



Effects of long-term straw retention on soil microorganisms under a rice–wheat cropping system

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Received: 23 November 2019 / Revised: 24 April 2020 / Accepted: 11 May 2020 / Published online: 25 May 2020
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Abstract

The objective of this study was to investigate how straw-incorporating practices affect bacterial communities and carbon source utilization capacity under a rice–wheat rotational farming practice in central China. To clarify the effect of long-term straw incorporation in microbial abundance and carbon metabolism, a long-term field experiment was initiated in May 2005 (rice-planting season). Soil bacterial communities were revealed by high-throughput sequencing technology. After ten cycles of annual rice–wheat rotation (2005–2015), 2 M (straw incorporation) and 2 M + NPK (high straw incorporation + chemical fertilizer) treatments had significantly more bacterial phyla compared with CK (non-fertilization) and NPK (chemical fertilizer) treatments. Taxonomic analysis revealed that 2 M and NPK + 2 M treatments had a significantly greater abundance of microbial communities, especially the *Gemmatimonadetes*, *Acidobacteria*, *Firmicutes*, and *Actinobacteria*. In the NPK versus 2 M, 2 M treatment had a significantly greater abundance of *Rozellomycota* ($P < 0.05$). In the NPK + 2 M versus NPK, NPK + 2 M treatment also had significantly greater abundance of *Ascomycota* ($P < 0.05$). Principal component analysis (PCA) analysis showed that 2 M treatment was separate from other treatments. Using biogeochemistry (biog-ECO) method, the metabolic diversity and functional characteristics of microbial communities were used to indicate the ability of microorganisms to utilize carbon source. The carbon utilization ability of soil microorganisms in 2 M + NPK treatment was significantly higher than that of CK treatment ($P < 0.05$). The utilization ability of carboxylic acids, polymers, and other mixtures of carbon sources in 2 M treatment was higher than those of other treatments. These findings suggest that long-term straw incorporation affects the abundance and carbon utilization ability of soil microorganisms within 0–20 cm soil depths, among which, *Gemmatimonadetes*, *Firmicutes*, and *Actinobacteria* may play crucial roles in bacterial communities and carbon source utilization capacity.

Keywords Straw returning · High-throughput sequencing · Soil bacterial communities · Carbon utilization ability · Central China

Communicated by Erko Stackebrandt.

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s00203-020-01899-8>) contains supplementary material, which is available to authorized users.

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Introduction

The decline in agricultural productivity due to climate change factors and longtime continuous cropping practices has created the need to use different forms of organic and inorganic fertilizers to boost the capacity of farms to produce higher crop yields (Cui et al. 2010). However, over-usage of inorganic fertilizers has been confirmed to cause destruction to the soil environment, a situation that not only results in the degradation of soil quality, but also poses increased health risks to humans and animals such as the soil microorganisms (Dusenbury et al. 2008). Due to this, studies have continued to focus on the appropriate organic forms of soil amendments techniques that can increase the agricultural yields while promoting the soil ecological integrity and improved environmental condition (Cui et al. 2010; Bastida

et al. 2008). Soil microorganisms are the kernel of soil fertility, and the major forms of ecologically significant microbial communities found within soil are the bacteria and fungi (Bastida et al. 2008). Specifically, ammonia-oxidizing bacteria (AOB) are the primary microbial groups found in soil, and they provide significant ecological benefits to the soil (Mahajan and Balachandran 2012).

The practice of soil amendment using the straw incorporation procedure has been shown to be a better way of enhancing soil quality. Indeed, one study has confirmed its high potential in increasing the enzymatic activity and regulating the functions of soil microbiota (Bastida et al. 2008). As demand for food increases under this changing climatic conditions and degraded soil quality, the effects of straw incorporation in soil bacterial communities have become a crucial practice for improving soil quality. This has thus continued to attract the attention and interest of most soil scientists, with the aim of providing a better understanding on the effects of straw returning farming practice on the general quality, and with much emphasis on its ability to promote the soil's microbial communities and impact-related functions (Cui et al. 2010). The sustainability of a rice–wheat cropping system is highly negatively affected by soil degradation and pollution. Additionally, the long-term use of conventional management practices, such as the removal of crop residue, burning crop residues, or intensive soil tilling has also been confirmed to have greater effects on the productivity of the rice–wheat cropping system (Guo et al. 2010). The full understanding of these phenomena has not been achieved for the efficient management of rice–wheat cropping systems. One factor that has for a long time contributed to such low understanding on the rice–wheat cropping system and microbial interactions has been due to low economic and technical know-how on carrying out full characterization of the soil's bacterial communities in such cropping system, which requires large experimental fields and many years of experimental runs (Bastida et al. 2008).

To provide an in-depth understanding of the microbial communities in soil, high-throughput sequencing technologies have been introduced to characterize the soil's microbial community structures (Ogilvie et al. 2008). However, the response of the soil bacterial community to fertilization has varied considerably between studies, and no clear trends have emerged from the existing studies. As described previously, the use of high-throughput sequencing technology in two cycles of rice–wheat rotation under no-tillage and straw-incorporating practices can promote soil organic carbon (SOC) within the 0–5-cm soil layer. This may presumably be caused by increases in the abundance of bacterial genera (Guo et al. 2016a). Indeed, a study by Govaerts et al. found that tillage practices and straw-returning methods can drastically affect topsoil bacterial communities and organic carbon under a rice–wheat cropping system (Govaerts et al. 2007a).

Therefore, further investigation is needed to provide a clearer understanding of the relative contributions of soil bacterial communities to soil quality under the straw-incorporating practice. Furthermore, information about the influence of straw returning on the microbial community and carbon metabolism in soil is scarce. To bridge this gap, the present study investigated the effect of long-term straw incorporation in soil microorganisms (bacteria, fungi, and AOB) and carbon metabolism using high-throughput 16S rRNA sequencing technology and the *biolog-ECO* method. The ultimate objective of the study was to reveal the direct response of the microbial communities and carbon metabolism in soil on straw-returning practices to obtain the ecological and internal functional relationship mechanisms to guide future agricultural practices.

Materials and methods

Experimental site

The experiment was undertaken within a field experimental site located in Haokou Town (30°22'55.1" N, 112°37'15.4" E) in Qianjiang, Hubei Province, China. The topography was alluvial plain in nature, featuring the tidal soil-type compost of the river alluvial parent material with a pH of 7.44–8.41. The soil layer was deep with a light texture. The planting system was annual rotational rice–wheat. The study site had a humid, subtropical monsoon climate (Hu et al. 1999).

Experimental setup and designs

To provide clear information on the effects of long-term straw-returning practices on microbial abundance and carbon metabolism, a long-term field experiment (involving the application of manure/straw incorporation and a control treatment) was initiated in May 2005 (rice-planting season). The cropping regime was occupied by two crops: summer rice (sown in early May) and winter wheat (sown in early November). The study was undertaken during ten cycles of annual rice–wheat rotation (2005–2015).

