Effect of long-term fertilization on bacterial community in a sandy loam soil and its relation to organic carbon accumulation

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Abstract. Fertilization can affect the transformation of soil organic carbon (SOC) and soil microbial community composition. However, thus far, how SOC accumulation in association with bacterial community is still unclear. We collected arable soils (aquic inceptisol) from a long-term fertilization experiment (20 years) including compost (CM), inorganic nitrogen + phosphorus + potassium (NPK), half compost N plus half inorganic fertilizer N (HCM), NP, NK, PK, and untreated (Control). We investigated the relationship between the SOC accumulation rate and bacterial community composition measured by high-throughput sequencing. The highest SOC accumulation rate was observed in the compost treatments. Furthermore, compost and balanced NPK treatments increased soil carbohydrate content significantly (P < 0.05), while no such enhancement was observed following NK and PK application. Compared with the Control, fertilization substantially reduced the effective diffusion coefficient of oxygen in soil. Meanwhile, fertilization lowered the relative abundance (RA) of Bacteroidetes but increased the RA of Proteobacteria. Compost application increased the RA of Firmicutes, while inorganic fertilizers reduced it. The RA of Proteobacteria and Firmicutes were significantly and positively correlated with the SOC and carbohydrate content and the SOC accumulation rate (P < 0.05). SOC accumulation was also accompanied with the reduction in the effective diffusion coefficient of oxygen in soil. Our results indicated that poor aeration may induce a shift in the microbial community composition and a transition from aerobic to anaerobic degradation of SOC, thereby favoring SOC accumulation.

Keywords: Long-term fertilization; High-throughput sequencing; Microbial community; Organic C accumulation.

1. Introduction

Bacteria play significant roles in biogeochemical cycles in agricultural ecosystems, such as decomposition and conversion of soil organic carbon (C) and accompanied release of nutrients for plant growth [1]. Soil microbial communities are greatly impacted by soil chemical and physical properties such as nutrient level, pH, quantity and quality of organic C, water content, and oxygen level. In agricultural ecosystems, fertilizer management practices can affect nearly all these edaphic factors, leading to shifts in the microbial community composition. Although, in recent years, the response of soil microbial community to organic and inorganic fertilization have been extensively investigated [2], the information about the relation between alterations in bacterial community composition and soil organic carbon (SOC) sequstration as affected by different soil fertilization treatments is still limited.

Organic fertilization may positively influence microbial diversity, biomass, activity, and help maintain or increase the SOC content, while inorganic fertilization is less effective relative to organic fertilization [3]. Several researches have revealed that soil bacterial community is highly sensitive to organic and inorganic fertilizations, but such responses differ among phyla [1]. Nonetheless, some studies also revealed that current application of inorganic fertilizers has a major deleterious impact on the inherent soil microbial community, such as decreases of microbial biomass [4] and microbial diversity [5]. For instance, Jangid et al. [1] revealed that inorganic fertilization in croplands and pastures significantly reduced the microbial diversity and altered the composition of bacterial phyla, involving *Acidobacteria*, *Bacteroidetes*, *Firmicutes*, *Betaproteobacteria* and *Gammaproteobacteria*. The overloading of nitrogen (N) fertilizer reduced microbial biodiversity and enhanced nitrification [6]. However, it was found that variations in the soil bacterial community structure resulting from

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inorganic fertilization could be resumed by organic fertilization [2].

Fertilization-related alterations in microbial community structure can be related to variations in the soil environmental conditions. However, the response of diverse bacterial communities to the varying environment in arable soils has not been clearly stated. Here, we evaluated variations in the bacterial community composition in a sandy loam soil as influenced by various long-term organic and inorganic fertilizations. This study aimed to elucidate the key factors regulating the shifts in the bacterial community composition and to understand the relationships between SOC accumulation and bacterial community composition. The hypothesis was that the bacterial community composition corresponds to variations in soil properties, which will in turn change the SOC accumulation rate.

