



Comparing the Effects of Biochar and Straw Amendment on Soil Carbon Pools and Bacterial Community Structure in Degraded Soil

Chengsen Zhao¹ · Yuepei Zhang¹ · Xibo Liu¹ · Xiaowei Ma¹ · Yutian Meng¹ · Xiaoqing Li¹ · Xin Quan¹ · Jiangrong Shan¹ · Wei Zhao¹ · Hongyan Wang¹ 

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Abstract

The degradation of soil often occurs due to the depletion of organic matter. Both biochar and straw have value as two primary means of remediating soil. In this study, we compared the effects of biochar and straw on soil organic carbon pools and on microbial communities in degraded soil. We added straw (maize) and biochar (maize-derived) to the degraded soil at the ratios of total soil weight (0, 1, 2, or 4%), respectively. Soil samples were collected after 180 days. We determined that upon straw addition, there was an increase in microbial biomass carbon (MBC), dissolved organic carbon (DOC), and easily oxidizable carbon (EOC). Upon biochar addition, there was an increase in soil total organic carbon and recalcitrant organic carbon. Analysis of bacterial community was conducted via 16SrDNA sequencing with an Illumina MiSeq platform and revealed that the relative abundance of *Actinobacteria* increased, but the *Bacteroidetes* and *Chloroflexi* decreased with straw addition. We further found that the addition of straw altered the Shannon and Simpson diversity index values, whereas biochar did not impact soil bacterial diversity. Nonmetric multidimensional scaling and canonical correspondence analyses revealed that bacterial community structure was influenced by both biochar and straw addition. Mantel testing further revealed that this community structure was associated with soil EOC ($r = 0.286$, $P = 0.001$), DOC ($r = 0.174$, $P = 0.002$), and MBC ($r = 0.299$, $P = 0.002$) upon straw treatments. These results suggested that straw can improve soil labile organic carbon pools and soil bacterial communities better than biochar, whereas biochar (via pyrolysis at 550 °C, for 2 h) can improve carbon sequestration better than straw in degraded soil.

Keywords Soil carbon pool · Bacterial relative abundance · Community structure and diversity · Illumina MiSeq

1 Introduction

Degraded land is widely recognized as an important issue relating to food security and agricultural production (Lambin et al. 2013). Owing to its high-intensity agricultural utilization, Rashid et al. (2016) estimated that 30% of cultivated land worldwide will be converted into degraded soil by 2020. The degradation of soil often occurs due to the depletion of organic matter within the soil matrix (Smith et al. 2001). A lack of such matter can readily lead to nutrient depletion and

structural variations and decreases in both fertility and the capacity to hold water (Wander et al. 2004). Owing to its high-intensity utilization over extended periods of time, soil fertility in Northeastern China has been decreasing annually in many cases (Xu et al. 2010). Such reductions in fertility correspond to marked drops in surface organic matter content, as well as significant deterioration of the normal ecological, chemical, and physical properties of the soil (Fan et al. 2008; Cheng et al. 2012).

The soil samples used in this study were taken from a region of degraded black soil with 40 years of cultivation history. Black soil is classified into the Phaeozems soil type according to the Soil Taxonomy of the World Reference Base for Soil Resources (WRB 2015). Phaeozems that are about 30 cm thick with a dark surface horizon, a high base saturation, and no secondary carbonates are widespread in Northeastern China (WRB 2015). Yang et al. (2003) reported that the content of organic carbon in uncultivated soil was about twice that of soil with

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✉ Hongyan Wang
zcsen333@126.com

¹ College of Resources and Environment, Northeast Agricultural University, Harbin 150030, People's Republic of China

50 years of cultivation history. Liu et al. (2010) reported that the average annual decrease rate of organic matter is 0.5% in Northeastern China.

The levels of organic carbon present in soil are a key determinant of the quality of the soil and its overall ability to support sustainable land use (Leifeld 2005; Smith 2008). This organic carbon pool was able to markedly shape the chemical, physical, microbiological, and overall structural properties of soil (Pete and Changming 2010). Soil organic carbon pool is divided into two major parts: a labile organic carbon (LOC) pool and a recalcitrant organic carbon (ROC) pool (Changming et al. 2005). The soil LOC pool is a very active portion of the carbon pool, which can easily be utilized and decomposed by microorganisms, making this carbon the main factor regulating plant nutrient supplies (Cotrufo et al. 2013). The soil LOC pool is further subdivided into dissolved organic carbon (DOC), microbial biomass carbon (MBC), and easily oxidizable carbon (EOC) according to different methods of measurement (Zou et al. 2005). The soil ROC is a very stable organic carbon fraction that cannot be readily mineralized in the short term (Dungait et al. 2012). The residence time of the ROC in soil ranges from hundreds of years to thousands of years (Cheng et al. 2015). The soil ROC plays a very important role in soil carbon pool stability and global carbon cycle (Dungait et al. 2012). The soil ROC fraction is separated from soil organic carbon pool by 6 N HCl hydrolysis, and the organic carbon remaining in the residue fraction (after hydrolysis) represents the soil ROC, which can then be determined by the method for the determination of the SOC (Campbell et al. 1967; Leavitt et al. 1996). In addition, humus carbon (HC) is also one of the commonly used evaluation indicators of the soil ROC pool (Berg and McLaugherty 2013).