Each treatment plot had an area of 5 × 4 m, with four replications under a randomized block group arrangement. The treatment plots were separated by field ridges, fixed drainage, and irrigation between the groups. The groove width was 40 cm, and each cell could be independently drained. The experiment was designed as a randomized block with three replications, which involved five treatments: CK, NPK, 2 M, M + NPK, and 2 M + NPK. (1) For the CK treatment, rice and wheat were not fertilized during the seasons and straw incorporation was also not practiced. Ploughing was performed at depths of about 20 cm. (2) For

the NPK treatment, rice and wheat were only subjected to chemical fertilization in two seasons with no straw returning; the amounts of N, P₂O₅, and K₂O treatments used were 150, 90, 90, and 120, 75, and 60 for rice and wheat, respectively. (3) For 2 M treatment, the rice and wheat crops were not applied with chemical fertilizer, and straw return was undertaken at an application rate of 6000 kg/ha per season. To ensure consistency between treatments, the straw was obtained from the same farm plot within the experimental location. (4) For the M+NPK treatment, chemical fertilizer and straw return were undertaken, and the amount of NPK was the same under treatment 2, and straw return was undertaken at an application rate of 3000 kg/ha per season. (5) For 2 M+NPK treatment, chemical fertilizer and straw return were undertaken, and the amount of NPK was the same under treatment 2, and straw return was undertaken at an application rate of 6000 kg/ha per season. The experimental design is provided in Fig. 1.

Soil sampling

Soil samples were taken in replicate from selected plots at a soil profile depth of 0–20 cm using a soil sampler after the wheat harvesting season of May 2018. After sampling, visible plant residues and stones were removed, and large soil clods were gently broken by hand. The soil samples were sieved through a 2 mm sieve and stored in a refrigerator at – 80 °C.

Bacterial count using a dilution plate method

The soil samples were treated with an analytical sieve with a pore size of 1 mm. Then a 10 g sample was taken into an Erlenmeyer flask containing 90 mL of sterile water and oscillated for 20 min. After standing for 3–4 min, the upper soil suspension was used for the plate count test of bacteria. The bacteria were incubated at a constant temperature in a 30 °C incubator for 1 day. The bacteria were counted using

serial dilutions of 10⁻⁶, 10⁻⁷, and 10⁻⁸. Each dilution was repeated five times.

High-throughput 16S rRNA sequencing

High-throughput sequencing technology was used in the identification of soil bacteria. Polymerase chain reactions (PCRs) were performed on the soil samples as previously described (Caporaso et al. 2011). Samples with major bright strips of between 400 and 450 bp were chosen for further experiments. The PCR products were mixed in equidensity ratios and sequencing analysis was performed as previously described (Caporaso et al. 2010; Edgar 2013; Magoc and Salzberg 2011). The sequences were assigned to Operational Taxonomic Units (OTUs) with 97% similarity. A previously described protocol (Caporaso et al. 2010) was used to determine the composition and diversity of the bacterial communities under different treatments. A representative sequence for each OTU was selected, and the ribosomal database project classifier was used to assign taxonomic data to each representative sequence (40,000). To compute alpha diversity, the OTU table was ratified and then three metrics were calculated: the Chao1 metric to estimate metrics of richness and observed OTUs, which included the counts of unique OTUs in the samples; the Shannon index; and the Abundance-based Coverage Estimator (ACE) were calculated.

Determination of metabolism ability using biologi-ECO

In this study, the ecological characteristics of the microbial community i.e., the 31 carbon source substrates of biologi-ECO board were divided into 6 categories: amino acids, sugar, amine carbon sources, carboxylic acids, polymers, and other carbon source mixtures. The preparation of the inoculum of the ECO plate was carried out by first activating the soil sample at 25 °C for 24 h, and then 3 g of soil was placed in 27 mL of 0.85 mol/L NaCl solution and shaken at 200 r/min for 30 min. After mixing, 3 mL of the supernatant

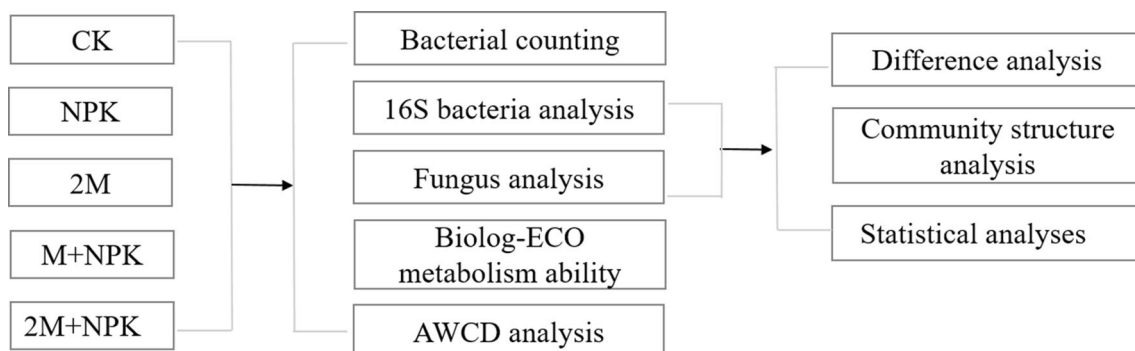


Fig. 1 Schematic workflow of the experimental design and procedure

was added to 27 mL of the NaCl solution, with a final dilution ratio of 1:1000. After the addition of 150 μ L of the dilution to each ECO plate well, and after the dilution of each soil sample was set according to the method requirements (Govaerts et al. 2007b), the inoculated microplate was put in a moisturizing container and then placed in a constant temperature incubator set at 25 °C. Measurements were then recorded at 24, 36, 48, 72, 96, 120, 144, and 168 h on an ELxS08-Biolog microplate reader (Bio-Tek Instruments Inc, Winooski, VT, USA) at wavelengths of 590 nm (color + turbidity) and 750 nm (turbidity), respectively.

Statistical analyses

Data were processed and calculated using Microsoft Excel 2007 (Microsoft Corporation, Redmond, WA, USA), and statistical analysis was performed using one-way analysis of variance (ANOVA). Crop yields and nutrient uptake were counted in two ways: first, through the calculation of the total amount of rice and wheat yields, and nutrient uptake in each plot for ten seasons, as well as the annual average yield and annual nutrient uptake of the crops in each plot. The four annual (2005–2015) average data of the different treatments were counted, and the results were provided as the statistical value of “community” yield and nutrient uptake, which eliminated the interannual variation. These results reflected the variation between repetitions of different treatments—that is, spatial variation. Second, the average yield of crop and nutrient uptake for each year and each treatment was calculated, as were the data of ten replicates (ten seasons). The results obtained are the “annual” yield and nutrient uptake statistics, which eliminated the variation between repetitions and reflected the variation between different treatments, that is, the time variation. For the nutrient content of crop grains and straw, the average value of four replicates per treatment per year was first determined; following this, the number of years (10) was used as the repeat number for statistical analysis.