2. Materials and methods

2.1. Field experiments and soil property analysis

Fengqiu Agro-ecological Experimental Station was located in Henan province, China (35°00′N, 114°24′E). A long-term fertilization experiment was established in the Agro-ecological Experimental Station in September 1989. The soil was originated from alluvial sediments of the Yellow River with a sandy loam texture. The mean annual temperature was 13.9 °C and the mean annual precipitation was 615 mm, representing a semi-arid, sub-humid monsoon climate in this region. In 1989, the soil (0–20 cm) parameters were: organic carbon, 4.48 g·kg⁻¹; total nitrogen, 0.43 g·kg⁻¹; total phosphorus, 0.50 g·kg⁻¹; and total potassium, 18.60 g·kg⁻¹; pH, 8.65.

In the long-term experiemnt, seven fertilization treatments with four replicates were included: (1) only compost (CM), (2) half compost nitrogen plus half inorganic nitrogen fertilizer (HCM), (3) combined inorganic nitrogen + phosphorus + potassium fertilizers (NPK), (4) combined inorganic nitrogen + phosphorus fertilizers (NP), (5) combined inorganic nitrogen + potassium fertilizers (NK), (6) combined inorganic phosphorus + potassium fertilizers (PK), and (7) no fertilization (Control). A total of 28 plots were analyzed. Table 1 presents the details of N, P, and K application rates for each treatment. Each plot had a size of 9.5 m in length and 5 m in width. The experiment design was a randomized block for all the plots. The compost was made by fermenting cakes of soybean and cottonseed, and wheat straw for 2 months and had 422 g C·kg⁻¹. The cropping system was a rotation of summer maize (*Zea mays* cv. Zhengdan 958) and winter wheat (*Triticum aestiv �l um* cv. Xinmai 19). Basal fertilizers were evenly applied in the respective plots before tillage which was conducted by hoes to a soil depth of 20 cm every season. Then the maize and wheat were sowed after tillage in early June and early October, respectively. Moreover, the soil surface was treated with supplemental N fertilizer in HCM, NPK, NP and NK treatments in late July and in late February for maize and wheat,

respectively, followed by irrigation or rainfall. All the plots applied same field management practices other than fertilization during the experiment. Detailed information regarding the experiment management has been reported by Yu et al. [7].

An auger with 2.5-cm-diameter was used to collect soil samples in each plot to a depth of 20 cm on 7 June 2009. The soil cores were homogenized, stored at 4 °C, and taken to the lab as soon as possible for further analysis. Fresh soil samples were gently ruptured along natural fissures and sieved to < 8 mm, and then visible plant residues and organic debris were carefully eliminated by forceps. These fresh samples were utilized for molecular analyses. An air-dried subsample passing through a 2 mm sieve was prepared to measure soil properties.

A pH meter (DMP-2, Quark Ltd., Nanjing, China) was applied to determine soil pH. The wet oxidation-redox titration method were performed to measure SOC content and the micro-Kjeldahl method were performed to measure total N content in soil. The soil carbohydrate content was determined following Puget et al. [8].

2.2. Effective oxygen diffusion coefficient

In each plot eight undisturbed soil core samples with volume of 100 cm³ were collected. The ceramic pressure plate method was employed at equilibrium matric potentials of −1, −2, −10, −35, −60, −100, −330, −500, −1000, −2000, −5000, and −15000 hPa to measure soil water retention curve.