Maize is the primary crop in much of Northeastern China and is responsible for substantial straw production, with maize straw being the most abundant and economical raw material for biochar carbonization this region (Chen et al. 2011). The returning of straw carbon to the soil plays a very practical role in increasing soil fertility, improving soil structure, and promoting crop yield in the context of agricultural production (Badía et al. 2013; T Fan et al. 2018; Hoang and Marschner 2019). Soil organic carbon levels have been shown to significantly rise following the return of maize residues (Christensen 2010), with the corresponding prevention of biodegradation (Zavalloni et al. 2011). Sampietro and Vattuone (2006) reported that long-term straw application can further prevent the degradation of soil in intensively utilized farmland. However, some studies have found that the organic carbon in straw is readily mineralized, with corresponding increases in CO₂ emissions (Badía et al. 2013). Biochar is an additional and stable source of sequestered carbon that has similarly been added to soil, thereby increasing its quality

(Lehmann et al. 2011), and similarly enhancing the microbial activity therein (Han et al. 2019). At present, biochar is widely used in the remediation of degraded and polluted soil. However, biochar cannot be readily utilized by microorganisms, and its improvement of soil activity is limited (Elzobair et al. 2015).

Many studies have focused on the improvement in soil properties, carbon storage, CO₂ emission, and climate change associated with straw or biochar application. However, few have studied the relative effects of straw and biochar addition on the makeup of the soil carbon pool, or the relationship between the soil organic carbon pool fractions and soil microbial communities. Therefore, in the present study, we sought to compare the relative effects of biochar and straw on soil organic carbon pools and microbial communities in context of degraded soil.

2 Materials and Methods

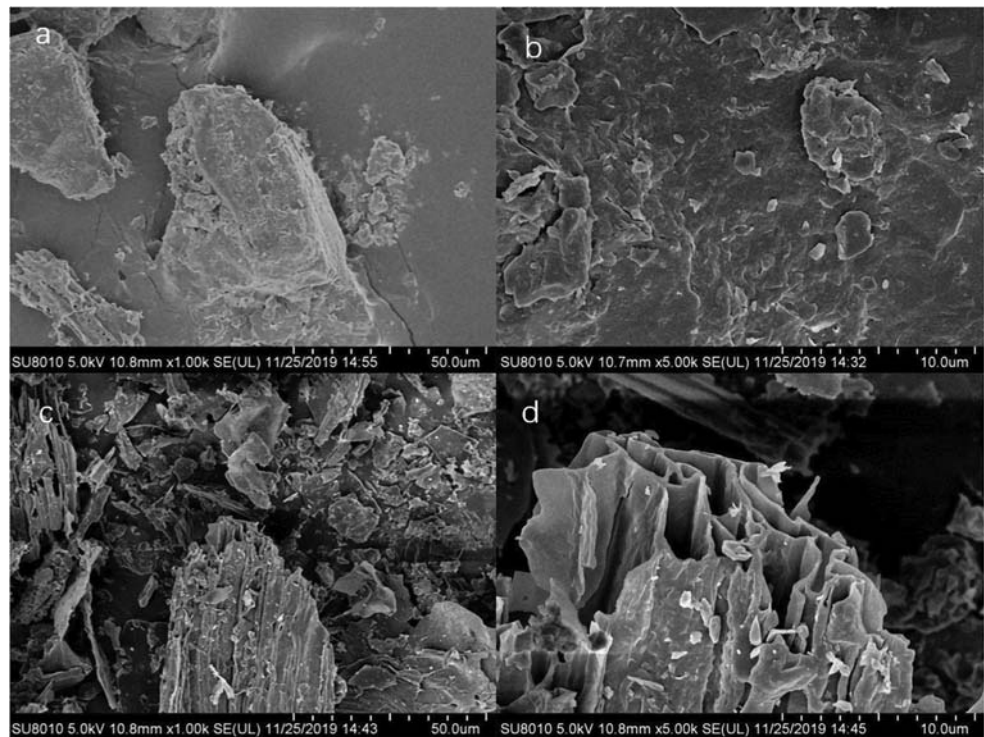
2.1 Soil, Straw, and Biochar

The soil samples used in this study were taken from a region of degraded black soil with 40 years of cultivation history (Acheng farm, Harbin, China). Before land reclamation, the organic matter content of this black soil was approximately 40–60 g kg⁻¹. At present, the content of organic matter in this soil is only 20–30 g kg⁻¹ (Liu and Yan 2009). The characteristics of this soil were as follows: total carbon (TC), 19.31 g kg⁻¹; total nitrogen (TN), 1.54 g kg⁻¹; total phosphorus (TP), 0.68 g kg⁻¹; total potassium (TK), 19.86 g kg⁻¹; and pH, 6.24 (water/soil = 2.5/1, volume/weight (v/w)). The above properties were measured in accordance with the methods described reported by Bao (2000), Jones and Willett (2006), and Miranda et al. (2001). The clay mineral particles in this black soil are layered in structure, with the surface being very rough as shown in scanning electron microscope (SEM) images (Fig. 1a, b).

Straw was also obtained from Acheng farm following a corn harvest. Part of this straw was used to produce biochar. Biochar was produced by processing the straw for 2 h under limited oxygen conditions at 550 °C (Runnong Ltd., China). Both biochar and straw were air-dried, crushed, and then sieved through a 1-mm mesh.

