Effects of Short-term Application of Moutai Lees Biochar on Nutrients and Fungal Community Structure in Yellow Soil of Guizhou

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Abstract

In order to realize the resource utilization of Guizhou sauce-flavor distiller's grains and the improvement of yellow soil fertility, a field experiment was carried out to study the effects of short-term application of vinasse biochar on soil nutrients and the diversity of fungal community structure by setting five biochar dosages of 0% (MB_0), 0.5% ($MB_{0.5}$), 1.0% ($MB_{1.0}$), 2.0% ($MB_{2.0}$), and 4.0% ($MB_{4.0}$). The results showed that the application of lees biochar increased the pH, soil organic matter (SOM), total nitrogen (TN), ammonium N (AN), nitrate N (NN), available phosphorus and available potassium of the yellow soil to varying degrees, but decreased the microbial biomass carbon (MBC) and microbial biomass N (MBN) by 12.36%-26.49% and 34.10%-59.95% respectively. The application of lees biochar significantly reduced the number of fungal OTUs and community diversity. Compared with MB_0 treatment, the application of lees biochar significantly changed the structure of the fungal community. The relative abundances of Mortierellomycota, Basidiomycota, Glomeromycota, and Chlorophyta were all increased in varying degrees, but the relative abundance of Ascomycota was significantly reduced by 23.86%-29.06%. At the same time, the application of lees biochar also increased the relative abundance of some functional bacteria, such as Mortierella and Chaetomium, and reduced the relative abundance of some pathogenic bacteria, such as Aspergillus and Fusarium. In addition, the results of redundant analysis showed that SOM, AN and NN were the main environmental factors that affect the change of yellow soil fungal community structure. In summary, the short-term application of lees biochar can increase the nutrient content of soil, change the structure and diversity of soil fungal communities, and also can reduce the relative abundance of some pathogenic bacteria, which can inhibit the growth and reproduction of harmful plant pathogens.

Introduction

The dry-land yellow soil in Guizhou has more than 4.6 million ha^2, accounting for about 46% of the dry land area in the province (Guo et al., 2019; Luo et al., 2020). Yellow soil is not only sticky in texture and strong in acidity, and due to the shallow soil layer, soil nutrient leaching is also very easy to occur. Most of the dry-land yellow soil in Guizhou is mainly planted with high-value crops, such as pepper, sorghum and flue-cured tobacco. The continuous cropping obstacle caused by the continuous cropping of the soil has increased the obstacles to the soil, which seriously restricts the improvement of crop yield and quality. How to realize the improvement of yellow soil fertility and ease the obstacles of continuous cropping is one of the important problems that need to be solved urgently (Cheng et al., 2020; Ding et al., 2019). At the same time, as the by-product of the production of Guizhou sauce-flavor liquor, the sauce-flavored lees has an annual output of about 2 million tons, but the actual treatment of lees is less than 1 million tons per year, and about 50% of the lees are still idle or abandoned (Yang et al., 2019). Therefore, the comprehensive utilization of lees has become a major problem facing the development of the liquor industry in Guizhou, and it is also the current key development task and research direction of the utilization of agricultural organic waste.

Biochar is prepared from solid agricultural and forestry waste through anaerobic high-temperature carbonization and can be used in agricultural production. It can not only realize the rational utilization of waste resources, but also play a role in soil improvement and regulation of soil micro-ecological environment. It can enable agricultural production to achieve good green, ecological and sustainable development (Dai et al., 2017; Kumuduni et al., 2019; Zheng et al., 2019). Because of its special physical and chemical properties, biochar can

directly provide soil microorganisms with a good habitat and nutrients required for growth, and it plays an important role in regulating the diversity of soil microbial community structure (Sheng et al., 2018; Yu et al., 2018; Zheng et al., 2016). Fungi are an important part of soil microbes, which play an important role in decomposing the energy flow and material circulation of soil ecosystems (Nguyen et al., 2018). At present, there have been reports on the effects of biochar on soil fungal community structure. It has been found that the addition of 3.0% or 6.0% biochar can increase the activity of N mineralization enzymes, and the addition of biochar can affect the response of the fungal community to alfalfa plant restoration (Zhang et al., 2018). It has been shown that the application of biochar increases the soil pH and nutrient content of rubber trees, and also affects bacterial and fungal communities, and the fungal community is more affected than the bacterial community (Herrmann et al., 2019). It has also been shown that application of biochar can effectively control brucellosis by trapping more C and N, enriching specific beneficial bacteria, and reducing the abundance of pathogenic bacteria (Chen et al., 2020). It was found that biochar significantly increased the α diversity of rice soil bacteria but decreased the fungal community structure through continuous application of biochar for 4 years, and that biochar-induced changes in soil chemistry (such as pH, SOC, and C/N) were important factors in the changes in community composition (Zheng et al., 2016). It can be seen that biochar has obvious advantages in improving soil fertility and improving soil microecology.

The improvement effect of biochar on soil microenvironment is obvious, but the current research on the impact of biochar on soil microorganisms is still mainly based on the diversity of bacterial community structure (Abujabhah et al., 2018; Gao et al., 2019; Senbayram et al., 2019). The influence of fungal community structure and its inherent relationship with soil physical and chemical properties still need further exploration. Therefore, this article uses Guizhou sauce-flavor distiller's grain biochar as a test material and carried out a short-term cultivation test. This experiment qualitatively studied the effect of different lees biochar application on the nutrient of yellow soil and the diversity of fungal community structure, and the relationship between the change of soil physical and chemical characteristics and the diversity of soil fungal community. It is hoped that this experiment will provide a theoretical reference for the improvement of the fertility of Guizhou yellow soil and the rational utilization of lees.

Materials And Methods

Experimental site

This experiment was conducted in the experimental base of Guizhou Academy of Agricultural Sciences from April to June in 2019. During the experiment, the average daily temperature was 20.4℃ and the daily rainfall was 2.89 mm. The tested soil is a typical zonal yellow soil in Guizhou. The basic physical and chemical properties are: pH 6.4, organic matter (SOM) 26.8 g kg^{-1}, total nitrogen (TN) 0.7 g kg^{-1}, ammonium N (AN) 0.3 mg kg^{-1}, nitrate N (NN) 11.5 mg kg^{-1}, available phosphorus (AP) 48.6 mg kg^{-1}, available potassium (AK) 175.0 mg kg^{-1}. The test biochar was Maotai distillers grain biochar, which was prepared at 550 ℃ using special carbonization equipment. The basic physical and chemical properties of biochar are: pH 8.8, total carbon (TC) 281.3 g kg^{-1}, TN 7.5 g·kg^{-1}, AN 1.6 mg kg^{-1}, NN 24.3 mg kg^{-1}, AP 1.4 mg kg^{-1}, AK 4.6 g kg^{-1}.

