Li *et al. Annals of Microbiology* (2024) 74:16
https://doi.org/10.1186/s13213-024-01758-7

Annals of Microbiology

UNIVERSITÀ DEGLI STUDI DI MILANO

ORIGINAL ARTICLE Open Access

Responses of soil microbial community activities and soil physicochemical properties to coal fly ash soil amendment

Fangze Li[1], Tianqi Qi[2], Ge Zhang[1], Xingjie Lin[1*], Xiaohua Li[3], Zhenqing Wu[4], Shuhui Men[5], Hongchao Liu[3], Shiwei Zhang[6] and Zhanbin Huang[7*]

Abstract

Background Hundreds of millions of tons coal fly ash are produced annually to support economic development and industrial production. However, directly applying coal fly ash to agricultural production can decrease the land productivity and pose a threat to the ecosystem due to the poor physicochemical properties and seriously heavy metal pollution.

Methods In this study, a field experiment to investigate the effects of coal fly ash as a soil amendment was conducted in Hebei province, China. The coal fly ash (CFA) soil field was mixed with the carrier soil (CS, without containing coal fly ash) at different rates (0–40% mass content) in the 0–20 cm layer of top soil and then mixed with a rotovator. The soil was then amended with 0.45–1.80 kg·m^{-2} of G1 soil amendment for planting corn.

Purpose The purpose of this study is to investigate the response mechanism of soil microbial community activities, and soil physicochemical properties to soil amendment and carrier soil in coal fly ash soil.

Key results The study found that the G1 amendment, which consisted of humic acid, polyacrylamide, zeolite powder, and $FeSO_4 \cdot 7H_2O$, improved the soil chemical properties and physical structure by increasing soil bulk density and macroaggregates. The highest corn yield was observed in B5 (20% CS and 1.3500 kg·m^{-2} G1). Meanwhile, the abundance of microorganisms that facilitate the circulation of soil nutrients such as *Acidobacteria* (77.05%), *Sphingomonas* (25.60%), *Nitrospira* (20.78%), *Streptomyces* (11.32%), and *Gaiella* (10.20%) was increased.

Conclusions Overall, our results indicate that the use of coal fly ash soil as a amendment can enhance soil sustainability by improving soil microbial functions. These findings provide a reference for the development and application of coal fly ash soil amendments.

Keywords Coal fly ash, Soil amendment, Soil microbial community, Land productivity enhancement, Humic acid

*Correspondence:
Xingjie Lin
215229854@qq.com
Zhanbin Huang
zbhuang202208@126.com

Full list of author information is available at the end of the article

Introduction

The consumption of coal has been rapidly increasing due to economic and industrial development, and resulting in hundreds of millions of tons coal fly ash (CFA) are produced annually worldwide (Qin et al. 2020). Solid and gaseous pollutants are produced in the process of burning coal, which mainly consist of ash and slag (Guo 2018). Fine coal fly ash, as a typically solid waste, is collected from dust removers during the process of coal burning in thermal power plants (Ahmaruzzaman 2010). In addition, continuous mining is also an important source of fine coal fly ash, which greatly increase the storage difficulty and efficiency of coal fly ash.

Currently, coal fly ash has various applications, such as backfilling mining subsidence, serving as raw materials for cement production, and acting as an absorbent for waste water treatment. The specific application depends on the composition and quality of the ash (Gollakota et al. 2019; Preethi et al. 2023; Teixeira et al. 2019; Wang et al. 2019). The aforementioned reuse methods can reduce the environmental risks associated with coal fly ash accumulation. From the perspective of circular economy, coal fly ash can be used as a raw material for subsequent utilization. Although coal fly ash has showed some potential to improve the soil structure and increase soil organic matter (Ahmaruzzaman 2010; Coudert et al. 2019; Han et al. 2022; Shaheen et al. 2014), the abuse of coal fly ash still was observed and cause multiple environmental damages. For example, excessive coal fly ash has been shown to weaken soil capacities, such as soil water holding capacity and nutrient storage function in soil (Chen et al. 2023; Roy et al. 2018; Tsiridis et al. 2015). Moreover, due to its high concentration of heavy metals, it can lead to pollution of groundwater and soil with the addition of coal fly ash (Awoyemi et al. 2019; He et al. 2019; Mahedi et al. 2019; Zhang et al. 2023). The addition of coal fly ash often leads to a significant decrease in soil bulk density and macroaggregates. According to our survey, coal fly ash has been used for crop plant in some regions of China. However, the local coal fly ash soil has already suffered from low economic crop yields and severe soil nutrient loss. Therefore, it is essential to explore strategies to improve agricultural productivity in coal fly ash soil.

In view of the above, we used the technology of carrier soil and organic amendments to improve the fly ash agricultural soil in Shxian County. It is used to improve the physical structure of fly ash soil by carrier soil technology. Meanwhile, it is accompanied by the addition of special amendments to increase nutrients of coal fly ash soil. The field experiment of corn planting was conducted in Shexian county, China. It aims to increase the local crop yields. Moreover, the purpose of this study is to investigate the response mechanism of soil microbial community activities and soil physicochemical properties to soil amendment and carrier soil in coal fly ash soil. It provides technical support for the recycle utilization of fly ash in ecological restoration and agricultural production. In this way, the problem of fly ash storage difficulty and topsoil shortage in some areas will be solved.

Materials and methods

Experimental site

The experimental area was located in Qingjian River Basin, Shexian County, Hebei Province, China (36°29′45″–36°30′45″N, 113°42′40″–113°43′50″E). In 1996, a severe flood caused soil and water loss in the local farmland. As a result, 4 local villages including Zhuangshang, Huyu, Shigang, and Lianquan had to use the coal fly ash from local power plant for crop planting. The coal fly ash soil layer ranged from 40 to 60 cm. Preliminary investigation showed that the contents of cadmium (Cd), lead (Pb) and mercury (Hg) in the local coal fly ash farmland exceeded Hebei average contents in top soil. Crop yield directly planted in the coal fly ash soil was very low. In addition, the drought resistance and other damage resistance of crops were poor, and Cd and other heavy metals contained in some vegetables produced from coal fly ash soil exceeded the standard of food safety limit. The physicochemical properties of coal fly ash soil investigated are shown in supplement Table S1.

Experimental design

Carrier soil (CS) was taken from the 0–20 cm top soil layer and the detailed physical-chemical properties shown in supplement Table S2; Soil amendment of G1 was developed by China University of Mining and Technology-Beijing, which was consist of humic acid, polyacrylamide, zeolite powder, and $FeSO_4 \cdot 7H_2O$.

Briefly, 9 experiment groups were designed including control group (labeled as B0) and 8 treatment groups (labeled as B1to B8). B0 was the local coal fly ash soil without CS and G1 addition; B1 was that the local coal fly ash soil added with G1 but without CS; B2-B8 were that the local coal fly ash soil added with different proportions of CS (10–40% mass content in 0–20 cm layer of top soil) and G1, respectively. All groups were added with chemical fertilizer at 0.12 $kg \cdot m^{-2}$ (N: P_20_5: K_2O=18:9:9). The detailed experimental design is shown in Table 1.

The 31.5 m × 22 m field was divided into 9 plots (3.5 m× 2 m each plot with a 50 cm passage between plots). Corn seeds (Suodan 20#, from Junxian Institute of Agricultural Sciences, Henan province, China) were planted after one day of the addition of carrier soil and soil amendment G1. The Corn was planted at the row spacing 40 cm×30 cm (8 plants$\cdot m^{-2}$), and all the samples were harvested after 118 days.

