Water Air Soil Pollut (2024) 235:519
https://doi.org/10.1007/s11270-024-07320-0

# Physical and Chemical Properties of Soils Derived from Different Parent Rocks Mediate Microbial Carbon Cycling

**Hongmei Wu · Sen Chang · Qihang Li · Heng Wang · Cheng Chen · Xuefeng Wen**

Received: 11 December 2023 / Accepted: 29 June 2024 / Published online: 12 July 2024


**Abstract** Parent rock is a key factor contributing to differences in soil physical and chemical properties. However, the mechanism of microbial carbon cycle mediated by soils with different physical and chemical properties based on parent rock are unclear. In this study, the physical and chemical properties of weathering soils of different parent rocks and the characteristics of soil carbon content were analysed. The composition of soil bacteria and fungi and the genes associated with carbon cycle were analysed via genome sequencing. The results showed that the highest abundance and diversity of soil microbes was detected in purple sandstone, followed by limestone and the least in basalt. Further, the predominant bacterial phyla in the three parent rocks were *Proteobacteria*, *Chloroflexi*, *Acidobacteria*, and *Actinobacteria*. The predominant fungi were those belonging to phyla *Basidiomycota*, *Ascomycota*, and *Mortierellomycota*. Soil organic carbon (SOC) and available nitrogen (AN), available potassium(AK) and available phosphorus (AP) were the main factors affecting the composition of soil bacteria, while soil soil water content (SWC) pH and AP were the main factors affecting the composition of soil fungi. Similarly, the relative abundance of functional genes associated with soil carbon cycle was the greatest in the purple sandstone, followed by limestone and the least in basalt. The variation in relative abundance of the genes was correlated with the soil physico-chemical properties, especially soil SWC, pH, and AP, which limited carbon metabolism of the soil microbes. Our results show that soil physical and chemical properties of the parental rock regulate microbial composition and carbon cycling.

**Keywords** Parent rock · Soil physical and chemical properties · Soil organic carbon · Microbial community composition · Carbon cycle function genes

H. Wu · S. Chang · X. Wen (✉)
College of Agriculture, Guizhou University, Guiyang 550025, Guizhou, China
e-mail: wenxuefeng104@163.com

Q. Li
College of Resource and Environment Engineering, Guizhou University, Guiyang 550025, Guizhou, China

H. Wang · C. Chen
School of Public Administration, Guizhou University of Finance and Economics, Guiyang 550025, Guizhou, China

## 1 Introduction

The global soil organic carbon (SOC) stock is three times larger than the atmospheric or biospheric carbon stock. It is the largest carbon reservoir in terrestrial ecosystems. About 1500 PgC of the global organic carbon pool is stored in the top 100 cm of soil layer, and a small variation in the SOC pool significantly affects the atmospheric $CO_2$

concentration (Amundson, 2001; Lehmann & Kleber, 2015; Schmidt et al., 2011). Therefore, fixing atmospheric $CO_2$ into the soil and increasing SOC storage to reduce $CO_2$ emissions are key challenges. Currently, soil mineral adsorption, soil aggregate encapsulation, and biochemical resistance are the primary mechanisms stabilising SOC fixation(Chen & Cui, 2022). Soil-forming parent rocks contribute significantly to soil formation and development (Vestin et al., 2006).Soil mineral composition and physico-chemical properties differ among parent rocks after soil weathering. Therefore, the parent rock regulates a series of physical, chemical, and biochemical processes of SOC transformation by influencing the physico-chemical properties of the soil, which in turn alters the SOC levels (Barré et al., 2017; Fu et al., 2023).

However, recent studies suggest that soil microorganisms also play an important role in biogeochemical processes such as elemental cycling, organic matter degradation, mineral dissolution (Fomina & Skorochod, 2020), and soil aggregate formation (Xiong et al., 2021). Whether soil is a carbon "sink" or a carbon "source" is determined by microbial catabolism (respiration) and anabolic (biomass synthesis) trade-offs (Zeng et al., 2022). In addition, recent studies suggest that microorganisms themselves are an important part of SOC stabilization. Most of the persistent carbon in the soil is produced by pumping soil microbial carbon. The dead residues of microorganisms have longer turnover time in the soil. They directly attach to the surface of mineral particles, thereby generating new organic-mineral composites that stabilise the accumulation of soil carbon pool (Ma et al., 2018).In addition, studies have shown that parent rocks affect the characteristics of soil microbial community by regulating the soil physical and chemical properties (Zhao et al., 2021). Therefore, we speculate that soil formed by the weathering of different parent rocks not only affects its physical and chemical properties, but also changes the assembly mechanism of soil bacteria. Thus, the formation, transformation, and stability of organic carbon during soil formation show specific differences. However, the dominant underlying mechanisms, especially the microbial carbon cycling mediated by the physicochemical properties of soils under specific climatic conditions in different parent rocks are rarely analysed.

In order to investigate the role of soil microorganisms in SOC accumulation, transformation and stabilisation in different matrices, the soils derived from limestone, basalt, and purple sandstone in Weining County, Guizhou Province, were selected for analysis. Active and stable components of organic carbon, and the characteristics of the soil microbial communities in different matrices were analysed. Further, the relationship between organic carbon content of each component and the physico-chemical and microbiological properties of the soil were determined via regression and redundancy analyses. The study elucidated the physico-chemical properties of soils in different matrices contributing to microbial carbon cycling. The findings serve as a standard of reference for the management of soil carbon cycle in different rocky areas.

## 2 Materials and Methods

### 2.1 Study Area

Weining County (103°36 ’-104°45’ E, 26°36 ’-27°26’ N) is located in the northwest of Guizhou Province. It is the largest and the highest county in Guizhou Province, with a total area of 6,298 sq.km. It has a subtropical monsoon humid climate, with an annual rainfall of 926 mm, a large variation in daily temperature, and an average elevation of 2,200 m. Its parent rock is mainly composed of basalt, limestone, and purple sandstone (Fig. 1). Its soil type is mainly mountain yellow brown and purple soil.

### 2.2 Sample Collection and Pretreatment

Fieldwork and sample collection were conducted in July 2022 (Table 1). We selected three different parent rocks: limestone of the Permian Maokou Formation, basalt of the Permian Emeishan Formation, and purple sandstone of the Triassic Feixianguan Formation. Two sampling points were chosen for each parent rock type. At each sampling point, three natural soil profiles were randomly excavated using a spade, with the profile depth ranging from 0–100 cm. The layers were stratified into intervals of 0–10 cm, 10–20 cm, 20–40 cm, 40–60 cm, and 60–100 cm. Soil samples from each layer were collected using a ring knife to determine the bulk density (BD) and soil

