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Diversity of soil bacteria in alpine coal slag mountain grassland in different vegetation restoration years

Rina Dao*, Ying Zhang*, XiLai Li, Linxiong Ma, Xiaolong Tie and Shengyan Lei

Abstract

Purpose This study aimed to investigate changes in the bacterial diversity of the rhizosphere soil of slag mountains in different years of revegetation restoration.

Methods Seven soil samples were selected from different years of revegetation restoration in Qinghai, China. The bacterial community of each soil was analyzed via high-throughput sequencing using the Illumina MiSeq platform.

Results Statistical analyses revealed that the diversity of the soil bacterial community was higher in the soil that was restored in 2017 than that in the soils restored from other years. 16S rRNA sequencing revealed that Proteobacteria and Actinobacteria were the dominant phyla. *Sphingomonas* was the dominant genus. Total nitrogen, available nitrogen, and total potassium influenced the horizontal community structure of the phylum, whereas total nitrogen, organic matter, and pH had a great influence on the horizontal community structure of the phylum. The richness and diversity of the bacterial community in the soils that underwent revegetation restoration were greater in the third year (2017) than in other years. In the seventh year of recovery, the richness and diversity of the bacterial community began to decline.

Conclusion The bacterial diversity of the soil in the coal mine slag mountain improved with the increase in vegetation restoration years.

Keywords Coal slag mountain, High-throughput sequencing, Microbial diversity, Proteobacteria, Vegetation restoration

Introduction

Soil is the main limiting factor that affects the restoration of degraded ecosystems in coal mining areas (Du et al. 2009; Yin et al. 2010). Soil microorganisms, such as bacteria, participate in the decomposition of organic matter, growth of plants, and other critical ecological processes (Lu et al. 2022). The influence of the microenvironment is more significant when the soil environment changes (Chen et al. 2016); the soil microbial community can make a rapid response, and the biological community structure can change. The soil community structure is therefore a crucial indicator of soil quality change. Soil bacteria participate in the transformation of most nutrients in the soil (An et al. 2017) and occupy an absolute dominant position among soil microbes, with the proportion reaching over 95% (Li et al. 2013). Therefore, soil bacterial diversity can be used to measure soil quality levels after revegetation restoration in mining areas (Li et al. 2014; Sharma et al. 2011; Yao et al. 2013).

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The Jiangcang coal mining area is the largest coal mining area in Qinghai Province. It is located approximately 110 km northwest of Gangcha County toward the south of the upper reaches of Datong River. It is approximately 3800 m above sea level and has a cold climate. Mechanical piling up of past slag mountain has caused serious damage, including exhaustion of grassland resources, land desertification, and soil and water loss (Chang et al. 2003; Liu and Liu 2020), leading to irreversible destruction of the ecosystem; therefore, developing the structure and function of an ecosystem has a considerable effect, completely changing the growth of the vegetation survival environment. The soil microbial ecosystem has also been severely damaged by serious soil erosion, significant changes in the composition of the microbial community, and massive loss of microbial diversity, thereby affecting the material and nutrient cycling in the soil, structure and fertility of the soil, vegetation growth, and the entire ecosystem (Fan et al. 2011; Murphy et al. 2003). The alpine mining area ecosystem has suffered serious, long-term damage in the permafrost environment, which will not recover without intervention.

Most studies on ecological restoration in mining areas have focused on determining soil physical and chemical properties and vegetation reconstruction, and there are few studies on the use of soil microorganisms to analyze the soil conditions in mining areas (Zhang et al. 2014). Studies on soil bacterial diversity in China are primarily conducted in farmlands and jungles (Sun et al. 2012); however, few studies have been conducted in alpine regions. Studies on vegetation restoration in mining areas have mostly been conducted in loess hilly-gully and low-altitude regions (Jin et al. 2019). Most studies focus on soil enzyme activity and soil biomass. However, relevant studies have shown that revegetation restoration affects soil properties (Kumar et al. 2015) and that soil bacteria can accurately reflect the restoration of degraded land (Izquierdo et al. 2005). Regarding the methods used for microbial diversity research, traditional research methods, such as the plate culture method, BIOLOG microplate method, phospholipid fatty acid analysis, gradient gel electrophoresis technology, nucleic acid molecular hybridization-based method, PCR-based method, and Sanger sequencing, have been used in previous studies (Zhao et al. 2015; Lin et al. 2010; Cai et al. 2011; Ke et al. 2011; Gao et al. 2009). These traditional methods detect relatively low bacterial community abundance and have a small range, complex operation, and high cost (Mao et al. 2015). In contrast, high-throughput sequencing technology, with the advantages of high sensitivity and quick throughput, enables simple, quick, and accurate acquisition of soil microbial information (Jones et al. 2009). Therefore, high-throughput sequencing technology was used in this study to analyze the response characteristics of soil bacterial diversity in the compound green grassland and to measure soil nutrients. This study used the grassland of the slag mountain of the Jiangcang mining area that had been planted in different years as the research objects. The relationship between the soil nutrients and soil bacterial diversity of the slag mountains of mining areas with different planting years was investigated to provide a theoretical basis for future construction and ecological reconstruction in the alpine mining area.

