characterized by a semi-arid climate with a mean annual precipitation of 46.5 cm occurring mostly from April through October (NOAA, 2010). The average daily temperature ranges between 7.9 and 22.9 °C. The coolest month is January with an average low temperature of −4.4 °C, and the warmest month is July with an average high temperature of 33.3 °C. Between January and just prior to sampling in July 2010, the study site received 40.6 cm of precipitation. Two of the three agroecosystems were ICLs initiated in 2004 with three field replicates totaling 42 ha and the third agroecosystem was managed for at least four years as a continuous cotton (CTNc) system. All agroecosystems were established on Pullman clay loam soil (fine, mixed, superactive, thermic Torrertic Paleustolls) with an average of 38% clay, 28% silt, and 34% sand and a pH of 7.7 in the top 20 cm.

The first ICL is a forage-cotton (FRG_CTN) system comprised of three non-irrigated paddocks and one irrigated paddock. The non-irrigated paddocks included one paddock of perennial native grasses (PNG) (4.5 ha) and two paddocks of annual crops (1.7 ha each) that rotated between cotton [Ct; *G. hirsutum* L.] and foxtail millet [Mi; *Setaria italica* (L.) P. Beauv.]. Dominant grasses within the PNG included blue grama [*Bouteloua gracilis* (Willd. ex Kunth) Lag. ex Griffiths], sideoats grama [*Bouteloua curtipendula* (Michx.) Torr.], buffalograss [Buchloe dactyloides (Nutt.) J.T. Columbus], and green sprangletop [*Leptochloa dubia* (Kunth) Nees]. The irrigated paddock contained 'WW-B. Dahl' old world bluestem (OWB1) [*Bothriochloa bladhii* (Retz.) S.T. Blake] (2.1 ha), which originally was managed from 2004 to 2008 as part of the irrigated second ICL system described below but in 2009, was incorporated as part of the FRG_CTN system to assist in cattle retention during drought years (Zilverberg, 2012). Steers grazed PNG, foxtail millet, and OWB1, before moving to the feedyard for finishing. Average stocking density for 2009–2010 in PNG, OWB1 and in the millet of the Mi–Ct rotation were 6.6, 14.5, and 5.7 steers ha^{-1}, respectively. The PNG paddocks received a total of 60 kg ha^{-1} N, 11 kg ha^{-1} P and 18 kg ha^{-1} S in 2009, while no fertilizer was applied in 2010. In 2009 and 2010, OWB1 received an average of 200 mm of irrigation and 477 mm of precipitation per year, which is equivalent to an average of 39% replacement of evapotranspiration (i.e., deficit irrigated). This paddock also received 67 kg N ha^{-1} and 12 kg S ha^{-1} each year in the last two years prior to sampling. Each crop of the millet–cotton rotation (Mi–Ct) received 56 kg N ha^{-1}, 11 kg P ha^{-1} and 17 kg S ha^{-1} annually. The cotton variety was 'FiberMax 9058F'.

The second ICL is a deficit-irrigated (average of 49% replacement of evapotranspiration) three-paddock agroecosystem consisting of two types of perennial warm-season grasses: 'WW-B. Dahl' old world bluestem and bermudagrass [*Cynodon dactylon* (L.) Pers.] (OWB_BER). One paddock (2.1 ha) contains OWB (OWB2) and the remaining two paddocks contain 'Tifton-85' bermudagrass (BER) on 0.89 ha each. Because the two BER paddocks were similarly managed, only one bermudagrass paddock was sampled to conserve costs of analyses. Excess growth of bermudagrass was harvested