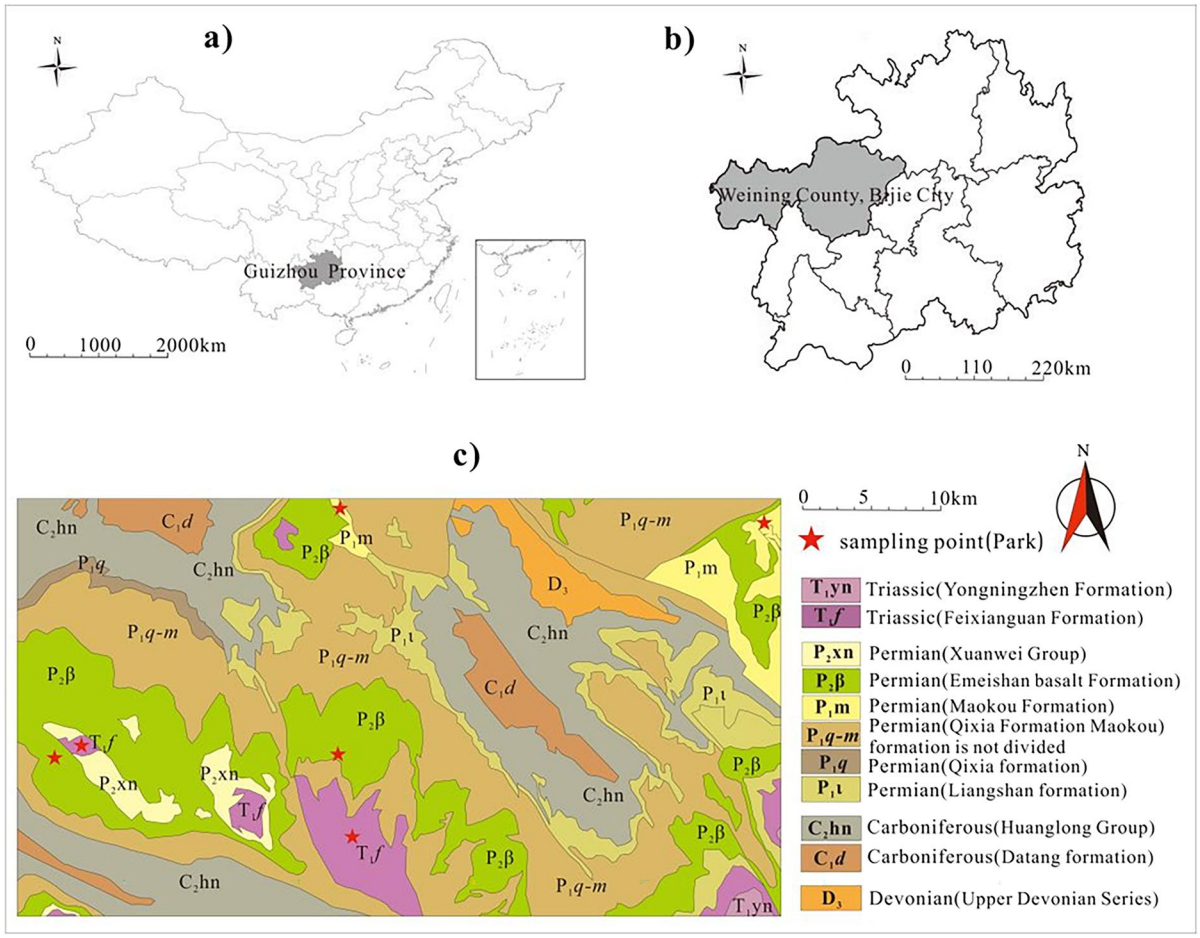


**Fig. 1** Geological sketch of the sampling area

**Table 1** Basic information of sampling points

| Sampling point number | stratum | Parent rock | Soil type | vegetation type | Longitude and latitude | Altitude (m) |
|---|---|---|---|---|---|---|
| $L_1$ | $P_1m$ | Limestone | yellow brown soil | deciduous mixed irrigation forest | 26°86′84″N, 104°65′72″E | 2290 |
| $L_2$ | | | | | 26°81′74″N, 104°38′17″E | 2148 |
| $B_1$ | $P_2\beta$ | Basalt | yellow brown soil | Evergreen coniferous forest | 26°49′35″N, 104°37′57″E | 2076 |
| $B_2$ | | | | | 26°49′28″N, 104°24′10″E | 2150 |
| $P_1$ | $T_1f$ | Purple sandstone | purple soil | Deciduous mixed irrigation forest | 26°50′16″N, 104°24′48″E | 2001 |
| $P_2$ | | | | | 26°48′14″N, 104°36′10″E | 2013 |

water content (SWC). The same soil layer from the three profiles was combined with a single soil sample in a sterile sealed bag. The sample information and number were recorded. A total of 27 soil samples were obtained, which were immediately transferred to a car refrigerator for transportation to the laboratory to remove plant roots, gravels, and other debris. Subsequently, each sample was divided into three

portions. The first portion was passed through a 2 mm sieve and stored in a refrigerator at -20 °C for 16S rRNA and its gene sequencing. The second portion was also passed through a 2 mm sieve and refrigerated at 4 °C for measuring microbial biomass carbon (MBC) and dissolved organic carbon (DOC) content. The remaining portion was air-dried and passed through a 0.15 mm and 2.00 mm sieve to measure soil pH, mineral-associated organic carbon (MOC), organic matter (SOM), available nitrogen (AN), available phosphorus (AP), and available potassium(AK).

### 2.3 Analysis of Physical and Chemical Properties of Soils

SWC was determined by drying method. BD was determined by ring knife method. SOM and SOC were estimated by potassium dichromate-external heating method. DOC was determined by extraction method. AN levels were measured by alkaline dissolution diffusion. AP was determined by $NaHCO_3$ leaching-molybdenum antimony antimony colorimetry. AK levels were measured by neutral $NH_4OAc$ leaching-flame photometry. Soil pH was determined via potentiometric methods used to determine soil pH (soil–water ratio = 1:5, M/V) (Li et al., 2015).

MOC was determined via chemical separation (Eusterhues et al., 2003), weighing 3.00 g of air-dried soil through a 0.15 mm sieve. It was transferred to a 100 ml centrifuge tube, and mixed with 25 ml of 10 mol/L HF/1 mol/L HCl (2:1, V/V) for 24 h. The centrifuge tube was washed 3 to 5 times with distilled water followed by centrifugation. The supernatant was mixed with 15 mL of 10 mol $L^{-1}$ HCl and left to stand for 24 h. The washing step was repeated 3 to 5 times. The final precipitate obtained was dried at 60ºC, weighed, and then filtered through a 0.15 mm sieve. The organic carbon content was determined and designated as nMOC (organic carbon not bound to minerals), whereas MOC refers to the organic carbon lost during HF treatment. The MOC content is equal to the total organic carbon content minus the nMOC content.

MBC levels was determined via chloroform fumigation leaching method. Fresh soil samples weighing > 10.00 g (Calculate the weight of fresh soil for 10 g of dry soil according to the conversion formula for fresh and dry soil) were transferred to 50 ml beakers for determination of MBC levels via chloroform fumigation leaching method. The soil moisture content was adjusted to about 45% of the water holding capacity of the field. The beaker was then incubated with shaking. A beaker containing 50 ml of deionised water and a beaker with 50 ml of 0.1 mol/L NaOH (to maintain the air humidity in the incubator bottle and to absorb released $CO_2$) were pre-culture for 7 days under dark at 25ºC.The samples were then removed and transferred to a vacuum desiccator in a beaker containing 50 mL of de-ionised water and a beaker containing approximately 50 ml of chloroform (with glass beads to prevent boiling) at the bottom of the desiccator. The rim of the desiccator was coated with petroleum jelly and closed with a lid. The chloroform at the bottom of the desiccator was allowed to boil using a vacuum pump for 5 min, and the process was repeated three times. The vacuum desiccator was transferred to a 25ºC incubator and incubated under dark conditions for 24 h, after which the soil was again repeatedly pumped with a vacuum pump until the chloroform flavour was completely removed from the soil. At the end of the fumigation, all the soil was transferred to a 100 mL plastic shock bottle containing 40 ml of 0.5 mol/L $K_2SO_4$ solution (1:4 soil–water ratio). The extract was shaken and leached for 30 min on an oscillator and then filtered, and the filtrate was measured immediately. Carbon in the extract was determined via $K_2Cr_2O_7$-$H_2SO_4$ external heating method (Islam et al., 1997). The conversion factor used to determine the microbiological amount of carbon was 0.45(Islam et al., 1997; Liang et al., 2010; Witt et al., 2000).