The characteristics of the maize straw and biochar were measured by the methods reported by Bao (2000), Jones and Willett (2006), and Miranda et al. (2001). The straw: TC, 431.54 g kg⁻¹; TN, 2.28 g kg⁻¹; TK, 4.75 g kg⁻¹; and pH, 6.81 (water/biochar = 10/1, v/w). The biochar: TC, 811.34 g kg⁻¹; TN, 1.32 g kg⁻¹; TK, 24.42 g kg⁻¹; and pH, 9.11 (water/biochar = 10/1, v/w). Biochar had a loose structure and large number of pores as shown in SEM images (Fig. 1c, d).

Fig. 1 Scanning electron micrographs (SEM) images of the degraded black soil (Phaeozems) and maize-derived biochar (pyrolysis at 550°C, 2 h) with different magnifications; a and b are the degraded black soil with a magnification of 1000 and 5000 times, respectively; c and d are the degraded black soil with a magnification of 1000 and 5000 times, respectively



2.2 Experimental Setup and Sample Collection

All the experiments were conducted using three replicates of seven treatments in a Horticulture Station (Harbin, China). Soil was obtained from Acheng farm as details above. All clearly visible plant and fauna residue were removed from soil samples before the experiment began. Boxes (length 50 cm, width 50 cm, and height 20 cm) were filled with 2.5-kg soil that had been mixed with either biochar or straw at 0, 1, 2, or 4% of the soil weight (i.e., 0, 2.5, 5, and 10 kg m⁻²). These treatments were coded as CK (0%), B1 (1% biochar), B2 (2% biochar), B3 (4% biochar), S1 (1% straw), S2 (2% straw), and S3 (4% straw), respectively. The boxes were then incubated in a greenhouse at 25–28°C with the temperature being maintained using air conditioners. A hygrometer was inserted into the middle of each box to check the soil moisture. An appropriate amount of water was added to each box to ensure that the soil moisture was maintained at 50–55%. The greenhouse was transparent, with the sun as the light source. In order to mimic a tillage period, soil samples were collected after 180 days (frost-free period), obtaining a total of five 15-cm deep soil cores per box (in the center and four quadrant corners). The soil samples were placed in sterile plastic bags, put in a box with dry ice, and immediately transferred to the laboratory. Approximately 15 g per soil sample was then put into a sterile plastic bag and stored at –80 °C for soil DNA extraction. Approximately 100 g per soil sample was stored at 4 °C for soil MBC and DOC determination. The remaining soil samples were air-dried for the others measurements of carbons pools.

2.3 Analysis of Soil Properties

Potassium dichromate oxidation and ferrous ammonium sulfate titration were used for the measurement of SOC (Bao 2000). The 333-mmol L⁻¹ KMnO₄ oxidation method was used for EOC measurements (Blair and Lefory 1995). The CH₃Cl₃ fumigation–extraction method was used for MBC measures (Monz et al. 1991). To extract DOC, 2 M KCl was used followed by assessment with a total organic carbon analyzer (Shimadzu TOC-5050A) (Jones and Willett 2006). For ROC, the 6 N HCl acid hydrolysis method that was reported by Leavitt et al. (1996) was employed. The composition of humus carbon was extracted with a mixture of 0.1 mol L⁻¹ Na₄P₂O₇ and 0.4 mol L⁻¹ NaOH and measured according to methods previously reported by Kumada (1987) and Nakamura et al. (2007). Soil pH was determined via soil liquid extraction (water/soil = 2.5/1, v/w) using a pH meter (Bao 2000). Soil total nitrogen (TN) was determined with an elemental analyzer (Vario EL III, Germany) (Jones and Willett 2006). Soil total potassium (TK) was determined with a flame photometer (FP6410, China) (Bao 2000). Soil total phosphorus (TP) was determined with an ultraviolet spectrophotometer (UV2600, Shimadzu, Japan) (Miranda et al. 2001). The structure and surface of samples were observed and analyzed by scanning electron microscope (SEM) instrument (SU8010, HITACHI, Japan) with a voltage of 5 kV (Brodowski et al. 2005).

2.4 Microbial Sequencing and Data Analysis

Soil sample gDNA extraction was conducted using a MiSeq Reagent Kit v3 (Illumina, USA) for soil based on manufacturer's direction. PCR was then used to amplify the V4-V5 hypervariable bacterial 16S rDNA genes with the 515F and 907R universal primers in a 25- μ L volume reaction with the following thermocycler settings: 98 °C for 30 s; 25 cycles of 98 °C for 15 s, 55 °C for 30 s, and 72 °C for 30 s; and 72 °C for 300 s. Triplicate samples were independently amplified (Jiang et al. 2013).

16S rDNA-amplified sequences were compared against those generated by the National Center for Biotechnology Information (NCBI), with taxonomic classifications in samples determined using BLAST followed by comparison with GenBank (Quast et al. 2012). An operational taxonomic unit (OTU) cluster analysis was conducted at 97% similarity with USEARCH V10.0, and chimeric sequences were removed via the Denovo template within USEARCH. An equal level analysis was used to select the minimum number of random sequences per sample. Total 16S rDNA sequences have been uploaded in the NCBI gene bank (SRP218956).