Methods

Site description and soil sampling

The research site is located in the Jiangcang coal mine area, Gangcha County, Haibei Prefecture, Qinghai Province, China. It is located in the alpine zone at an altitude of 3800–4200 m (Jin et al. 2019). Its geographical coordinates are 99°27′–99°35′E and 38°02′–38°03′N. The annual average temperature is − 2.8 ℃, ranging from − 35.6 ℃ to 19.8 ℃. A large number of alpine meadows and marshes are distributed in the Jiangcang mining area, which are classified as alpine marsh wetland. The matrix of the slope surface is composed of coal gangue and accumulated residue. On the sunny slope, cofferdams have been built along the bottom edge of the slag mountain to increase the stability of the slope surface. The planting methods for all plots were the same, where *Elymus nutans*, *Poa crymophila*, and *Puccinellia tenuiflora* were planted artificially at a ratio of 2:1:1. The proportion of 1 was planted in May 2015, May 2017, and late May 2019, respectively, at a sowing rate of 8.0943 kg/hm^2, and plants were covered with a nonwoven fabric after sowing. During this period, no fertilization, watering, or grazing activities were performed. The elevation of the undisturbed original vegetation in the mine area is 3788 m, and the geographical coordinates are 99°38′E and 38°03′N. The dominant species in this area are *Kobresia pygmaea*, *Kobresia humilis*, and *Carex rigescens*.

In the experiment area (Fig. 1), the vegetation restoration duration from 2013 to 2019 was selected, and the grasslands had vegetation restoration durations of 1 year (2019), 2 years (2018), 3 years (2017), 4 years (2016), 5 years (2015), 6 years (2014), and 7 years (2013). We also collected samples of native vegetation soil (YS) from the undisturbed original vegetation area. Three soil samples of 0–20 cm were collected from each area, stones, and residual plant roots were removed, and samples were placed into ziplock bags before being brought to the laboratory for determination of their physical and chemical properties. Then, ground vegetation and surface coverings were removed

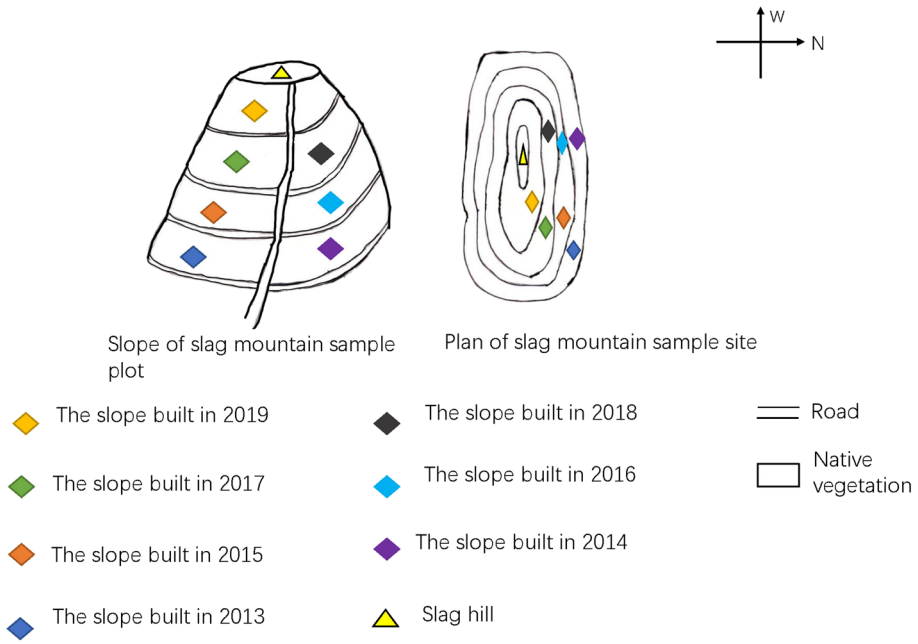

Fig. 1 The geographical location of the layout of the sample plot

from the sample site, and sterile soil samples were collected using a sterilized shovel. The sterile samples were returned to the laboratory at low temperature (− 5 ℃) and placed in the refrigerator for correlation analysis of soil chemical properties and soil microorganisms. The sterile soil of native vegetation was soil that had not been applied to guest soil and had not undergone revegetation restoration in the coal mine slag mountain.

Soil chemical property measurements

Soil pH was measured using a pH meter in a suspension of soil and water with a soil:water ratio of 1:2.5. Total nitrogen (TN) content was measured using the potassium dichromate sulfuric acid boiling method. Total phosphorus (TP) content was determined using the sulfuric acid and perchloric acid boiling and molybdenum antimony resistance colorimetric methods. Total potassium (TK) content was determined using the molten NaOH and flame photometry method. Available nitrogen (AN), available phosphorus (AP), and available potassium (AK) contents were measured using the alkaline hydrolysis diffusion, molybdenum blue, and flame photometry methods, respectively. Soil organic matter (SOM) was determined using the potassium dichromate volumetric method. All methods were followed according to a previous report (Chao and Bunge 2002).