The effective soil oxygen diffusion coefficient (D, m²·s⁻¹) was computed as follows [9]:

$$D = \frac{1}{N^2} \times \left[\left(D_{a0} \times Q_a{}^p \right) + \left(KH \times D_{w0} \times Q_w{}^p \right) \right]$$

Table 1 Amount of nutrient inputs (N, P, and K) through organic or inorganic fertilization in each cropping season under different treatments

| Treatment | Basal fertilizer | | | | | | Supplementary fertilizer urea (kg N·ha⁻¹) |
| | N (kg N·ha⁻¹) | | P (kg P₂O₅·ha⁻¹) | | K (kg K₂O ha⁻¹) | | |
	Compost	Urea	Compost	Calcium superphosphate	Compost	Potassium sulfate	
Maize							
Control	0	0	0	0	0	0	0
HCM	75	0	25.5	49.5	32.5	117.5	75
CM	150	0	51	24	65	85	0
NPK	0	60	0	75	0	150	90
NP	0	60	0	75	0	0	90
NK	0	60	0	0	0	150	90
PK	0	0	0	75	0	150	0
Wheat							
Control	0	0	0	0	0	0	0
HCM	75	15	22.5	52.5	31.5	118.5	60
CM	150	0	45	30	63	87	0
NPK	0	0	0	75	0	150	60
NP	0	0	0	75	0	0	60
NK	0	0	0	0	0	150	60
PK	0	0	0	75	0	150	0

where N is the soil porosity (%) calculated by soil bulk density (ρ) and particle density (2.65 g·cm⁻³); D_{a0} is the free diffusion coefficient of oxygen in the air at 20 °C

$(1.8 \times 10^{-5}$ m$^2\cdot$s$^{-1})$; *KH* is Henry's equilibrium constant at 20 °C (0.03); D_{w0} is the free oxygen diffusion coefficient in the water at 20 °C (2.2×10^{-9} m$^2\cdot$s^{-1}); Q_a is the ratio of soil porosity filled with air and Q_w is the ratio of soil porosity filled with water, i.e., $Q_a + Q_w =$1; and *p* is a power constant (3.4). The Q_w was calculated by:

$$Q_w = \rho \times \theta_m / N$$

where θ_m is the water content of soil (cm$^3\cdot$g^{-1}).

2.3. Measurement of the specific C mineralization rate

To measure the specific C mineralization rate (SCMR), 10 g soil seieved to < 2 mm was put in a glass jar with volume of 150-mL. The moisture content of soil was regulated to 60% of WHC (water-holding capacity) for all soil samples during the incubation. The jars covered by ventilated film were placed in an incubator at 25 °C and the deionized water was added once every two days to maintain soil moisture content the same as initial condtion during the incubation. The CO_2 emission rate was measured on the 0.5, 1, 2, 3, 5, 7, 9, 11, 13, 15, 18, 21, 24, 28, and 32 days of the incubation. For measuring CO_2 emissions, the jar was plugged with a rubber lid perforated by centered Perspex tubes. Then, an hermetic syringe was utilized to collect 1 mL headspace gas immediately and at 6 h after closure to dertermine the CO_2 concentration by a gas chromatograph (Agilent 7890, Santa Clara, CA, USA). The CO_2 emission rate representing organic C mineralization rate (CMR) was computed by assuming the CO_2 concentration was linearly changed during the 6-h incubation in the airtight jar at temperature of 20 °C. The SCMR was calculated using the following equation [7]:
SCMR = CMR/SOC content.

2.4. Soil DNA extraction

Fresh soil samples of 0.5 g (on the oven-dried basis) was used to extract total DNA by a Fast DNA Spin Kit for Soil (MP Biomedicals, CA, USA) based on the manufacturers' protocols. The gel electrophoresis and NanoDrop spectrophotometer (NanoDrop Technologies, Wilmington, USA) were employed to measure the quality and concentration of the extracted DNA, respectively, and then the extracted DNA was subsequently preserved at –20 °C.