Experimental design and management

This test was conducted using open field cultivation methods, and the test device was a PVC pipe with a diameter of 20 cm and a height of 35 cm. First fill the bottom of the PVC pipe with 5 cm thick quartz sand, and wrap the bottom of the PVC pipe with gauze to prevent the loss of soil or quartz sand. Then mix the yellow soil with the lees biochar and put it in a PVC tube, and press it properly to avoid overflow. The soil weight was 10 kg, and the biochar ratios were 0% (MB_0), 0.5% ($MB_{0.5}$), 1.0% ($MB_{1.0}$), 2.0% ($MB_{2.0}$) and 4.0% ($MB_{4.0}$). The test device was placed in the field and soil was collected for analysis after 60 days of cultivation. Each treatment was repeated three times.

Collection of soil samples

After the test, the soil in each PVC tube was mixed thoroughly and soil samples were collected. The soil sample was divided into three parts. The first part was wrapped in foil, quickly placed in a centrifuge tube, put into liquid N for freezing and transportation, and then transferred to a refrigerator at -80 ℃ for storage, used for high-throughput sequencing analysis of soil microorganisms. The second part of the fresh soil sample was used for the determination of AN, NN and microbial biomass C and N. The third part of the soil sample was used to determine the soil pH, SOM, TN, AP, and AK.

Determination of soil physical and chemical properties

Soil pH was measured in 1:2.5 (soil: water ratio, w/v) extraction with a pH meter (FE20K, Mettler Toledo, Switzerland). SOM was determined by wet combustion method. TN was determined using Kjeldahl method. AN and NN were measured by 1 $mol \cdot L^{-1}$ KCl solution immersion-continuous flow analyzer. Microbial biomass C (MBC) and N (MBN) were determined by chloroform fumigation-K_2SO_4 extraction method. AP was determined by sodium bicarbonate method. AK was extracted with ammonium acetate and boiling nitric acid, and determined with a flame photometer (FP640, Jingke, Shanghai, China) (Bao 2000).

Soil microbial DNA extraction and high-throughput sequencing

Microbial community genomic DNA was extracted from soil samples using the E.Z.N.A.® soil DNA Kit (Omega Bio-tek, Norcross, GA, U.S.) according to manufacturer's instructions. The DNA extract was checked on 1% agarose gel, and DNA concentration and purity were determined with NanoDrop 2000 UV-vis spectrophotometer (Thermo Scientific, Wilmington, USA). The hypervariable region ITS2 of the fungi gene were amplified with primer pairs ITS3F (5'-GCATCGATGAAGAACGCAGC-3') and ITS4R (5'-TCCTCCGCTTATTGATATGC-3') by an ABI GeneAmp® 9700 PCR thermocycler (ABI, CA, USA). The PCR amplification of 16S rRNA gene was performed as follows: initial denaturation at 95 ℃ for 3 min, followed by 27 cycles of denaturing at 95 ℃ for 30 s, annealing at 55 ℃ for 30 s and extension at 72 ℃ for 45 s, and single extension at 72 ℃ for 10 min, and end at 4 ℃. The PCR mixtures contain 5 × *TransStart* FastPfu buffer 4 μL, 2.5 mM dNTPs 2 μL, forward primer (5 μM) 0.8 μL, reverse primer (5 μM) 0.8 μL, *TransStart* FastPfu DNA Polymerase 0.4 μL, template DNA 10 ng, and finally ddH_2O up to 20 μL. PCR reactions were performed in triplicate. The PCR product was extracted from 2% agarose gel and purified using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, USA) according to manufacturer's instructions and quantified using Quantus™ Fluorometer (Promega, USA).

Purified amplicons were pooled in equimolar and paired-end sequenced (2 × 300) on an Illumina MiSeq platform (Illumina, San Diego, USA) according to the standard protocols by Majorbio Bio-Pharm Technology Co. Ltd. (Shanghai, China). The raw reads were deposited into the NCBI Sequence Read Archive (SRA) database.

Statistics and Analysis

Mothur software was used to calculate the richness index Ace, Chao1 and the diversity index Shannon, Simpson index. Origin 8.0 was used for mapping, SPSS 20.0 was used for variance analysis, and Canoco 4.5 was used for redundancy analysis (RDA).

Results And Analysis

Soil nutrients

Compared with MB_0 treatment, the soil pH, OM, TN, NN, AP and AK was increased by 0.31%-1.69%, 81.77%-508.83%, 35.79%-365.26%, 122.96%-171.80%, 4.97%-146.17% and 59.36%-847.71% (Table 1). The variation trend was $MB_{4.0}$>$MB_{2.0}$>$MB_{1.0}$>$MB_{0.5}$>MB_0. AN also was increased by 45.76%-128.81%, but the difference between treatments was not significant. Compared with MB_0, MBC and MBN showed a decreasing trend, and MBC decreased by 12.36%-26.49%, among which $MB_{4.0}$ treatment showed the most significant decrease. MBN decreased by 34.10%-59.95%, among which $MB_{1.0}$, $MB_{2.0}$ and $MB_{4.0}$ were significantly reduced.

Table 1
Effects of different biochar dosages on nutrient of yellow soil.

Treatment	pH	SOM ($g \cdot kg^{-1}$)	TN ($g \cdot kg^{-1}$)	AN ($mg \cdot kg^{-1}$)	NN ($mg \cdot kg^{-1}$)	AP ($mg \cdot kg^{-1}$)	AK ($mg \cdot kg^{-1}$)	MBC ($mg \cdot kg^{-1}$)	MBN ($mg \cdot kg^{-1}$)
MB_0	6.51 ± 0.05 c	7.02 ± 0.39 e	0.95 ± 0.06 c	0.59 ± 0.15 a	34.75 ± 21.36 b	7.45 ± 0.93 d	14.00 ± 2.84 e	322.52 ± 75.34 a	76.16 ± 23.61 a
$MB_{0.5}$	6.53 ± 0.07 bc	12.76 ± 2.15 d	1.29 ± 0.01 c	1.04 ± 0.56 a	77.48 ± 11.50 a	7.82 ± 0.48 cd	22.31 ± 2.94 d	282.67 ± 35.46 ab	50.19 ± 8.11 ab
$MB_{1.0}$	6.53 ± 0.08 bc	18.25 ± 0.52 c	1.57 ± 0.05 c	1.08 ± 0.15 a	82.25 ± 7.62 a	10.01 ± 1.02 c	46.90 ± 4.92 c	280.71 ± 40.70 ab	32.48 ± 17.83 b
$MB_{2.0}$	6.59 ± 0.05 ab	25.74 ± 3.46 b	2.70 ± 0.76 b	0.86 ± 0.45 a	89.39 ± 10.41 a	12.72 ± 2.18 b	84.03 ± 2.48 b	250.87 ± 10.18 ab	30.50 ± 16.17 b
$MB_{4.0}$	6.62 ± 0.07 a	42.74 ± 2.81 a	4.42 ± 0.59 a	1.35 ± 0.60 a	94.45 ± 3.21 a	18.34 ± 1.43 a	132.68 ± 5.58 a	237.07 ± 31.65 b	33.84 ± 9.89 b

Note: Different lowercase letters in the same column indicate significant differences between treatments ($P < 0.05$).