DNA extraction, sequencing, and data analysis

Nucleic acid extraction was performed using the TGuide S96 magnetic bead method soil genomic DNA Extraction Kit (DP812). The concentration of extracted nucleic acid was detected using a microplate reader (Synergy HTX). The integrity of the amplified PCR products was detected via electrophoresis in a 1.8% agarose gel.

Excel 2007 was used for data collation, and SPSS Statistics 26 was used for one-way analysis of variance of soil nutrients. Duncan's complex range method was used to test significant differences ($P < 0.05$). Using a 70% confidence threshold, the phylogenetic relationship of each 16S rRNA gene sequence was analyzed against the SILVA (SSU123) 16S rRNA database using a ribosomal database project (RDP) classifier for taxonomic analysis. Operational taxonomic units (OTUs) with similarities of at least 97% were selected for OTU cluster analysis and species taxonomy analysis to generate a dilution curve, and Mothur was used to calculate the Chao1, ACE richness, and Shannon and Simpson diversity indices (Schloss et al. 2011). The RDP classifier Bayesian algorithm was used for the taxonomic analysis of representative OTU sequences, and each sample's community composition was determined at the classification levels of phylum and class (Wang et al. 2007). The relationships between the fungal community structure and soil factors were analyzed using the redundancy analysis of the Baimaike Cloud platform.

Results

Soil chemical properties

The analysis was based on the data of the physical and chemical properties of the soil from the study plots with different vegetation restoration years, as shown in Table 1. The pH values of all soil samples were within the range of 7.6–8.6, indicating that all soils were slightly alkaline. The SOM initially increased and then decreased with the increase in the duration of vegetation restoration and reached a maximum value at the fourth vegetation restoration year (2016). There were no significant differences in TN, AK, and AN contents among the greenfield plots. The AP index reached the highest value in the soil from restoration year 2019. The maximum value of TP was 1.67 ± 0.16 in the soil from restoration year 2015. The TN, AN, AK, and SOM were higher in YS (native vegetation soil) than in the other soil samples, whereas the TK content in YS was lower than that in the other soil samples. The nutrient status of YS was significantly different from that of other soils. YS was neither applied to the guest soil nor was it greened, resulting in a significant difference from the greened soils. Therefore, there was a correlation between soil nutrients and vegetation, and changes in vegetation also change soil nutrients.

Alpha diversity of soil bacterial communities

As shown in Table 2, bacteria isolated from the 2017 soil had the highest Chao1 and ACE indices among the eight samples in this study, indicating the highest bacterial community richness, while YS had the lowest. The soil planted in 2017 had the highest Shannon value (8.594). The Shannon indices of the YS and 2019 soils were lower than those of the other samples, indicating that the bacterial community diversity was relatively low.

Composition of the soil bacterial community

As shown from the analysis in Fig. 2, 146 OTUs were obtained from sample bacteria after OTU clustering, and 63 OTUs were common. Each sample had an OTU count ranging from 4 to 67, with YS having the most (64). The lowest OTU counts were found in the soils planted in 2014 and 2016, both of which had OTU values of 4. The number of OTUs in YS accounted for approximately 33% of the total number of OTUs, indicating that the bacteria in YS did not have a high similarity with the bacteria in the other soils.

At the phylum level, 11 bacterial phyla were detected among the eight samples, as depicted in Fig. 3. The distribution of the soil bacterial community was uniform in various plots. The planted samples were mainly dominated by Proteobacteria, Actinobacteria, Bacteroidetes,