Results

Soil microbial biomass

The abundance of soil bacteria under CK, NPK, 2 M, M + NPK, and 2 M + NPK conditions is shown in Fig. 2. Based on the above information, the soil bacterial abundance was the highest with the 2 M treatment followed by 2 M + NPK treatment then M + NPK treatment, NPK treatment and lastly CK treatment. The changes in soil bacteria across the different fertilization treatments showed that the number of bacteria in 2 M-treated soil was significantly higher than that for other fertilization treatments ($P < 0.05$),

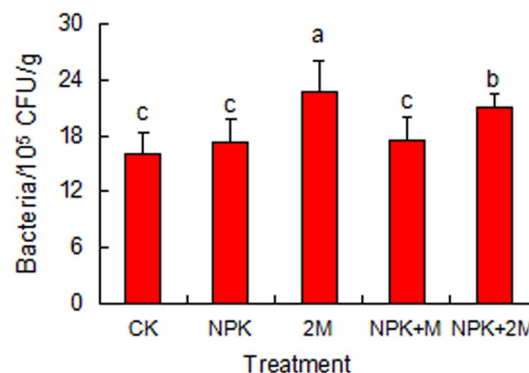


Fig. 2 The abundance of soil bacteria under CK, NPK, 2 M, M + NPK and 2 M + NPK conditions. The x-axis represents different treatments; the y-axis represents amount of bacteria. Different small letters indicated significant difference at $P < 0.05$ (color figure online)

followed by NPK + 2 M treatment; CK treatment had the lowest amount of soil bacteria.

Soil bacterial community structure

The hierarchical clustering analysis of the top 50 genera is shown in Fig. 3. To further compare the microbiota between the different treatments, taxonomic analysis and PCA was performed on the relative abundance. In Fig. 4a, *Proteobacteria*, *Acidobacteria*, and *Chloroflexi* were the three most dominant phyla, accounting for more than 50% of the reads. When comparing the 2 M versus CK, 2 M treatment had a significantly greater abundance of *Fibrobacteres* and WS2 ($P < 0.05$). Comparing the 2 M versus NPK, 2 M treatment had a significantly greater abundance of *Armatimonadetes*, *Cyanobacteria*, *Microgenomates*, *Bacteroidetes*, and *Firmicutes* ($P < 0.05$). For the NPK + 2 M versus CK, NPK + 2 M treatment had a significantly greater abundance of *Gemmatimonadetes* and *Saccharibacteria* ($P < 0.05$). For the NPK + 2 M versus NPK, NPK + 2 M treatment had a significantly greater abundance of *TM6 (Dependentiae)*, *Cyanobacteria*, *Actinobacteria*, and *Saccharibacteria* ($P < 0.05$). The PC1 and PC2 accounted for 48.28 and 20.03% of the total variation, respectively (Fig. 4b).

AOB community structure within the soil

The hierarchical clustering analysis of the top four genera of AOB communities is shown in Fig. 5. Taxonomic analysis and PCA were performed on the relative abundance. Based on the information provided in Fig. 6a, *Proteobacteria* and *Nitrospirae* were the two most dominant phyla, accounting for more than 80% of the reads. When comparing the NPK + 2 M versus CK, NPK + 2 M treatment had a significantly greater abundance of *Proteobacteria* and *Nitrospirae* ($P < 0.05$). When comparing the NPK + 2 M versus NPK,

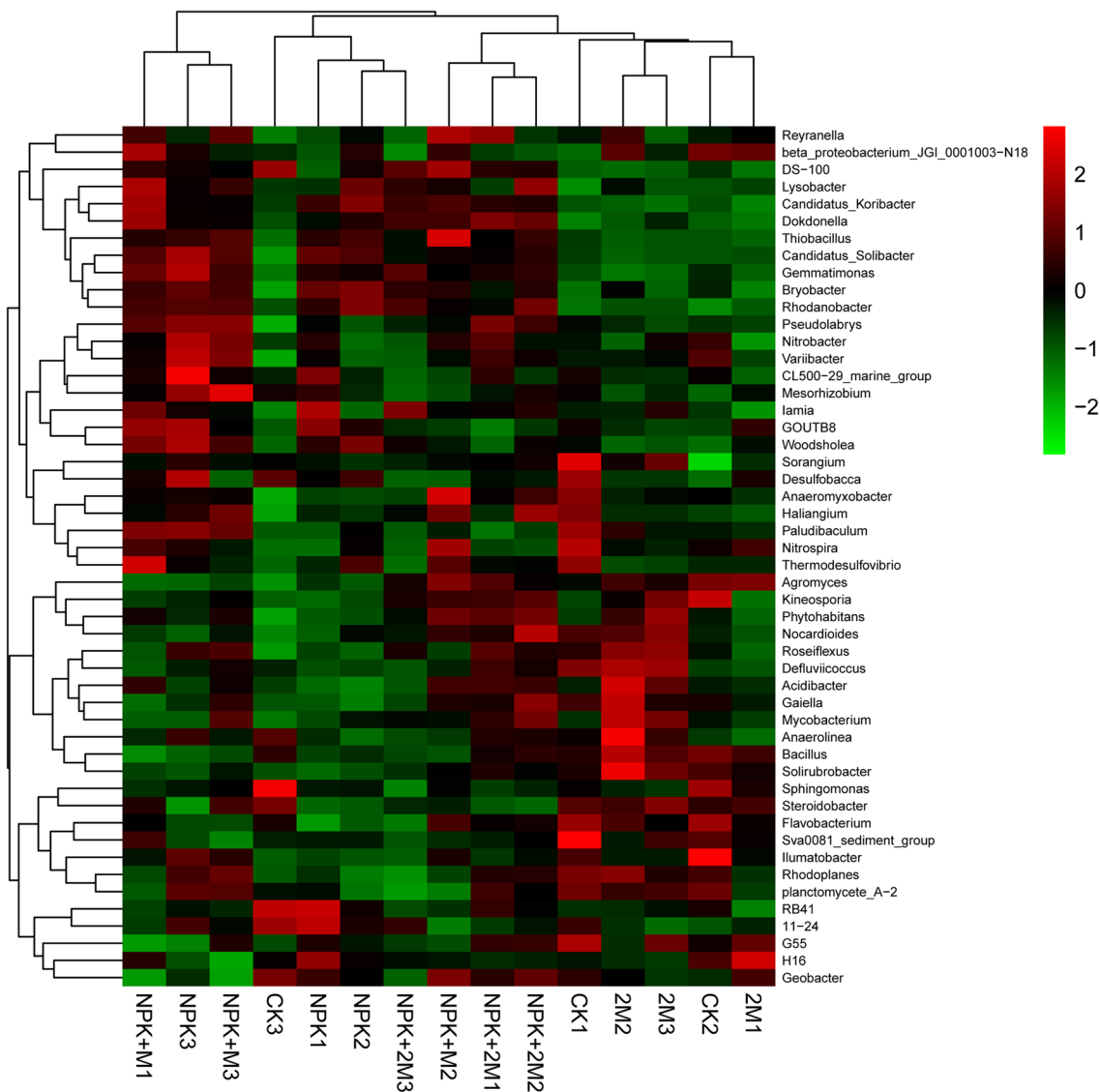


Fig. 3 Hierarchical clustering analysis of top 50 bacterial genera between different treatments. Row and column represent genera and different treatments, respectively. The color scale indicates the abun-

dance of genera. Red and green color indicate high and low abundance, respectively (color figure online)