Fungal community composition

After screening and filtering fungal sequences in soil samples, it was found that the average base length was 315.0 bp, and the average sequencing coverage rate reached 99.91%. As can be seen from Fig. 1, the OTUs dilution curve of fungi measured in the soil sample tends to be flat, indicating that the OTUs measured tends to be saturated, and the OTU quantity was MB_0 > $MB_{1.0}$>$MB_{0.5}$>$MB_{4.0}$>$MB_{2.0}$ (Fig. 1).

A total of 3234 OTUs were detected in the soil samples (Fig. 2), among which the OTUs with MB_0, $MB_{0.5}$, $MB_{1.0}$, $MB_{2.0}$ and $MB_{4.0}$ were 1548, 1479, 1510, 1294 and 1380, respectively. The public OTUs of the five treatments were 499, accounting for 32.24%, 33.74%, 33.04%, 38.56% and 36.16% of the total OTUs of MB_0, $MB_{0.5}$, $MB_{1.0}$, $MB_{2.0}$ and $MB_{4.0}$ respectively. The unique OTU numbers of MB_0, $MB_{0.5}$, $MB_{1.0}$, $MB_{2.0}$ and $MB_{4.0}$ were 402, 329, 403, 217 and 265 respectively, accounting for 25.97%, 22.24%, 26.69%, 16.77% and 19.20% of the total OTU of the corresponding treatment.

NMDS analysis of fungal community structure

The non-metric multidimensional scaling analysis (NMDS) of the fungal community composition in the yellow soil showed that (Fig. 3) the NMDS Stress coefficient value was 0.22, indicating that NMDS analysis could accurately reflect the degree of difference between the samples. The MB_0 treatment was mainly on the left side of NMDS and could be completely separated from the fungal community treated with other treatments, indicating that the application of distillage biochar could significantly affect the fungal community structure of yellow soil. However, the distances between various points treated with $MB_{0.5}$, $MB_{1.0}$, $MB_{2.0}$ and $MB_{4.0}$ were relatively close and overlaps existed, and the species similarity coefficient was high, indicating that different biochar application amounts could promote the growth of some of the same species in the composition of the yellow soil fungus community.

Fungal community diversity index

Compared with MB_0 treatment, Ace and Chao1 indexes treated with distillers' grains biochar decreased by 5.12%-0.23% and 5.29%-11.59% respectively, but the differences were not significant (Table 2). With the increase of biochar application amount, Simpson index increased, while Shannon index showed no significant difference. Compared with MB_0 treatment, Simpson index of $MB_{0.5}$, $MB_{1.0}$, $MB_{2.0}$ and $MB_{4.0}$ treatment increased by 10.25%-91.30%, among which $MB_{4.0}$ treatment was significantly higher than that of MB_0, $MB_{0.5}$ and $MB_{2.0}$ treatment.

Table 2
Effects of different biochar dosages on fungal community diversity index in yellow soil.

Treatment	Coverage (%)	Ace	Chao1	Shannon	Simpson
MB_0	99.93 ± 0.02 a	391 ± 22 a	397 ± 22 a	2.85 ± 0.25 a	0.1034 ± 0.0230 b
$MB_{0.5}$	99.92 ± 0.03 a	371 ± 15 a	376 ± 16 a	3.05 ± 0.26 a	0.1140 ± 0.0336 b
$MB_{1.0}$	99.91 ± 0.03 a	361 ± 44 a	364 ± 39 a	2.84 ± 0.24 a	0.1309 ± 0.0437 b
$MB_{2.0}$	99.92 ± 0.02 a	351 ± 15 a	357 ± 22 a	3.06 ± 0.17 a	0.1468 ± 0.0431 ab
$MB_{4.0}$	99.87 ± 0.03 b	359 ± 19 a	351 ± 24 a	2.87 ± 0.26 a	0.1978 ± 0.0766 a

Richness and diversity of fungal communities

Phylum level fungal community structure

We detected a total of 18 bacterial species and undetermined groups at the gate level, among which 16, 17, 15, 16 and 16 gates were treated with MB_0, $MB_{0.5}$, $MB_{1.0}$, $MB_{2.0}$ and $MB_{4.0}$ respectively. The results showed that the relative abundance of Ascomycota, Chytridiomycota and Mortierellomycota were 47.31%-76.37%, 11.72%-21.45% and 2.07%-23.34% respectively, belonging to the dominant fungal group, and the relative abundance was 81.43%-90.16% in total (Fig. 4). The relative abundance of Ascomycota was significantly reduced by 23.86 to 29.06 percentage points. The relative abundance of Mortierellomycota showed an obvious increasing trend with the increase of biochar applied to lees, which was 5.27–11.27 times higher than MB_0 treatment. In the relative abundance of other smaller fungus door, vinasse biochar improves the relative abundance of Basidiomycota and Glomeromycota, whereas Chlorophyta deal with highest $MB_{2.0}$ treatment.

Genus level fungal community structure

At the genus level, we detected a total of 444 fungal species and undetermined groups, among which 287, 277, 254, 257 and 271 genera were treated with MB_0, $MB_{0.5}$, $MB_{1.0}$, $MB_{2.0}$ and $MB_{4.0}$ respectively. The relative abundance of Unassigned fungi, Aspergillus, unclassified_Chaetomiaceae, Mortierella, Spizellomyces, Penicillium, Fusarium, unclassified_Chromista and Chaetomium was relatively high. The total relative abundance was 87.08%-92.03% (Fig. 5). Compared with MB_0 treatment, the relative abundance of Aspergillus and Fusarium decreased by 8.80%-22.11% and 1.77%-12.44% respectively, but significantly increased the relative abundance of Mortierella and Spizellomyces. In addition, the relative abundance of Wallemia and Purpureocillium of $MB_{4.0}$ treatment were significantly reduced, while the relative abundance of Chaetomium, Geomyces and unclassified_Trichocomaceae showed a significant increasing trend with the increase of biochar application amount of distillates.

LefSe analysis of fungal community structure

LefSe analysis of the fungal community (Fig. 6) showed that the fungi with significant differences in MB_0 treatment was Ascomycota, while fungi with significant differences in $MB_{0.5}$, $MB_{1.0}$, $MB_{2.0}$ and $MB_{4.0}$ treatment were Coprinellus_ellisii, Pestalotiopsis, Emerallopsis and Mortierellomycota.

Richness and diversity of fungal communities

De-trend correspondence analysis (DCA) of the relative abundance data for the top 15 dominant genera of the fungal community showed that the maximum value of the gradient was 2.42 in the four axes (< 3). Further RDA redundancy analysis of the 15 dominant genera with soil chemistry Results showed that SOM, AN, and NN were the main factors influencing the structure of the fungal community in yellow soil (Fig. 7). Axis 1 interpretation of RDA analysis was 49.1% and axis 2 interpretation was 25.1%, for a cumulative interpretation rate of 74.2%.

