Applied Soil Ecology 101 (2016) 107–116

Contents lists available at ScienceDirect

Applied Soil Ecology

journal homepage: www.elsevier.com/locate/apsoil

Soil amendments yield persisting effects on the microbial communities—a 7-year study

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ARTICLE INFO

Article history:
Received 15 September 2015
Received in revised form 23 December 2015
Accepted 29 December 2015
Available online xxx

Keywords:
Soil amendment
Soil enzyme activity
Fungi
Bacteria
Community

ABSTRACT

Soil microbial communities are sensitive to carbon amendments and largely control the decomposition and accumulation of soil organic matter. In this study, we evaluated whether the type of carbon amendment applied to wheat-cropped or fallow soil imparted lasting effects on the microbial community with detectable differences in activity, population size, or community structure after a period of seven years post-amendment. The microbial communities from the top 10 cm of soil were analyzed for activity related to C-cycling (glucosidase, galactosidase), P-cycling (acid phosphatase), S-cycling (arylsulfatase), and N-cycling (β-glucosaminidase, arylamidase), in addition to fungal and bacterial abundance and structure. The amendments were applied at similar carbon rates for five years under annual wheat or continuous fallow and included cotton linters, sucrose, wheat residue, composted wheat residue, brassica residue, wood sawdust, alfalfa feed pellets, manure, biosolid and a no treatment control. Two crops, brassica and grass, were in the fallow treatments. The majority of the communities in the amended soils were not distinguishable from the no-treatment control. For amendments and crops that produced changes, significant differences in the population size and community structure were observable for fungi but not bacteria. Wood, sugar, and grass cropping produced the most pronounced effects on enzyme activity, fungal abundance and structure. Overall, the species of the planted crop had a significant effect on the soil enzyme activity and population size of fungi, with the greatest values under grass compared to wheat or brassica. The microbial communities were differentially affected by C source amendments in which the persistency of change and the aspect of the community affected (i.e. function, size, structure, kingdom) were dependent on amendment type.

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1. Introduction

The capacity of soil to store carbon (C) is largely influenced by the role of soil microbes in the formation and decomposition of organic matter (Paul, 2007; Six et al., 2006). The chemical composition (or quality) and quantity of detritus or C substrate has a strong impact on the rate and mode of decomposition. For example, litter with high lignin such as wood will decompose at much slower rates than cytoplasmic sugars and amino acid compounds. The type of substrate can also affect soil C and nitrogen (N) in which amendments of disparate composition produce different C/N ratios in soil when added as a surface amendment (Wuest and Gollany, 2013). Soil management strategies including fertilization, soil amendment, and selection of crop species will impact the rates of turnover in addition to the structure and function of the resident microbial communities (Acosta-Martínez et al., 2007; Acosta-Martínez and Tabatabai, 2001; Angers et al., 1993; Dodor and Tabatabai, 2002).

Extracellular soil enzymes have a key role in the stabilization and destabilization of organic matter and are important in the decay of insoluble plant materials such as cellulose and lignin. Soil management practices, environmental factors such as temperature and pH (Speir et al., 1980; Tabatabai, 1994), and the C and N status of the microbes (Allison and Vitousek, 2005; Geisseler and Horwath, 2009) affect the activity of enzymes in the soil. Enzyme synthesis is controlled under different regulatory mechanisms. Soil enzymes may be either constitutively expressed or responsive to the chemical environment, i.e. substrate availability may induce enzyme production (Geisseler and Horwath, 2009; Mobley and Hausinger, 1989; Suto and Tomita, 2001) or result in feedback inhibition. Enzyme activity can yield information regarding the substrate status of soil and may provide insight to the microbial community composition or abundance. As such, activities of several enzymes have been correlated to C and N mineralization

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http://dx.doi.org/10.1016/j.apsoil.2015.12.013
0929-1393/Published by Elsevier B.V.

rates (Allison and Vitousek, 2005; Ekenler and Tabatabai, 2002; Geisseler and Horwath, 2009), microbial respiration (Frankenberger and Dick, 1983) and microbial biomass of soils (Frankenberger and Dick, 1983; Taylor et al., 2002).

Microbial communities are dynamic and change rapidly in response to a disturbance such as an amendment. For example, changes in the community composition can be measured as quickly as 12 h post-addition (Cleveland et al., 2007). Most communities are sensitive to carbon amendments, meaning some aspect such as structure, composition, or function change in response to the addition. While some communities may remain unchanged after a perturbation (resistance), others may change and then revert back to the original composition (resilience) (Allison and Martiny, 2008). In a survey of 41 studies, the mean length of the studies showing sensitivity to disturbance (83% of studies) was far greater (4.9 ± 12.6 years) than studies showing resistance (0.15 ± 0.09 years) (Allison and Martiny, 2008). The difference in the response compared to the study duration suggests that a lag time may occur between C addition and community change, and that studies too short in length may miss key transformations. The resiliency of communities sensitive toward soil amendments is influenced by several factors including the type of carbon applied (Orwin et al., 2006), the dose (Saison et al., 2006), and the frequency of application (Saison et al., 2006). It is unclear how the microbial community resiliency is affected in farm production systems where the soil amendments may be infrequently applied or used as “pulse” applications and whether amendment type influences the response longevity.

