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Potential legacy effects of biofuel cropping systems on soil microbial communities in southern Wisconsin, USA

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ABSTRACT

Soil microbial community structure is clearly linked to current plant species composition, but less is known about the legacy effects of plant species and agricultural management practices on soil microbial communities. Using microbial lipid biomarkers, we assessed patterns of community-level diversity and abundance at depths of 0-10 and 10-25 cm from three hay (alfalfa/orchardgrass) and two corn plots in southern Wisconsin. Principal components analysis of the lipid biomarkers revealed differential composition of the soil microbial communities at the two depths. Despite similar abundance of fungi, bacteria, actinomycete, protozoa, and total microbial lipids in the hay and corn at 0-10 cm, community structure differed with a significantly higher absolute abundance of arbuscular mycorrhizal fungi and gram-negative bacteria in the hay plots. No significant microbial lipid mass differences were detected between the two management regimes at 10-25 cm, but the proportional dominance of bacterial gram type differed with depth. These results indicate the potential for legacy effects of annual and perennial cropping systems management on microbial community composition and suggests the importance of considering past land-use when initiating long-term agroecological trials.

KEYWORDS

Lipid Biomarker; Alfalfa; Hay; Corn; Agroecosystem

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