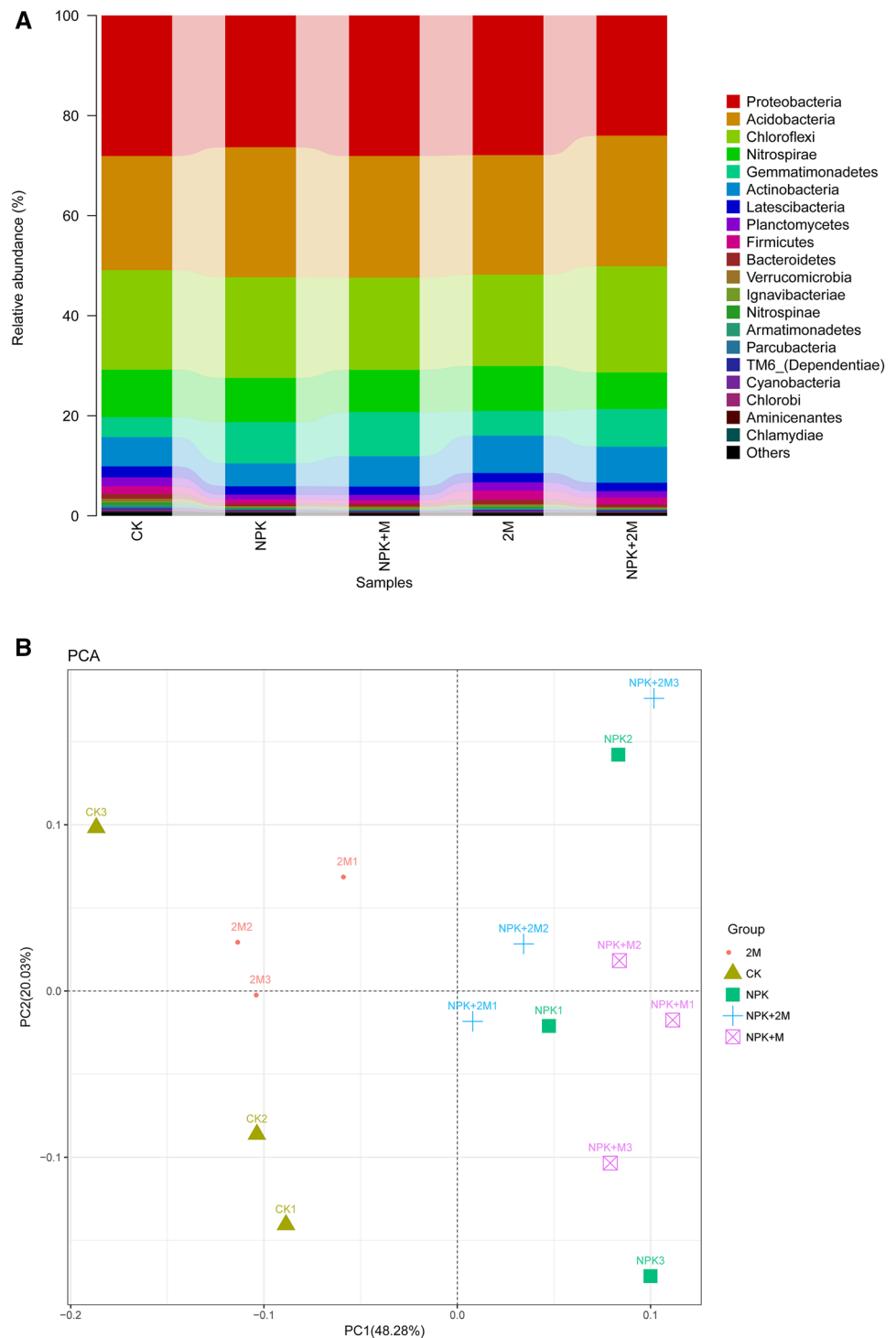
NPK + 2 M treatment also had a significantly greater abundance of *Proteobacteria* and *Nitrospirae* ($P < 0.05$). The information in Fig. 6b indicates that PC1 and PC2 accounted for 97.74 and 2.18% of the total variation, respectively. There were significant differences between the five treatments ($P < 0.05$).

Soil fungal community structure

The hierarchical clustering analysis of the top 50 genera of the fungal community is shown in Fig. 7. To further compare the microbiota between the different treatments, taxonomic analysis and PCA were performed on the relative

abundance. As indicated in Fig. 8a, in all samples, it was found that *Ascomycota*, *Basidiomycota*, *Zygomycota*, and *Cercozoa* were the four most dominant phyla, accounting for more than 80% of the reads. Through a comparison of NPK versus 2 M, the 2 M treatment had a significantly greater abundance of *Rozellomycota* ($P < 0.05$). Additionally, when examining the comparisons between NPK + 2 M versus NPK, it was found that NPK + 2 M treatment also had a significantly greater abundance of *Ascomycota* ($P < 0.05$). The results provided in Fig. 8b indicate that PC1 and PC2 accounted for 50.57 and 25.03% of the total variation, respectively.

Fig. 4 Taxonomic analysis and principal component analysis (PCA) on the relative abundance of bacterial. **a** Taxonomic analysis of five treatments in the phylum level. The X-axis represents different treatments, the Y-axis represents different genera. **b** Component analysis (PCA) on the relative abundance (color figure online)



Comparison of carbon source utilization capacity

Straw incorporation had great effects on the carbon metabolism of soil bacteria. The Average Well Color Development (AWCD) changes of soil microbes in different fertilization treatments showed that the AWCD value of soil microbes in NPK + 2 M treatment was slightly higher than that in other

fertilization treatments, followed by 2 M treatment, while the AWCD value of soil microorganisms in CK treatment was lowest (Supplementary Fig. 1).

The carbon (which consisted of amino acids, sugar, and amine carbon sources, as well as carboxylic acids, polymers, and other mixtures of carbon sources) metabolism ability of CK, NPK, 2 M, M + NPK, and 2 M + NPK soil