### 2.4 DNA Extraction and Bioinformatics Analysis

Total bacterial and fungal DNA was extracted from soil samples using the Fast DNA® spin kit extraction kit (MP Biomedicals, Cleveland, Ohio, USA), according to the manufacturer's instructions. Bacterial primers 388F (ACTCCTACGGGGAGGCAGCA) and 806R (GGACTACHVGGGTWTCTAAT) were used to amplify the standard bacterial 16S V3V4(a) region. Fungal primers Tts5F (GGAAGTAAAAGTCGT AACAAGG) and Its1R (GCTGCGTTCTTCATC GATGC) were used to amplify the standard fungal ITS1(a) region. The products obtained were recovered, purified, quantified, and homogenised using a PCR product purification kit to develop sequencing libraries (recovery concentration > 0.5 ng/μL required

for library construction). The libraries that passed the quality control were sequenced using the NovaSeqPE250 platform at Shanghai Personalbio Technology Co., Ltd. (Shanghai, China).

Sequencing raw data were saved in FASTQ format. The primer fragments of sequences were excised with qiime cutadapt trim-paired in the QIIME2 (2019.4) analytical software. The sequences with unmatched primers were discarded. DADA2 was used for qiime dada2 denoise-paired quality control, denoising, splicing, and de-chimerisation; to obtain clusters of high-quality sequences at 97% similarity using Vsearch; and obtain the representative sequences and OTU tables (Callahan et al., 2016). Based on the bacterial 16S rRNA: Greengenes (http://greengenes.secondgenome.com/) (DeSantis et al., 2006) and fungal ITS: UNITE (https://unite.ut.ee/) (Kõljalg et al., 2013), taxonomic databases were obtained for taxonomic annotation of OTUs.

### 2.5 Statistical Analysis

BM SPSS Statistics version 26.0 was used to determine the soil physicochemical parameters and the microbial diversity index. Origin 2018 and Corel Draw 2018 were used to analyse and obtain the histogram of soil carbon content. The ASV/OTU table after draw levelling was used to calculate the Bray–Curtis distance matrix. The PCoA coordinates of the sample points were determined using R scripts for PCoA analysis in R language and plotted as a two-dimensional scatter plot. Percentage stacked histograms were obtained using QIIME2 (2019.4) to determine species composition, and self-written perl scripts were developed to analyse microbial species composition. PICRUSt2 was used to predict the potential metabolic function of the microbial community. The genes related to carbon cycling (carbon metabolism and carbon fixation) were identified based on the KEGG database. Vegan software package was utilised to plot heat maps of genes related to carbon cycling. Pearson's correlation analysis of soil physicochemical properties and genes related to carbon cycling was conducted ($p < 0.05$ or 0.01). Redundancy analysis (RDA) of dominant OTUs and soil physicochemical parameters was performed using CANOCO for Windows 5.0 (Ithaca, NY, US) to determine the effects of soil parameters on bacterial and fungal community structure.

## 3 Results

### 3.1 Soil Physical and Chemical Properties and Organic Carbon Characteristics

The physico-chemical properties of soil differ among different parent rocks. The limestone soil had the highest levels of SM, SOM, AN, and AK. The basalt soil had significantly higher BD than the other parent rocks ($P < 0.05$) but the lowest levels of AP. In contrast; the purple sandstone had the highest levels of AP, but the lowest levels of SWC and SOM. In addition, the soil pH (6.08–6.80) of purple sandstone was weakly acidic-to-neutral, while the soil pH (5.29–6.16) of limestone and basalt were acidic (Table 2). This indicates that the physico-chemical properties of the soils differ significantly between different parent rocks and that the nutrient content is unbalanced.

The soil carbon content also varied because the soil-forming parent rock determines the physicochemical properties of the soil. The soil carbon content of all three parent rocks showed a decreasing trend with increasing soil depth vertically (Fig. 2).The SOC content ranges of limestone, basalt, and purple sandstone were 11.67–38.54 g/kg, 9.76–32.99 g/kg, and 8.67–23.47 g/kg, respectively. The ranges of MBC content were 96.65–320.02 mg/kg, 84.83–287.60 mg/kg, 50.87–187.46 mg/kg, respectively. The DOC content ranged from 32.00–154.80 mg/kg, 5.72 -115.60 mg/kg, and 3.99–70.00 mg/kg, respectively. The soil carbon content decreased in the following order: limestone > basalt > purple sandstone. In addition, the MOC levels of inert organic carbon fractions of limestone, basalt and purple sandstone ranged from 2.44–8.25 g/kg, 2.92–9.64 g/kg, and 2.17 -5.87 g/kg, respectively, with basalt soils containing the highest MOC content, followed by limestone, and purple sandstone containing the least amount.

### 3.2 Characteristics of Diverse Soil Microbial Communities

Microbial alpha diversity emphasises the heterogeneity within the microbial community. The higher the alpha diversity, the more stable the microbial community is likely to be (Whittaker, 1972). The microbial alpha diversity of all soil samples varied (Table 3). The Chaol index, Shannon index and