Table 1 Experimental design

Treatments	CS	G1
B0	–	–
B1	–	1.35 $kg{\cdot}m^{-2}$
B2	10%	1.35 $kg{\cdot}m^{-2}$
B3	30%	1.35 $kg{\cdot}m^{-2}$
B4	40%	1.35 $kg{\cdot}m^{-2}$
B5	20%	1.35 $kg{\cdot}m^{-2}$
B6	20%	0.45 $kg{\cdot}m^{-2}$
B7	20%	0.90 $kg{\cdot}m^{-2}$
B8	20%	1.80 $kg{\cdot}m^{-2}$

Note CS (carrier soil)

Soil physiochemical properties and crop growth

On harvest day, soil samples for all 9 groups were collected from the 0~20 cm layer soil. The soil pH was measured using the glass electrode method (m_{soil}: v_{water} = 1:2.5). Total organic carbon (TOC) was measured by an elemental analyzer (vario MACRO cube, Elementar, Germany), total nitrogen (TN) by the semi-micro Kjeldahl method (Sankar 2018), total P (TP) by the acid-perchlorate and sulfuric acid-perchloric acid digestion method, and total K (TK) by the flame photometer colorimetric method. The available N was determined by the alkali-hydrolysis diffusion method using an elemental analyzer (UV-1100 Spectrophotometer, Shanghai Meipuda Instrument Co., LTD, China), the available phosphorus by $NaHCO_3$ extraction molybdenum-antimony colorimetric method (Alhaj Hamoud et al. 2019), and the available K by the flame spectrophotometry method (Xiao et al. 2017). The soil bulk density and moisture content were determined by the cutting ring method. The particle-size distribution of aggregates was determined by an aggregate analyzer (DM200, Jinwei Hardware Factory, Shangyu Economic Development Zone, China). Soil specific gravity was determined by the pycnometer method (Holthusen et al. 2018).

The plant height was measured with a ruler. The fresh weight was directly measured by electronic scale. Hundred grain weight, moisture, and dry weight were determined by drying method in the oven (48 h, 80°C). The number of kernels per spike was counted, and the mean kernel number per spike per plot was calculated.

Microbial community activities and DNA extraction and sequencing

Microbial DNA was extracted from soil samples using the E.Z.N.A.® Soil DNA Kit (Omega Bio-tek, Norcross, GA, U.S.). The V3-V4 region of bacterial 16S ribosomal RNA gene was amplified by PCR using the primer pair 338F (5'-GTA CTC CTA CGG GAG GCA G-3') and 806R (5'-CCG TCA ATT CMT TTR AGT TT-3'). PCR procedures were as follows: 95°C for 2 min, followed by 25 cycles at 95°C for 30 s, 55°C for 30 s, and 72°C for 30 s; and a final extension at 72°C for 5 min. PCR was performed in triplicates in reaction system containing 4 μL of 5 × FastPfu Buffer, 2 μL of 2.5 mM dNTPs, 0.8 μL of each primer (5 μM), 0.4 μL of FastPfu Polymerase, and 10 ng of template DNA. Amplicons were extracted and purified with 1.2% agarose gels using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, U.S.) according to the manufacturer's instructions, and quantified using QuantiFluor™-ST (Promega, U.S.). The purified amplicons were pooled in equimolar, and paired-end sequenced (2×250) on an Illumina MiSeq platform according to standard protocols. The sequencing data were submitted to the NCBI Sequence Read Archive (SRP222851).

Data analysis

Raw fastq files were demultiplexed and quality-filtered using QIIME (version 1.17) according to the following criteria: (i) the 300-bp reads were truncated at any site receiving an average quality score < 20 over a 50 bp sliding window, with the truncated reads shorter than 50 bp discarded; (ii) exact barcode matching was required, with reads containing 2 nucleotide mismatches and ambiguous characters removed; and (iii) only those sequences with >10 bp overlapping were assembled according to their overlap sequence. Reads that could not be assembled were discarded. Operational Units (OTUs) with 97% similarity were clustered using UPARSE (version 7.1 http://drive5.com/uparse/), and chimeric sequences removed using UCHIME. The 16 S rRNA gene sequence was analyzed by RDP Classifier (http://rdp.cme.msu.edu/) against the SILVA (SSU115) 16 S rRNA database using a confidence threshold of 70% (Didonato et al. 2016). One-way ANOVA (SPSS software package) was performed to reveal difference in the soil parameters, stem dry weight, plant height, species richness, and root nutrient element contents among groups. The mean values were compared with least significant difference (LSD). Stepwise multiple linear regressions were used to further identify the most important factor affecting species richness. All statistical analyses were performed using SPSS 21.0. $P<0.05$ was considered as statistically significant.

Results

Effects of CS and G1 application on soil physical and chemical properties

Figure 1 shows that CS and G1 have significant effects on the soil bulk density, specific gravity, and porosity. The soil bulk density in B1 to B8 groups was significantly increased by 40.78–54.47%, compared with that in the control B0 ($p=0.000$, $P<0.001$). The soil specific gravity in B1 to B8 was 4.14–16.00% lower than that in the control group (B0), respectively, ($P>0.05$), but the porosity in

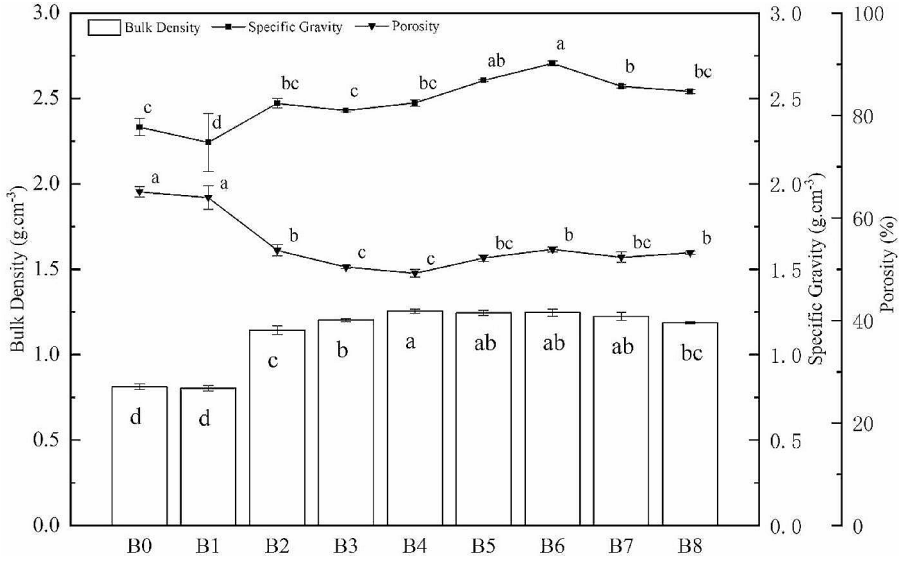

Fig. 1 Effects of CS and G1 application on soil physical properties. Different lower-case letters indicate significant differences ($P < 0.05$) based on a one-way ANOVA followed by LSD ($p < 0.05$)

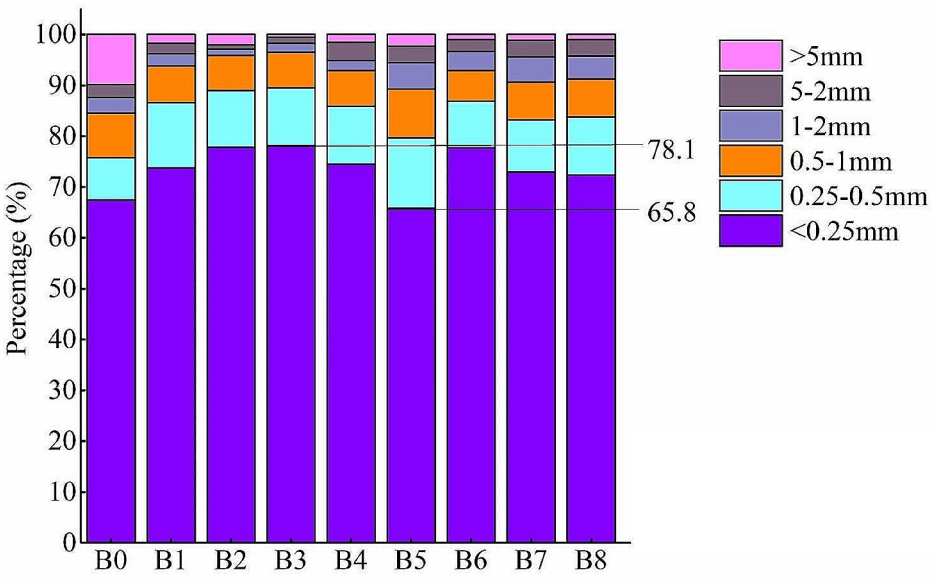

Fig. 2 Particle-size distribution of soil aggregates under different treatments

B1 to B8 was 17.17–24.39% higher than that in B0 group ($p = 0.001$, $P < 0.05$). Of all the treatment groups, B5 group exhibited the optimal bulk density, specific gravity, and porosity, and its bulk density reached up to 1.25 g·cm^{-3}, which was close to China national second soil census nutrient classification standards. The bulk density in the control B0 was only 0.87 g·cm^{-3}, which was far lower than the average level of local farmland soil (1.26 g·cm^{-3}) (Li et al. 2019). Bulk density in B1 group was lower than that in B0 group, which might be due to the fact that B1 group was added with G1 but with no CS, and humic acid, as one main component of G1 amendment, significantly increased the content of soil organic matter, thus decreasing soil bulk density (Li et al. 2019).