3 Statistical Analysis

The alpha diversity, including Chao1 richness, Shannon diversity, Simpson diversity, and Good's coverage, were calculated using the "vegan" package in R v.4.3.2 according to the method reported by Jost (2007). SPSS v17.0 was used to conduct one-way ANOVAs with least significant difference (LSD) tests which were used to compare soil carbon pools, relative bacterial abundance, and diversity between samples. The response ratio is the percentage of increase or decrease in the value of each treatment compared with the control. The "vegan" package in R v.4.3.2 was used for nonmetric multidimensional scaling (NMDS) and Canonical Correspondence Analyses (CCA) of the link between bacterial community structure and soil carbon pools. Excel 2016 and SigmaPlot12.5 were used for figure generation. $P < 0.05$ was the significance threshold.

4 Results

4.1 Changes in Soil Organic Carbon Pools

We found that the addition of straw and biochar to soil for 180 days had a significant impact on soil organic carbon pools in degraded soil samples. The contents of soil TOC increased by 52.08%, 38.69%, and 26.24% in response to biochar treatments (B3, B2, and B1, respectively) compared with CK, while the contents of soil TOC slightly increased by 8.91%,

5.81%, and 1.84% in response to straw treatments (S3, S2, and S1, respectively) compared with CK (Table 1). We further found that the soil EOC, DOC, and MBC all significantly increased with straw addition, with the highest increases upon straw addition of 4% soil weight (Fig. 2). However, biochar did not impact on soil EOC, DOC, and MBC in this study (Fig. 2). We further found that the contents of soil ROC increased by 53.92%, 37.03%, and 22.74% in the B3, B2, and B1 treatments as compared with CK, whereas straw had no obvious impact on soil ROC (Table 1). We also found that the content of soil HC had a slight increase with the straw addition, whereas the content of soil HC was not influenced by biochar amendment in degraded soil. In addition, soil pH significantly increased with biochar addition, whereas straw had no obvious impact on soil pH (Table 1).

The response ratio of the biochar and straw addition to soil organic carbon pools is shown in Fig. 2. The response ratio is the percentage of increase or decrease in the index value of each treatment compared with the control. Briefly, the addition of 4% soil weight in straw yielded the best increases (39.23%) in soil EOC in degraded soil, and the addition of 4% soil weight in biochar yielded the best increases in soil ROC (53.92%) in degraded soil.

4.2 Changes in the Relative Abundance and Diversity of Soil Bacterial Communities

We assessed soil bacteria at the phylum level in order to gauge differences in bacterial relative abundance and changes in overall soil bacterial community structure. We found that the dominant phyla in most soil samples were *Proteobacteria*, *Acidobacteria*, *Bacteroidetes*, *Actinobacteria*, *Chloroflexi*, *Gemmatimonadetes*, and *Planctomycetes*, which represented >80% of the total bacteria (Fig. 3). Their relative abundances ranged from 25.73 to 29.49%, 17.12 to 20.84%, 3.95 to 4.86%, 4.52 to 5.84%, 3.12 to 5.54%, and 2.47 to 4.37%, respectively (Fig. 3). Upon straw addition, the relative abundance of *Actinobacteria* rose significantly, with a corresponding decrease in the relative abundance of *Bacteroidetes* and *Chloroflexi* in degraded soil samples (Fig. 4). We also observed a slight decrease in the relative abundance of *Acidobacteria* in response to biochar addition (Fig. 4).

We further found that the dominant classes (average of relative abundance >2%) across most of these soil samples were *Betaproteobacteria*, *Alphaproteobacteria*, *Sphingobacteriia*, *Actinobacteria*, *Acidobacteria_Gp4*, *Deltaproteobacteria*, *Gemmatimonadetes*, *Gammaproteobacteria*, *Acidobacteria_Gp6*, *Anaerolineae*, *Planctomycetia*, and *Acidobacteria_Gp7*, which represented >70% of the total bacteria (Table 1s). Upon biochar addition, the relative abundance of *Actinobacteria* and *Alphaproteobacteria* increased significantly, with a