**Table 2** Physico-chemical properties of soils derived from different parent rocks

| Parent rock grouping | Soil depth (cm) | SWC (%) | BD (g/cm$^3$) | pH | SOM(g/kg) | AN(mg/kg) | AP(mg/kg) | AK(mg/kg) |
|---|---|---|---|---|---|---|---|---|
| Limestone | 0–10 | 40 ± 0.00aA | 0.95 ± 0.02dC | 5.77 ± 0.01cB | 66.66 ± 0.12aA | 118.41 ± 2.25aA | 7.20 ± 0.25aB | 261.33 ± 0.29aA |
| | 10–20 | 39 ± 0.00bA | 1.07 ± 0.04cB | 5.95 ± 0.01bB | 57.08 ± 2.27bA | 114.18 ± 2.82aA | 6.84 ± 0.38aB | 226.46 ± 4.08bA |
| | 20–40 | 35 ± 0.00cA | 1.17 ± 0.01bB | 5.96 ± 0.01bB | 46.72 ± 0.56cA | 90.43 ± 4.88bA | 3.3 ± 0.17bB | 100.64 ± 0.29cA |
| | 40–60 | 27 ± 0.00 dB | 1.21 ± 0.02bC | 6.16 ± 0.03aB | 44.3 ± 2.51cA | 62.78 ± 2.82cA | 2.75 ± 0.02bcB | 72.85 ± 0.29 dB |
| | 60–100 | 22 ± 0.00eB | 1.32 ± 0.00aB | 5.38 ± 0.02dC | 20.12 ± 0.77dA | 36.92 ± 0.47dA | 2.57 ± 0.08cB | 62.24 ± 3.50eB |
| Basalt | 0–10 | 38 ± 0.01aB | 1.04 ± 0.00eB | 5.33 ± 0.01cC | 56.88 ± 1.84aB | 56.28 ± 0.56aB | 10.45 ± 0.08aA | 78.91 ± 0.59aC |
| | 10–20 | 33 ± 0.00bB | 1.06 ± 0.01 dB | 5.29 ± 0.00cC | 37.30 ± 1.45bB | 28.95 ± 2.07bC | 1.74 ± 0.15cC | 61.73 ± 0.87 dB |
| | 20–40 | 33 ± 0.00bB | 1.11 ± 0.01cB | 5.48 ± 0.08bC | 26.62 ± 0.69cB | 25.05 ± 2.44bcC | 1.81 ± 0.02cC | 65.27 ± 0.87cB |
| | 40–60 | 31 ± 0.01cA | 1.30 ± 0.01bB | 5.84 ± 0.02aC | 22.22 ± 1.03 dB | 24.07 ± 1.13bcB | 1.85 ± 0.13cC | 74.62 ± 0.44bA |
| | 60–100 | 27 ± 0.01dA | 1.32 ± 0.01aB | 5.92 ± 0.01aB | 16.83 ± 0.43eB | 22.77 ± 0cB | 2.97 ± 0.02bB | 76.64 ± 0.44bA |
| Purple sandstone | 0–10 | 19 ± 0.01aC | 1.27 ± 0.00eA | 6.08 ± 0.00dA | 40.41 ± 1.03aC | 41.31 ± 0.56bC | 7.67 ± 0.31 dB | 81.69 ± 1.02aB |
| | 10–20 | 18 ± 0.01aC | 1.38 ± 0.01dA | 6.16 ± 0.01cdA | 21.47 ± 0.20bC | 41.96 ± 2.07bB | 12.22 ± 0.10aA | 48.09 ± 0.58bC |
| | 20–40 | 16 ± 0.00bC | 1.43 ± 0.01cA | 6.24 ± 0.00bcA | 20.28 ± 1.07bC | 54.86 ± 8.35aB | 10.6 ± 0.50bA | 36.97 ± 0.58cC |
| | 40–60 | 16 ± 0.00bC | 1.56 ± 0.01bA | 6.80 ± 0.00aA | 17.44 ± 0.03cB | 24.40 ± 0.19cB | 8.68 ± 0.10cA | 30.41 ± 0.29dC |
| | 60–100 | 14 ± 0.01cC | 1.64 ± 0.01aA | 6.31 ± 0.10bA | 14.97 ± 0.16dC | 17.49 ± 0.33cC | 10.38 ± 0.21bA | 34.45 ± 1.46cC |

Values are mean ± standard error (mean ± SE)($n = 3$). Statistical significance was assessed by one-way analysis of variance followed by LSD multiple comparison tests. Different lowercase letters in each column indicate significant differences in an index between different soil layers of the same parent rock. Different uppercase letters in the same column indicate significant differences in an index between different mother rocks of the same soil layer ($P < 0.05$). The same below

Pielous evenness index of bacteria and fungi in purple sandstone were significantly higher than in limestone and basalt ($P < 0.05$), indicating that the richness, diversity and evenness of soil bacterial and fungal communities in purple sandstone were the highest, followed by limestone and basalt. In addition, the bacterial Goods coverage index of basalt was significantly higher than that of the other two types of rocks, indicating that the bacterial community coverage of basalt was the highest. However, no significant difference was found in the Goods coverage index of the developing soil fungi of the three parent rocks.

Beta diversity refers to the degree of similarity and differences between microbial communities (Whittaker, 1960). PCoA analysis reveals the similarities and dissimilarities of microbial communities between soils derived from different parent rocks. (Fig. 3).The scattered distribution of limestone indicates that the soil bacterial community levels varied between the surface (0–20 cm) and the bottom locations (20–100 cm). However; the distribution of basalt and purple sandstone was more concentrated, and the projection distance between the two was farther away along the PCo1, which indicates significant differences in the bacterial species composition. The difference in species composition based on the principal components of PCo1 was 37.4%. The fungal communities of limestone, basalt and purple sandstone included three independent assemblages separated between the first and second coordinates. The purple sandstone and basalt soil fungi were projected farther away from each other along the first coordinate. The PCoA1 principal component explained 23.6% of the difference in fungal species composition. The purple sandstone and limestone bacterial species were projected farther away from each other on the second coordinate axis and the explanation degree of PCoA2 principal component was 19.7%.

### 3.3 Characteristics of Soil Microbial Community Composition

The predominant bacterial phyla in the limestone soil were *Proteobacteria* (21.77–46.19%), *Chloroflexi* (11.27–26.08%), and *Acidobacteria* (7.83–25.90%). The dominant bacterial phyla in the basalt soil were *Proteobacteria* (65.07–89.68%), *Chloroflexi* (4.03–22.78%), and GAL15 (1.25–8.03%). The dominant bacterial phylum in the purple sandstone soil were *Proteobacteria* (25.45–30.25%), *Actinobacteria* (15.91–29.71%), and *Acidobacteria* (8.69–20.12%) (Fig. 4 A and B).The dominant fungal phyla in the limestone soil were *Basidiomycota* (65.14–89.58%),