A study on the effect different C source amendments on the soil C/N ratio in a wheat-fallow system revealed that the amendment composition had a large and lasting effect (3.5 yr) on the soil C/N ratio when application frequency and dose were constant (Wuest and Gollany, 2013). The study selected 9 different soil amendments with varying solubility, C structures, and nutrient and lignin contents to test the hypothesis that the amendment type, rather than specific dose, affects the soil organic carbon (SOC). The amendments included plant residues and compost, sugar, wood, cotton, manure and biosolid in addition to different living crops. Of the diverse amendments, wood produced a much higher C/N ratio than the other amendments including manure, compost and biosolid. The authors attributed the increased C/N ratio in the wood-amended soil to changes in the microbial community, presumably enhanced fungal populations (Wuest and Gollany, 2013). Although it is likely that many, if not all, of the amendments impacted the microbial communities to some degree, it is unknown whether the amendments produce lasting effects, particularly after the plots returned to cropping. Since the amendments were applied at similar doses based on C content and the same frequency (once a year for five years), it is possible to evaluate whether different carbon types influence microbial resiliency. The experiment initiated by Wuest and Gollany (2013) provided a unique opportunity to determine whether “pulse” amendments yield lasting effects on the microbial communities in a field setting rather than lab incubations. In the current study, we assessed the soil microbial communities of the amended plots of Wuest and Gollany (2013) which have been treated uniformly for the past 7 years post-amendment, with the final 2.5 years in crop rotation.

Community function was assessed based on the activity of extracellular enzymes functioning in C, N, phosphorous (P), and sulfur (S) cycling. Hydrolytic enzymes β-glucosidase, α-galactosidase, and β-glucosaminidase were used to query the C-cycling capacity of the soil. β-glucosidase is involved in cellulose degradation and produces glucose through the hydrolysis of the terminal, nonreducing ends (Deng and Popova, 2011). Similarly, α-galactosidase catalyzes the degradation of hemicellose and oligosaccharides by the hydrolysis of the terminal, nonreducing α-D-galactose residues (Adl, 2003; van den Brink and de Vries, 2011). The chitinase, *N*-acetyl-β-D-glucosaminidase, is involved in both C and N cycling through the release of the terminal *N*-acetyl-β-D-glucosamine residues from chitooligosaccharides (Ekenler and Tabatabai, 2002). Arylamidase catalyzes the release of the N-terminal amino acid from a peptide, amide or arylamide (Acosta-Martínez and Tabatabai, 2000a), and has been suggested as an index for net soil N-mineralization (Dodor and Tabatabai, 2002). Phosphatase produces plant available inorganic P through the hydrolysis of organic phosphomonoester (Tabatabai, 1994). Phosphatases are ubiquitous and pH sensitive, therefore the acid phosphatase was selected based on the pH range of the soil. Finally, arylsulfatase produces plant available sulfate by cleaving the O—S bond of ester sulfates, which is considered the dominant form of organic S in soil (Knauff et al., 2003; Scherer, 2009; Tabatabai, 1994). This subset of soil enzymes, in addition to assessment of the fungal and bacterial communities, was selected to determine whether the diverse composition of the amendments differentially impacted the microbial communities with persisting changes in function, structure, and/or abundance.

2. Materials and methods

2.1. Experimental design

Soil characteristics, annual precipitation averages, and previous management history of the research site located 15 km northeast of Pendleton, OR, USA is provided in Wuest and Gollany (2013). The plots were managed under no-till with crops planted in October and harvested late July according to regional practices. The experiment was initiated in 2002 in a split-plot design with two main factors of annual winter wheat (*Triticum aestivum* L.) or continuous fallow (referred to as main plots, or wheat or fallow main) and 12 subplots of 10 soil treatments and two different plant species (fallow only). The main plot locations were randomized within each of four block locations and were continuous (no rotation) throughout the experiment. The blocks were divided into randomly assigned subplots 9.29 m^2 (1.52 m × 6.10 m) with 0.15 m borders. Amendments were selected based on the common regional surface residues (wheat straw, brassica residue, alfalfa foliage) or amendments (manure and biosolids) in addition to other sources not typical of farming practices but high in concentration of different crop residue components (cotton linter is >85% cellulose [Han, 1998], sucrose is 100% sugar, wood is high in lignin). The 9 soil amendments were cotton (*Gossypium hirsutum* L.) linters, sucrose, wheat residue, composted wheat residue (referred to as compost), brassica residue (*Brassica napus* or *Brassica juncea*), wood sawdust (bark-free conifer species with 90% <1 mm size), alfalfa (*Medicago sativa* L.) feed pellets, cattle manure (un-aged, soil- and straw-free), dry biosolid from a municipal sewage treatment plant, and a no-amendment control (check). Additional amendment properties including C, N, and S contents are provided in Wuest and Gollany (2013). The amendments were added to the soil surface at targeted application rates of 250 g C m^{-2} at the end of summer 2002 just prior to planting the wheat main. The compost treatment received a lesser amount of C and N since the application rate was based on the pre-composted content of the wheat straw. The two different plant species (or crops), perennial grass tall fescue (*Festuca arundinacea* Schreb.) and winter brassica (*B. napus* or *B. juncea* L.), failed as intercrops in the wheat main and were therefore only present the fallow main. The grain drill used for planting and fertilization of the wheat was driven through the fallow plots for equal soil disturbance for the two main plots. The wheat main plots, excluding high N treatments of biosolid, manure and alfalfa, received fertilizer containing 58 g N m^{-2}, 9 g S m^{-2}, and 5 g P m^{-2} total over the five year period.