Agriculture, Ecosystems and Environment 216 (2016) 82–88

Contents lists available at ScienceDirect

Agriculture, Ecosystems and Environment

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

Changes in soil microbial community, enzyme activities and organic matter fractions under long-term straw return in north-central China

Shicheng Zhao[a], Kejiang Li[c], Wei Zhou[a], Shaojun Qiu[a], Shaowen Huang[a], Ping He[a,b,*]

[a] Ministry of Agriculture Key Laboratory of Plant Nutrition and Fertilizer, Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences (CAAS), Beijing 100081, PR China
[b] CAAS-IPNI Joint Laboratory for Plant Nutrition Innovation Research, Beijing 100081, PR China
[c] Dryland Farming Institute, Hebei Academy of Agricultural and Forestry Sciences, Hengshui 053000, PR China

ARTICLE INFO

Article history:
Received 1 December 2014
Received in revised form 21 September 2015
Accepted 25 September 2015
Available online 8 October 2015

Keyword:
Straw return
Soil microbial community structure
Soil extracellular enzyme
Light fraction organic carbon
Heavy fraction organic carbon

ABSTRACT

Field nutrients management practices influence soil biological properties and organic matter fractions. A long-term experiment (30-year) was conducted to investigate changes in soil microbial community, enzyme activities and organic carbon fractions under straw return in north-central China. Treatments included no-fertilizer control (CK) and maize straw return at rates of 0 (S0), 2250 (S1), 4500 (S2), and 9000 kg ha^{-1} (S3) under combined nitrogen and phosphorus fertilization. All fertilization treatments increased total phospholipid fatty acid (PLFA) and the abundances of Gram-negative (Gm^-) bacteria and fungi over the CK treatment. The S3 treatment increased total PLFA compared with the S0 treatment. The S2 and S3 treatments increased Gm^- bacterial abundance by 11.6 and 9.3%, respectively, and increased fungal abundance by 68.2 and 113.6%, respectively, compared with the S0. Fertilization increased the activities of β-glucosidase (BG), β-xylosidase (XYL), and N-acetyl-glucosaminidase (NAG) over the CK. The S2–S3 increased the activities of BG, XYL, and NAG by 10.5–20.7, 19.0–32.5, and 21.6–32.8% compared with the S0, respectively. Although the S1 and S3 had lower activities of phenol oxidase than the CK, the activities did not differ among the S0–S3 treatments. The S0–S3 treatments increased the concentration of total organic C (TOC) than the CK, and the S2–S3 increased TOC than the S0. There were no differences in soil light fraction (LF) and the light fraction organic C (LFOC) among the CK, S0, and S1. The LF and LFOC in the S2 increased by 14.7 and 33.9%, respectively, and these values in the S3 increased by 48.0 and 81.3%, respectively, relative to the S0. The S0–S3 treatments increased the heavy fraction organic C (HFOC) over the CK and the HFOC in the S2–S3 increased by 39.2–43.1% compared with the S0. The LFOC/TOC ratio was lower than the HFOC/TOC ratio for each treatment. Overall, low rates of straw return did not affect, while high rates of straw changed microbial community structure and increased the activities of most hydrolytic enzymes and the concentration of LFOC and HFOC under chemical fertilizer application.

1. Introduction

Soil organic matter (SOM) is the center of soil function and quality. High SOM can increase soil nutrients supply (Rochette et al., 1999), improve soil physical and biological properties (Gong et al., 2009; Guo et al., 2012), and enhance soil buffering capacity (Yang et al., 2012). Therefore, maintenance of SOM is particularly important for sustaining the productivity of agroecosystems. The enhancement of SOM increases soil carbon (C) sequestration (Lal, 2004). Many agricultural management practices such as fertilization, tillage, and straw return significantly influence SOM (Smith et al., 2005; Ludwig et al., 2011; Malhi et al., 2011). Total SOM is not sensitive to changes in soil management practices; however, one labile fraction, light fraction organic matter, which is dominated by newly incorporated plant-derived materials, and is central to nutrient cycling and microbial maintenance, responds rapidly to changes in soil management (Murata and Goh, 1997). Accordingly, this fraction is considered to be an early indicator of changes in soil quality (Haynes, 2000; Malhi et al., 2011). The SOM is most commonly estimated by soil organic carbon (SOC) content, and changes in SOC affect the C and nitrogen (N) cycle in terrestrial ecosystem (Malhi et al., 2011; Grandy et al., 2013). Changes in organic C and N of different organic matter fractions are the result of combined effects of soil chemical and biological properties.