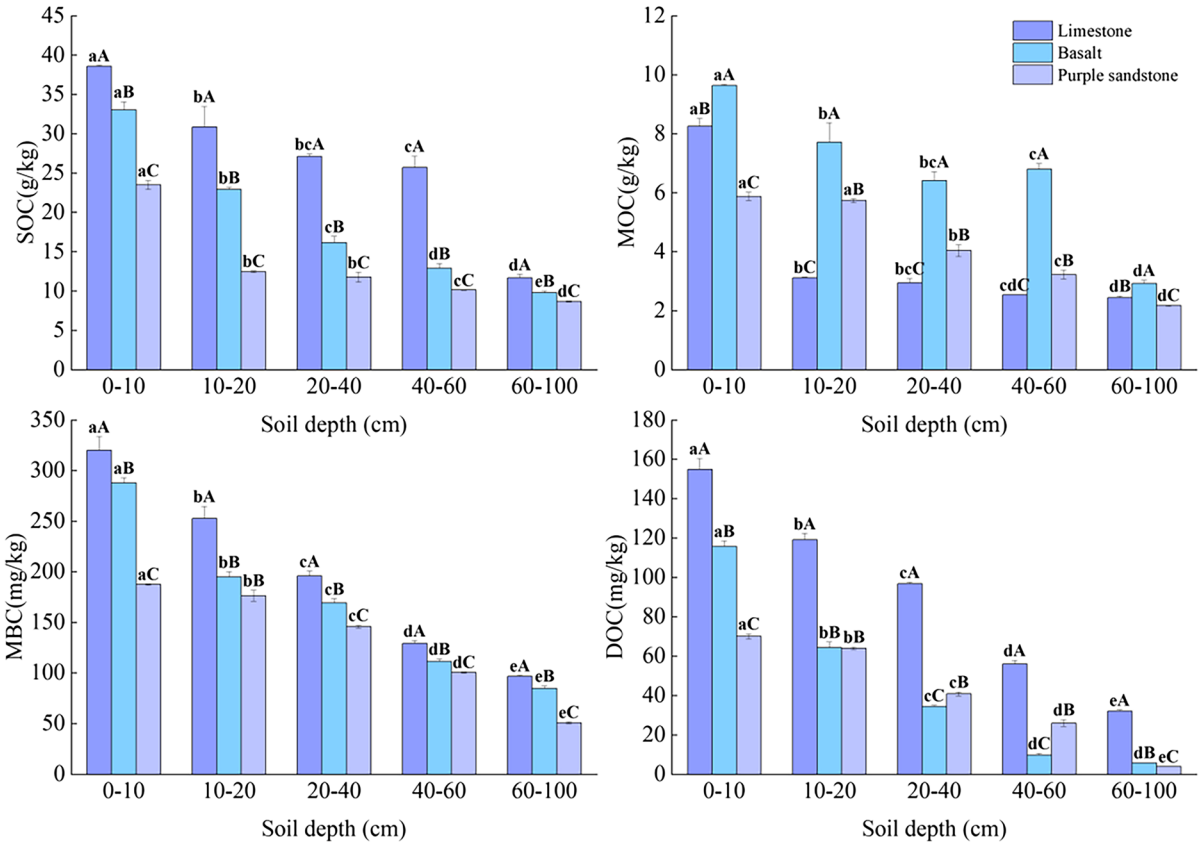


**Fig.2** Contents of soil organic carbon and carbon components in different parent rocks

**Table 3** Microbial alpha diversity in soil profiles with different parent rock development

| Parent rock grouping | Soil depth (cm) | bacteria | | | | Fungi | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Chao1 | Shannon | Goods coverage | Pielous evenness | Chao1 | Shannon | Goods coverage | Pielous evenness |
| Limestone | 0–10 | 2943.65 ± 1.71aB | 10.28 ± 0.14aB | 0.9978 ± 0.00bB | 0.89 ± 0.00bB | 341.33 ± 1.42aB | 3.90 ± 0.09aB | 0.9996 ± 0.00bB | 0.47 ± 0.00bB |
| | 10–20 | 3418.38 ± 1.81bB | 10.62 ± 0.10aA | 0.9960 ± 0.00cB | 0.91 ± 0.00aA | 292.36 ± 1.29bB | 3.67 ± 0.23abB | 0.9997 ± 0.00bA | 0.45 ± 0.00cB |
| | 20–40 | 2201.84 ± 1.33cB | 9.48 ± 0.10bB | 0.9971 ± 0.00bB | 0.86 ± 0.00cB | 176.64 ± 1.18cA | 2.61 ± 0.10cB | 0.9999 ± 0.00aA | 0.35 ± 0.00 dB |
| | 40–60 | 1284.73 ± 2.48 dB | 8.19 ± 0.10cB | 0.9989 ± 0.00aB | 0.79 ± 0.00 dB | 118.14 ± 1.03dC | 1.28 ± 0.10dC | 0.9999 ± 0.00aA | 0.19 ± 0.00eC |
| | 60–100 | 455.45 ± 1.71eB | 6.91 ± 0.11 dB | 0.9997 ± 0.00aA | 0.78 ± 0.00eB | 95.39 ± 0.99eC | 3.39 ± 0.09bB | 0.9999 ± 0.00aA | 0.52 ± 0.00aB |
| Basalt | 0–10 | 229.77 ± 3.03aC | 5.40 ± 0.10aC | 0.9999 ± 0.00aA | 0.69 ± 0.00bC | 97.70 ± 1.46eC | 3.02 ± 0.09bC | 0.9999 ± 0.00aA | 0.46 ± 0.00aC |
| | 10–20 | 206.9 ± 2.16bC | 5.41 ± 0.08aB | 0.9997 ± 0.00aA | 0.71 ± 0.00aB | 150.76 ± 1.18cC | 2.44 ± 0.07cC | 0.9998 ± 0.00aA | 0.34 ± 0.00cC |
| | 20–40 | 95.32 ± 1.11dC | 4.17 ± 0.09cC | 0.9998 ± 0.00aA | 0.64 ± 0.00cC | 111.54 ± 0.96dC | 1.53 ± 0.06dC | 0.9999 ± 0.00aA | 0.22 ± 0.00eC |
| | 40–60 | 173.57 ± 2.02cC | 4.73 ± 0.05bC | 0.9997 ± 0.00aA | 0.64 ± 0.00dC | 176.56 ± 1.01bB | 2.3 ± 0.07cB | 0.9998 ± 0.00aB | 0.31 ± 0.00 dB |
| | 60–100 | 92.75 ± 1.30dC | 3.41 ± 0.08dC | 0.9998 ± 0.00aA | 0.53 ± 0.00eC | 308.26 ± 1.17aB | 3.69 ± 0.11aB | 0.9996 ± 0.00bB | 0.45 ± 0.00bC |
| Purple sandstone | 0–10 | 4261.99 ± 1.68aA | 10.78 ± 0.11aA | 0.9923 ± 0.00dC | 0.90 ± 0.00bA | 650.01 ± 1.18aA | 6.09 ± 0.12bA | 0.9995 ± 0.00aB | 0.65 ± 0.00eA |
| | 10–20 | 3974.62 ± 4.04bA | 10.78 ± 0.11aA | 0.9940 ± 0.00cC | 0.90 ± 0.00aA | 313.40 ± 1.6dA | 6.46 ± 0.10aA | 0.9999 ± 0.00aA | 0.78 ± 0.00aA |
| | 20–40 | 3007.24 ± 1.18cA | 10.28 ± 0.08bA | 0.9975 ± 0.00bB | 0.89 ± 0.00cA | 165.50 ± 1.24eB | 4.99 ± 0.10cA | 0.9998 ± 0.00aA | 0.68 ± 0.00cA |
| | 40–60 | 1990.01 ± 2.09eA | 9.60 ± 0.05dA | 0.9983 ± 0.00aB | 0.88 ± 0.00eA | 606.14 ± 0.90cA | 6.27 ± 0.09abA | 0.9997 ± 0.00aC | 0.68 ± 0.00dA |
| | 60–100 | 2381.19 ± 1.20dA | 9.88 ± 0.07cA | 0.9975 ± 0.00bB | 0.88 ± 0.00dA | 626.61 ± 1.01bA | 6.4 ± 0.08abA | 0.9997 ± 0.00aAB | 0.69 ± 0.00bA |