2.5. Illumina sequencing and data analysis

The primers 802R (5′-TACNVGGGTATCTAATCC-3′) and 520F (5′-AYTGGGYDTAAAGNG-3′) were utilized for amplifying the V4 hypervariable regions of bacterial 16S rRNA gene, with a sample-specific 12 bp barcode added to 520F. The PCR reaction was conducted in the thermal cycler (Bio-Rad Laboratories, Hercules, CA, USA). Library quality was assessed by an Agilent Bioanalyzer 2100 and a Qubit 2.0 fluorometer. At last, high-throughput sequencing of 16S rRNA genes was performed by Illumina MiSeq (Personalbio Technology Co. Ltd., Shanghai, China) and 300-bp paired-end reads were obtained. The data were submitted to the NCBI (number: PRJNA763332).

Read pairs from raw data were initially merged in FLASH version 1.2.7, in which forward and reverse reads had more than 10-bp overlaps and no base mismatches. Illumina sequence reads were processed by the quantitative insights into microbial ecology (QIIME) pipeline. In briefly, low-quality sequence reads were removed, and the 12-bp barcode was inspected to allocate the multiplexed reads to samples. Chimeric sequences were identified with the Uchime algorithm in a chimera-free reference database using the Usearch tool. The high-quality sequences with a 97% similarity were allocated to OTUs (operational taxonomic units) with Uclust clustering method. A representative sequence from each OTU was aligned with PyNAST against the GreenGene Database (v13_5). The taxonomic classification of OTUs was conducted with the RDP Classifier against the GreenGene Database (v13_5) with a percent similarity threshold of 97%.

2.6. Statistical analysis

The soil organic C accumulation rate was computed as follows:
Accumulation rate = (organic C content in 2009 – organic C content in 1989)/20.
One-way analysis of variance was employed to assess the effects of long-term fertilization on soil properties. The least significant difference method was carried out using SPSS 18 for Windows (SPSS Inc., Chicago, IL, USA) to test statistically significant differences among treatments at the 5% level. The relations between the soil microorganisms and soil properties as well as the effects of long-term fertilization on microbial community composition were evaluated using canonical correspondence analysis (CCA).

3. Results

3.1. Soil properties

The SOC and total N contents increased to a greater extent after 20-year compost application than inorganic fertilization (Table 2). The CM treatment had the highest accumulation rate of SOC (0.39 g C kg$^{-1}\cdot$yr^{-1}), followed by HCM (0.24 g C kg$^{-1}\cdot$yr^{-1}), while the NK treatment presented the lowest accumulation rate of SOC (0.04 g C kg$^{-1}\cdot$yr^{-1}). The CM, HCM and NPK treatments also presented significantly greater soil carbohydrate content than the Control ($P < 0.05$), while the NK and PK application did not. The highest SCMR was 0.52 mg C$\cdot$g^{-1} SOC$\cdot$day^{-1} in the PK treated soil, while the lowest was in the CM treated soil (0.32 mg C$\cdot$g^{-1} SOC$\cdot$day^{-1}). Compost and inorganic N treatments decreased the soil pH significantly ($P < 0.05$).

Table 2 Soil properties, organic C accumulation rate and SCMR in soil following 20 years of organic and inorganic fertilizer application.

Treatment	pH	SOC (g C·kg⁻¹)	Total N (g N·kg⁻¹)	C/N	Carbohydrates (g C·kg⁻¹ soil)	SOC accumulation rate (g C·kg⁻¹ soil·yr⁻¹)	SCMR (mg C·g⁻¹ SOC·d⁻¹)
Control	8.39 (0.02)a	4.45 (0.03)e	0.47 (0.02)f	9.47 (0.34)a	0.49 (0.04)e	0.00 (0.00)f	0.34 (0.01)c
CM	8.06 (0.06)c	12.20 (0.08)a	1.56 (0.03)a	7.82 (0.10)c	1.00 (0.04)a	0.39 (0.00)a	0.32 (0.02)c
HCM	7.90 (0.01)d	9.28 (0.08)b	1.10 (0.03)b	8.44 (0.19)b	0.78 (0.06)b	0.24 (0.01)b	0.41 (0.00)b
NPK	8.00 (0.05)c	7.00 (0.04)c	0.80 (0.03)c	8.75 (0.23)b	0.60 (0.02)c	0.13 (0.01)c	0.43 (0.02)b
NP	8.24 (0.00)b	6.64 (0.05)c	0.76 (0.02)d	8.74 (0.15)b	0.58 (0.04)d	0.11 (0.01)c	0.38 (0.00)bc
NK	8.03 (0.09)c	5.22 (0.06)d	0.88 (0.02)c	5.93 (0.07)a	0.55 (0.03)e	0.04 (0.00)e	0.32 (0.02)c
PK	8.34 (0.01)a	5.80 (0.10)d	0.62 (0.01)e	9.35 (0.01)d	0.51 (0.04)e	0.07 (0.00)d	0.52 (0.05)a