Discussions

Effect of biochar on soil nutrient effectiveness

Biochar is produced from agricultural organic waste through high temperature charring. Most biochar is alkaline, has a loose texture, and is rich in N, phosphorus, potassium and many other elements, as well as many mineral nutrients. Such as calcium, magnesium, zinc and other trace elements. When biochar is applied to the soil, it can not only change the physical properties of the soil, improve soil porosity, but also raise the nutrient content of the soil. It is favorable to the balanced supply of multiple nutrients (Zhang et al., 2017; Zhang et al., 2019). The results of this paper showed that short-term application of lees biochar can significantly improve the pH, SOM, TN, AN, NN, AP and AK content of the yellow soil in Guizhou, which is similar to the results of previous studies (Liu et al., 2019; Zhang et al., 2019). Maotai lees are a by-product of sorghum and other by-products formed after many high temperature fermentations. The pH of biochar was weakly acidic, rich in nutrients, and contains a large number of residual fats, proteins, cellulose and vitamins. trace elements and N-free leachables (Dai et al., 2020). The lees were prepared into biochar after high temperature charring, and its own pH changed to alkaline (8.78). The content of SOM, TN and AK was significantly increased, thus the fertility of yellow soil could be improved after application to the soil. However, short-term application of lees biochar reduced the microbial mass carbon (MBC) and microbial mass N (MBN) content of the yellow soil. One reason may be due to the high C/N of biochar, which disrupted the microbial C/N balance when applied to the soil, thus suppressed the number and activity of microorganisms (Xu et al., 2014; Zhu et al., 2917). Another reason, the application of organic materials generally increases the C and N content of soil microbial mass (Foster et al., 2016). However, biochar is rich in inactive organic C that is stable in nature. Although the application of biochar directly increases the soil organic C content, it decreases the proportion of activated C available to the microorganisms, resulting in the soil microbial quantity C/N decreased (Johannes et al., 2006; Zwieten et al., 2010).

MBC/MBN can be used to reflect structural information about the soil microbial community. Bacteria have C/N ratios ranging from 3 to 6, while fungi have C/N ratios ranging from 7 to 12 (Vries et al., 2006). In this study, MB0, MB0.5, MB1.0, MB2.0, MB4.0 treated MBC/MBN 4.50, 5.65, 10.07, 8.23, and 7.01, respectively. This indicates that the yellow soil microorganisms were predominantly bacterial under no biochar (MB_0) or low application ($MB_{0.5}$) conditions. At high application rates ($MB_{1.0}$, $MB_{2.0}$, $MB_{4.0}$), the fungus was predominant. It has been shown that N fertilizer paired with biochar can increase the proportion of bacteria in the microbial community. When the total amount of soil flora remains constant, the rate of bacterial growth and reproduction increases, which leads to a decrease in soil microbial C/N (Wang et al., 2010). In the present study, MBC/MBN tended to decrease when biochar was applied above 1.0%. Although the soil microorganisms were still dominated by fungal communities, the bacterial growth and reproduction rate gradually increased, resulting in

a soil microbial C/N decrease. Soil microbial communities are gradually changing from "fungal" to "bacterial", which means that biochar application can improve the quality of soil microorganisms. Soil microhabitat environment to alleviate soil continuum barriers (Chen et al., 2012).

Effect of biochar on soil nutrient effectiveness

Fungi are important members of the soil microbial community that drive energy flow and material cycling in soil-vegetation ecosystems. It plays an important role in the ecosystem. The results of this study found that short-term application of lees biochar significantly increased the fungal Simpson index, but Ace, Chao1 and Shannon indices had no effect. This indicates that the application of lees biochar can reduce the diversity of yellow soil fungal communities, but has no effect on species diversity, which is consistent with the results of previous studies (Hu et al., 2014). It has been shown that soil fungal richness and diversity indices were significantly reduced after charcoal-based fertilization, which may be related to the different pathways of soil microorganisms to decompose soil organic matter. Biochar application can not only affect soil fungal community diversity, but also improve the fungal community structure and reduce the species with pathogenic potential, which in turn can lead to the development of soil fungi towards beneficial flora (Bai et al., 2019). In the present study, application of lees biochar significantly reduced the relative abundance of Fusarium and increased the relative abundance of Mortierella, which is similar to the results of a previous study (Yao et al., 2017). Fusarium is the main causative agent of soil-borne diseases of crops, and application of biochar can significantly reduce the gene copy number and relative abundance of Fusarium in the soil, which may be related to the increase in soil pH and decrease in the effectiveness of some phenolic acids in the soil after application of biochar (Jaiswal et al., 2017; Wu et al., 2020). Mortierella promotes an increase in soil organic matter and nutrient content, thereby promoting crop root growth and development (Curran et al., 2000). In addition, the application of lees biochar also increased the relative abundance of some functional genera of bacteria such as Chaetomium. It has been found that the increase in Chaetomium not only promotes the uptake of active substances from the soil, but also produces antibiotics and cell wall-degrading enzymes, thus acting to alleviate soil continuity disorders and inhibit the occurrence of soil-borne diseases (Ingrid et al., 2015).

Relationship between fungal community structure and soil environmental factors

Soil microbial community structure is not only influenced by physical factors such as soil moisture and aeration conditions, but also soil chemical factors such as pH, SOM and TN are key factors influencing the changes in soil microbial community structure (Liu et al., 2019). Results of RDA redundancy analysis in this study showed that SOM, AN, and NN were important factors influencing the structural changes of fungal communities in yellow soil. It has been noted that the fungi prefer to grow in acidic environments. The application of biochar increased the soil pH and therefore was associated with other soil influences (such as TC content, TN content, electrical conductivity) compared to pH as the main factor influencing changes in soil microbial communities (Chen et al., 2015; Nielsen et al., 2014). However, it has also been found that soil pH is the dominant factor influencing changes in soil fungal community structure, which is influenced by soil nutrients much more than soil pH (Dai et al., 2016), and some studies have confirmed the significant correlation between the effective nutrient content of soil and fungal community composition (Zhang et al., 2019). Thus, the response of environmental factors and fungal community structure differed according to soil type, crop type, and biochar type. In addition, there are few studies on the effect of Maotai lees biochar on the fungal

diversity of yellow soil, and the soil microbial environment will certainly change with the time of biochar application and the aging process of biochar itself. Therefore, more experiments need to be conducted to explore the short- and long-term effects of lees biochar on the diversity of fungal communities, so as to provide theoretical reference for the improvement of loess geology and the rational utilization of wine lees in Guizhou.