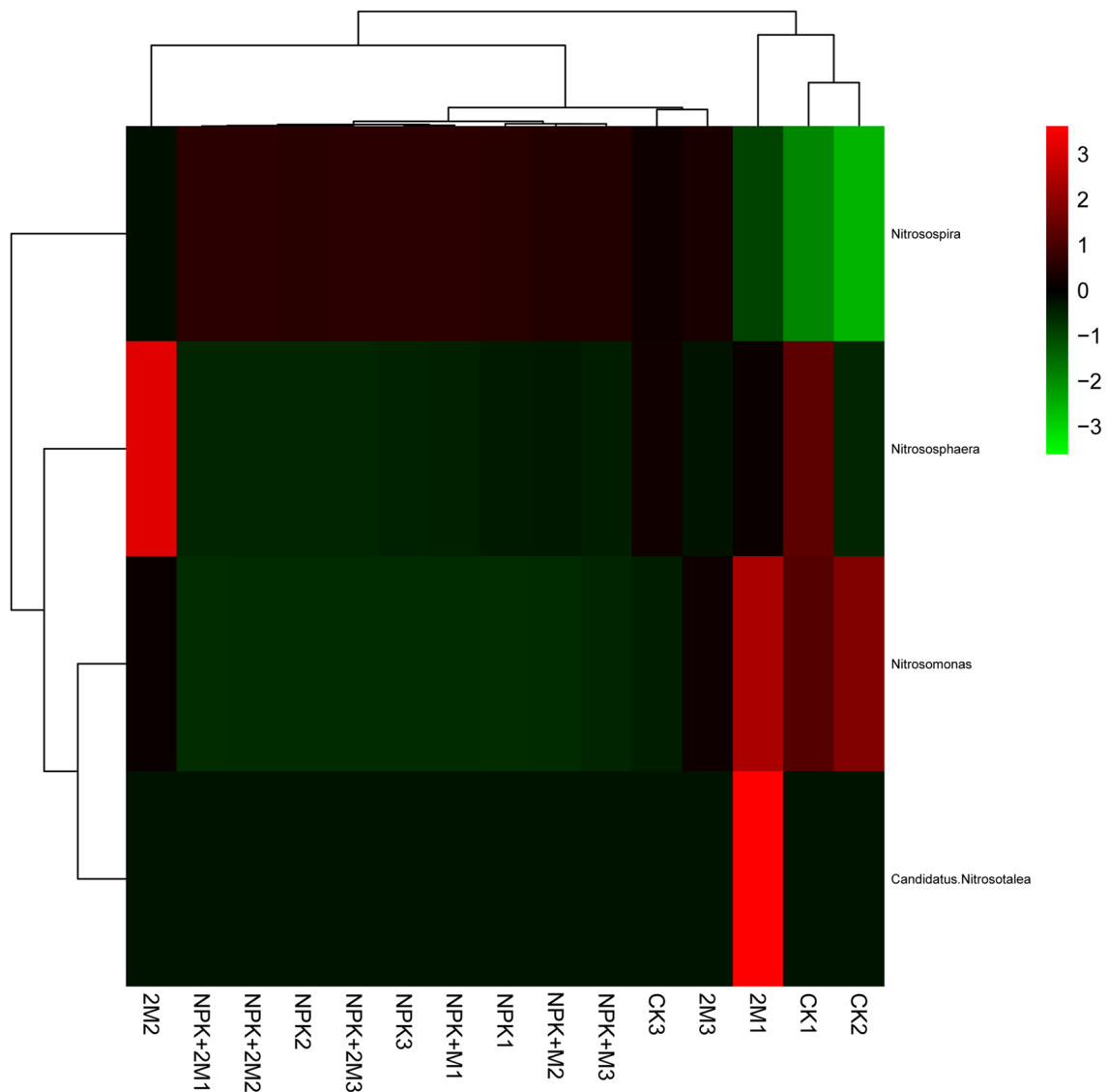


Fig. 5 Hierarchical clustering analysis of top four ammonia oxidizing bacterial genera between different treatments. Row and column represent genera and different treatments, respectively. The color scale

indicates the abundance of genera. Red and green color indicate high- and low-abundance, respectively (color figure online)

treatments is shown in Fig. 9. Based on the figure, the carbon utilization ability of soil microorganisms following 2 M + NPK treatment was significantly higher than that associated with CK treatment ($P < 0.05$). It was found that the microorganisms in 2 M-treated soil tended to utilize carboxylic acids, polymers, and other mixtures of carbon sources to a greater degree than soils treated with other treatments; this difference was significant when compared to CK treatment ($P < 0.05$). For the carbon source utilization diversity index, the diversity index and evenness index of microbial carbon source utilization in soil following NPK + M treatment was significantly higher than those obtained for other treatments ($P < 0.05$). Furthermore, the

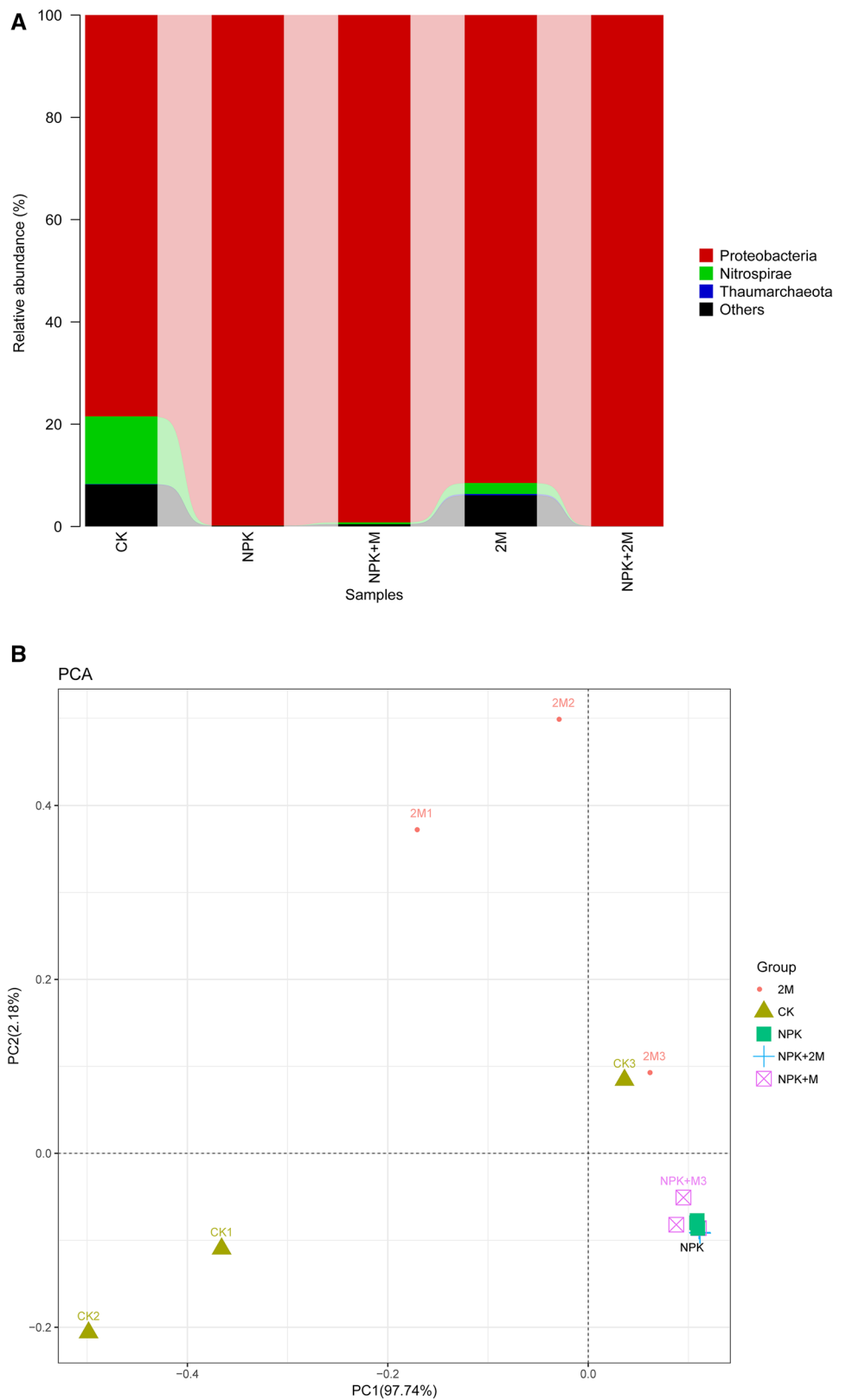
soil microbial carbon source utilization diversity index was the lowest in the CK treatment (Supplementary Fig. 2).