The standard deviations (sd) are shown in parentheses (n = 4). Different letters represent significant differences between treatments at $P < 0.05$.

The Control treatment had significantly greater D (5.19 × 10⁻⁶ m²·s⁻¹, Fig. 1) than the other treatments ($P < 0.05$), while the CM treatment had the lowest vaule (1.30 × 10⁻⁶ m²·s⁻¹). The D significantly differed among treatments ($P < 0.05$) and were in the order of CM < HCM < PK, NP and NPK < NK < Control.
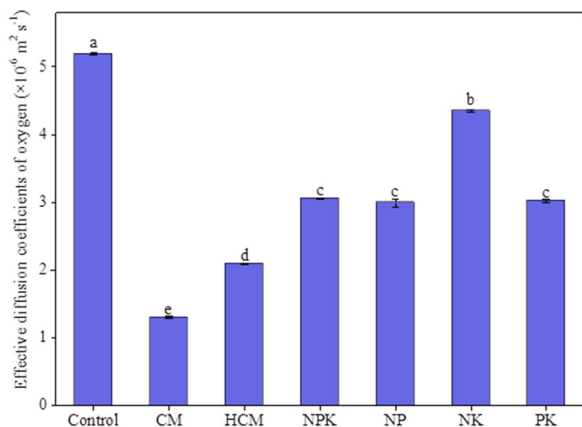

Fig. 1 The effective diffusion coefficient of oxygen (D) in different long-term (20 years) fertilization treatments. Vertical bars indicate the sd (n = 4). Different letters represent significant differences between treatments at $P < 0.05$.

3.2. Bacterial community composition

The 16S rRNA Illumina sequencing generated 517,660 high-quality sequences in total, with 73,951 sequences and 8372 unique OTUs per sample on average (OTUs are defined as sequences with 97% similarity), and the average read length was 225 bp. Eleven phylum-level groups were selected for the statistical analysis (Fig. 2). Of these, the most predominant phylum was *Proteobacteria* in all treatments, and accounted for 25.4−32.7% of the total abundance. *Actinobacteria*, *Bacteroidetes*, and *Acidobacteria* also constituted a large proportion of the total microbial abundance in all treatments and accounted for 17.1−21.4%, 8.4−23.4%, and 9.2−16.2% of the total abundance, respectively. Fertilization treatments presented lower relative abundance (RA) of *Bacteroidetes* and higher *Proteobacteria* and *Verrucomicrobia* than the Control. The RA of *Firmicutes* was augmented by 90.47% and 68.32%, respectively in the CM and HCM treatments but reduced by 52.47%−78.18% in the inorganic fertilization treatments. Relative to the Control treatment, the change of the RA of *Firmicutes* was mainly due to the variation in *Bacillales* in fertilizer-treated soil (Fig. 3). Nonetheless, the RA of *Acidobacteria* decreased slightly in the compost treatments (CM and HCM) but increased by 49.0% under NPK treatment and by 11.8−13.1% under unbalanced fertilization treatments relative to the Control.
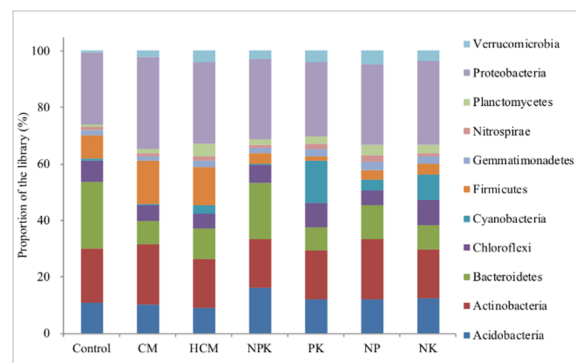