Generally, the aggregates with particle size of >0.25 mm were defined as macroaggregates. The particle size of macroaggregates in all the groups except control group was within the range of 2-0.25 mm. Figure 2 shows that soil macroaggregates (>0.25 mm) in B5 group accounts for 34.2%, and those in the control B0 accounts for 32.6%. However, the percentage of the macroaggregates (with particle size of 0.25-5 mm) in B5 group was 31.9%, which was the highest in all the treatment groups, while it was the lowest in B0 group (22.74%). Our results

showed that the addition of the CS and G1 effectively increased the percentage of the 0.25-2 mm aggregates in the soil, which was very important for soil drought resistance and soil moisture conservation (Chen et al. 2019; Ju et al. 2023).

The soil chemical properties are shown in Table 2. Soil pH in all treatment groups was not significantly decreased, relative to that in B0 ($p=0.124$, $P>0.01$). Meanwhile, the soil available P in B1 to B8 groups was significantly increased by 13.95–55.69%, compared with that in B0, respectively ($p=0.000$, $P<0.01$), which showed G1 and CS had slow release on available P. B5 exhibited the highest soil available P (124.39 mg·kg^{-1}). The available N in B1 to B8 groups was significantly decreased by 5.34–50.67%, compared with that in B0 ($p=0.048$, $P<0.05$). The reason might be that the available N in the soil was absorbed and fixed by the crops. The soil available K in B1 to B8 groups was significantly increased by 1.33–388.37% compared with that in B0, respectively ($p=0.000$, $P<0.01$). The soil organic matter in B2 to B8 groups was decreased by 35.71%, to 90.63%, compared with that in B0, while B1 was not decreased. It was suggested that CS could decease soil organic matter content by Table 2, respectively ($p=0.0002$, $P<0.01$). Compared with control B0, only B1 (added G1without carrier soil) exhibited an increase in soil organic matter (by 50.89%) while B2-B8 (added G1 and carrier soil) were lower than B0, indicating that G1 could increase soil organic matter concentration.

Table 2 Soil chemical properties

Properties	B0	B1	B2	B3	B4	B5	B6	B7	B8
pH	7.76 ± 0.0125a	7.76 ± 0.028a	7.67 ± 0.012ab	7.58 ± 0.012ab	7.59 ± 025ab	7.57 ± 0.025b	7.71 ± 0.01ab	7.74 ± 0.03ab	7.75 ± 0.005ab
AN (mg kg^{-1})	72.60 ± 1.29a	68.72 ± 1.69a	60.71 ± 3.95b	60.93 ± 1.81b	38.64 ± 2.27d	35.81 ± 1.52d	46.47 ± 1.8c	63.41 ± 2.8ab	64.38 ± 1.7ab
AP (mg kg^{-1})	28.07 ± 1.24e	31.98 ± 1.24 cd	35.20 ± 1.27 cd	43.70 ± 2.93b	41.00 ± 3.01b	152.46 ± 2.95a	28.19 ± 1.9e	38.64 ± 1.0bc	29.10 ± 3.3 cd
AK (mg kg^{-1})	125.46 ± 1.20f	160.32 ± 4.96e	148.64 ± 3.53ef	328.26 ± 15.26b	258.78 ± 17.45c	610.08 ± 41.21a	131.68 ± 25.7f	208.15 ± 11.1d	226.86 ± 18.8 cd
TN (g kg^{-1})	1.33 ± 0.043a	1.36 ± 0.113a	0.80 ± 0.011c	0.70 ± 0.020 cd	0.38 ± 0.009 f	1.06 ± 0.031b	0.53 ± 0.002de	0.56 ± 0.003de	0.60 ± 0.002 de
TP (g kg^{-1})	0.92 ± 0.03a	0.84 ± 0.002ab	0.65 ± 0.001bc	0.69 ± 0.001b	0.61 ± 0.003bc	0.82 ± 0.002a	0.58 ± 0.001c	0.67 ± 0.009bc	0.63 ± 0.005bc
TK (g kg^{-1})	1.30 ± 0.037c	1.36 ± 0.004c	1.77 ± 0.021b	1.92 ± 0.003ab	2.05 ± 0.001a	1.95 ± 0.010ab	1.92 ± 0.004a	1.87 ± 0.003ab	1.94 ± 0.01a
OM(g^{-1}kg)	10.67 ± 0.08b	16.10 ± 0.97a	6.86 ± 0.036c	4.76 ± 0.045d	1.00 ± 0.059f	3.64 ± 0.041d	3.09 ± 0.03e	3.45 ± 0.01de	4.33 ± 0.04de

Notes TN, total nitrogen; TP, total phosphorus; TK, total potassium; AN, available nitrogen; AK, available potassium. AP, available phosphorus. Different lower-case letters indicate significant differences ($P<0.05$) among different samples based on a one-way ANOVA, followed by an LSD test

Bacterial α-diversity and taxonomy of bacterial communities

After chimeras were removed, the sequence data were analyzed at the OTU level. A total of 3,857 OTUs were generated from 9 samples sequenced on an Illumina MiSeq, and the number of OTUs ranged from 2,215 to 2,771 when sequence data were clustered at 97% similarity (Fig. 3a). The coverage ranged from 97.01% (B3) to 97.47% (B7), indicating that more than 97% of the bacterial species were detected from each sample. These results suggested that the data collected were adequate to capture the diversity of the bacteria associated with each sample (Fig. 3b). The ACE and the Chao1 indexes were calculated to estimate the bacterial abundance. As shown in Fig. 3c, e, the overall bacterial abundance in the B3 estimated were higher than other treatments. Among all the groups treatments, it was showed that bacterial diversity was the highest in treatment B3 while it was the lowest diversity in treatment B4 (Fig. 3d and f). This suggests that the bacterial α-diversity was strongly influenced by the addition of CS.

Nine dominant phylogenetical phyla were identified including Proteobacteria (26.46–37.18%), Actinobacteria (16.36–23.47%), Chloroflexi (14.63–19.22%),