Discussion

Soil microbial biomass under different treatments

Soil microbial biomass is based on a unifying driver or set of environmental drivers that need to be adequately understood (Bastida et al. 2008). The current study investigated the effects of straw-incorporating practices on bacterial communities in soil and their relationship with carbon metabolism

Fig. 6 Taxonomic analysis and principal component analysis (PCA) of the relative abundance of ammonia-oxidizing bacteria. **a** Taxonomic analysis of five treatments in the phylum level. The X-axis represents different treatments; the Y-axis represents different genera. **b** Component analysis (PCA) on the relative abundance (color figure online)



following a 10-year rice–wheat cropping cycle in central China. The results supported the study hypotheses, insofar as straw-incorporating practices increased the bacterial

abundance, and they also led to an increased abundance of AOB and fungi within the topsoil. Previous studies reported that straw-incorporating practices generally increased the

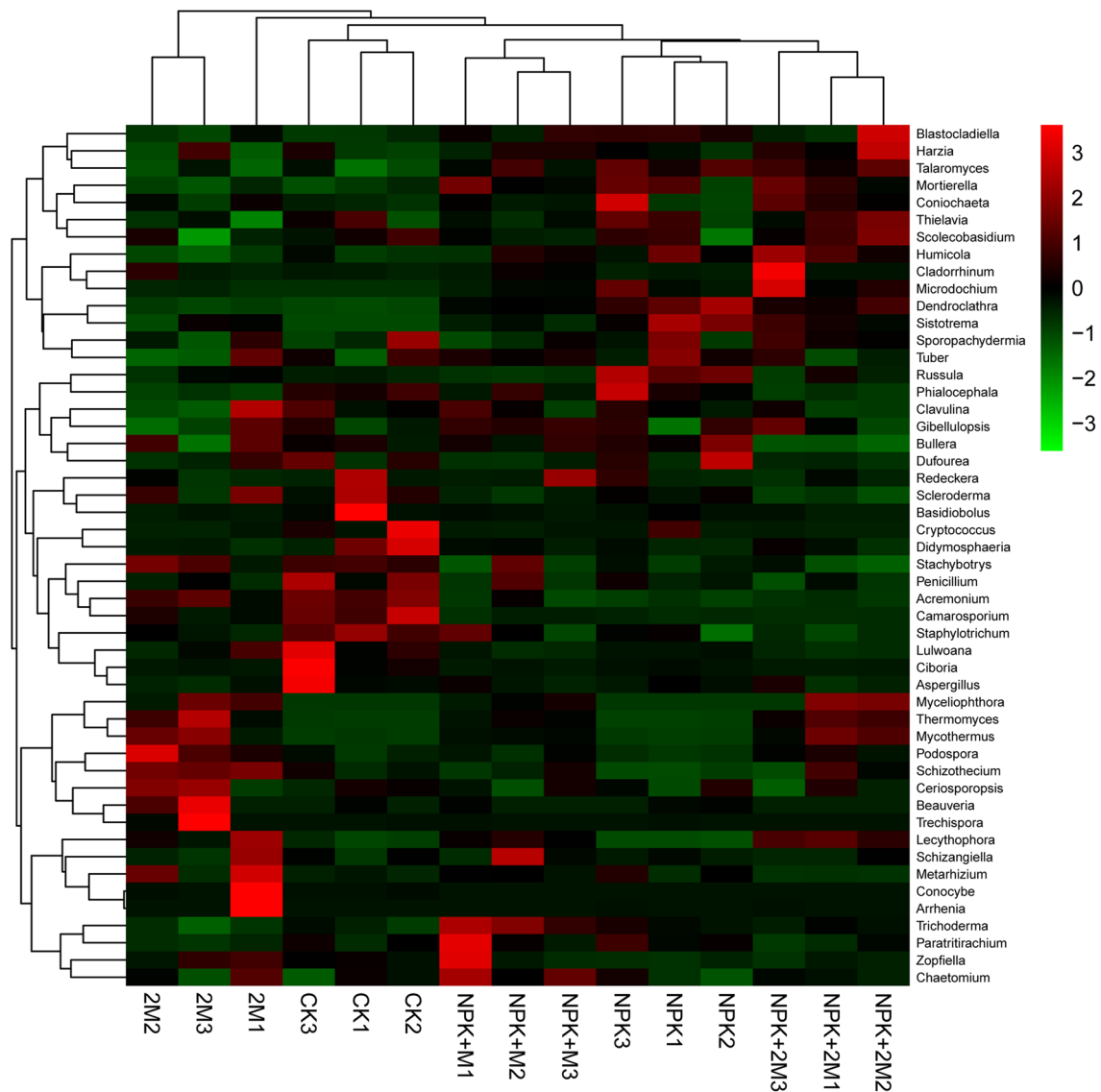


Fig. 7 Hierarchical clustering analysis of top 50 fungal genera between different treatments. Row and column represented genera and different treatments, respectively. The color scale indicates the

