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Crop rotation complexity regulates the decomposition of high and low quality residues

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ABSTRACT

While many ecosystem processes depend on biodiversity, the relationships between agricultural plant diversity and soil carbon (C) and nitrogen (N) dynamics remains controversial. Our objective was to examine how temporal plant diversity (i.e. crop rotation) influences residue decomposition, a key ecosystem function that regulates nutrient cycling, greenhouse gas emissions, and soil organic matter formation. We incubated soils from five long-term crop rotations, located at W.K. Kellogg Biological Station LTER in southwestern Michigan, USA, with and without four chemically diverse crop residues. Increasing crop biodiversity increased soil potentially mineralizable C by 125%, increased hydrolytic enzyme activity by 46%, but decreased oxidative enzyme activity by 20% in soils before residue was added. After residue additions, soils from more diverse cropping systems decomposed all residues more rapidly (0.2–8.3% greater mass loss) compared to monoculture corn. The fast-cycling, 'Active C' pool and microbial biomass N increased with higher cropping diversity, but the differences among rotations in Active C pools was higher for the most recalcitrant residues. Further, the ratio of the cellulose degrading enzyme (β-glucosidase) to the lignin degrading enzyme (phenol oxidase) was highest in the two most diverse crop rotations regardless of residue additions, providing additional evidence of enhanced microbial activity and substrate acquisition in more diverse rotations. Our study shows that crop diversity over time influences the processing of newly-added residues, microbial dynamics, and nutrient cycling. Diversifying crop rotations has the potential to enhance soil ecosystem functions and is critical to maintaining soil services in agricultural systems.

1. Introduction

Decades of research shows that the loss of aboveground biodiversity and associated ecosystem functions and services is one of humanity's major challenges (Tilman et al., 1997; Cardinale et al., 2012; Hooper et al., 2012). However, few studies link plant biodiversity to belowground communities and ecosystem processes, limiting our capacity to predict whether future changes in plant communities will influence decomposition and other critical belowground functions. Given that soils sequester carbon (C), store water, support crop growth, and provide other services to our growing population, we have an imperative to better understand the relationships between plant biodiversity and soil processes.

We know that plant species richness may influence soil C accrual, nutrient cycling, and microbial biomass dynamics, but specific relationships vary across sites and systems (Zak et al., 2003; Eisenhauer et al., 2010; Mueller et al., 2013). For example, Zak et al. (2003) found that increasing species richness from 1 to 16 species in a Minnesota grassland increased soil microbial biomass, nitrogen (N) mineralization, and respiration per-unit-biomass after 7 years. However, they found no effect of plant species richness on bulk soil C or N, and other studies have shown inconsistent effects of plant diversity belowground. Eisenhauer et al. (2010) found that soil microbial biomass, but not respiration rate, was greater with increasing plant species richness. Soil inorganic N has shown both decreasing (Mueller et al., 2013) and increasing (Oelmann et al., 2007) relationships with plant richness. These divergent responses come as no surprise to soil scientists, who have been wrestling for more than a century with soils' staggering biological diversity (Fierer et al., 2007; Caporaso et al., 2011), complex physical structure (Grandy and Robertson, 2007; Tiemann and Grandy, 2014), and dynamic organic matter chemistry (Heckman et al.,

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2013), all of which confound predictions of aboveground biodiversity effects on soil function across time and space.

Converting complex natural communities to highly simplified agricultural systems is driving global declines in biodiversity (Heywood, 1995; Sala et al., 2000; Tilman et al., 2001). In agroecosystems, successive, single crop plantings (i.e. crop rotations) create temporal rather than spatial biodiversity. In many industrialized regions, this temporal diversity consists of rotating two crops in two years (e.g. corn-soybean), although both monocultures and longer rotations are not uncommon. Rotational diversity may be further augmented by planting cover crops. Cover crops are not harvested for economic gain but are instead grown to increase soil N, decrease erosion, and increase soil C inputs. Thus, rotations with and without cover crops are used to increase plant species richness, primarily by substituting temporal for spatial diversity. This "temporal biodiversity" makes agroecosystems a unique and tractable testing ground for examining the effects of plant biodiversity on soils.

Although the mechanisms are unclear, increased temporal plant biodiversity may provide some of the same belowground benefits as spatial diversity. These benefits include increased soil N availability (Drinkwater et al., 1998; Sanchez et al., 2001; Tonitto et al., 2006), increased soil organic matter (SOM) concentrations (Mitchell and Entry, 1998; Grandy and Robertson, 2007; Kou et al., 2012), increased soil microbial biomass (Ekenler and Tabatabai, 2002; McDaniel et al., 2014) and increased soil microbial diversity (Lupwayi et al., 1998; Suzuki et al., 2012; Xuan et al., 2012). However, despite this evidence of crop rotation's benefits, their centuries of use in agriculture (Bullock, 1992), and current prevalence in U.S. cropping systems (82% of current agricultural land; Padgitt et al., 2000), little is known about the mechanisms by which crop rotations affect soil biogeochemical processes.