Conclusion

It is concluded that in the short term, lees biochar resulted in stronger improvements in nutrient and fungal diversity of yellow soil. The present study provided evidence that lees biochar increased the soil organic matter positively influenced the growth of fungal community, and could inhibit the growth and reproduction of pathogenic bacteria of harmful plants. However, long term field studies are needed to assess the effect of Moutai less biochar on nutrient availability and microbial community.

Declarations

Authors' contributions All authors contributed to the study conception and design. Meng Zhang conceived the experiments; Meng Zhang and Yanling Liu performed the experiments and analyzed the data; Quanquan Wei contributed materials; Meng Zhang wrote the paper; and Jiulan Gou revised the paper.

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Data availability All data generated or analyzed during this study are included in this published article.

Compliance with ethical standards

Competing interests The authors declare that they have no competing interests.

Ethical approval Not applicable

Consent to participate Not applicable

Consent to publish All authors have read the manuscript and approve of its submission to Environmental Science and Pollution Research.

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Figures

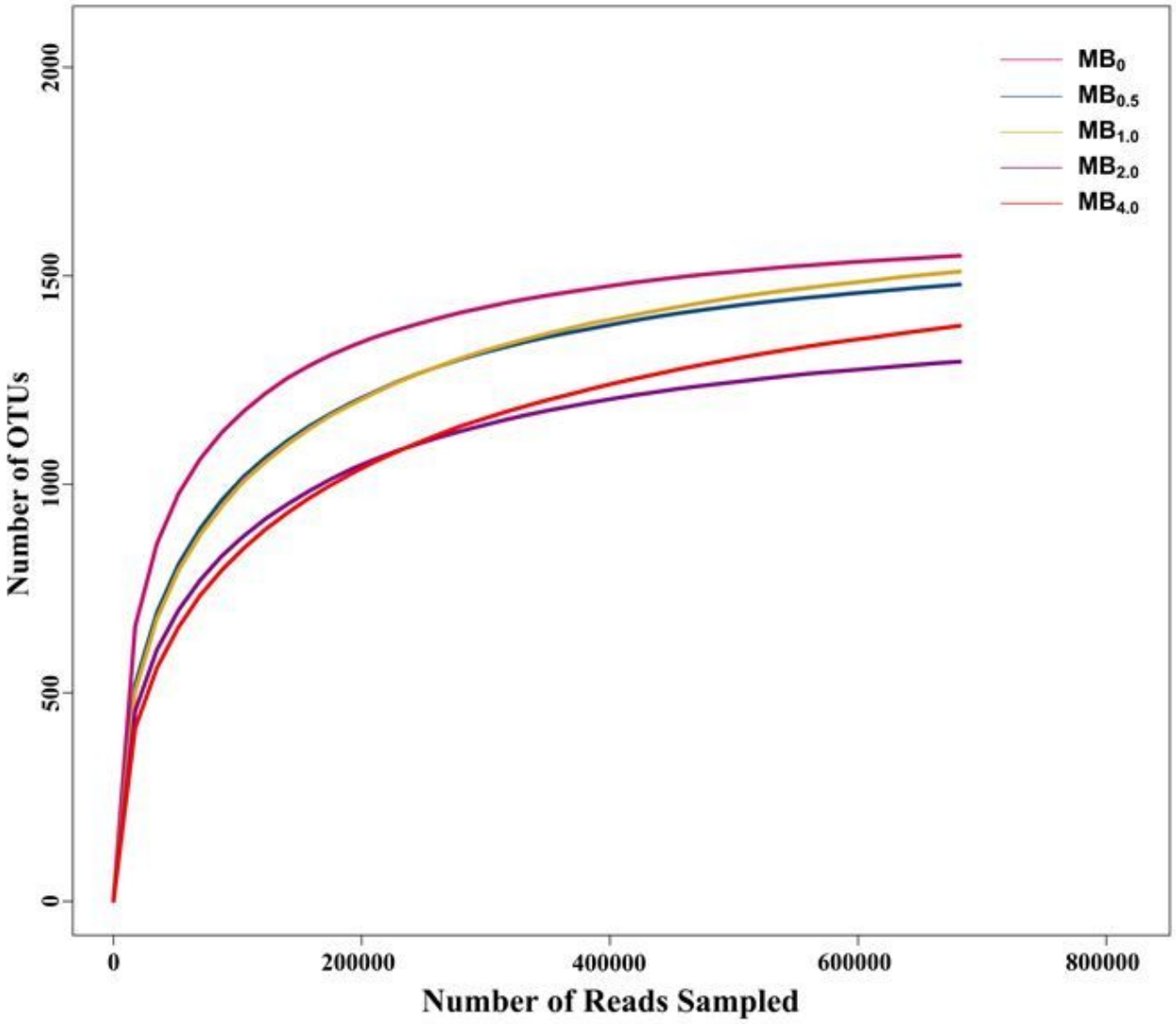

Figure 1

The OTUs rarefaction curves of soil.