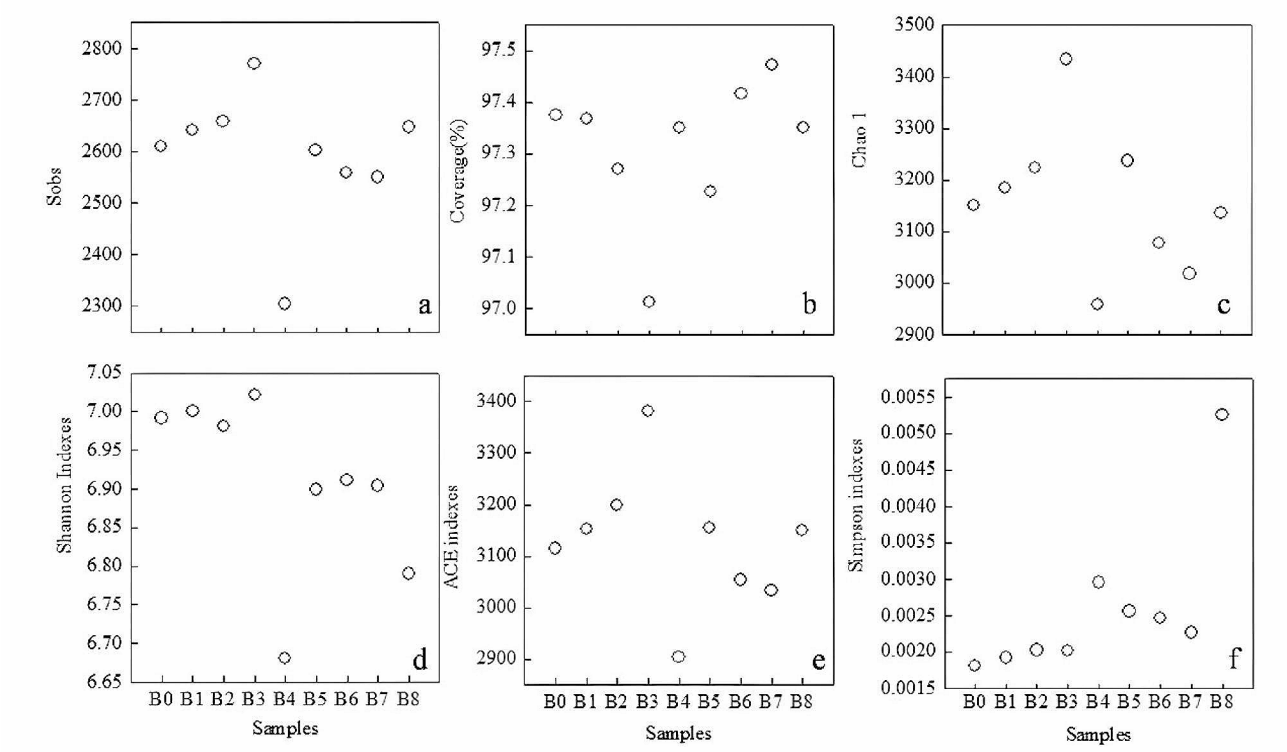

Fig. 3 Estimated community richness and community diversity indexes. (**a**) Sobs. (**b**) Coverage. (**c**) Chao1 indexes. (**d**) Shannon indexes. (**e**) ACE indexes. (**f**) Simpson indexes

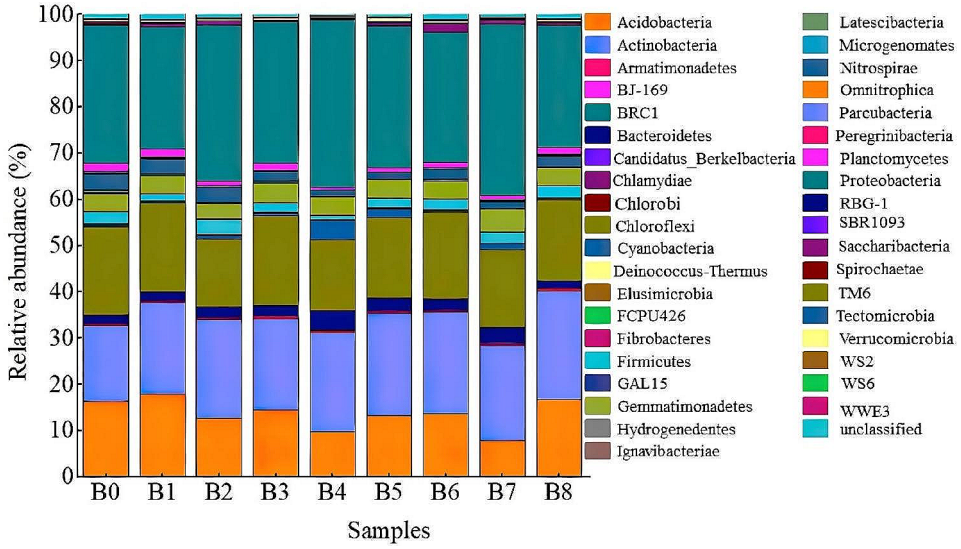

Fig. 4 Relative abundance of soil microbial community in all 9 samples under different treatments at the phylum level

Acidobacteria (7.93–17.89%), Gemmatimonadetes (3.25–4.97%), Bacteroidetes (1.51–4.28%), Nitrospirae (1.36–3.47%), Firmicutes (0.77–3.34%), and Planctomycetes (0.51–1.68%) (Fig. 4). The soil bacterial communities differed slightly between treatments and the control. The abundance of Armatimonadetes (0.39–0.53%), Bacteroidetes (1.74–4.28%), and Cyanobacteria (0.36–4.27%) in soil samples of treatment groups was increased, compared with that in soil sample of control group (0.34%, 1.71%, and 0.33%, respectively). The abundance of Chlamydiae (0.01–0.05%), FCPU426 (0.00–0.01%), Ignavibacteriae (0.00–0.05%), Latescibacteria (0.04–0.51%), Nitrospirae (1.35–3.21%), Omnitrophica (0.01–0.09%), Parcubacteria (0.05–0.34%), Planctomycetes

(0.51–1.59%), and RBG-1__Zixibacteria (0.00–0.09%) in treatment groups was decreased, compared with that in B0 (0.08%, 0.02%, 0.08%, 0.59%, 3.47, 0.19%, 0.38%,1.68%, and 0.26%, respectively).

A hierarchical cluster tree of the bacterial communities was constructed by the UPGMA at a 97% OUT similarity level. This tree showed that the bacterial communities were clustered into four distinct clades (Fig. 5a). Clade 1 contained bacterial communities from the sample of B4, Clade 2 included those from B5 and B7. Clade 3 included those from B3 and B8, and Clade 4 included those from B0, B1, B2 and B6. Afterwards, a principal coordinate analysis (PCoA) of the major bacterial clades was performed with 46.77% of the observed variation explained. As Fig. 5b shows, the B4 sample was separated from other 8 samples, and B0 was located on the left of the graph along PC1, and B4 was located on the right of the graph along PC1, whereas the other seven samples were distributed in the middle of the graph between B0 and B4. Bacterial sequences were assigned to a total of 585 classified and unclassified genera. The 50 genera with highest abundance were displayed in a heatmap (Fig. 5c), which revealed complex patterns in the genera abundances across samples. Some of the genera, such as *Acidobacteria* (77.05%), *Sphingomonas* (25.60%), *Nitrospira* (20.78%), *Streptomyces* (11.32%), and *Gaiella* (10.20%), were abundant in all 9 samples, with a total abundance of 10.20–77.05%.

Effects of soil amendments on corn growth in coal fly ash soil

After the corn samples were harvested, the root dry weight, the plant height, the stem dry weight, and the corncob dry weight were determined (Fig. 6a and b), respectively. The results showed that the root dry weight was significantly decreased by 7.98–68.90% in B1 and B3-B8, respectively, while B2 was significantly increased by 52.59%, compared with that in B0 ($P=0.004$, $P<0.01$) (Fig. 6a). The root moisture content was significantly increased by 5.65%, 8.04%, 14.91%, 47.77%,