* Corresponding author at: Chinese Academy of Agricultural Sciences, Institute of Agricultural, Resources and Regional Planning, 12 South Zhongguancun Street, Beijing 100081. Fax: +86 10 82106206.
E-mail addresses: phe@ipni.net, phe@caas.ac.cn (P. He).

http://dx.doi.org/10.1016/j.agee.2015.09.028
0167-8809/

Soil microorganisms play key roles in organic matter decomposition and soil nutrient biogeochemical cycling in ecosystems (Leininger et al., 2006; Cusack et al., 2011). Soil microbial diversity is also important in maintaining soil health and quality (Garbeva et al., 2004; Janvier et al., 2007). Different microbial communities are responsible for specific functions in the decomposition of crop residues. For example, bacteria dominate in the initial phases, while fungi dominate in the later stages of crop residues decomposition (Paterson et al., 2008; Marschner et al., 2011), and saprotrophic fungi is an important source of soil oxidative enzymes (Cusack et al., 2011). Soil microbial community structure also varies with agricultural management practices (He et al., 2007; Ai et al., 2012; Navarro-Noya et al., 2013). Long-term application of organic fertilizer was shown to increase total microbial biomass and fungal abundance, but decrease bacterial abundance in a fluvo-aquic soil in Northern China (Ai et al., 2012). No-tillage practice increased soil fungal abundance in Northeastern China (Zhang et al., 2012). Crop residues retention significantly affected bacterial community structure and increased the abundances of *Bacteroidetes*,*Betaproteobacteria*, and *Gemmatimonadetes* relative to residue removal in central Mexico (Navarro-Noya et al., 2013). Moreover, changes in microbial community structure also affect the C and N transformation in soil ecosystem (Cusack et al., 2011; Grandy et al., 2013).

Soil extracellular enzymes are synthetised and secreted by soil microorganisms, and are the proximate agents of organic matter formation and decomposition (Burns et al., 2013). Soil enzyme activities can provide useful insights into the mechanisms of microbial sensitivity to added N and C. Soil enzymes can be divided into hydrolytic enzymes which are responsible for the acquisition of C, N, and phosphorus (P) to support primary metabolism, and oxidative enzymes, which degrade recalcitrant compounds like lignin in cometabolic acquisition of nutrients (Sinsabaugh and Moorhead, 1994; Tiemann and Billings, 2011). These groups of enzymes may respond differently to the addition of C and N to soil and field management practices (Grandy et al., 2008, 2013; Sinsabaugh et al., 2008; Cusack et al., 2011). Cusack et al. (2011) found that N addition increased the activities of some hydrolytic enzymes, but decreased oxidative enzyme activities in two tropical forests. Wang et al. (2015) reported that the increasing N inputs increased *N*-acetyl-glucosaminidase activity, but decreased β-glucosidase activity in three sizes of soil aggregate in a semi-arid grassland, China.