Table 1 Straw and biochar impact on soil carbon pools

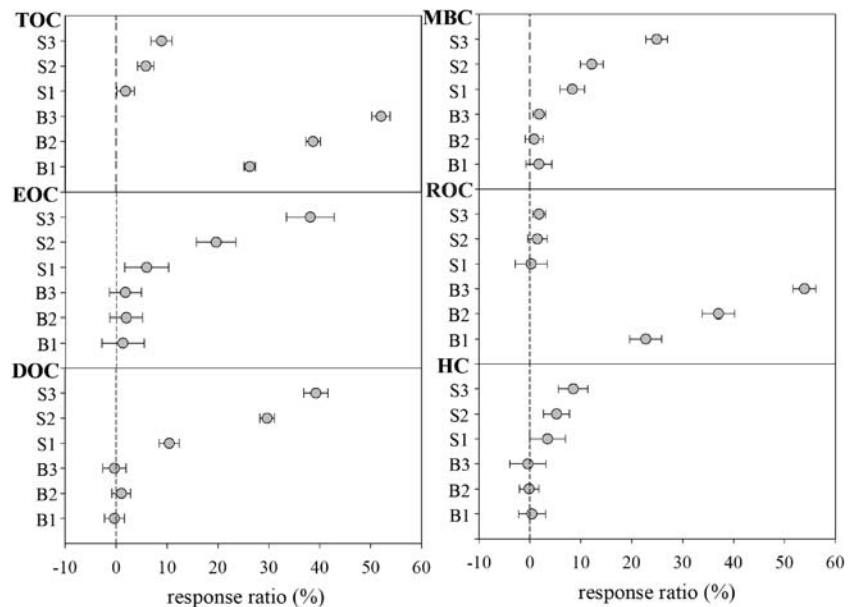
Treatment	TOC† (g kg ⁻¹)	EOC (g kg ⁻¹)	DOC (mg kg ⁻¹)	MBC (mg kg ⁻¹)	ROC (g kg ⁻¹)	HC (g kg ⁻¹)	pH
CK	19.39 ± 0.25e‡ (0%)	3.57 ± 0.18c (0%)	110.81 ± 2.55d (0%)	104.46 ± 2.15c (0%)	11.27 ± 0.14d (0%)	4.15 ± 0.09c (0%)	6.24 ± 0.07d (0%)
B1	24.47 ± 0.21c (26.24%)	3.61 ± 0.15c (-0.37%)	110.4 ± 2.19d (1.31%)	106.29 ± 2.64c (22.74%)	13.83 ± 0.36c (1.75%)	4.17 ± 0.11bc (0.32%)	6.35 ± 0.08d (1.76%)
B2	26.89 ± 0.28b (38.69%)	3.64 ± 0.12c (1.01%)	111.93 ± 2.03d (1.96%)	105.32 ± 1.86c (37.03%)	15.44 ± 0.36b (0.82%)	4.14 ± 0.08c (-0.24%)	6.33 ± 0.06d (1.44%)
B3	29.48 ± 0.35a (52.06%)	3.63 ± 0.11c (-0.35%)	110.42 ± 2.53d (1.78%)	106.36 ± 1.31c (53.92%)	17.35 ± 0.25a (1.81%)	4.13 ± 0.15c (-0.48%)	6.32 ± 0.08d (1.28%)
S1	19.74 ± 0.33e (1.84%)	3.78 ± 0.15c (10.4%)	122.34 ± 2.14c (5.98%)	113.15 ± 2.52b (0.24%)	11.30 ± 0.35d (8.32%)	4.29 ± 0.15bc (3.37%)	6.51 ± 0.07c (4.33%)
S2	20.51 ± 0.31d (5.81%)	4.27 ± 0.14b (29.64%)	143.66 ± 1.61b (19.63%)	117.14 ± 2.36b (1.45%)	11.43 ± 0.22d (12.13%)	4.37 ± 0.11ab (5.14%)	6.79 ± 0.12b (8.81%)
S3	21.11 ± 0.4d (8.91%)	4.93 ± 0.17a (39.23%)	154.28 ± 2.64a (38.14%)	130.47 ± 2.23a (1.77%)	11.47 ± 0.14d (24.9%)	4.50 ± 0.12a (8.43%)	7.14 ± 0.09a (14.42%)

†TOC, total organic carbon; EOC, easily oxidizable carbon; ROC, recalcitrant organic carbon; DOC, dissolved organic carbon; MBC, microbial biomass carbon. The values in brackets represent the percentage of increase compared to the control (CK). ‡Different letters correspond to a significant difference measured via one-way ANOVA with LSD testing at a *P* < 0.05

corresponding decrease in the relative abundance of *Sphingobacteriia* and *Anaerolineae* in degraded soil samples. Upon biochar addition, *Acidobacteria_Gp4* and *Acidobacteria_Gp6* decreased significantly, whereas *Alphaproteobacteria* increased in these degraded soil samples. Among them, the *Alphaproteobacteria* genus belongs to the *Proteobacteria* phylum; the *Acidobacteria_Gp4* and *Acidobacteria_Gp6* genera belong to the *Acidobacteria* phylum; and the *Actinobacteria*, *Sphingobacteriia*, and *Anaerolineae* genera belong to *Actinobacteria*, *Bacteroidetes*, and *Chloroflexi* phyla, respectively (Table 1s).

Further taxonomic classification revealed that more than 300 (data not shown) bacterial genera were detectable in this study. There were 23 genera with a relative abundance (average) > 0.5%. Of these, five genera increased, and three genera decreased in relative abundance in response to straw addition, while three genera increased, and four genera decreased in relative abundance in response to biochar addition in degraded soil samples. Most of these bacteria belonged to the four dominant *Proteobacteria*, *Acidobacteria*, *Bacteroidetes*, and *Actinobacteria* phyla (Table 2s).

Fig. 2 Response ratios in soil organic carbon pools following biochar and straw addition. Values represent biochar (B1, B2, B3) and straw (S1, S2, S3) treatments compared with CK treatment. Error bars represent 95% confidence intervals. Differences are considered significant when the confidence intervals do not include zero. TOC-total organic carbon, EOC-easily oxidizable carbon, ROC-recalcitrant organic carbon, DOC-dissolved organic carbon, MBC-microbial biomass carbon.