Fig. 2 Relative abundance (RA) of bacteria phyla in different long-term (20 years) fertilization treatments.
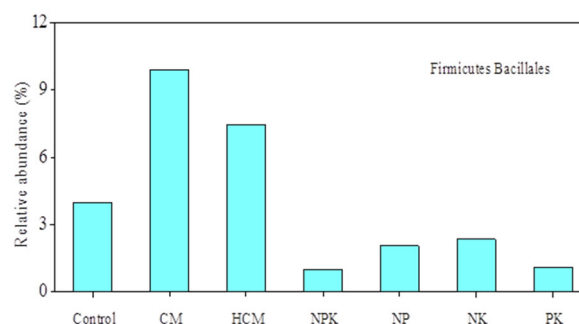

Fig. 3 Relative abundance (RA) of order Bacillales within phylum Firmicutes in different long-term (20 years) fertilization treatments.

For classes within phylum *Proteobacteria*, *Alpha*-proteobacteria augmented in the NPK and CM treatments relative to the Control (Fig. 4). The RA of *Beta-proteobacteria* augmented in all fertilization treatments except NPK. The RA of *Gamma-proteobacteria* augmented in the CM treatment while

reduced in the other treatments. On the contrary, the RA of *Delta-proteobacteria* remained relatively stable in the CM treatment, but increased by 46.87%−74.33% in the other treatments. Finer taxonomic divisions revealed that the CM treatment presented the greatest RA of the order *Xanthomonadales* within *Gamma-proteobacteria* (Fig. 5).
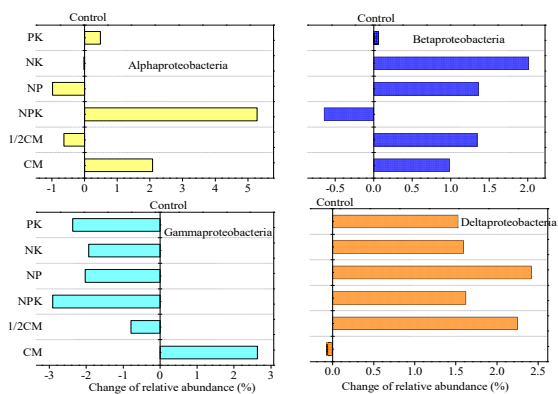

Fig. 4 Changes in the relative abundance (RA) of four classes of *Proteobacteria* (*Alpha-proteobacteria*, *Beta-proteobacteria*, *Gamma-proteobacteria*, and *Delta-proteobacteria*) in soil treated with compost and inorganic fertilizer application for 20 years compared with the Control.
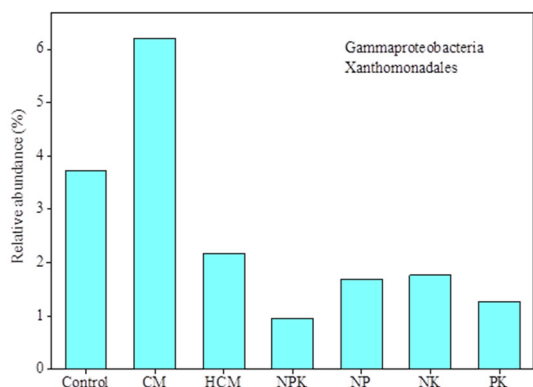

Fig. 5 Relative abundance (RA) of order *Xanthomonadales* within *Gamma-proteobacteria* in different long-term (20 years) fertilization treatments.