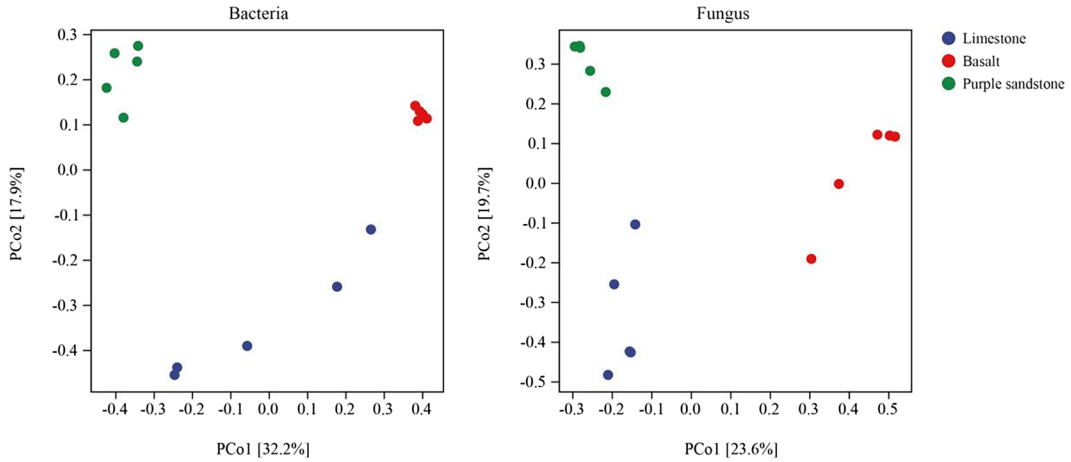


**Fig. 3** Results of PCoA analyses of microbial communities in soil developed from different parent rocks

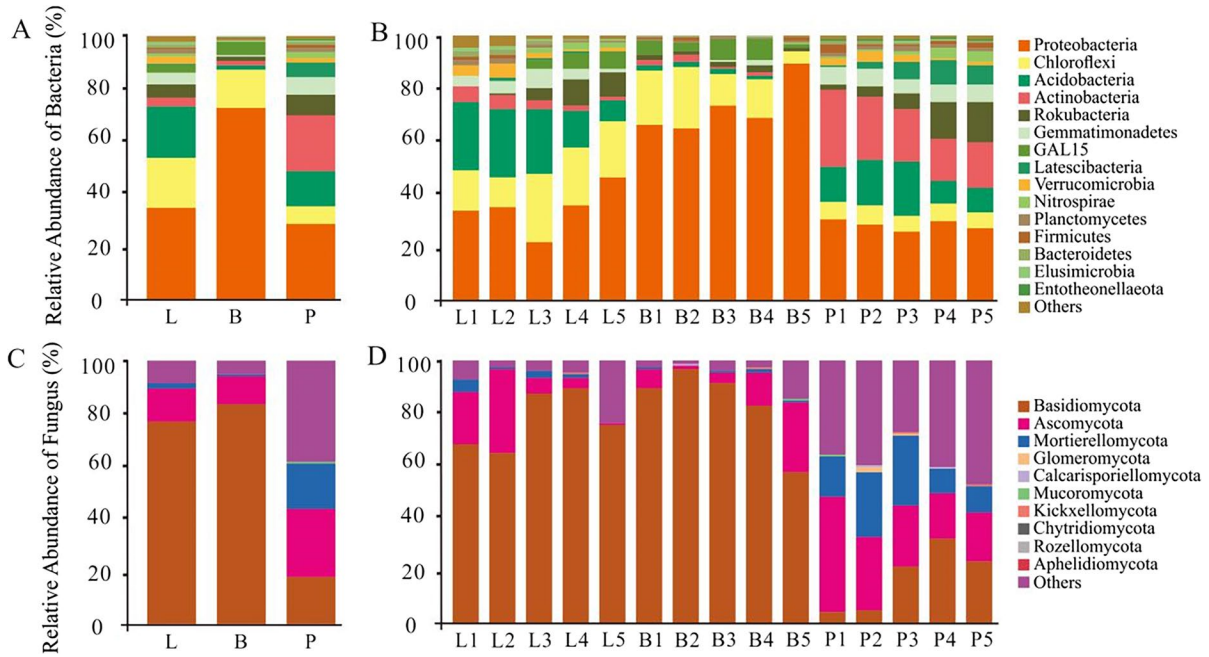


**Fig. 4** Composition of microbial communities in soil with different parent rock development. Note: L, B and P represent the soil profiles of limestone, basalt and purple sandstone respectively; L1-L5, B1-B5, and P1-P5 represent different soil depths of the corresponding parent rock development soil profile, namely 0–10 cm, 10–20 cm, 20-40 cm, 40–60 cm, and 60–100 cm. The same below

*Ascomycota* (0.61–31.55%), and *Mortierellomycota* (0.06–4.67%). The dominant fungal phyla in the basalt soil were *Basidiomycota* (57.84–96.96%), Ascomycota (1.08–26.42%), and *Mortierellomycota* (0.31–1.35%). The dominant fungal phyla in the purple sandstone soil were *Ascomycota* (17.51–43.95%), *Basidiomycota* (4.40–32.10%), and *Mortierellomycota* (9.49–26.51%) (Fig. 4 C and D). At the phylum level, *Proteobacteria* bacteria and *Basidiomycota* fungi were the most abundant groups in almost all soil samples.

### 3.4 Relationship Between Edaphic Characteristics and Microbes

According to the RDA map, the two first axes explained 73.81% and 85.77% of the variation in bacterial and fungal community structure, respectively (Fig. 5).The main soil variables affecting soil bacterial community composition were SWC ($r^2=0.67$, $p=0.002$), BD ($r^2=0.70$, $p=0.002$), pH ($r^2=0.59$, $p=0.005$), SOM ($r^2=0.42$, $p=0.035$), AN ($r^2=0.60$, $p=0.006$), AP ($r^2=0.56$ $p=0.012$), SOC ($r^2=0.42$, $p=0.031$), and DOC ($r^2=0.39$, $p=0.044$). The main soil parameters affecting the soil fungal composition of the 16 phyla in all soil samples were: SWC ($r^2=0.85$, $p=0.001$), pH ($r^2=0.46$, $p=0.025$), SOM ($r^2=0.43$, $p=0.034$), AP ($r^2=0.54$, $p=0.011$), AK ($r^2=0.52$, $p=0.012$) and SOC ($r^2=0.41$, $p=0.036$), which were significantly correlated, indicating that soil physico-chemical properties were the main drivers influencing the dominant soil microbial communities.

### 3.5 Characterization of Functional Genes Associated With Soil Microbial Carbon Cycling

In order to further understand the differences in the function of microbial communities in soils derived from different parent rocks, PICRUSt2 was used to predict the functional annotation of microbial communities. A total of 188 functional groups were obtained after functional annotation. The genes associated with carbohydrate metabolism and carbon fixation were identified according to the KEGG database. Among them, the relative abundance of soil microbial carbon in purple sandstone was the highest, followed by limestone, and basalt was the least (Fig. 6).

The abundance of different functional genes in the microbial carbon cycle correlated with soil physico-chemical parameters (Fig. 6). Specifically, SWC, BD, pH, SOM, AN, AP, MOC, AK, SOC, MBC, and DOC were significantly correlated ($p=0.05$ or 0.01) with the abundance of genes related to microbial carbon cycling.