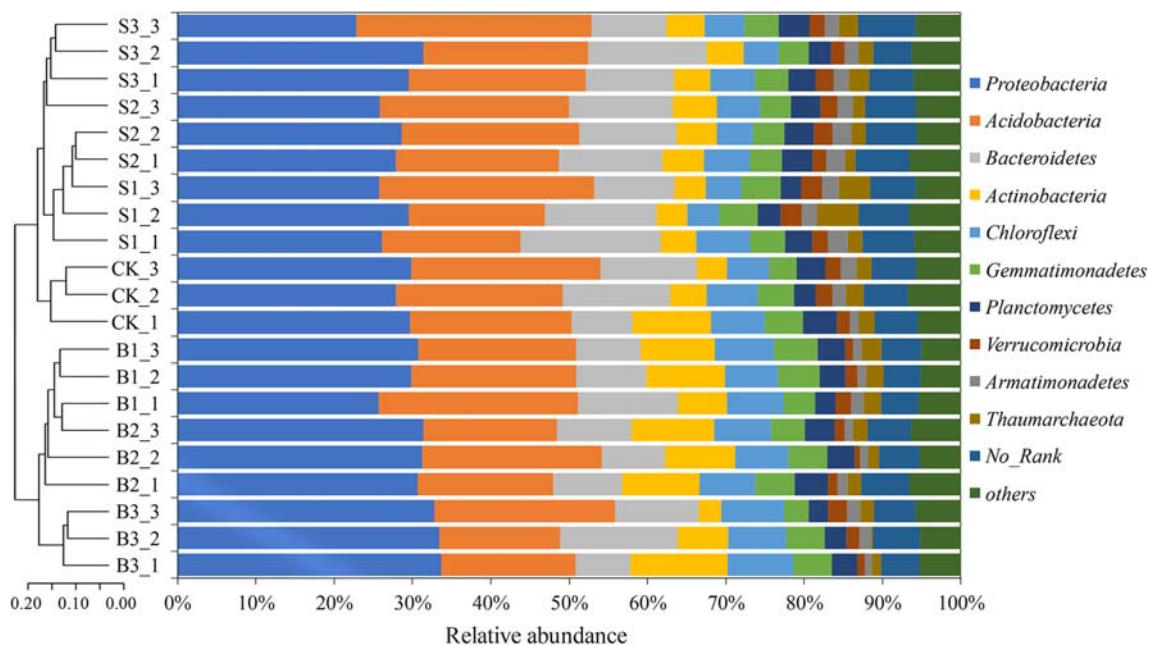


Fig. 3 Phylogenetic relationships and relative abundances of bacterial communities across all soil samples at the phylum level. Others correspond to all low-abundance bacteria ($\leq 0.01\%$) combined

The Chao1 richness, Shannon, and Simpson diversity indices were used to gauge overall microbial community α -diversity (Table 2). There was no difference in these indexes between the three biochar treatments (B1, B2, and B3) and the control (CK) in degraded soil. Therefore, biochar did not significantly impact soil bacterial diversity in this study. However, there were significant increases in the Shannon and Simpson diversity of degraded soil following straw addition (S1, S2, and S3) relative to controls (CK) (Table 2).

4.3 The Relationship Between Soil Carbon Pools and Bacterial Community Structure

In order to estimate overall soil bacterial community structure, NMDS was employed, with treatments separating into two distinct clusters along the MDS1 (Fig. 5). On the left were

the biochar treatments (B1, B2, B3) along MDS2. Similarly, on the right were the straw treatments (S1, S2, S3) along MDS2.

CCA revealed that soil TOC and ROC were near CCA1, while EOC, DOC, and MBC were close to CCA2 (Fig. 5). TOC and ROC levels were more closely associated with biochar treatments (B1, B2, and B3), whereas AOC, DOC, MBC, and HC were more closely associated with straw treatments (S1, S2, and S3). A Mantel test analysis revealed that there was a significant correlation between soil bacterial community structure and soil EOC ($r = 0.286$, $P = 0.001$), DOC ($r = 0.174$, $P = 0.002$), and MBC ($r = 0.299$, $P = 0.002$) (Table 3) in the conditions wherein straw was added to degraded soil. There was a significant correlation between soil bacterial community structure and soil pH ($r = 0.312$, $P = 0.001$) (Table 3) in the conditions wherein biochar was added to degraded soil.

Fig. 4 Shifts in relative bacterial abundance in response to straw and biochar treatments at phylum level. Different letters correspond to a significant difference measured via one-way ANOVA with LSD testing at a $P < 0.05$.