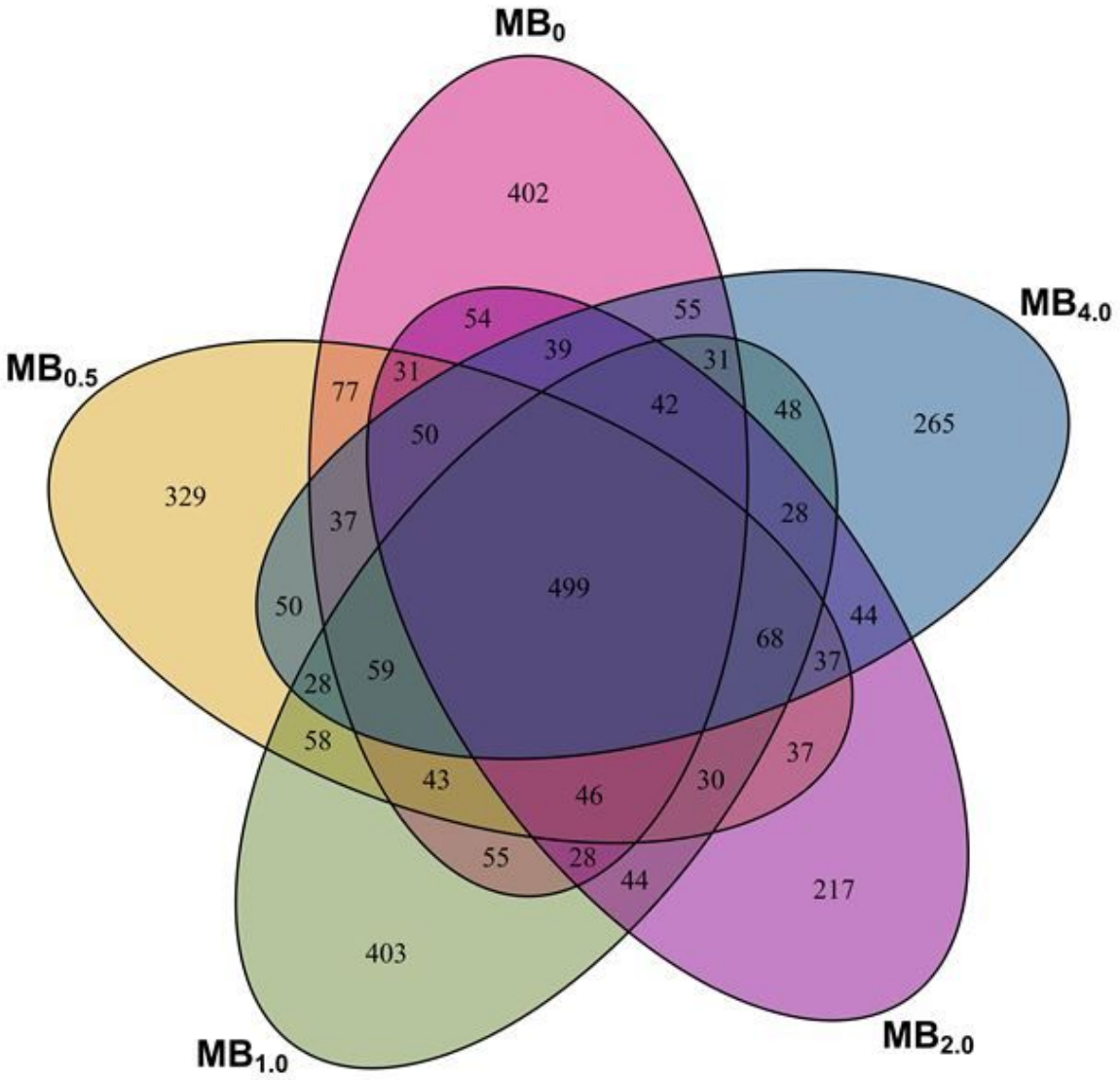

Figure 2

The venn figure of fungus OTU in soil.

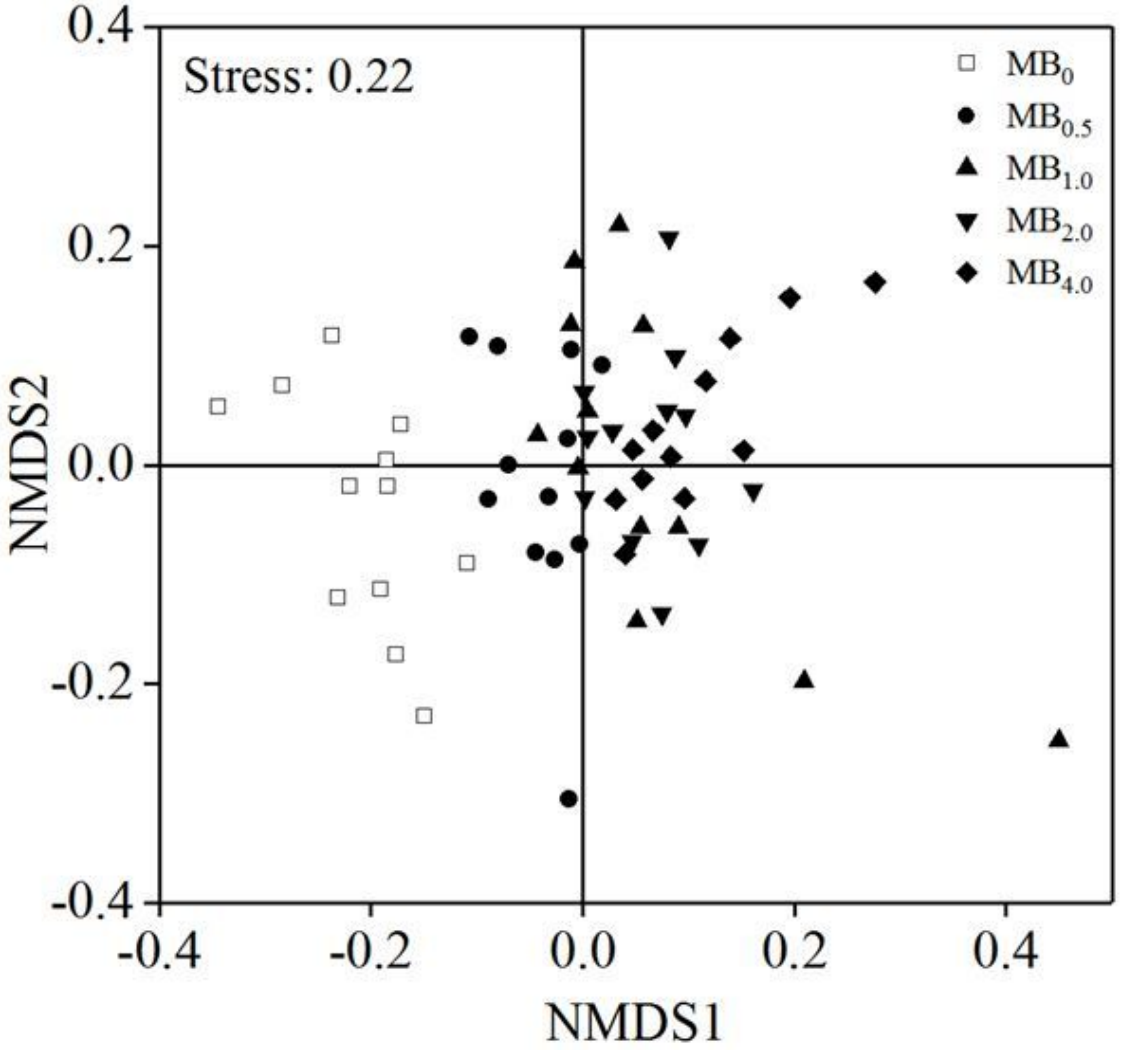

Figure 3

The nonmetric multidimensional scale analysis of soil fungus community structure.