Table 1 Physical and chemical materials of soil

	TN(g·kg^{-1})	TP (g·kg^{-1})	TK(g·kg^{-1})	AN(m g·kg^{-1})	AP(m g·kg^{-1})	AK(m g·kg^{-1})	OM(g·kg^{-1})	pH
Y13	0.86 ± 0.02^{b}	1.04 ± 0.24^{abc}	23.32 ± 1.87^{abc}	28.00 ± 0.00^{b}	10.77 ± 2.36^{c}	124.00 ± 3.47^{ab}	24.02 ± 2.06^{d}	8.21
Y14	1.99 ± 0.84^{b}	0.84 ± 0.12^{c}	24.22 ± 2.71^{ab}	68.00 ± 38.74^{b}	16.40 ± 9.55^{bc}	148.33 ± 47.65^{ab}	66.02 ± 12.71^{c}	8.54
Y15	0.94 ± 0.05^{b}	1.67 ± 0.16^{a}	27.27 ± 1.10^{ab}	38.67 ± 12.90^{b}	21.57 ± 11.05^{abc}	145.00 ± 20.08^{ab}	75.10 ± 1.80^{c}	7.99
Y16	1.62 ± 0.25^{b}	0.80 ± 0.14^{c}	24.59 ± 1.34^{ab}	27.00 ± 10.39^{b}	13.90 ± 4.00^{bc}	127.67 ± 53.72^{ab}	158.93 ± 49.57^{b}	8.42
Y17	1.32 ± 0.11^{b}	1.12 ± 0.20^{abc}	23.90 ± 2.63^{ab}	25.67 ± 4.04^{b}	29.93 ± 7.82^{ab}	129.33 ± 18.56^{ab}	81.98 ± 10.03^{c}	7.62
Y18	1.41 ± 0.18^{b}	0.89 ± 0.22^{c}	23.32 ± 0.90^{abc}	35.33 ± 9.45^{b}	21.23 ± 11.02^{abc}	153.7 ± 7.64^{ab}	80.68 ± 5.79^{c}	8.14
Y19	1.02 ± 0.10^{b}	0.99 ± 0.23^{bc}	21.22 ± 1.38^{bcd}	26.00 ± 1.73^{b}	34.77 ± 17.72^{a}	118.67 ± 15.01^{ab}	56.79 ± 0.89^{cd}	8.48
YS	9.62 ± 5.73^{a}	1.63 ± 0.92^{ab}	18.76 ± 3.95^{d}	425.6 ± 220.26^{a}	13.17 ± 4.30^{c}	164.33 ± 25.81^{a}	328.68 ± 27.28^{a}	8.46

TN Total nitrogen, *TP* Total phosphorus, *TK* Total K, *AN* Available nitrogen, *AP* Available phosphorus, *AK* Available K, *OM* Organic matter. Different lowercase letters for the same index indicate significant difference ($P < 0.05$)

Table 2 Soil bacterial data of grassland with different vegetation restoration years in slag mountain of coal mine

Sample name	ACE indices	Chao1 indices	Shannon indices	Simpson indices	Coverage indices
Y13	1383.8049	1415.75	8.1788	0.9904	0.9981
Y14	1019.2238	1060.0769	7.0091	0.9782	0.9975
Y15	1342.3753	1340.6783	8.3371	0.9909	0.9983
Y16	1183.5284	1193.3942	7.3217	0.9748	0.9975
Y17	1438.892	1459.2844	8.594	0.9942	0.9974
Y18	1322.5432	1374.0964	8.3281	0.9925	0.9975
Y19	1149.3683	1198.8571	6.3991	0.9455	0.9969
YS	257.3057	231.8571	6.7737	0.9857	0.9997

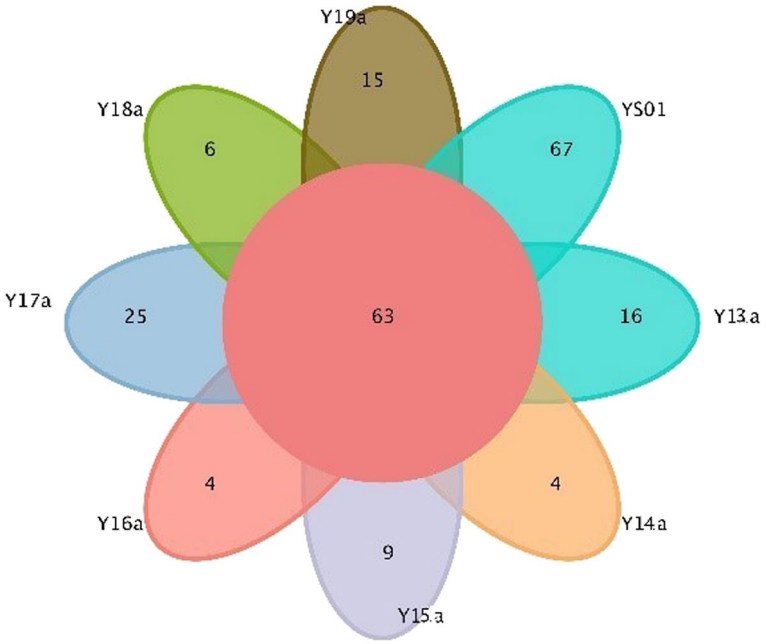

Fig. 2 Venn diagram of bacterial operational taxonomic unit distribution in the sample