Increasing the diversity of plant inputs to SOM with crop rotation may increase microbial community size, functioning, and biodiversity by creating more habitable resource niches (Zak et al., 2003; Hättenschwiler et al., 2005). Viewed in light of new concepts emphasizing microbial biomass as the key to SOM formation (Simpson et al., 2007; Grandy and Neff, 2008; Liang and Balser, 2010), such increases may be more likely to retain residue C in SOM. Furthermore, residue cometabolism with SOM, and conversion of that residue to SOM (Paterson et al., 2009; Kuzyakov, 2010), may be influenced by long-term rotation effects on soil decomposer communities and SOM. Ultimately, the strong linkage between aboveground biodiversity and soil functioning in crop rotations lies in the quantity, quality, and temporal diversity of crop inputs to soil, because at any one time the spatial plant richness is one.

The general objective of this study was to examine how crop rotational diversity alters the decomposition dynamics of newly-added residue inputs. More specifically, we used crop residues varying in quality to determine how crop rotation history influences C and N cycling and soil microbial communities. In a year-long laboratory incubation, we examined the decomposition of four crop residues (Red clover, *Trifolium pretense*; Soy, *Glycine max*; Corn, *Zea maize*; and Wheat, *Triticum aestivum*) in agricultural soils managed for over a decade with five different corn-based crop rotations. Combining rotations varying in diversity from one to five crops with different litter combinations allows us to test the longer-term rotation effects on processing of newly-added crop residues. Our specific research objectives were three-fold: first, we tested variations in potentially mineralizable soil and residue C pools among rotations by modeling respiration rates determined at 30 time points over a 360 day laboratory incubation; second, we examined soil inorganic N produced at 3 time points along the 360 day incubation; and third, we measured microbial biomass C and N (proxies for biological stimulation, short-term C and nutrient processing) and soil enzyme activities (proxies for microbial C and nutrient demand) to understand the microbial regulation of C and N cycling in response to residue and cropping system diversity. We predicted that increased crop diversity would enhance soil biogeochemical cycling in general, but especially for poor-quality residues where there may be resource constraints and/or biochemical obstacles (e.g. high lignin) to decomposition.

2. Methods and materials

2.1. Site and experiment description

Soils for this incubation experiment were collected from the Cropping Biodiversity Gradient Experiment (CBGE) located at the W.K. Kellogg Biological Station (KBS) Long-term Ecological Research site. Mean annual temperature and precipitation at the site are 9.7 °C and 890 mm, respectively. The two main soil series found at the site are Kalamazoo, a fine-loamy, mixed, mesic Typic Hapludalf, and Oshtemo, a coarse-loamy, mixed, mesic Typic Hapludalf (KBS, 2013). The CBGE crop rotation experiment was initiated in 2000, with biodiversity increased through the systematic addition of crops in rotations ranging from single crop monocultures to complex rotations with three different grain crops and two cover crops for a total of five species in a 3-year rotation sequence. The experimental set-up was a randomized block design consisting of 9.1 × 27.4 m plots with each crop rotation replicated across four blocks. The plots received no external chemical amendments (i.e. fertilizer or pesticides) and the same annual chisel plow tillage to a depth of 15 cm. For further details on the experimental design and agronomic management practices see Smith et al. (2008).

Soils were collected on November 15, 2011 after corn harvest from the following rotations: monoculture corn (mC), corn-soy (CS), corn-soy-wheat (CSW), corn-soy-wheat with red clover cover crop (CSW1), and corn-soy-wheat with red clover and cereal rye (*Secale cereale)* cover crops (CSW2). All soils were collected from plots coming out of the corn phase in order to avoid confounding effects of current crop differences. Three soil cores were collected within each plot (0–10 cm), homogenized in the field, and stored on ice in a cooler until arrival at the laboratory. Fresh soils were sieved to 2 mm, brought to 50% water holding capacity (WHC), then pre-incubated at 25 °C for 5 days to decompose labile substrates released during soil processing.

2.2. Crop residues and laboratory soil incubation

We collected wheat crop residues during spring 2011 and corn, soy, and red clover residues in fall 2011 (Table 1). Residues were dried at 60 °C for 3 days, ground to fragments of ~2 mm, and stored until mixed with the soils. To obtain the relative chemical composition of the crop residues we used pyrolysis gas chromatography/mass spectrometry (py-GC/MS; Grandy et al., 2007). After residue addition (at 1.2 g of residue per 100 g of dry soil) and thorough mixing, each soil-residue mixture was divided evenly into three analytical replicates for destructive sampling over the course of the incubation. Each replicate soil sample was placed in a 50 ml test tube, and all three replicate test tubes were placed into a 1 quart canning jar. Jars were placed in a dark environmental chamber set at 25 °C and were capped to prevent moisture loss, but caps were frequently removed to prevent CO_2 build-up. Soil moisture was monitored and maintained at 50% WHC by adding deionized water.