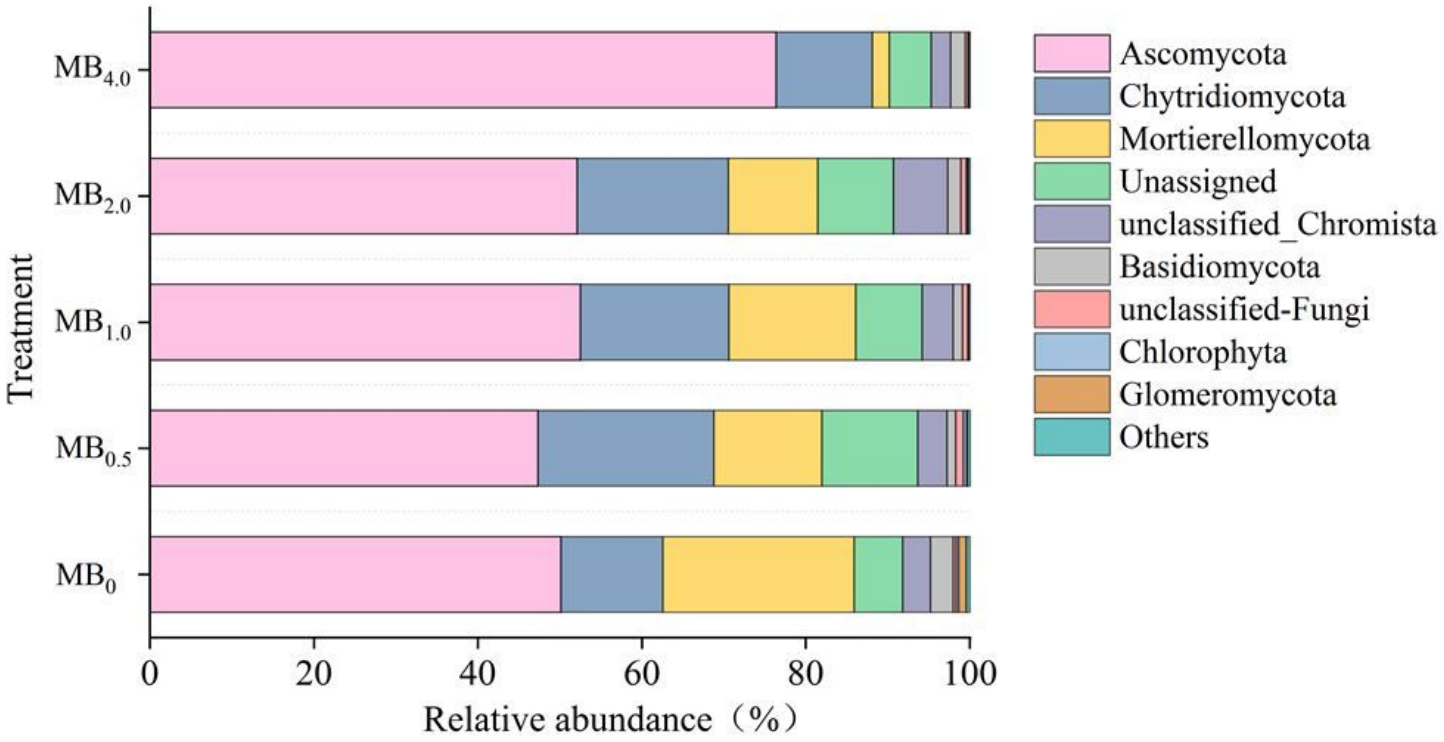

Figure 4

The relative abundance of fungi at phylum level in soil under different biochar dosages.

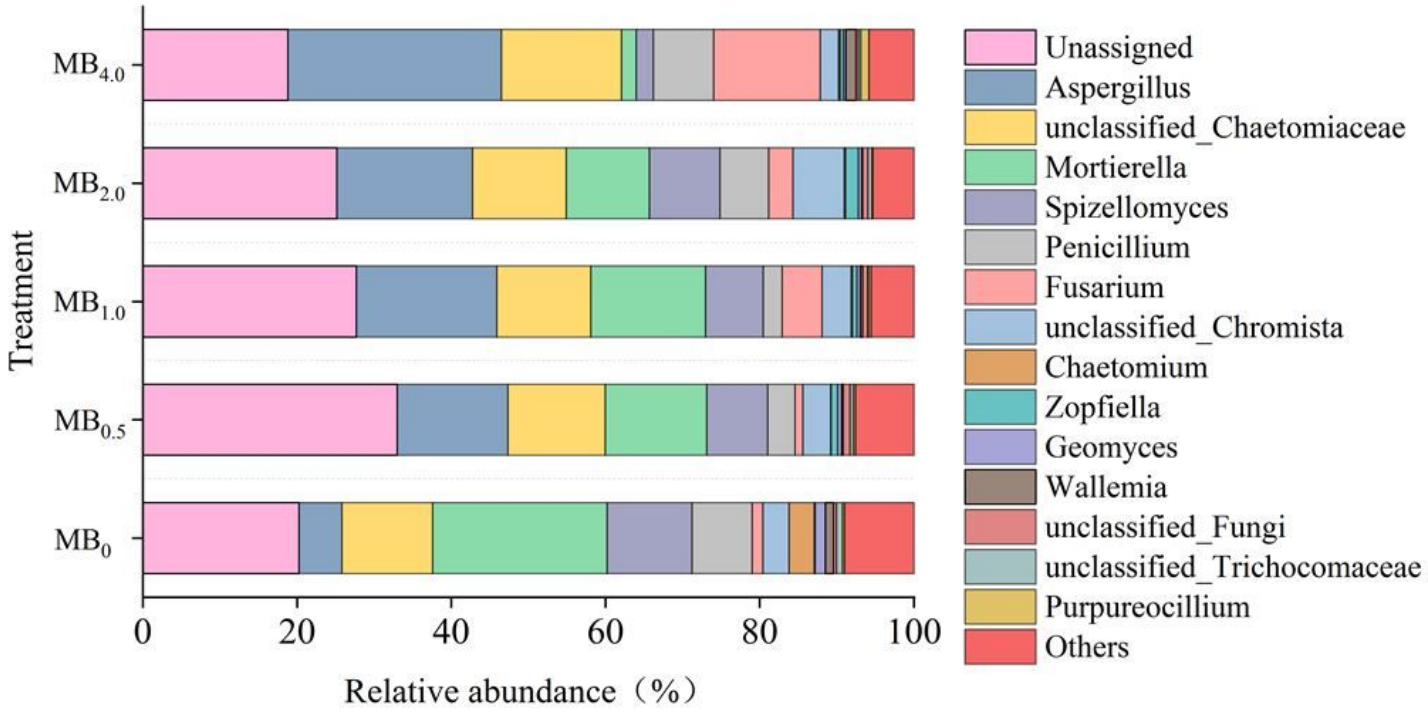

Figure 5

The relative abundance of fungi at genus level in soil under different biochar dosages.