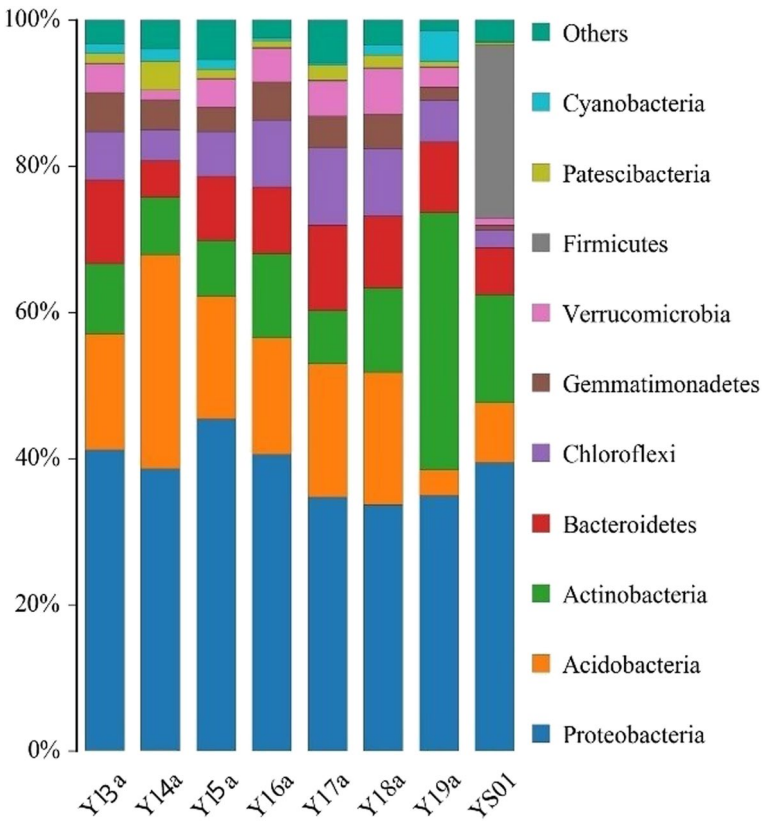

Fig. 3 Distribution map of bacterial communities at the phylum level

Chloroflexi, and Acidobacteria, while Proteobacteria, Firmicutes, and Acidobacteria were the dominant phyla in YS. Proteobacteria accounted for 39% of the soil bacteria in YS and 33%–54% of the soil bacteria in the other samples. Proteobacteria species can degrade complex pollutants and repair soil. The proportion of Acidobacteria was less than 10% in the 2019 and YS samples and more than 15% in the other samples. Actinomycetes accounted for the highest proportion of bacteria in the 2019 samples. Actinobacteria play a role in nitrogen cycling, and the proportion of Actinobacteria in native vegetation soils was approximately 6%. Firmicutes accounted for 23.7% of soil bacteria in YS and approximately 1% in the other samples.

As shown in Fig. 4, the dominant genera in the 2013–2018 soil samples were *Sphingomonas* and *Ellin6067*. In the 2019 and YS samples, *Sphingomonas* was the dominant genus. *Sphingomonas* strains have a high metabolic capacity and strong adaptability to the environment (Tai et al. 2011) and accounted for approximately 5% of the bacteria in YS and more than 6% of the bacteria in the 2013–2019 samples. The genus *Ellin6067* accounted for less than 0.01% of the bacteria in YS and between 0.1% and 7% of the bacteria in the other samples. The proportion of *Gemmatimonas (Blomonas)* in the 2011–2019 samples was more than 0.7%, while it was not found in YS.

The link between diversity and composition of bacterial communities and soil environmental variables

In this study, the physical and chemical soil properties were analyzed at the phylum and genus levels, respectively, and the analysis results are shown in Fig. 5. At the bacterial phylum level (Fig. 5a), TN, AN, and TK had longer rays, indicating that they significantly influenced the community structure at the phylum level. TP showed a significant positive correlation with the dominant Proteobacteria and a negative correlation with Actinobacteria, Bacteroidetes, and Acidobacteria. Total potassium was positively correlated with Proteobacteria, Bacteroidetes, and Acidobacteria, while Actinobacteria was positively correlated with AP and pH. At the genus level (Fig. 5b), TN, SOM, and pH had longer rays, indicating that they significantly influenced the bacterial community structure at the genus level. SOM, TP, TN, pH, and AK were positively correlated with *Ochrobactrum*, while *Sphingomonas* was positively correlated with AP and pH. Total potassium was associated with *Ferruginibacter*, *Hymenobacter*, *Terrimonas*, *Ellion6067*, and *Haliangium* but was negatively correlated with *Ochrobactrum* and