3.3. Relations between soil properties and microbial taxa

The SOC, SOC accumulation rate, carbohydrate content, and the total N were significantly ($P < 0.05$) correlated with the RA of *Firmicutes* and *Proteobacteria* (Fig. 6). The CCA ordination plots showed that the D was significantly ($P < 0.05$) related with the SOC, carbohydrate content, and SOC accumulation rate (Fig. 7). OTUs identified as *Mogibacterium* in the *Clostridiales* order, *Bacillus asahii* in the *Bacillales* order, and *Xanthomonadaceae* in the *Xanthomonadales* order were significantly related with the SOC accumulation rate, SOC, and carbohydrate content ($P < 0.05$), but a negative correlation was observed between the D and the above OTUs.
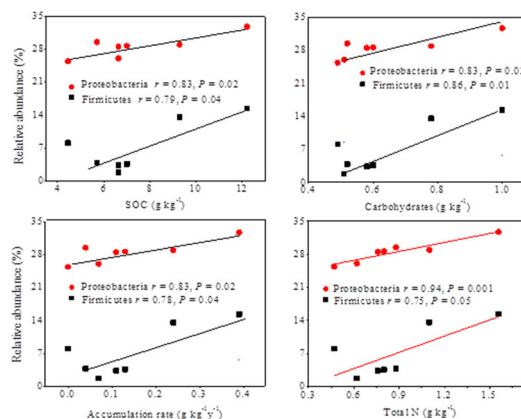

Fig. 6 Relation between the relative abundance (RA) of two bacterial groups, SOC, carbohydrate content, total N content, and organic C accumulation rate in different long-term (20 years) fertilization treatments.
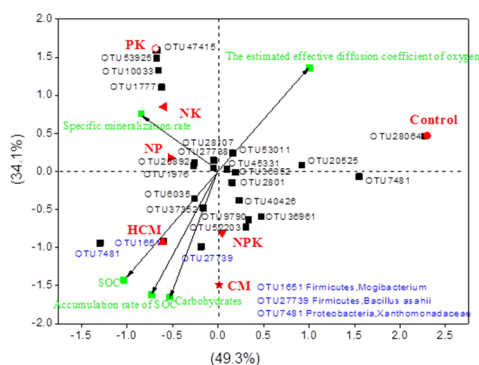

Fig. 7 Canonical correspondence analysis (CCA) illustrating the relation between microorganisms and some soil properties such as SOC, carbohydrate, accumulation rate of organic C, specific mineralization rate of organic C, and the effective oxygen diffusion coefficient at the OTU level.

4. Discussion

Proteobacteria and *Bacteroidetes* are generally considered to be copiotrophic taxa which likely flourish in soils as the availability of SOC increases. Our result showed that long-term fertilization enhanced the RA of *Proteobacteria* but reduced that of *Bacteroidetes* in soil relative to the Control (Fig. 2). However, an analysis of the finer taxonomic divisions revealed that the RA of order *Xanthomonadales* within *Gammaproteobacteria* increased only in the CM-treated soils, where the SOC (12.20 g C·kg^{-1}) was greater than the other treatments (Fig. 5). Similarly, in previous studies, *Xanthomonadales* were reported to be more plentiful in long-term N-fertilized treatment than the Control or unfertilized treatment when the SOC content was grerater than 12 g C·kg^{-1} [1]. More importantly, Li et al. [10] reported that the RA of *Xanthomonadales* increased with decreasing oxygen content of soil. Thus, we speculated that the SOC, particularly the effective oxygen diffusion coefficient, determined the growth of *Xanthomonadales* in our study. Our result showed that the Control

treatment presented the highest abundance of *Bacteroidetes*. Similar to our findings, Li et al. [10] and Zeng et al. [2] also revealed that the abundance of *Bacteroidetes* decreased in soils treated with fertilizer (inorganic fertilizer combined with wheat straw or inorganic fertilizer alone). This may be because *Bacteroidetes* were not only positively correlated to availability of C or N but also negatively correlated with soil pH.