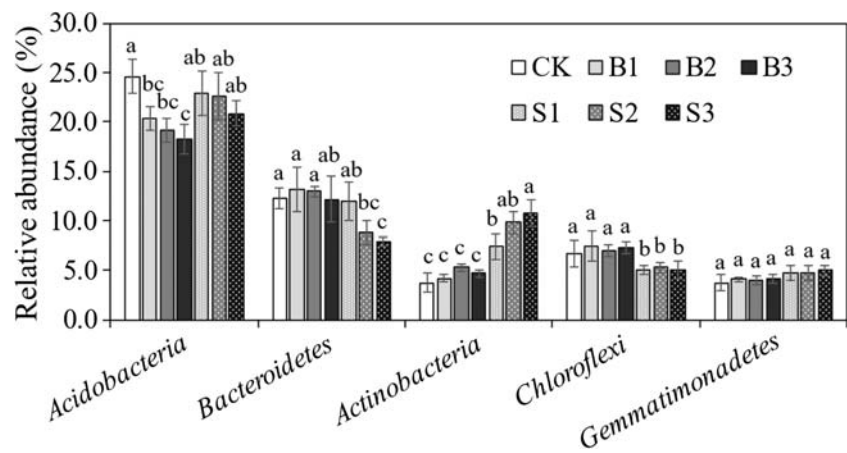


Table 2 Straw and biochar impact on bacterial community diversity

Treatment	Observed sequences	Chao1 richness	Shannon diversity	Simpson diversity	Coverage† (%)
CK	3779 ± 314a‡	5215 ± 278a	6.48 ± 0.06c	0.0037 ± 0.0002b	97.85
B1	3780 ± 475a	5205 ± 307a	6.48 ± 0.09c	0.0038 ± 0.0006b	97.79
B2	3827 ± 237a	5393 ± 450a	6.60 ± 0.07bc	0.0037 ± 0.0005b	97.71
B3	3941 ± 323a	5417 ± 357a	6.70 ± 0.15abc	0.0038 ± 0.0006b	97.69
S1	4103 ± 190a	5723 ± 199a	6.75 ± 0.08ab	0.0047 ± 0.0007ab	97.53
S2	4055 ± 122a	5568 ± 233a	6.73 ± 0.01a	0.0065 ± 0.0012a	97.63
S3	4059 ± 150a	5504 ± 294a	6.80 ± 0.10a	0.0064 ± 0.0017a	97.72

Coverage, Good’s nonparametric coverage estimator. Data were generated based upon 57,094 bacterial sequences per soil sample. ‡Different letters correspond to a significant difference measured via one-way ANOVA with LSD testing at a $P < 0.05$

5 Discussion

5.1 Changes in Soil Organic Carbon Pools

Previous reports have found that soil TOC increases significantly following the short-term application of straw (Christensen 2010; Ye et al. 2015). However, in this study, the soil TOC increased slightly upon straw addition. This may be because most straw had undergone microbe-mediated mineralization after a tillage period (Yemadje et al. 2017). Yan et al. (2007) reported that large amounts of straw were degraded to form activated organic carbon. This is the reason that the soil LOC pools (EOC, DOC, and MBC) increased significantly in all straw-amended treatments. The impact of straw addition on soil HC had a slight increase in soil; Fan et al. (2018) found that crop residues increased the content of humic acid and fulvic acid in a 112 day-long incubation experiment.

Upon biochar addition, we observed a significant increase in both soil TOC and ROC in degraded soil, whereas biochar failed to have a profound impact on soil EOC, DOC, MBC, or HC. This is presumably due to most of the biochar carbon being recalcitrant (Wang et al. 2016), thus limiting its ability

to contribute to EOC, DOC, and MBC levels. Biochar was able to increase the content of soil ROC, whereas it could not increase the content of soil HC. Microorganisms play an essential role in the formation of humus (Berg and Mcclougherty 2013). Biochar is not readily utilized by microorganisms (Reddy 2015), and it is therefore not easily converted into humus in the short term.

In summary, these results indicate that biochar is a more reliable mean of increasing soil ROC pools, while straw offers a reliable mean of increasing soil LOC pools.

5.2 Changes in the Relative Abundance and Diversity of Soil Bacterial Communities

The most dominant phyla of soil bacteria identified in this study were largely consistent with those in previous studies of soil bacteria communities in different types of soil (Blanc et al. 2006; Yao et al. 2017). However, there were differences in the ratios of soil bacteria communities in this study. The changes in the relative abundance of soil bacteria at the class and genus levels were similar with those at the phylum level. The changes in the bacterial relative abundance were mainly

Fig. 5 Nonmetric multidimensional scaling (NMDS) and canonical correspondence analysis (CCA) of the relationship between soil carbon pools and bacterial community structure. TOC-total organic carbon, EOC-easily oxidizable carbon, ROC-recalcitrant organic carbon, DOC-dissolved organic carbon, MBC-microbial biomass carbon.

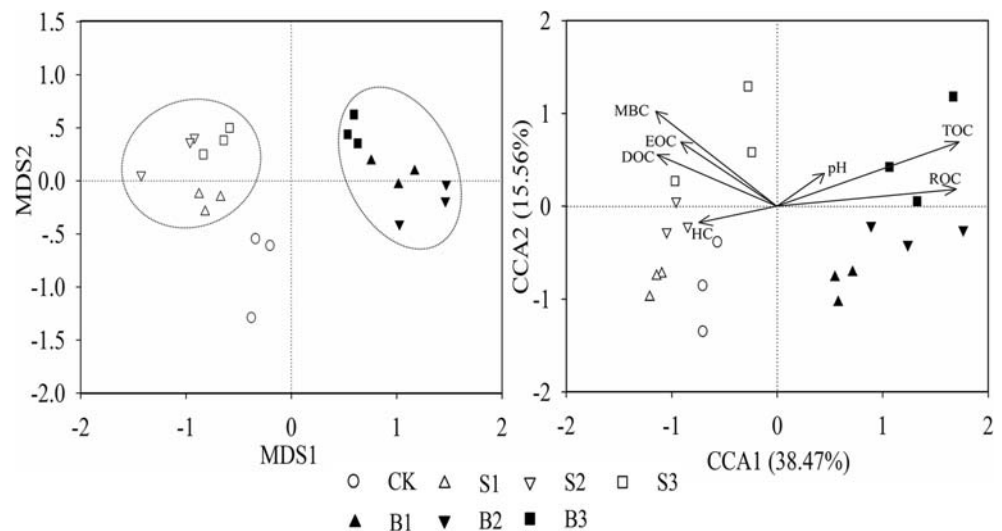


Table 3 Correlation (r) and significance (P) between bacterial communities and soil carbon pools using the Mantel test

