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Soil microbial communities under model biofuel cropping systems in southern Wisconsin, USA: Impact of crop species and soil properties

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ABSTRACT

Biofuel-induced landscape change will have an enormous impact on terrestrial ecosystems in the near future due to globally escalating energy demands, but investigations into the biological properties of soil under potential biofuel crops have not been well documented. The soil microbiota plays a significant role in ecosystem services and especially their regulation of carbon and nutrient cycles. To improve our knowledge about the structure of soil microbial community and the factors that influence it, we analyzed microbial lipids and various soil physicochemical factors under model biofuel cropping systems of corn, switchgrass and mixed prairie in southern Wisconsin, USA. Principal component analysis of lipid biomarkers from soil microbial communities indicated that there were consistent differences among the crop species. Microbial biomass was significantly lower in corn than prairie soils, with switchgrass intermediate to these systems. An increase in fungi to bacteria ratio was coinciding with a net growth in fungal biomass when converting conventionally managed corn system to perennial systems, which indicates the microbial community change could be affected by the creation or expansion of niches for certain functional groups, rather than rebalancing of competitive interactions among these groups. The soil microbial community structure under corn was distinct from the perennial systems with markers indicative of greater *in situ* stress in annual corn sites and a reduced proportional abundance of arbuscular mycorrhizal fungi and an increased of gram-positive bacteria. Redundancy analysis (RDA) using 21 lipid biomarkers concurrently with 17 physicochemical indices showed that these properties correlated with different subsets of the microbial communities. We conclude that the cropping system shifted the microbial community composition at this regional scale, which may also affect the microbial processes associated with these differing communities. This may be significant when scaled up from regional to national, continental or global scales.

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1. Introduction

The transformation of agricultural landscapes to include cellulosic bioenergy crops poses a historic opportunity to promote environmentally beneficial farming practices while addressing our energy demands (Robertson et al., 2008; Tilman et al., 2006). However, many of the agroecosystem elements likely to be impacted by adoption of cellulosic feedstock cropping systems remain insufficiently understood to predict their effects (Dauber et al., 2010; Groom et al., 2008). In particular, the soil microbial communities mediate processes that are important to plant productivity as well as ecosystem services, but these communities and their link to processes remain poorly characterized.

Progress towards a sustainable bioeconomy may be achieved by exploring novel production systems and the associated ecosystem services such as carbon sequestration, enhanced biodiversity, improved water quality and reduced greenhouse gas emissions. Most of these services are directly catalyzed or indirectly modulated by the microbial communities (Nannipieri et al., 2003; Schimel and Gulledge, 1998; Strickland et al., 2009; Zak et al., 2003). Different cropping systems, including different biofuel crops

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such as corn, switchgrass and prairie (Robertson et al., 2011; Perlack et al., 2005), can select different populations of bacteria and fungi, which in turn have differing capabilities to utilize substrates and withstand stresses (Strickland and Rousk, 2010; Ushio et al., 2010). Identifying land use and land cover effects on soil microbial communities together with knowledge of community-specific functions will improve understanding of fundamental controls on communities and their processes. Hence, one of the opportunities provided by biofuel production studies is to identify those characteristics and functions of soil microbial communities that are central to maintaining soil ecosystem services (Balser and Firestone, 2005; Schimel and Gulledge, 1998; Steenwerth et al., 2002).

Former studies indicate that soil attributes are important in determining the structure and function of bacterial communities (Bossio et al., 1998; da C. Jesus et al., 2010; Lauber et al., 2008; Wakelin et al., 2008). However, there still remains a scarcity of detailed knowledge about the specific factors that influence soil microbial communities. Such knowledge can provide important information for agroecosystem management and environment impact assessment. Lipid analysis is a proven tool to measure microbial abundance and composition (Vestal and White, 1989), and can be used to aid management for beneficial yield and sustainable ecosystem services (Kong et al., 2010; Steenwerth et al., 2002). In this study, we used microbial lipids to determine microbial community structure and biomass under model biofuel crops on soils representative of a 30,000 km^2 region in southern Wisconsin. The main objectives were (1) to determine the effects of three biofuel crops on belowground microbial community structure, and (2) to determine if and how differences in the microbial community structure are correlated with physicochemical factors, such as pH value, organic matter, texture and mineral elements.