In contrast to *Bacteroidetes* and *Proteobacteria*, *Acidobacteria* can grow at low pH and utilize nutrient-poor and recalcitrant C substrates. In our study, *Acidobacteria* had the greatest RA in the NPK treatment, probably due to its relatively low pH. Although the HCM treatment presented lower pH than the NPK treatment, it had a higher SOC, consequently inhibiting the growth of *Acidobacteria* as members of this phylum favor oligotrophic conditions. In current study, the RA of *Firmicutes*, especially *Bacillus* spp., augmented by compost application but decreased following inorganic fertilizer treatment, which is in consistent with the results of the previous study [10]. Feng et al. [11] found that compost application not only increased the abundance of *Bacilli* significantly but also changed its composition, while NPK did not. It is likely that the soil environment established in the compost-treated soil provided a more suitable niche for the growth of indigenous *Bacillus* spp. [11].

We found that the RA of *Firmicutes* and *Proteobacteria* was significantly related with the SOC, carbohydrate content, and SOC accumulation rate (Fig. 6), in accordance with the results reported in previous studies. A major part of the identified anaerobic respiration genes have been allocated to the *Firmicutes*, *Proteobacteria*, and *Actinobacteria* phyla, which decomposed SOC at lower rates under anaerobic conditions than under aerobic conditions. In the present study, fertilization treatments, especially compost application, decreased the effective oxygen diffusion coefficient due to the changes in the pore systems and enhanced the RA of *Proteobacteria* and *Firmicutes*. Our results suggest that there was a gradual transition of SOC degradation from aerobic to anaerobic with increasing SOC [11]. In addition, *Actinobacteria*, *Bacteroidetes*, and *Verrucomicrobia* accounted for >70% of genes that were allocated to the three main groups of polysaccharide degradation (cellulases, endohemicellulases, and debranching enzymes). Thus, the significant decline in the abundance of *Bacteroidetes* in fertilized soils may have favored polysaccharide accumulation.

For finer divisions, we found that the *Mogibacterium*, *Bacillus* and *Xanthomonadaceae* showed positive correlations with the accumulation rate of SOC (Fig. 7). Previous researches have illustrated that the increase in the abundance of *Bacillus* significantly improved the activities of both lipase and polyphenol oxidase in soil, and then promoted soil organic matter to be transformed into humus, which is the main component of SOC. Thus far, however, how *Mogibacterium* and the *Xanthomonadaceae* family favor organic C accumulation remains to be understood and the function

of these bacteria requires to be elucidated in future studies.

5. Conclusion

In conclusion, 20-year compost application was more favorable in augmenting the SOC content compared with inorganic fertilizer application. However, the Control treatment presented significantly greater D than the other treatments, especially in compost-treated soils. The soil bacterial community structure was altered by the shifts in soil properties between fertilization treatments. Fertilizer application decreased the RA of *Bacteroidetes* but augmented the RA of *Proteobacteria*. Compost application increased the RA of *Firmicutes* but inorganic fertilizer application decreased it. The enhancement of the RA of *Proteobacteria* and *Firmicutes* indicated degradation of SOC was gradually shrifted from aerobic to anaerobic with the application of fertilizers, especially in compost treatment, which would favor SOC accumulation. However, the significant reduction of the RA of *Bacteroidetes* in fertilized soils may have favored polysaccharide accumulation. At the genus levels, the RA of *Bacillus* spp. was higher in compost-treated soils, which could improve the conversion of soil organic matter into humus. This study aids in clarifying the impact of long-term organic and inorganic fertilization on bacterial community and its relation to organic carbon accumulation in a sandy loam soil.

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