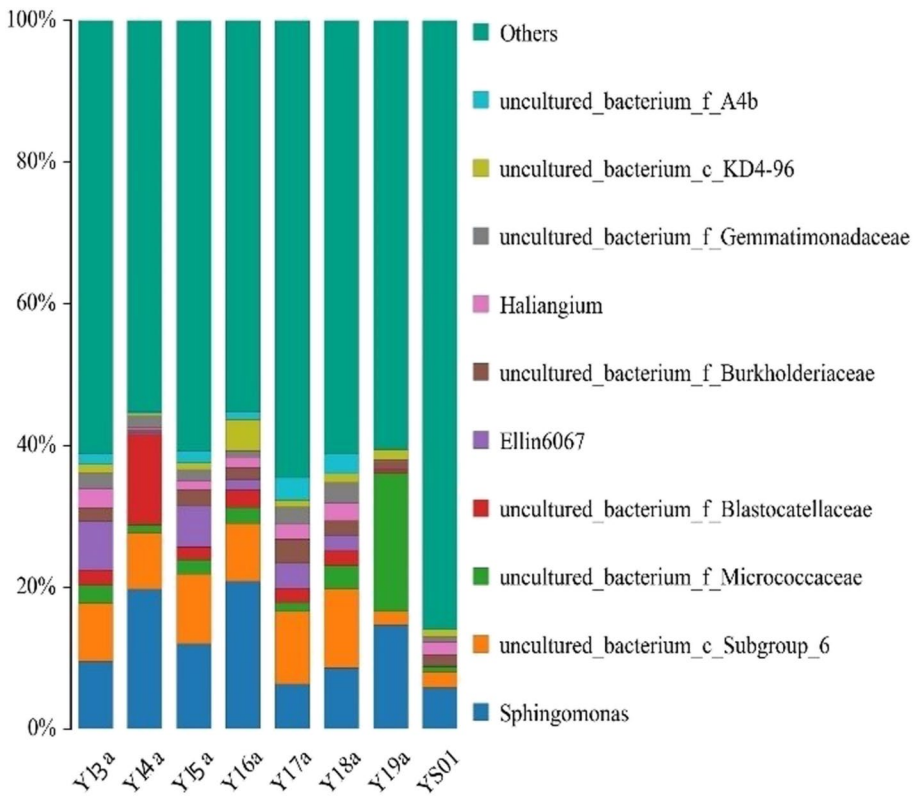

Fig. 4 Distribution of community structure of all samples at the genus level

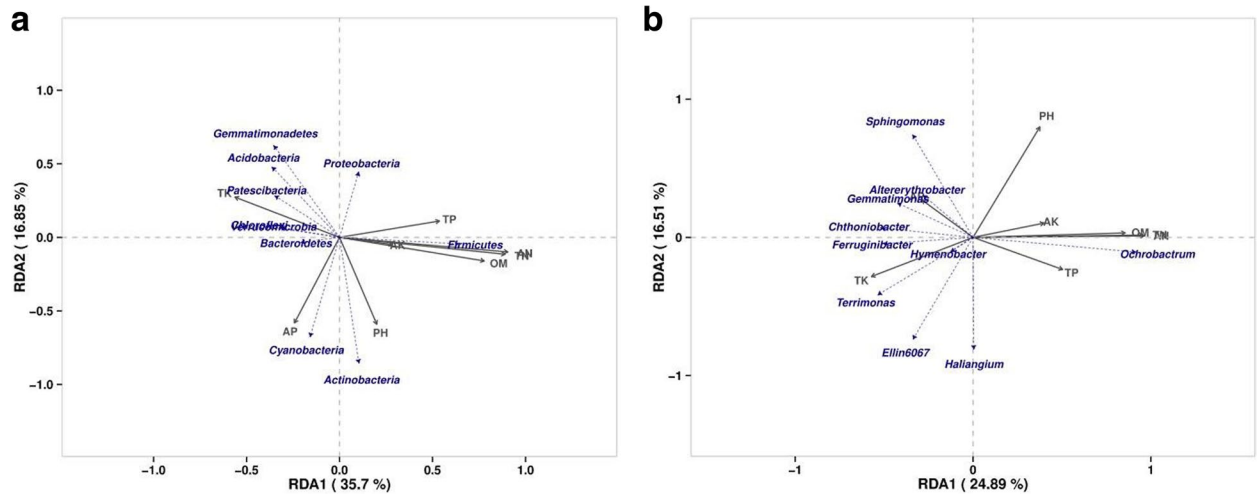

Fig. 5 RDA of soil microbial community structure and soil physicochemical properties. **a** Horizontal community structure of bacterial phylum. **b** Horizontal community structure of bacterial generic level

Sphingomonas. It can be seen that there is a specific interaction between soil bacterial community structure and the soil's physical and chemical properties in different restoration degrees of coal mine slag mountain grassland.

Linear discriminant analysis effect size

Linear discriminant analysis (LDA) effect size (LEfSe) can find important species with significant differences between groups, and the statistical results include three parts. The LDA value distribution histogram shows the significantly enriched species and their importance in each group, while the species branching evolution diagram shows the different species and their evolutionary relationships. It can be seen from Fig. 6 that there were 20 bacterial populations with significant differences in the treatment model. There were significant differences in species effect size (importance) in the top four taxa (Sphingomonadales, Sphingomonadaceae, *Sphingomonas*, and Bacteroidetes, respectively). There were 16 populations with significant differences to the control (YS). The bacteria with significant differences ranked in order of impact size (importance) were Lachnospiraceae, *uncultured-bacterium-f-SC-I-84*, *f-SC-I-84*, *uncultured-bacterium-f-SC-I-84*, and Rhizobiales. The number of microbial species significantly enriched in the treatment model was significantly higher than that in the control soil (YS).

In the treatment model, the bacterial taxa enriched with significant differences were *Sphingomonas*, *Micrococcus*, Chitinobacteriaceae, Blastocatellales, and Blastocatellaceae. In the control soil, Rokubacteriales, Firmicutes, *Clostridium*, Clostridiales, and Lachnospiraceae were the main bacterial taxa with significant differences and evolutionary relationships.