2. Materials and methods

2.1. Site description and sample collection

This study was conducted in southern Wisconsin, USA, and consisted of 10 corn (*Zea mays*) sites, 9 switchgrass (*Panicum virgatum*) sites and 10 mixed prairie sites chosen to represent the geographic area (Fig. 1). Corn sites are conventionally managed on working farms, while switchgrass and prairie stands have received minimal management, either for wildlife habitat or seed production. The type and density of plant species dominating each cropping system has been described in a recent report (Werling et al., 2011). The sites ranged from 12 to 60 ha for corn, 2 to 40 ha for switchgrass, and 4 to 40 ha for prairie. The average of management time for the three crops is over 10 years. Mean soil physicochemical properties of the three cropping systems are presented in Table 1. The soil series of the 29 sites are described in Appendix.

Soil sampling was completed over 2 days in late July 2009. Replicate samples, 5 per site, were taken by a 2 cm diameter soil corer to a depth of 10 cm, kept on ice, and transported back to the laboratory the same day. Replicate samples were combined and subsampled for microbial biomarker analyses, then sieved to 2 mm and dried at 60 °C for 48 h for physicochemical analyses. For subsampled soils, we subsequently freeze-dried and homogenized the samples for storage at −20 °C.

2.2. Physicochemical analysis

Soil samples were analyzed by the UW-Madison Soil and Plant Analysis Laboratory for Al, B, Ca, Cu, Fe, K, Mg, Mn, Na, P, S and Zn by inductively coupled plasma optical emission spectrometry (Jarrel Ash IRIS High Resolution ICP-OES). Soil pH was measured in a 1:1 water solution using a meter with a combination reference glass

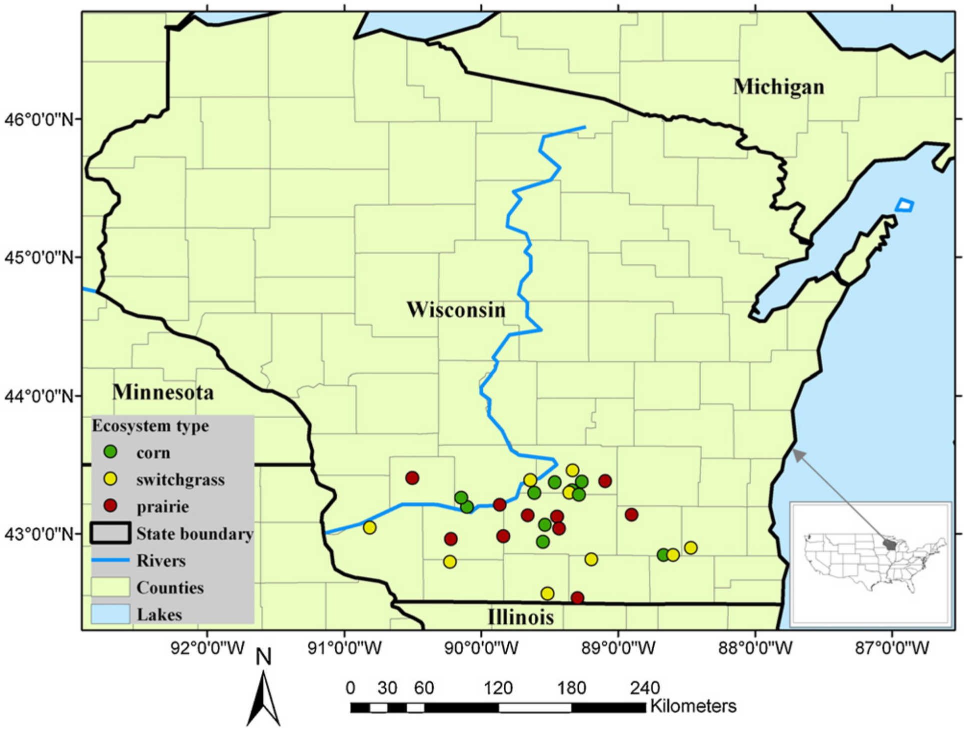

Fig. 1. Map showing the location of the corn, switchgrass and prairie sites scattered across southern Wisconsin, USA. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)