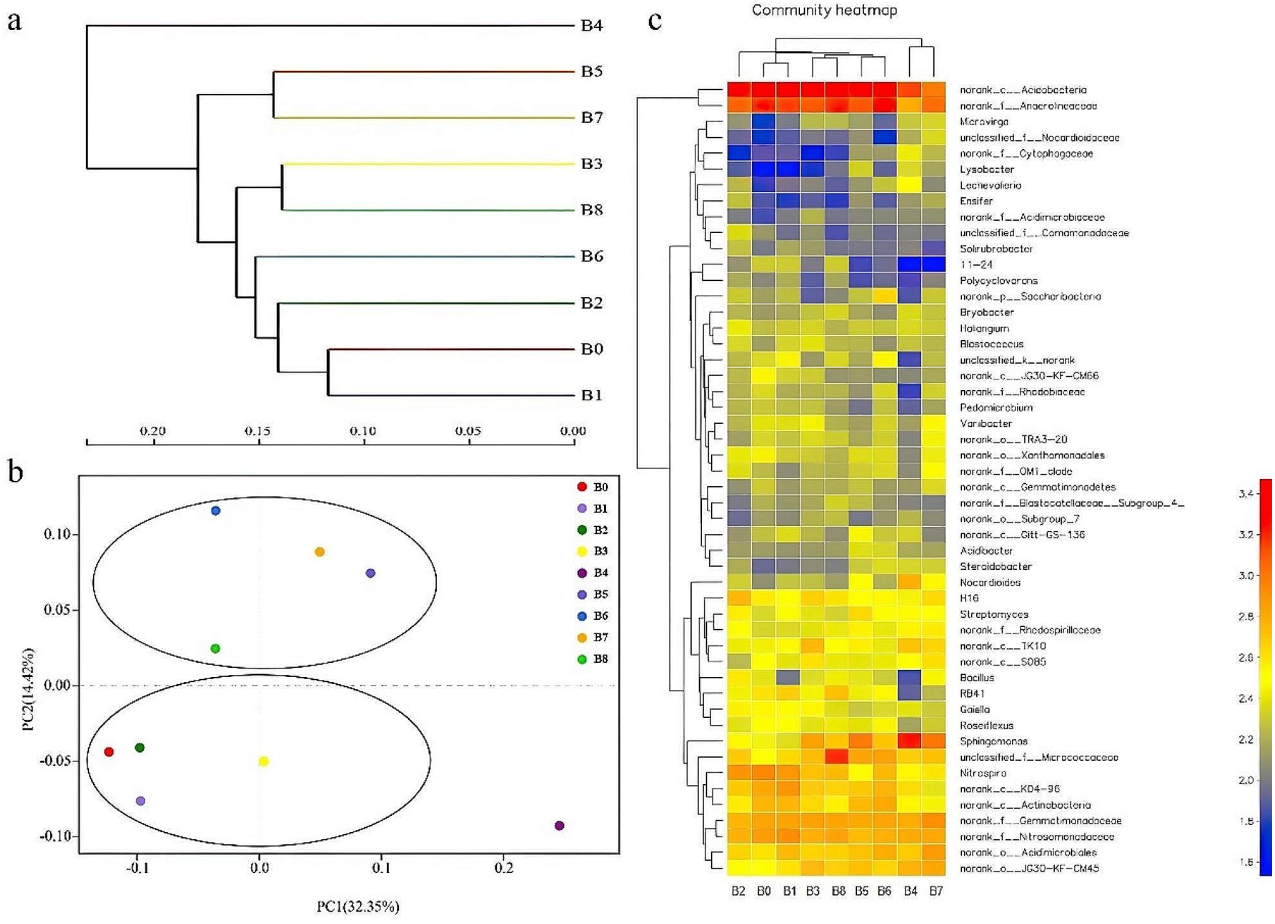

Fig. 5 Relationships among bacterial communities on each sample. (**a**) Hierarchical clustering tree of the bacterial community composition at the OTU level based on Bray-Curtis distances. (**b**) PCoA plot based on an OTU-based unweighted-Unifrac distance metrics derived from the different treatments. The two PCs (PC1 and PC2) extracted accounted for 46.77% of the total variance. (**c**) Heat map of mean relative abundances (%) of bacteria in samples

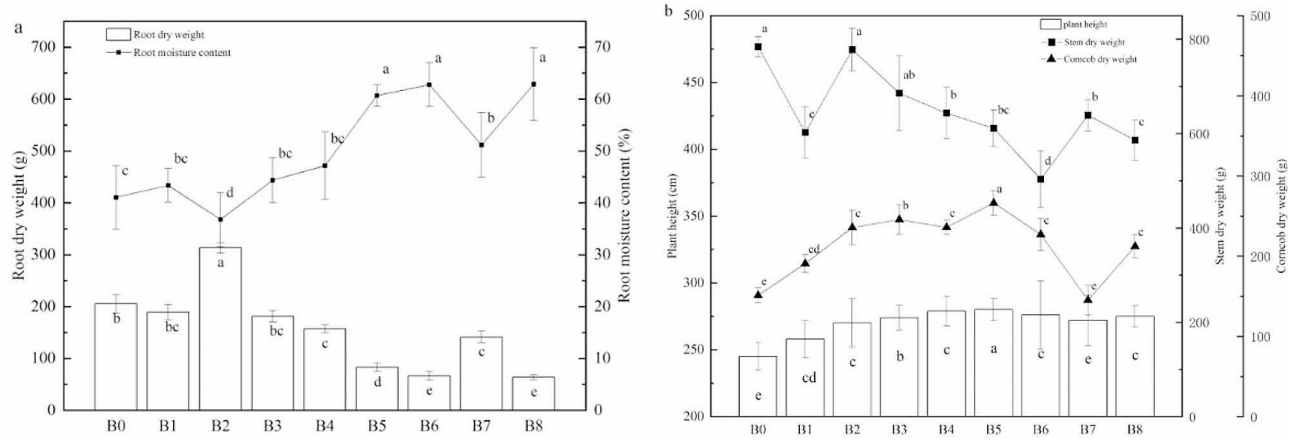

Fig. 6 Effects of soil amendments on maize growth. Different lower-case letters indicate significant differences among different treatments based on a one-way ANOVA followed by LSD ($p < 0.05$)

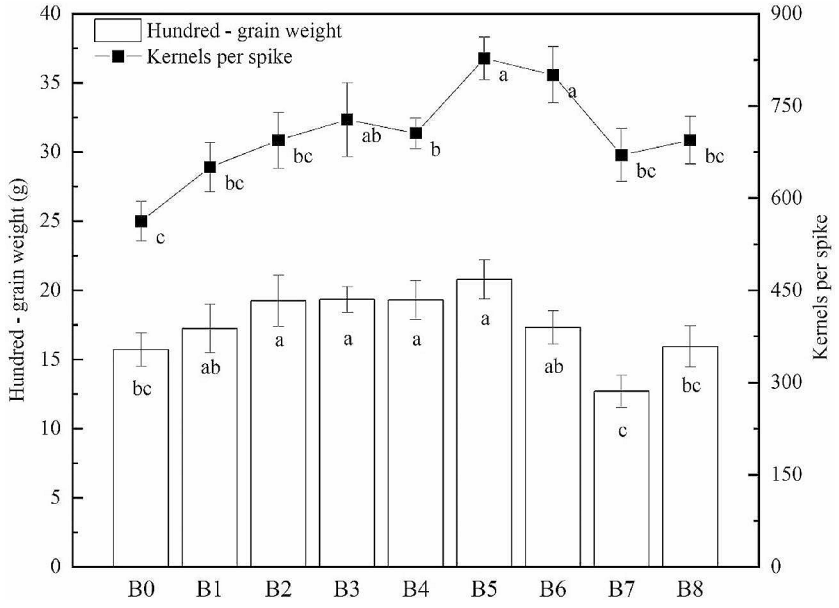

Fig. 7 Effects of soil amendment on hundred grain weight and kernel number per spike. Different lower-case letters indicate significant differences among different treatments based on a one-way ANOVA followed by LSD ($p < 0.05$)

52.91%, 24.68%, and 53.15% in B1, B3, B4, B5, B6, B7, and B8, respectively, whereas that of B2 was significantly decreased by 10.38%, compared with that in B0 ($P=0.002$, $P<0.01$) (Fig. 6a). The result showed that the addition of G1 could promote the growth and water retention ability of plant roots. The plant height was significantly increased by 5.31–12.24% in B1-B8, respectively, compared with that in B0 ($P=0.007$, $P<0.01$) (Fig. 6b). The corncob dry weight was significantly increased by 26.30–76.37% in B1-B6 and B8, respectively, whereas B7 was significantly decreased by 3.81%, compared with that in B0 ($P=0.004$, $P<0.01$) (Fig. 6b). The stem dry weight was significantly decreased by 23.16%, 0.77%, 12.55%, 17.94%, 22.03%, 35.80%, 18.52%, and 25.24% in B1, B2, B3, B4, B5, B6, B7, and B8, respectively, compared with that in B0 ($P=0.000$, $P<0.01$) (Fig. 6b).

Effect of soil amendments on corn yield in coal fly ash soil

The corn kernel number per spike and hundred grain weight were shown in Fig. 7. The hundred grain weight was significantly increased by 9.60%, 22.31%, 23.01%, 22.80%, 32.17%, 10.04%, and 1.33% in B1, B2, B3, B4, B5, B6, and B8, respectively, while hundred grain weight in B7 was significantly decreased by 19.26%, compared with that in B0 ($p=0.027$, $P<0.05$). The kernel number per spike was significantly increased by 15.73%, 23.52%, 29.49%, 25.50%, 47.20%, 42.39%, 19.21%, and 23.52% in B1, B2, B3, B4, B5, B6, B7, and B8, respectively, compared with that in B0 ($p=0.018$, $P<0.05$). The values of

hundred grain weight and kernel number per spike in B5 were higher than for the other groups, which were 32.17% and 47.2% higher than those in the control group, respectively.