Discussion

The primary method for restoring a fragile ecosystem is to conduct revegetation restoration, which promotes the recovery of the overground and underground soil quality, so that the ecosystem of the coal mine slag mountain can reach a stable state. Soil microorganisms can reflect the soil restoration status of the ecosystem and provide a scientific basis for future restoration. The methods for studying microbial diversity include biochemical techniques, which include traditional methods and molecular phylogenetic analysis techniques, such as high-throughput sequencing. This study aimed to investigate the bacterial communities in the grassland soils of coal mine slag mountains after various periods of vegetation restoration.

Jin (2019) found that after 4 years of restoration, nutrients in the soil increased to varying degrees compared with that in the bare land in the slag mountain before restoration, which is inconsistent with the results of this experiment. We found that the levels of nutrients in the soil 1–7 years after revegetation restoration were lower than those of native soil. In addition, although the pH of the soil decreased to varying degrees after 2 years of revegetation restoration, it remained weakly alkaline. This was because that the revegetation restoration period was short, the microbial species were few, and that nutrients were not replenished in this time, resulting in poor soil nutrient content and a continuous alkaline state.

Chen Laihong et al. (Chen et al. 2012) observed that the bacterial diversity changed irregularly after various reclamation periods. In the present study, differences in

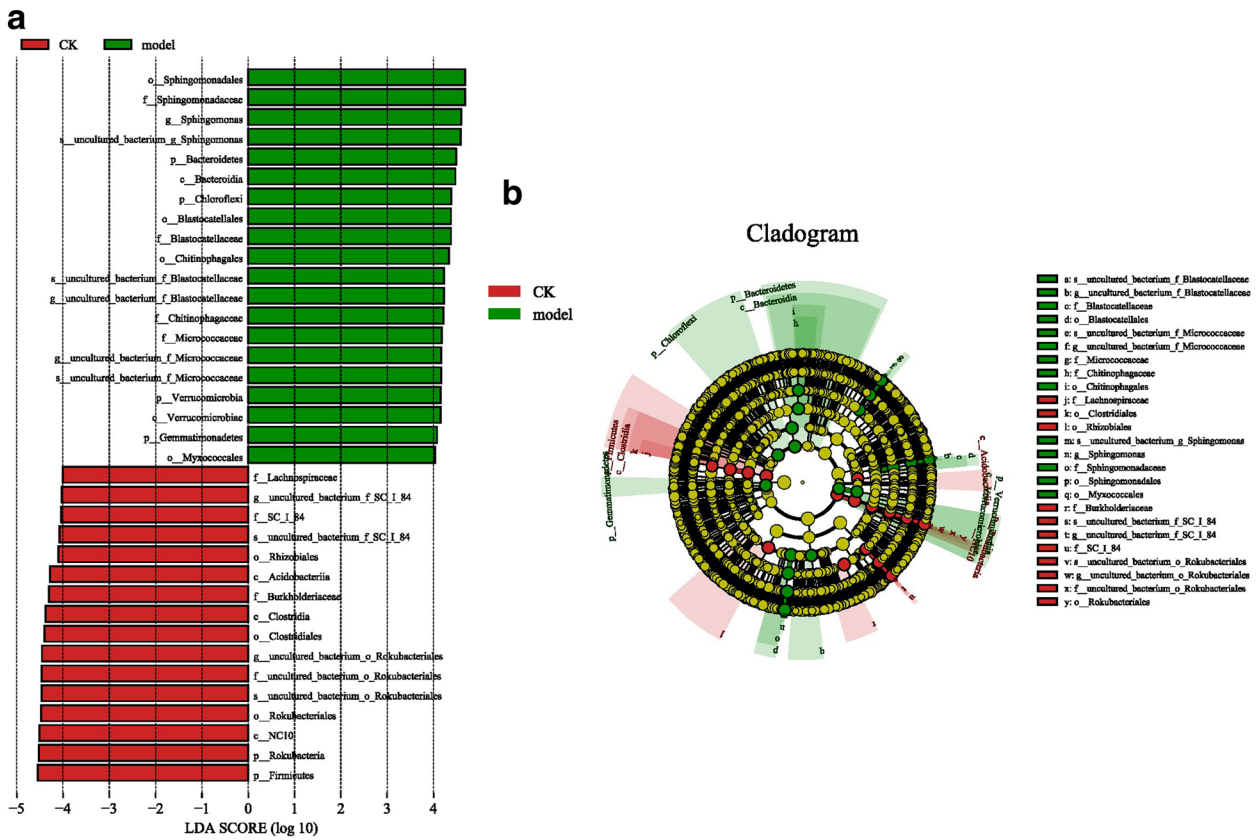

Fig. 6 Indicator microbes in groups with linear discriminant analysis (LDA) scores higher than 4. **a** LDA score of LDA effect size (LefSe). Evolutionary branch diagram of differential bacterial communities or species. **b** Cladogram of LEfSe. The size of the circle from inside to outside of the evolutionary branching graphs in a group indicates the importance of abundance from the phylum to genus or species levels, and groups with the same color indicate the importance of the phylum in this group. The LDA value (influence value of linear discriminant analysis) distribution histogram shows the bacterial community or species (biomarker) with LDA scores > 4. All the displayed bacterial communities or species exhibited significant differences among all groups. The letters k, p, c, o, f, g, and s indicate kingdom, phylum, class, order, family, genus, and species, respectively. Bacterial communities or species with significant abundance differences in different groups are shown, and the length of the histogram represents the influence of the biomarkers