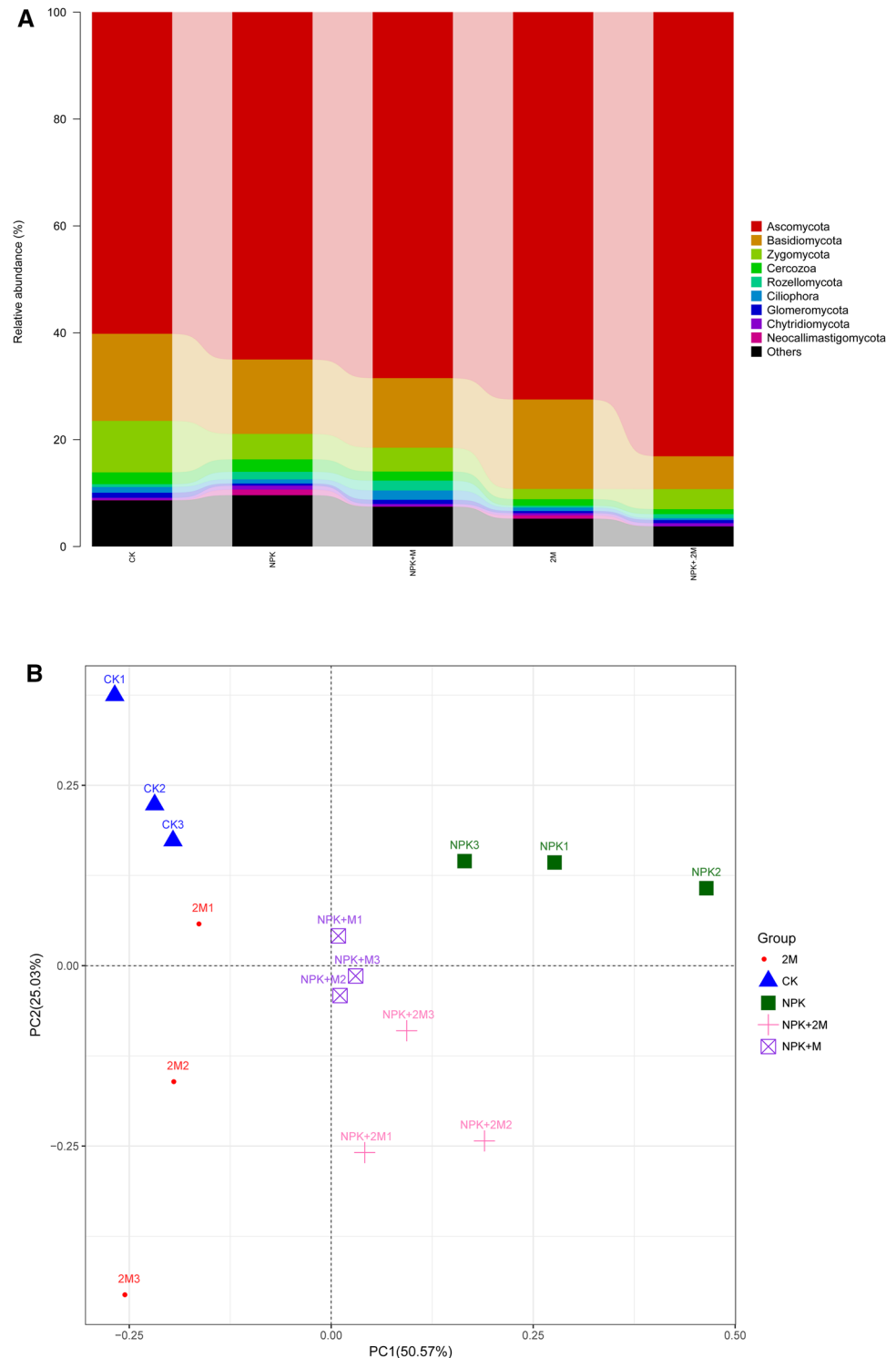
abundance of genera. Red and green color indicate high and low abundance, respectively (color figure online)

abundance, activity, and diversity of microbial communities in the topsoil layer, as this practice contributes to the greater accumulation of crop residues on the soil's surface when compared with the conventional tilling (Wolfarth et al. 2013). The present study indicated that straw incorporation promotes the growth and proliferation of certain groups of microbes, such as those that can play important ecological roles in decomposing cellulose. It was found that long-term straw incorporation can promote and enrich the soil microbes responsible for improving the properties of soil while consequently promoting crop productivity.

Straw incorporation involves the input of organic residues to improve the soil nutrition, which can increase

carbon and soluble organic carbon residues along the soil's surface, and provide energy sources for soil microbes, thus enhancing the microbial biomass in soil (Guo et al. 2016b). The input and accumulation of residues to the soils can improve the soil's moisture and temperature, which can consequently promote soil aggregation, thus boosting microbial growth (Cui et al. 2010; Guo et al. 2016a). In the present study, straw incorporation increased the diversity of different bacterial functional groups in soil, and the number of soil bacteria followed the order of 2 M > 2 M + NPK > M + NPK > NPK > CK. The five treatments showed significant differences ($P < 0.05$). 2 M > NPK indicated that straw returning increased the abundance of soil

Fig. 8 Taxonomic analysis and principal component analysis (PCA) on the relative abundance of fungus. **a** Taxonomic analysis of five treatments in the phylum level. The X-axis represents different treatments; the Y-axis represents different genera. **b** Component analysis (PCA) on the relative abundance (color figure online)



microorganisms. $2M + NPK > M + NPK$ indicated that the amount of straw returning also affected the abundance of soil microorganisms. It may be because straw returning increased the carbon resource, which can accelerate the growth and proliferation of soil microorganisms (Kandeler et al. 1999). Govaerts et al. reported that residue retention

induced higher population counts of total bacteria, fluorescent *Pseudomonas*, and actinomycetes when compared to residue removal under both zero tillage and conventional tillage (Govaerts et al. 2008). Indeed, the findings of the present study supported this fact while specifically showing that *Gemmatimonadetes*, *Acidobacteria*, *Firmicutes*,

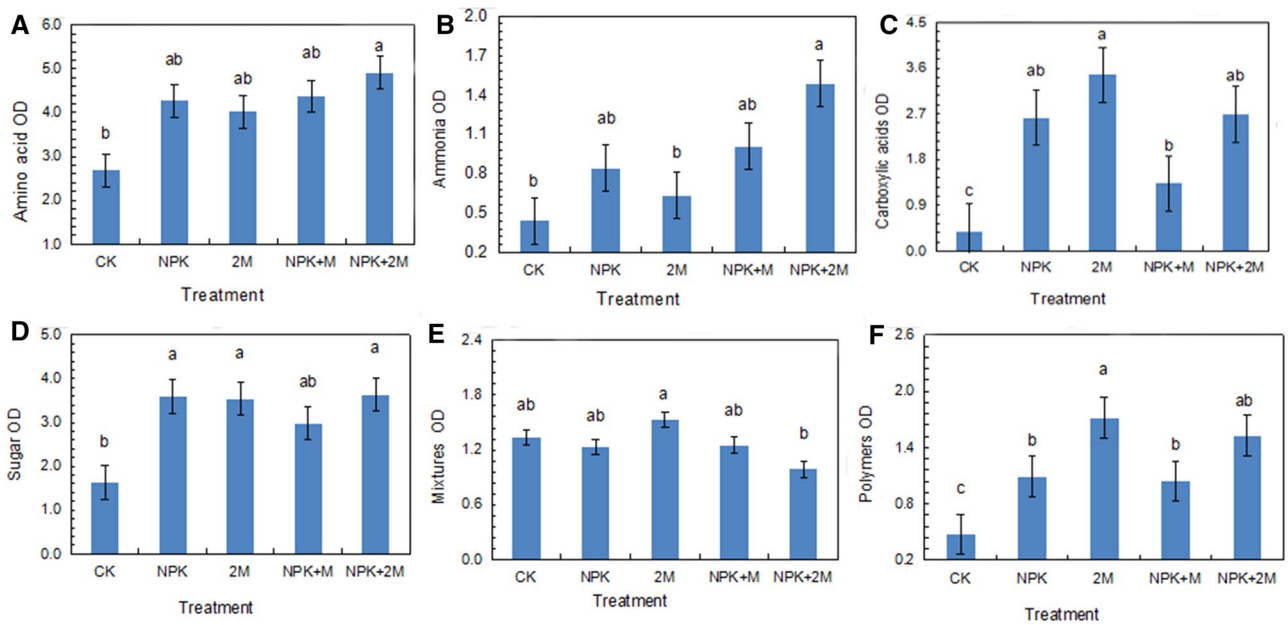


Fig. 9 Comparison of microbial carbon source utilization ability in different treatments. The X-axis represents culture times; the Y-axis represents the value of OD of different carbon sources. **a** Amino acid,

b ammonia, **c** carboxylic acids, **d** sugar, **e** mixtures of carbon sources, **f** polymers (color figure online)

and *Actinobacteria* were the groups to demonstrate the greatest advantages under straw-incorporating tillage.