Discussion

In this study, we investigated the responses of soil bacterial communities to the addition of carrier soil (CS) and soil amendment G1 under different level treatments in coal fly ash farmland. The results showed that the different treatments influenced the soil bulk density and other soil physicochemical properties, crop growth, crop yield, and soil bacterial community structure. In particular, soil amendment G1 had a great influence on soil microbial community structure (Chen et al. 2016; Ding et al. 2016; Hu et al. 2018).

Soil physical and chemical properties

It is commonly take several years to observe the effects of the continuous application of fertilizers on the total C and N, in particular, the effects of organic farm management, green manure, and organic soil amendment (Becker 2001; Lemke et al. 2010). Our results showed that soil pH was not obviously significantly different between all the treatment groups and control group after soil amendments. In addition, soil available N, available P, and total N, total P, and organic matter were all lower in treatment groups than in control group with an exception of soil total K and available K, which were slightly different among treatment groups but higher than those in control group. For example, the soil available nitrogen was decreased from 103.21 $mg{\cdot}kg^{-1}$ to 23.16 $mg{\cdot}kg^{-1}$ (a decrease of 77.56%). A possible reason for this result was that the use of soil amendments improved soil fertility and plant growth and development, thus promoting plant uptake and utilization of soil N, P, and other nutrients, and organic matter in soil. Our data also showed that the different addition amounts of G1 and CS had various effects on the available nutrients. Table 2 showed a soil available nitrogen decrease, which might be because additional amendments could promote the absorption of available nitrogen by the plants. Application of G1 fractions can increase the soil organic carbon content and soil C/N value, thus promoting the growth of crops (Kang et al. 2018). Furthermore, treatment with G1 fractions has been reported to enhance the compact structure of the surface soil and the high stability of soil aggregates, thus effectively inhibiting the dispersion of soil particles and effectively preventing soil erosion (Liu et al. 2019). One recent study has shown that soil nutrients are negatively correlated with the percentage of aggregates with particle size of >5 mm (Jiang et al. 2023). Consistently, in this study, 0.25-2 mm macroaggregates were significantly increased, which could be explained by the fact that G1 acted as a bonding material to aggregate small-grained particles into the large-grained ones. Due to its large specific surface area and negative surface charge, humic acid, as one G1 fraction, can adsorb and fix a variety of inorganic ions and polar or nonpolar organic compounds in the soil, thus increasing the viscosity of soil particles and enhancing its agglomeration (Didonato et al. 2016). Likewise, the applications of biosolids, as another G1 fraction, greatly increased the free Fe oxide content, thereby enhancing the formation of macro-aggregates.

Effects of soil amendment addition on soil microbial community under different conditions

Our results showed that the addition of G1 and CS significantly changed the abundance of soil microbial communities, which was consistent with some previous reports that humic acid treatment can significantly change soil bacterial community structure (Puglisi et al. 2009, 2013). In our study, the abundance of Armatimonadetes, Bacteroidetes, and Cyanobacteria in all the treatment groups was higher than that in control group. Low N/P ratio and a wide TN range can promote the blooms of N_2-fixing Cyanobacteria (González-Madina et al. 2019). One previous study has indicated that the growth of Cyanobacteria was limited by phosphorus, and an increase of phosphate will contribute to the increase of the abundance of Cyanobacteria (Bridgeman et al. 2012). In this study, most soil nutrients such as N and P in all treatment groups were lower than those in the control group B0. We speculated that this might be because G1 addition increased the abundance of nitrogen-fixing bacterial communities, thus promoting soil nutrient transformation, eventually enhancing the production of effective nutrients in the soil and their absorption and utilization by plants. Our speculation was confirmed by the results that the dry weight in the corn roots increased after the application of the modifier (Fig. 5). Among all the treatments, it was found that the main taxa of microbial communities existed were similar, but the abundance was different. Nitrospirae and Actinobacteria existed in all the samples but they were higher in B4 and B5, which might be because $FeSO_4$ and super absorbent polymer in G1 could promote the activities of soil microorganisms and enzymes, further accelerating the mineralization of organic matter and promoting the release of nutrients, eventually increasing the total abundance of soil microorganisms. Additionally, the addition of biochar with similar structure to humic acid can promote the transformation of NH_3 and NH_4^+ into NO_3^- in the soil, thus reducing the loss of available nitrogen in the soil (Lehmann et al. 2011).

These bacteria have different effects on the soil. For example, *Acidobacteria* has been reported to participate in the metabolism of soil single carbon compounds and promote their absorption by plants (Müller et al. 2016;

Radajewski et al. 2002). *Nitrospira* can oxidize nitrite into nitrate (Attard et al. 2010). *Sphingomonas*, which belongs to obligate aerobe, could promote the conversion of polysaccharides (pentose, hexose and disaccharide) to carboxylic acids to reduce the pH of fly ash soil (Delbrassinne 2016; Du et al. 2018; Kumari 2016; Xu et al. 2018). *Bacillu* has strong moisture retention capacity, and it can form a strong natural material called polyglutamic acid to protect the soil and prevent the loss of fertilizer and water (Das 2019; Delbrassinne 2016; Kumari 2016; Shen et al. 2015).

Effects of CS and G1 on crop growth and yield

The changes in microbial activity and compositions can influence plant growth by enhancing nutrient turnover (Wang et al. 2018). According to the results of Figs. 6 and 7, the root dry weight and stem dry weight of B0 are higher than other groups except B2, while its panicle dry weight and hundred-grain weight are lower than other groups. And the root dry weight of B2 (adding G1 and CS) was much higher than that of other treatments. It can be concluded that adding appropriate amounts of CS and G1 can increase the uptake of soil nutrients by plant roots and promote the accumulation of dry matter mass in corn grains. The application of soil amendment can improve microbial growth and activities in soil, in turn enhancing plant performance (Khoa et al. 2017; Santoyo et al. 2012; SHEN et al. 2014). Previous studies have demonstrated that the application of humic acid to corn can significantly improve soil physical properties and contribute to transferring micronutrients from the soil to the plant, thus enhancing water retention, increasing seed germination rate, and improving root penetration, finally stimulating the development of soil bacterial communities in soils (Canellas et al. 2015; Tahir et al. 2011). In the present study, hundred grain weight and kernel number per spike in all treatment groups were significantly higher than those in the control group. Our data showed that 20% CS in 0–20 cm top soil layer and 13,500 kg·ha^{-1} G1 addition (B5) exhibited the optimum fly ash soil modification effect, which resulted in a hundred grain weight of 20.79 g and kernels per spike of 827.56.

Taken together, our results imply that application of carrier soil (CS) and the soil amendment G1 to the coal fly ash farmland can improve soil physicochemical properties, especially bulk soil density, and raise crop yield, which are closely correlated with soil microbial community activities. This study lays a foundation for the study of the application of coal fly ash to the agriculture production and provides technical reference for the coal fly ash soil amendment.

Conclusion

The results showed that the addition of carrier soil and amendments improved the physicochemical properties of coal fly ash soil, thus increasing the corn yield. The abundance of microorganisms that facilitate the cycling of soil nutrient elements was increased after the addition of carrier soil and amendments. With the macro-aggregates, organic carbon and nitrogen increased by amendments, the coal fly ash soil could provide more air, water and nutrient elements for the survival, growth and reproduction of microorganisms. It leads to increased activity of carbon and nitrogen fixing microorganisms. The microbial community activities can improve the physical structure and increase fertility in coal fly ash soil, which is beneficial to the plant growth. Overall, this study reveals the response mechanism of microbial community activities and soil physiochemical properties to coal fly ash soil amendment strategy. Our results provide valuable reference for extensive applications of carrier soil and amendment to improve the agricultural productivity of coal fly ash soil. It provides technical support for recycle utilization of fly ash in ecological restoration and agricultural production. In this way, the problem of difficulty storage of coal fly ash, which is produced several hundreds of millions of tons, and topsoil shortage in some areas can be solved. With the reuse of coal fly ash, it can promote the realization of Zero-waste city and circular economy. This study is a contribution to the Sustainable Development Goal 7 "Affordable and Clean Energy" and 9 "Industry, Innovation and Infrastructure" of the 2030 by Agenda of the United Nations. It will reduce the industries production of solid waste and promote the development of other industries by recycling industrial solid waste fly ash in ecological restoration and agricultural production.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s13213-024-01758-7.