microorganisms in the soil of the revegetated grassland were not evident after 4–7 years of recovery, which may be due to the slow improvement of microorganisms in the coal slag mountain due to the cold climate, shallow surface soil, and poor nutrient supply of vegetation. Dangi et al. (2012) discovered that the soil microbial structure could recover to the normal soil structure after 5–14 years of revegetation restoration. In the current study, the soil bacterial community was found to return to the normal soil structure level after 5–8 years of revegetation restoration, which is consistent with Dangi's study but differed from the findings of Kumar's study (Kumar et al. 2015) on the revegetation restoration of coal gangue mountains in India, mainly because soil microorganisms are associated with changes in various related factors in the soil and the geographical structure and climatic conditions of the study area. In the current study, we discovered that regardless of the vegetation restoration year, bacteria dominated. This finding is consistent with the research conclusions of Tan (Tan et al. 2014) and Wang (Wang et al. 2016). Overall, soil disturbances, such as cultivation and revegetation restoration, cause significant harm to fungal populations, and it is common for bacterial dominance to increase after physical disturbances. The research of Li et al. (Li et al. 2015) showed that bacteria of the green bent phylum were dominant in different soil types in the mining area, which differed from the findings of the current study. This difference may be due to the dominant species of bacteria being different due to the different types of polygreen plants, soil structure, geographical structure, and climate between the two studies. In two other previous studies (Tai et al. 2011; Jin et al. 2019), it was discovered that Proteobacteria and Actinobacteria were the dominant bacteria in samples with different years of revegetation restoration

in the slag mountain of the permafrost mining area, which was consistent with the findings of the current study, where the main microbial dominant groups in the samples with different vegetation restoration years were Proteobacteria, Actinobacteria, Bacteroidetes, Chloroflexi, and Acidobacteria at the phylum level, and *Sphingomonas*, *uncultured-bacterium-c-Subgroup-6*, and *Ellin6067* were the dominant bacteria at the genus level. Among these bacteria, *Sphingomonas* gradually became the dominant microbial group as the number of revegetation restoration years increased. *Sphingomonas* has a high metabolic capacity, multi-functional physiological characteristics and a special degradation mechanism, strong adaptability to the environment, and has great application potential in environmental protection (Yang et al. 2015). More attention should be paid to *Sphingomonas* in future mine vegetation restoration projects.

The results of this study indicated that TN, AN, and TK had a significant influence on the bacterial phylum community structure. TP was significantly positively correlated with the dominant Proteobacteria and negatively correlated with Actinobacteria, Bacteroidetes, and Acidobacteria. TK was positively correlated with Proteobacteria, Bacteroidetes, and Acidobacteria, while Actinobacteria was positively correlated with AK and pH. These results contradict those of Li et al. (2018), who found that Chloroflexi was significantly positively correlated with AK and SOM, while Actinobacteria was negatively correlated with AP, SOM, and AK, and nitrate nitrogen had little effect. Soil nutrients and structure may be altered due to the various restoration mechanisms, and soil microbes may change accordingly.

In the Jiangcang coal mine area of Qinghai Province, the bacterial species composition of grassland soil in different vegetation restoration years (from 2013 to 2019) was rich, and the microbial community composition of grassland soil was significantly different in the soil from different vegetation restoration years. Land reclamation and ecological reconstruction in mining areas should not only restore the surface vegetation and organisms but should also restore the underground ecosystem. Soil microorganisms are extremely important for the stability of soil ecosystems and their related functions. The importance of ecological indicators, such as soil microorganisms, should be noted, and a comprehensive and scientific index of land reclamation and soil quality dynamic monitoring should be established. It is necessary to grasp the changing trend of reclaimed soil quality to realize the reconstruction and coordinated development of the above- and below-ground ecosystems and realize the highly coordinated and unified ecological economy and social benefits of land reclamation in mining areas.

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Authors' contributions
Rina Dao did the field sampling and physiochemical data analysis, and wrote the draft manuscript. Ying Zhang and XiLai Li did the field sampling. Xiaolong Tie, Linxiong Ma, and Shengyan Lei supervised the project and finalized the manuscript. All authors read and approved the final manuscript.

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Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
All authors of the manuscript have read and agreed to its content and are accountable for all aspects of the accuracy and integrity of the manuscript in accordance with ICMJE criteria. That the article is original, has not already been published in a journal, and is not currently under consideration by another journal. That you agree to the terms of the BioMed Central Copyright and License Agreement.

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

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