The north-central China is a highly intensive agricultural area with a winter wheat (*Triticum aestivum* L.)—summer maize (*Zea mays* L.) double-cropping system, the sustainable utilization of agricultural soil in this major grain-producing region could affect China's food security (Gong et al., 2009). In recent decades, crop straw return was widespread in this region (Li and Jin, 2011). Straw return increases the inputs of nutrients and organic C, and has great potential in enhancing soil fertility, SOM, and microbial population (Lal, 2004; Powlson et al., 2008). Soil C/N ratio is a critical factor influencing SOM decomposition and accumulation. We used a long-term field experiment consisting of various rates of straw return under chemical fertilizer application in north-central China, the objectives were to examine the effects of straw return on soil microbial community, enzyme activities, and organic C fractions. We hypothesized that (i) microbial biomass would increase and microbial community structure would change because of increased SOC and N inputs from fertilization and straw retention; (ii) hydrolytic enzyme activities would increase and oxidative enzyme activities would decrease under increasing soil N levels; and (iii) the increase in the light fraction organic C would be insignificant/negative in low straw return rates and be significant in high straw return rates under the increased microbial biomass and hydrolytic enzyme activities.

2. Materials and methods

2.1. Experimental site

The field experiment was established in October 1981 at the Hengshui Dryland Farming Experimental Station, Hebei province, north-central China (37°53′N, 115°42′E). This site has a warm temperate, sub-humid continental monsoon climate. The 30-year mean annual temperature and precipitation were 12.4 °C and 550 mm, respectively, and two-thirds of precipitation fell between June and September. The soil in this site is a sandy loam fluvo-aquic soil (Calcaric Cambisols, FAO). The physical and chemical properties of initial soil (0–20 cm) in 1981 were as follow: pH 8.7 (soil: water = 1:2.5), organic matter 11.5 g kg^{-1}, total N 0.83 g kg^{-1}, total P 1.03 g kg^{-1}, total K 20.31 g kg^{-1}, Olsen-P 12.3 mg kg^{-1}, and exchangeable K 110 mg kg^{-1}.

2.2. Experimental design

The experiment was conducted on a winter wheat-summer maize rotation system using a split-plot design with three replicates. The four main-plot treatments were different rates of N and P fertilizers, the four sub-plot treatments were different rates of maize straw return, and the plot size was 66 m^2 (6.6 m × 10 m) (Cao et al., 2008). We selected no-fertilizer control (CK) and maize straw return at rates of 0 (S0), 2250 (S1), 4500 (S2), and 9000 kg ha^{-1} (S3) under combined N and P fertilization at 360 N kg ha^{-1} yr^{-1} and 240 kg P_2O_5 ha^{-1} yr^{-1}, respectively. The N rate in each season was 180 kg N ha^{-1} and it was optimal for wheat and maize productions in this region. Starter N (one half of the total N) was surface broadcast-applied by hand before sowing and incorporated into the topsoil by moldboard plowing (20–25 cm depth in 1981–2001) or rotary tillage (10–15 cm depth since 2002), while topdressing N (the other half of the total N) was broadcast-applied at the shooting stage followed by an irrigation of 60 mm water in the wheat season. In the maize season, starter N (one third of the total N) was band-applied at the three-leaf stage, and topdressing N (two thirds of the total N) was applied at the ten-leaf stage in the same way as in wheat season. All P fertilizer was applied before wheat sowing, while no K fertilizer was applied. Fertilizers applied were urea (46% N) and calcium superphosphate (12% P_2O_5).

All wheat straws (except crop stubble) were moved out of the plots before maize sowing, and maize straw was crushed into pieces and incorporated into soil by tillage at designed rates in corresponding plots before wheat sowing. Local high-yielding varieties of wheat and maize were used in this experiment. Other field management practices followed standard farming practices.

2.3. Soil sampling and analysis

After wheat harvested in June 2012, five soil cores (0–20 cm depth, 2 cm in diameter) were collected in each plot. Fresh soil samples were mixed as a composite sample and then sieved to pass through a 2-mm mesh, after which they were immediately analyzed for enzyme activities. Additionally, a partion of the subsamples were stored at −70 °C for microbial phospholipid fatty acid (PLFA) analysis, while the other subsamples were air-dried and then passed through 0.25-mm mesh for separation of the light and heavy fractions organic matter, or passed through 0.15-mm mesh for total organic C (TOC) and total N (TN) determination.

2.4. PLFA determination

Microbial community structure were determined by PLFA analysis with the method of Wu et al. (2009). PLFAs were extracted