Soil microbial community structure

The *Proteobacteria*, *Acidobacteria*, and *Chloroflexi* were the three most dominant phyla in the five treatments. *Proteobacteria* is a major phylum of Gram-negative bacteria, which include many of the bacteria responsible for nitrogen fixation. *Acidobacteria* is a new bacterial group that has been identified through molecular research and is primarily considered to consist of acidophilic bacteria (Naether et al. 2012). It has been considered that the concentrations of soil nutrients (e.g., organic C, N, P, and K) are good indicators of soil quality and productivity because of their favorable effects on the physical, chemical, and biological properties of soil (Cao et al. 2011). Soil organic components, such as soil organic carbon (SOC) or total N (TN) are the most critical indices of paddy soil fertility (Liu et al. 2011). Dynamics of SOC and TN storage in agricultural soils drives microbial activity and nutrient cycles, promotes soil physical properties and water retention capacity, and reduces erosion (Martyniuk et al. 2019). Given the high frequency of nitrogen input and bacteria-sensitive responses to N change, we propose that *Acidobacteria* have a certain response to nitrogen input that is influenced by the form and dose of nitrogen. Indeed, *Proteobacteria* was one of the three most dominant phyla depicted in this study. Furthermore, the carbon utilization ability of soil microorganisms following 2 M + NPK

treatment was significantly higher than that associated with CK treatment. Therefore, we speculated that in this study, the long-term straw returning to the field affected the number of these bacteria, which further influenced the C and N contents of the soil.

Bacterial and fungal carbon source utilization capacity

Cellulose is the main structural component of higher plant cell walls and represents approximately 35–50% of a plant's dry weight (Ransom-Jones et al. 2012). Cellulose should be degraded by cellulolytic microorganisms that are present in soil. As such, one of the largest material flows in the soil is controlled by cellulolytic microorganisms (Lynd et al. 2002). Previous studies have indicated that straw-incorporating practices promote the accumulation of straw on the soil's surface, thereby ensuring that the major component present is cellulose, which can improve the physical conditions of soil while also providing carbon sources (specifically cellulose) for cellulolytic bacteria (Grosbellet et al. 2011; Koeck et al. 2014; Peng et al. 2008). In this way, straw incorporation promoted the growth of cellulolytic bacteria, thus increasing the decomposition of cellulose and subsequently the SOC. Cellulose-degrading bacteria are more frequently found within the aerobic phylum *Actinobacteria* and the anaerobic phylum *Firmicutes*. In the present study, the taxonomic analysis of bacteria revealed that the 2 M treatment had a significantly greater abundance

of *Firmicutes* ($P < 0.05$) when compared to NPK treatment. Moreover, the NPK + 2 M treatment was associated with a significantly greater abundance of *Actinobacteria* ($P < 0.05$) when compared to the NPK treatment. The result from this study suggest that straw incorporation can contribute to the increased abundance of cellulolytic microorganisms, thus resulting in improved soil quality, which is necessary for high plant yields and quality.

Both bacteria and fungi are major players in soil biogeochemical cycles (Wang et al. 2019). Soil fungi exhibit high extracellular enzyme activity and their enzyme types are relatively comprehensive, which means that they have a strong ability to degrade cellulose. Soil fungi play an important role in the process of straw incorporation; however, given that straw takes a great deal of time to degrade naturally, there is a consequential effect on the number and community structure of soil fungi, a situation that has not yet been adequately reported. Bardgett et al. (Bardgett et al. 1993) showed that fungi play a dominant role in the degradation of straw. Further, Marschner et al. (Marschner et al. 2011) analyzed the soil at the early stages of wheat straw degradation (within 30 days), and the results showed that the community structure of soil fungi changed significantly when the straw was being degraded within the first 1–2 weeks. In the present study, NPK + 2 M treatment was associated with a significantly greater abundance of Ascomycota when compared to NPK treatment. As a class of fungi that can decompose cellulose into Ascomycota, Chaetomium can decompose cellulase and xylanase, which play important roles in the carbon cycle of the natural ecosystem and can result in soil improvement. These findings indicated that long-term straw incorporation could promote and enrich the soil fungal community and subsequently improve the properties of soil.

Decomposition of exogenous crop straw provides carbon sources for soil microorganisms and, therefore, increases the microbial biomass of soil, which contributes to the development and increases of the soil's organic matter (Ayres et al. 2010). Yin et al. (Yin et al. 2010) also reported that bacteria play critical roles in the production of soil aggregates and they are involved in the conversion of plant residues to organic matter in soil. The results of present study revealed that the carbon utilization ability of soil microorganisms following 2 M + NPK treatment was significantly higher than that following CK treatment ($P < 0.05$). Within the 2 M-treated soil, the utilization for carboxylic acids, polymers, and other mixtures of carbon sources was higher than in the other treatments, and the difference was significantly greater than that of the CK treatment ($P < 0.05$). This finding also showed that the NPK + 2 M treatment had a significantly greater abundance of *Gemmatimonadetes* compared to the CK treatment ($P < 0.05$). *Gemmatimonadetes* can use metabolic products such as acetate and propionate as sole carbon sources (Glissmann and Conrad 2000, 2002;

Takaichi et al. 2010). The *Gemmatimonadetes* normally have a greater ability to use available carbon sources when compared with the other soil microorganisms. These findings suggested that straw incorporation may change the activities of *Gemmatimonadetes*, *Acidobacteria*, *Firmicutes*, and *Actinobacteria*, and consequently change the decomposition process of residue, thus affecting the carbon source utilization capacity of bacterial communities across the entire plough layer of soil (0–20 cm).

Conclusion

The results from this study showed that after ten cycles of rice–wheat rotation involving straw incorporation practices, the carbon source utilization capacity of bacterial communities was promoted across the entire plough layer of soil (0–20 cm), presumably by increasing the abundance of bacterial communities. However, the ability of bacterial communities to regulate these effects remains unclear. Therefore, further studies should be conducted to uncover the mechanism underlying these effects.

Acknowledgements We thank the National Natural Science Foundation of China (No. 31770660); the Key Laboratory of Fertilization from Agricultural Wastes; the Ministry of Agriculture and Rural Affairs, P. R. China (No. 31300518); and the Qianjiang Scientific Observing and Experimental Station of Agro-Environment and Arable Land Conservation, Ministry of Agriculture.

Compliance with ethical standards

Conflict of interest All authors declare that they have no conflicts of interest.

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