## 4 Discussion

### 4.1 Differences in Physical and Chemical Properties and Soil Carbon Content of Parent Rocks

The limestone soils in this study were acidic, with a heavy clayey soil texture and the highest soil carbon content (Table 2).Limestone soils are generally

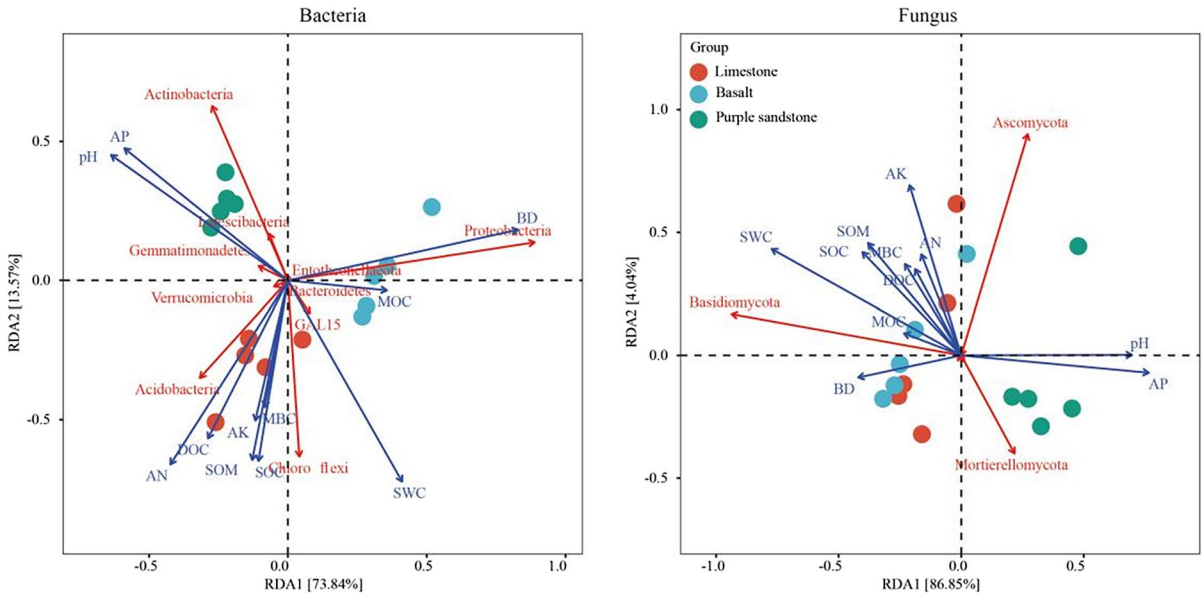


**Fig. 5** RDA analysis of soil microorganisms and soil environmental factors

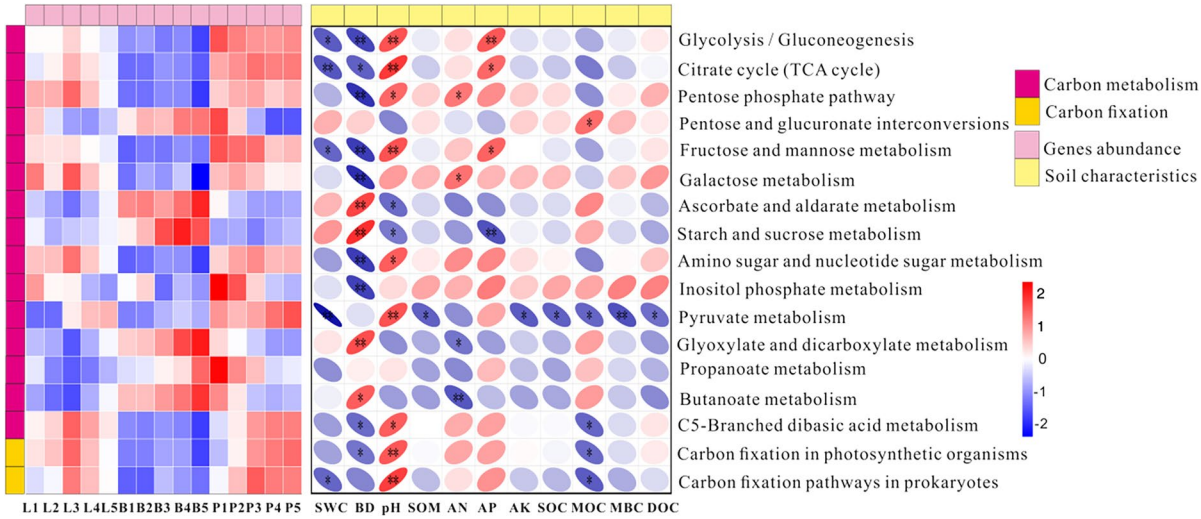


**Fig. 6** Heat map showing differences in relative abundance of carbon cycle functional genes in the KEGG database for soil microbial genomes from different parent rocks. Note: The colours represent the values of Pearson correlation coefficients, red means positive correlation, blue means negative correlation; * means $p \leq 0.05$, ** means $p \leq 0.01$

alkaline. However, the limestone soil pH is weakly acidic due to better hydrothermal conditions in the study area, severe desilication, and iron-rich aluminisation of the soils (Table 2).In addition, the high organic carbon content of limestone soils may be related to the high $Ca^{2+}$ and $Mg^{2+}$ levels of limestone weathered soils. $Ca^{2+}$ and $Mg^{2+}$ in soil solution can act as cationic bridges between negatively-charged carboxyl groups and negatively-charged adsorption sites on the soil surface (Mouvenchery et al., 2012). On the other hand, $Ca^{2+}$ and $Mg^{2+}$ facilitate the formation and stabilisation of soil macroaggregates (Bimüller et al., 2016). Their interactions reinforce the physical and chemical protection of soil against organic carbon. Therefore, limestone soils are considered to have a greater potential for organic carbon accumulation.

The basalt soils were also acidic, with a clayey texture and relatively high soil SOC and MOC content (Table 2).The high soil carbon content of basalt soils may be related to their iron and aluminium oxide levels, and soil iron oxides represent an important inorganic cement that binds fine particles to inorganic or organic molecules to form agglomerates (Mao, 2021, McNally et al., 2017). Soil aggregates can reduce the degree of organic carbon contact with soil microorganisms and enzymes, and thus enhance the physical shielding of organic carbon (Yang et al., 2023). In addition, soil Fe and Al oxides carry a large specific surface area and abundant hydroxyl sites, especially in acidic soil, and the low pH leads to protonation of hydroxyl groups on the surface of Fe and Al oxides, enhancing their ability to adsorb SOC (Chen & Cui, 2022). It can be seen that basalt-developed soil also has great potential in organic carbon accumulation. Previous studies have also shown that basalt weathering is a major carbon sequestration process of atmospheric $CO_2$ (Du et al., 2012). For example, the application of weathering mineral rock (basalt) clasts to farmland can enhance the effect of anthropogenic carbon sequestration (Wu et al., 2023).

The purple sandstone soil is neutral, with few soil nutrient levels and low soil carbon content (Table 2). This phenomenon may be due to the unique porosity and structure of sandstone, which leads to relatively sandy texture after weathering, resulting in a large loss of soil nutrients (Wang et al., 2018). In addition, the weathering of purple sandstone into soil leads to basically coarse bone soil, soil porosity and permeability, and strong microbial activity (Mao, 2021). Combined with few soil clay particles and weak physical strength of soil aggregates, the weathered purple sandstone soil exhibits rapid microbial decomposition of SOM and hinders the accumulation of organic carbon.

### 4.2 Differences in Microbial Communities in Soils Derived from Different Parent Rocks

In this study, the richness, diversity and evenness of soil bacterial and fungal communities in purple sandstone were the highest, followed by limestone and basalt (Table 3). Significant differences in soil microbial communities are associated with changes in specific soil characteristics. The higher microbial diversity of limestone soils may be attributed to the stable environment provided by soil microaggregates for microorganisms and their protection against predators in the soil. Therefore, small aggregates are more conducive to maintaining microbial diversity (Rashid et al., 2016).However, clay particles in basalt soil and micro-agglomerates were equally abundant, whereas the microbial diversity was the least, which may be related to the acidic nature of the soil and the high content of iron and aluminium ions. Aluminium ions may have a limiting effect on microorganisms in acidic soils (Tonneijck et al., 2010). In addition, microbial diversity was the highest in purple sandstone soil with low clay particle content, possibly due to increased competition resulting from nutrient deficiencies in purple sandstone soil, which exacerbated species replacement among communities (Qiu et al., 2020), and was more favourable for microbial activity in neutral soil environments (Averill & Waring, 2018). Neutral soils are generally unsuitable for most mineral adsorption mechanisms (Whittinghill & Hobbie, 2012), but provide the optimum pH for SOC mineralisation. Therefore, the organic matter of sandstone soils can be decomposed by microorganisms, resulting in decreased soil carbon content.