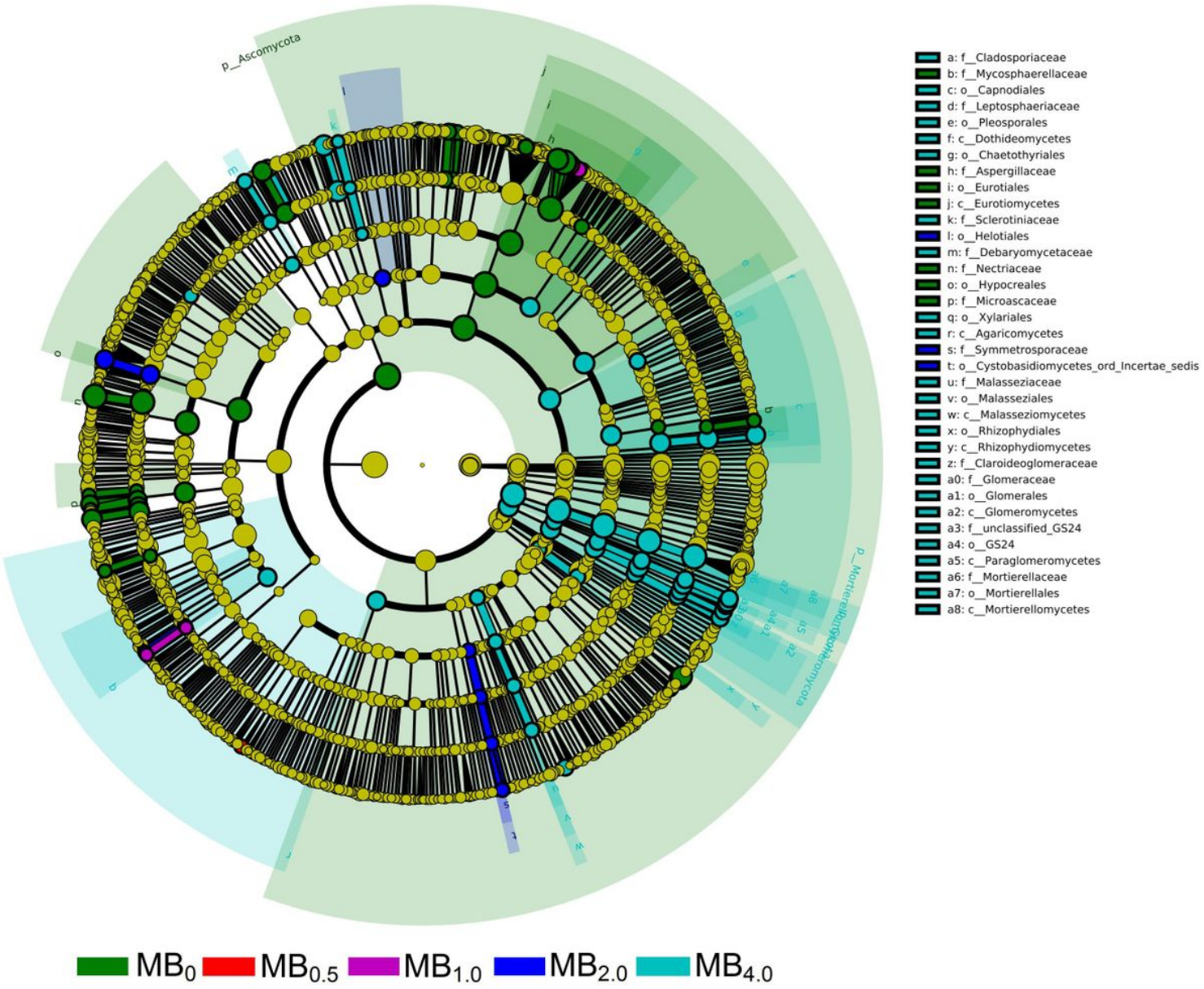

Figure 6

LefSe analysis of fungal community in soil.

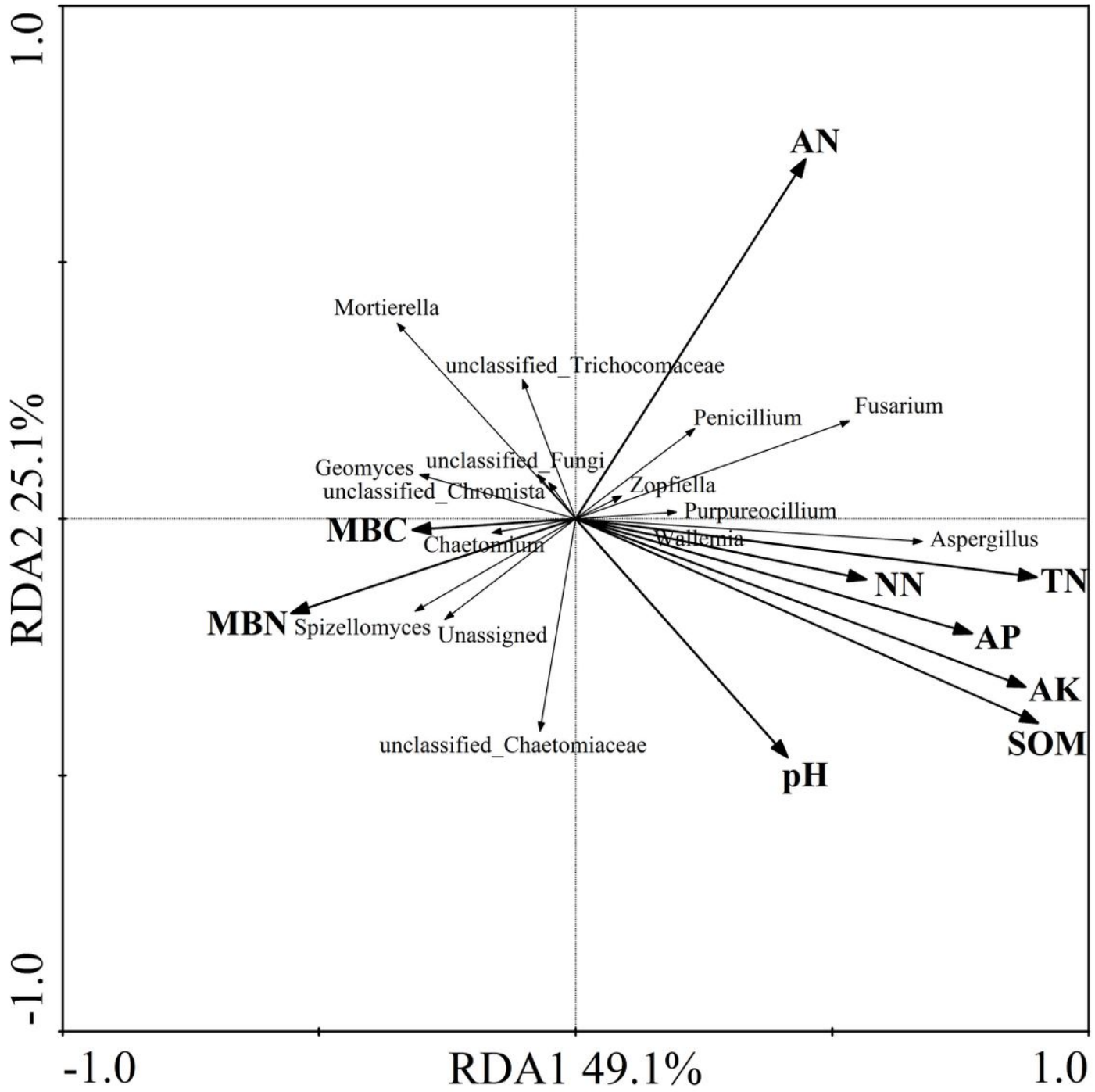

Figure 7

Redundancy analysis of fungi and chemical properties in yellow soil (genus).