Soil properties	Biochar treatments		Straw treatments		Total	
	r	P	r	P	r	P
TOC †	0.287	0.028	0.850	0.006	0.766	0.012
EOC	0.033	0.373	0.286	0.001	0.160	0.017
DOC	0.031	0.331	0.174	0.002	0.113	0.008
MBC	0.233	0.472	0.299	0.002	0.266	0.021
ROC	0.245	0.013	0.316	0.133	0.282	0.149
HC	0.065	0.356	0.186	0.012	0.104	0.218
pH	0.312	0.001	0.138	0.045	0.225	0.031

†TOC, total organic carbon; EOC, easily oxidizable carbon; DOC, dissolved organic carbon; MBC, microbial biomass carbon; ROC, recalcitrant organic carbon

in *Acidobacteria*, *Bacteroidetes*, and *Actinobacteria* phyla. Upon straw addition, the relative amounts of *Actinobacteria* increased, while the relative abundance *Bacteroidetes* and *Chloroflexi* decreased. Lewin et al. (2016) reported that the *Actinobacteria* was easy to colonize in in the environment of rich active organic carbon and straw application increased soil active organic carbon availability, thereby stimulating an increase in relative *Actinobacteria* abundance. Hengst and Buttner (2008) found that *Actinobacteria* were able to reproduce rapidly by utilizing cellulose from straw, which may explain the observed increase in *Actinobacteria* in our study. Yamada and Sekiguchi (2009) found that *Bacteroidetes* and *Chloroflexi* were anaerobic and that straw was able to increase the permeability of soil to air, thus potentially reducing the levels of *Bacteroidetes* and *Chloroflexi*.

Bertola et al. (2019) found that biochar could provide a shelter for protecting soil beneficial microorganisms against grazers or competitors. Gomez et al. (2014) determined that biochar application could alter soil microbial activity and community composition. In contrast, Liu et al. (2016) reported that biochar addition had no effect on the microbial community structure in the short term (several weeks) or long term (several years) in paddy soils. We observed a slight decrease in the relative abundance of *Acidobacteria* in the biochar-amended treatments. Lauber et al. (2009) found that *Acidobacteria* was very sensitive to soil pH. We found that biochar application raised the pH of the soil in our study, resulting in the loss of *Acidobacteria*. Although we did observe a slight change in the relative abundance of *Acidobacteria*, biochar overall did not significantly impact soil bacterial diversity in this study.

We found that straw addition had a significant impact on soil bacterial diversity. This is consistent with previous work wherein Schnecker et al. (2014) found that soil microbial diversity is largely governed by organic matter utilization. Musilova et al. (2017) reported that the LOC plays an

important role in changes in bacterial diversity. These results explain why straw was a more effective means of improving soil microbial diversity in degraded soil than was biochar addition.

5.3 The Relationship Between Soil Carbon Pools and Bacterial Community Structure

Through NMDS we observed that biochar and straw treatments separated into two distinct clusters. This is consistent with previous work wherein Kaminsky et al. (2017) found that different biomass sources resulted in different structures and distributions of soil bacterial communities, thus explaining why biochar and straw treatments were separated in this analysis. A Mantel test analysis and CCA indicated that soil EOC, DOC, and MBC were key mediators of soil bacteria community structure in the context of degraded soil and this finding is consistent with the previous work by Bending et al. (2000), who found that the fresh crop residues are easily available for utilization with a surge in microbial biomass. Similar findings were also reported by Musilova et al. (2017). In addition, soil pH was closely associated with changes in the structure of bacterial communities in the condition wherein biochar was added to degraded soil, and this finding is consistent with the previous work by Lauber et al. (2009), who found that the soil pH had a significant impact on the soil bacterial community composition at the relative levels of taxonomic resolution in a biochar amendment study.

6 Conclusion

Herein we found that straw addition was able to significantly increase the pool of labile organic carbon, whereas biochar addition increased the pool of recalcitrant organic carbon. Of the tested conditions, the addition of 4% soil weight in straw yielded the best increases in soil easily oxidizable carbon, while the addition of 4% soil weight in straw biochar yielded the best increases in soil recalcitrant organic carbon within degraded soil samples. Biochar did not impact soil bacterial diversity in degraded soil, whereas straw significantly increased soil bacterial diversity. These results also demonstrated that biochar and straw could significantly alter relative soil bacterial abundance and we found that overall bacterial community structure was associated with labile carbon pools. Overall our findings clearly emphasize that straw can significantly improve soil bacterial communities and soil labile organic carbon pools better than biochar, whereas biochar can improve carbon sequestration better than straw in degraded soil.

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Compliance with Ethical Standards

Conflict of Interest The authors declare that they have no conflict of interest.

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