Supplementary Material 1

Supplementary Material 2

Acknowledgements

We thank Prof. Ping Liu, Huazhong Agriculture University, for her linguistic assistance during the preparation of this manuscript.

Author contributions

All authors contributed to the study conception and design. Methodology, investigation, and supervision were performed by F.L.; Methods and analysis of soil microbial detection were performed by T.Q., G.Z. and S.Z. Field trials were designed, analyzed and tested by X.L., X.L., F.L., Z.W., Z.H. and H.L. Soil physical properties was performed by S.M. and F.L. Soil chemical properties were performed by H.L., G.Z. and X.L. The first draft of the manuscript was written by F.L., X.L. and Z.H. and all authors commented on previous versions of the manuscript. The revision of paper was performed by F.L., X.L., Z.H. and H.L. All authors read and approved the final manuscript.

Funding
This work was supported by Beijing Nova Program (20230484424). And also this work was sponsored by 2022 Youth Science and Technology Fund of BGRIMM Technology Group "Study on Copper Tailings-based Modified Reclamation Material and Organic Carbon Conversion" (04-2204).

Data availability
All data generated or analysed during this study are included in this published article [and its supplementary information files].

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors have no relevant financial or non-financial interests to disclose.

Author details
[1]Institute of Environment Engineering, BGRIMM Technology Group, Beijing 100160, China
[2]Department of Clinical Laboratory, Aerospace Center Hospital, Beijing 100049, China
[3]Exploration Unit of North China Geological Exploration Bureau, Sanhe 065201, China
[4]Eco-Development Research Center, BioMintec Environment (Shanghai) Co. Ltd. (BME), Shanghai 200333, China
[5]State Key Laboratory of Environmental Criteria and Risk Assessment, Chinese Research Academy of Environmental Sciences, Beijing 100012, China
[6]Olympic Village School, Heping Street No.1 Middle School, Beijing 100020, China
[7]School of Chemical & Environmental Engineering, China University of Mining & Technology - Beijing, Beijing 100083, China

Received: 27 October 2023 / Accepted: 15 March 2024
Published online: 27 April 2024

References

Ahmaruzzaman M (2010) A review on the utilization of fly ash. Prog Energy Combust Sci 36:327–363. https://doi.org/10.1016/j.pecs.2009.11.003
Alhaj Hamoud Y, Shaghaleh H, Sheteiwy M et al (2019) Impact of alternative wetting and soil drying and soil clay content on the morphological and physiological traits of rice roots and their relationships to yield and nutrient use-efficiency. Agric Water Manag 223:105706. https://doi.org/10.1016/j.agwat.2019.105706
Attard E, Poly F, Commeaux C et al (2010) Shifts between nitrospira- and nitrobacter-like nitrite oxidizers underlie the response of soil potential nitrite oxidation to changes in tillage practices. Environ Microbiol 12:315–326. https://doi.org/10.1111/j.1462-2920.2009.02070.x
Awoyemi OM, Adeleke EO, Dzantor EK (2019) Arbuscular mycorrhizal fungi and exogenous glutathione mitigate coal fly ash (cfa)-induced phytotoxicity in cfa-contaminated soil. J Environ Manage 237:449–456. https://doi.org/10.1016/j.jenvman.2019.02.103
Becker M, Johnson DE (2001) Cropping intensity effects on upland rice yield and sustainability in west africa. Nutr Cycl Agroecosyst 59:107–117. https://doi.org/10.1023/A:1017551529813
Bridgeman TB, Chaffin JD, Kane DD, Conroy JD, Panek SE, Armenio PM (2012) From river to lake: phosphorus partitioning and algal community compositional changes in western lake erie. J Great Lakes Res 38:90–97. https://doi.org/10.1016/j.jglr.2011.09.010
Canellas LP, Olivares FL, Aguiar NO et al (2015) Humic and fulvic acids as biostimulants in horticulture. Sci Hortic 196:15–27. https://doi.org/10.1016/j.scienta.2015.09.013
Chen C, Zhang J, Lu M et al (2016) Microbial communities of an arable soil treated for 8 years with organic and inorganic fertilizers. Biol Fertil Soils 52:455–467. https://doi.org/10.1007/s00374-016-1089-5
Chen X, Han X, You M et al (2019) Soil macroaggregates and organic-matter content regulate microbial communities and enzymatic activity in a Chinese mollisol. J Integr Agric 18:2605–2618. https://doi.org/10.1016/S2095-3119(19)62759-0
Chen Z, Chen Z, Liu J et al (2023) Optimizing co-combustion synergy of soil remediation biomass and pulverized coal toward energetic and gas-to-ash pollution controls. Sci Total Environ 857:159585. https://doi.org/10.1016/j.scitotenv.2022.159585
Coudert E, Paris M, Deneele D, Russo G, Tarantino A (2019) Use of alkali activated high-calcium fly ash binder for kaolin clay soil stabilisation: physicochemical evolution. Constr Build Mater 201:539–552. https://doi.org/10.1016/j.conbuildmat.2018.12.188
Das AJ, Kumar R (2019) Production of biosurfactant from agro-industrial waste by bacillus safensis j2 and exploring its oil recovery efficiency and role in restoration of diesel contaminated soil. Environ Technol Innov 16:100450. https://doi.org/10.1016/j.eti.2019.100450
Delbrassinne L, Mahillon J (2016) Bacillus: occurrence. In: Caballero B, Finglas PM, Toldrá F (eds) Encyclopedia of Food and Health. Academic, Oxford, pp 307–311
Didonato N, Chen H, Waggoner D, Hatcher PG (2016) Potential origin and formation for molecular components of humic acids in soils. Geochim Cosmochim Acta 178:210–222. https://doi.org/10.1016/j.gca.2016.01.013
Ding J, Jiang X, Ma M et al (2016) Effect of 35 years inorganic fertilizer and manure amendment on structure of bacterial and archaeal communities in black soil of northeast China. Appl Soil Ecol 105:187–195. https://doi.org/10.1016/j.apsoil.2016.04.010
Du P, Wu X, Xu J, Dong F, Liu X, Zheng Y (2018) Effects of trifluralin on the soil microbial community and functional groups involved in nitrogen cycling. J Hazard Mater 353:204–213. https://doi.org/10.1016/j.jhazmat.2018.04.012
Fangze L, Tianqi Q, Xiaohua L et al (2023) Responses of soil microbial community activities and soil physicochemical properties to coal fly ash soil amendment [Preprint]. https://doi.org/10.21203/rs.3.rs-3096007/v1. Research Square
Gollakota ARK, Volli V, Shu C (2019) Progressive utilisation prospects of coal fly ash: a review. Sci Total Environ 672:951–989. https://doi.org/10.1016/j.scitotenv.2019.03.337
González-Madina L, Pacheco JP, Yema L et al (2019) Drivers of cyanobacteria dominance, composition and nitrogen fixing behavior in a shallow lake with alternative regimes in time and space, laguna del sauce (maldonado, Uruguay). Hydrobiologia 829:61–76. https://doi.org/10.1007/s10750-018-3628-6
Guo F, Zhong Z (2018) Co-combustion of anthracite coal and wood pellets: thermodynamic analysis, combustion efficiency, pollutant emissions and ash slagging. Environ Pollut 239:21–29. https://doi.org/10.1016/j.envpol.2018.04.004
Han J, Yu D, Wang Q et al (2022) Beneficiation of coal ash from ash silos of six Chinese power plants and its risk assessment of hazardous elements for land application. Process Saf Environ Prot 160:641–649. https://doi.org/10.1016/j.psep.2022.02.058
He H, Fan C, Peng Q, Wu M, Zheng J, Wu G (2019) Bioaccumulation and translocation of rare earth elements in two forage legumes grown in soils treated with coal fly ash. Chem Geol:119284. https://doi.org/10.1016/j.chemgeo.2019.119284
Holthusen D, Brandt AA, Reichert JM, Horn R (2018) Soil porosity, permeability and static and dynamic strength parameters under native forest/grassland compared to no-tillage cropping. Soil Tillage Res 177:113–124. https://doi.org/10.1016/j.still.2017.12.003
Hu X, Liu J, Wei D et al (2018) Soil bacterial communities under different long-term fertilization regimes in three locations across the black soil region of northeast China. Pedosphere 28:751–763. https://doi.org/10.1016/S1002-0160(18)60040-2
Jiang W, Li Z, Xie H, Ouyang K, Yuan H, Duan L (2023) Land use change impacts on red slate soil aggregates and associated organic carbon in diverse soil layers in subtropical China. Sci Total Environ 856:159194. https://doi.org/10.1016/j.scitotenv.2022.159194
Ju W, Moorhead DL, Shen G, Cui Y, Fang L (2023) Soil aggregate development and associated microbial metabolic limitations alter grassland carbon storage following livestock removal. Soil Biol Biochem 177:108907. https://doi.org/10.1016/j.soilbio.2022.108907
Kang H, Gao H, Yu W, Yi Y, Wang Y, Ning M (2018) Changes in soil microbial community structure and function after afforestation depend on species and age:

case study in a subtropical alluvial island. Sci Total Environ 625:1423–1432. https://doi.org/10.1016/j.scitotenv.2017.12.180
Khoa N, Xạ TV, Hào LT (2017) Disease-reducing effects of aqueous leaf extract of kalanchoe pinnata on rice bacterial leaf blight caused by xanthomonas oryzae pv. Oryzae involve induced resistance. Physiol Mol Plant Pathol 100:57–66. https://doi.org/10.1016/j.pmpp.2017.06.005
Kumari S, Sarkar PK (2016) Bacillus cereus hazard and control in industrial dairy processing environment. Food Control 69:20–29. https://doi.org/10.1016/j.foodcont.2016.04.012
Lehmann J, Rillig MC, Thies J, Masiello CA, Hockaday WC, Crowley D (2011) Biochar effects on soil biota – a review. Soil Biol Biochem 43:1812–1836. https://doi.org/10.1016/j.soilbio.2011.04.022
Lemke RL, Vandenbygaart AJ, Campbell CA, Lafond GP, Grant B (2010) Crop residue removal and fertilizer n: effects on soil organic carbon in a long-term crop rotation experiment on a udic boroll. Agr Ecosyst Environ 135:42–51. https://doi.org/10.1016/j.agee.2009.08.010
Li S, Li Q, Wang C et al (2019) Spatial variability of soil bulk density and its controlling factors in an agricultural intensive area of Chengdu plain, southwest China. J Integr Agric 18:290–300. https://doi.org/10.1016/S2095-3119(18)61930-6
Liu J, Chen Z, Kanungo DP et al (2019) Topsoil reinforcement of sandy slope for preventing erosion using water-based polyurethane soil stabilizer. Eng Geol 252:125–135. https://doi.org/10.1016/j.enggeo.2019.03.003
Mahedi M, Cetin B, Dayioglu AY (2019) Leaching behavior of aluminum, copper, iron and zinc from cement activated fly ash and slag stabilized soils. Waste Manag 95:334–355. https://doi.org/10.1016/j.wasman.2019.06.018
Müller CA, Obermeier MM, Berg G (2016) Bioprospecting plant-associated microbiomes. J Biotechnol 235:171–180. https://doi.org/10.1016/j.jbiotec.2016.03.033
Preethi K, Ambika D, Janani S (2023) A preliminary study on production of roof tiles and paver blocks using wood and coal ash. Mater Today: Proceedings. https://doi.org/10.1016/j.matpr.2023.01.124
Puglisi E, Fragoulis G, Ricciuti P et al (2009) Effects of a humic acid and its size-fractions on the bacterial community of soil rhizosphere under maize (zea mays l). Chemosphere 77:829–837. https://doi.org/10.1016/j.chemosphere.2009.07.077
Puglisi E, Pascazio S, Suciu N et al (2013) Rhizosphere microbial diversity as influenced by humic substance amendments and chemical composition of rhizodeposits. J Geochem Explor 129:82–94. https://doi.org/10.1016/j.gexplo.2012.10.006
Qin P, Chen P, Zhang X, Xie L (2020) Coal taxation reform in China and its distributional effects on residential consumers. Energ Policy 139:111366. https://doi.org/10.1016/j.enpol.2020.111366
Radajewski S, Webster G, Reay DS et al (2002) Identification of active methylotroph populations in an acidic forest soil by stableisotope probing. Microbiol (Reading) 148:2331–2342. https://doi.org/10.1099/00221287-148-8-2331
Roy M, Roychowdhury R, Mukherjee P (2018) Remediation of fly ash dumpsites through bioenergy crop plantation and generation: a review. Pedosphere 28:561–580. https://doi.org/10.1016/S1002-0160(18)60033-5
Sankar AS, Patnaik A (2018) Impact of soil physico-chemical properties on distribution of earthworm populations across different land use patterns in southern India. J Basic Appl Zool 79:50. https://doi.org/10.1186/s41936-018-0066-y
Santoyo G, Del Carmen Orozco-Mosqueda M, Govindappa M (2012) Mechanisms of biocontrol and plant growth-promoting activity in soil bacterial species of bacillus and pseudomonas: a review. Biocontrol Sci Technol 22:855–872. https://doi.org/10.1080/09583157.2012.694413
Shaheen SM, Hooda PS, Tsadilas CD (2014) Opportunities and challenges in the use of coal fly ash for soil improvements – a review. J Environ Manage 145:249–267. https://doi.org/10.1016/j.jenvman.2014.07.005
Shen Z, Wang Y, Sun Q, Wang W (2014) Effect of vegetation succession on organic carbon, carbon of humus acids and dissolved organic carbon in soils of copper mine tailings sites. Pedosphere 24:271–279. https://doi.org/10.1016/S1002-0160(14)60013-8
Shen Z, Ruan Y, Wang B et al (2015) Effect of biofertilizer for suppressing fusarium wilt disease of banana as well as enhancing microbial and chemical properties of soil under greenhouse trial. Appl Soil Ecol 93:111–119. https://doi.org/10.1016/j.apsoil.2015.04.013
Tahir MM, Khurshid M, Khan MZ, Abbasi MK, Kazmi MH (2011) Lignite-derived humic acid effect on growth of wheat plants in different soils. Pedosphere 21:124–131. https://doi.org/10.1016/S1002-0160(10)60087-2
Teixeira ER, Camões A, Branco FG, Aguiar JB, Fangueiro R (2019) Recycling of biomass and coal fly ash as cement replacement material and its effect on hydration and carbonation of concrete. Waste Manag 94:39–48. https://doi.org/10.1016/j.wasman.2019.05.044
Tsiridis V, Petala M, Samaras P, Sakellaropoulos GP (2015) Evaluation of interactions between soil and coal fly ash leachates using column percolation tests. Waste Manag 43:255–263. https://doi.org/10.1016/j.wasman.2015.05.031
Wang M, Chen L, Li Y et al (2018) Responses of soil microbial communities to a short-term application of seaweed fertilizer revealed by deep amplicon sequencing. Appl Soil Ecol 125:288–296. https://doi.org/10.1016/j.apsoil.2018.02.013
Wang G, Jensen PA, Wu H et al (2019) Potassium capture by coal fly ash: k2co3, kcl and k2so4. Fuel Process Technol 194:106115. https://doi.org/10.1016/j.fuproc.2019.05.038
Xiao Y, Tang J, Wang M, Zhai L, Zhang X (2017) Impacts of soil properties on phosphorus adsorption and fractions in purple soils. J Mt Sci 14:2420–2431. https://doi.org/10.1007/s11629-017-4545-2
Xu Y, Niu L, Qiu J, Zhou Y, Lu H, Liu W (2018) Stereoselective accumulations of hexachlorocyclohexanes (hchs) are correlated with sphingomonas spp. In agricultural soils across China. Environ Pollut 240:27–33. https://doi.org/10.1016/j.envpol.2018.04.078
Zhang X, Dou H, Bai J et al (2023) Effect of phosphorus on viscosity-temperature behavior of high-sodium coal ash slag. Fuel (Lond) 343:127930. https://doi.org/10.1016/j.fuel.2023.127930

Publisher's Note