The dominant soil bacterial communities in the three parent rocks were *Proteobacteria*, *Chloroflexi*, *Acidobacteria*, and *Actinobacteria*, and the dominant fungal phyla were *Basidiomycota*, *Ascomycota*, and *Mortierellomycota* (Fig. 4). It may be attributed to the wider ecological niche of *Proteobacteria*, *Chloroflexi* and *Acidobacteria* and stronger adaptation to different soil environments as the dominant taxa (Davinic et al., 2012).In addition, soil properties play a key role in determining microbial composition (Sun et al., 2021; Zhu et al., 2021). In this study, we found that the development of soil bacteria in soils from different parent rocks was closely related to soil carbon and AN, AP and AK levels. The strong correlation between soil nutrient levels and bacterial distribution could be explained by the copiotrophic-oligotrophic strategies of soil bacteria. For example, *Proteobacteria* and *Actinobacteria* carry common nutrient profiles and were enriched in soils with high nutrient levels (Qu et al., 2020; Zheng, 2022). Thus the abundance of *Proteobacteria* was the highest in limestone and basalt soils, while *Actinobacteria* levels were significantly correlated with soil AP ($p = 0.05$). The abundance of *Actinobacteria* was the highest in purple sandstone soils (Fig. 5). In contrast, members of the phyla *Acidobacteria* and *Chloroflexi* exhibited poor trophic biostrategy (Gao et al., 2021; Zhang et al., 2019), and thus their abundance was the highest in purple sandstone soils.

In addition, SWC, pH and AP had the most significant effects on the fungal community (Fig. 5), which was consistent with previous studies (Cui et al., 2020; Hu et al., 2022; Yu et al., 2022). Among them, fungi belonging to phylum Basidiomycota showed a significant positive correlation with soil SWC ($p = 0.05$). They were mainly distributed in limestone and basalt soils; while those belonging to *Ascomycota* and *Mortierellomycota* showed a significant positive correlation with soil pH and AP ($p = 0.05$) and therefore mainly distributed in neutral purple sandstone soils with high phosphorus content. Changes in the structure of fungal communities such as *Ascomycota* and *Basidiomycota* accelerated the accumulation of soil-active and recalcitrant organic carbon content and promoted the alkylation of SOC and the formation of micro-aggregates and macro-aggregates in the soil (Fan, 2022).

### 4.3 Differences between Microbial Carbon Cycling Genes in Different Soil Types

In this study, the relative abundance of genes associated with microbial carbon cycling (carbon metabolism and carbon fixation) in purple sandstone soil was the highest, followed by limestone, and the least in basalt soil (Fig. 6). Environmental factors strongly regulate the function of microbial communities, and the relative abundance of genes is related to the physical and chemical properties of soil. The nutrient levels (SOC, AN, and AK) of limestone and basalt soils decreased in carbon metabolism and increased in carbon fixation genes, which was consistent with previous studies (Yan et al., 2020). In addition, the low abundance of genes related to microbial carbon

cycling in basalt soils was associated with high SWC content and low soil AP levels. Excessive soil SWC combined with insufficient oxygen levels reduces the microbial growth efficiency, which in turn affects the efficiency of carbon utilisation and hinders microbial biomass production and organic carbon accumulation (Stockmann et al., 2013). Similarly, soil microbial metabolism can be limited by low soil phosphorus levels (Cui et al., 2020).Various metabolic activities of soil microorganisms were also affected by soil acidity and alkalinity, including the low (acidic) pH of the limestone and basalt soils, weak activity of microorganisms, and the decreased abundance of functional genes associated with carbon metabolism, which facilitated the fixation of SOC. The pH of purple sandstone soil was neutral, which was more conducive to the activity of soil microorganisms. Therefore, the relative abundance of functional genes associated with microbial carbon cycling was the largest, which hindered soil carbon storage.

However, studies have shown that soil microorganisms can also affect soil physical and chemical properties. Soil microorganisms can affect the soil nutrient cycling process, improve the biological availability of soil nutrients, increase the availability of plant nutrients, promote plant growth, and indirectly change soil organic carbon content (Zhang et al., 2020). Although many studies have proved the remarkable effect of underground microorganisms in promoting the growth of above-ground plants, this effect has not been widely used in agriculture due to the limitations of theories and technical means.

## 5 Conclusions

This study revealed the effects of soil physical and chemical properties of different parent rocks on microbial composition and carbon cycle function genes. There are significant differences in soil organic carbon content among the three parent rocks, with the trend of limestone > basalt > purple sandstone. The change of soil organic carbon content is closely related to the properties of the parent rocks, in which the soil formed after weathering limestone and basalt is rich in clay particles, which play a physical and chemical protection role for soil organic carbon. Therefore, limestone and basalt-developed soils are considered to have great potential for organic carbon accumulation, especially basalt-basalt weathering, which is a major carbon sequestration process of atmospheric $CO_2$. In addition, in addition to the influence of mother rock on soil organic carbon content, soil microorganisms participate in several metabolic processes such as soil carbon cycle, and are important biological factors affecting soil organic carbon content. In this study, the main dominant bacteria of the soil bacterial communities developed from the three parent rocks were *Proteobacteria*, *Chloroflexi*, *Acidobacteria* and *Actinobacteria*, and the main fungal dominant phyla were *Basidiomycota*, *Ascomycota* and Mortierellomycota. Changes in the community structure of fungi such as Ascomycota and Basidiomycota can accelerate the accumulation of soil activity and inert organic carbon content, and promote the alkylation of soil organic carbon structure and the formation of microaggregates and macroaggregates in soil, thus playing a physical protection role for soil organic carbon. Through RDA analysis, it was found that SWC, BD, pH, SOM, AN, AP, AK, etc. were the main driving factors affecting the composition of soil microbial community. At the same time, soil microbial C metabolism and C-fixed gene abundance were significantly affected by soil physicochemical properties, especially soil SWC, pH and AP content limited the carbon metabolic activity of soil microbial communities.

In conclusion, soil physical and chemical properties of different parent rocks significantly affect soil organic carbon content, microbial community composition and metabolic activities, and soil microorganisms in turn affect soil organic carbon and soil physical and chemical properties. Soil microorganisms can affect the soil nutrient cycling process, improve the biological availability of soil nutrients, increase the amount of plant nutrients, promote plant growth, and indirectly change the soil organic carbon content. Therefore, soil organic carbon content is the result of the interaction between soil microorganisms and soil physical and chemical properties. This study can provide basic theoretical knowledge for the study of soil carbon sink regulation mechanism and the realization of China's "carbon neutrality" goal.

**Authors' Contributions** All authors contributed to the study conception and design. Material preparation was completed by Cheng Chen and Xuefeng Wen; data collection and analysis were performed by Hongmei Wu, Sen Chang, Qihang Li and Heng Wang. The first draft of the manuscript was written

by Hongmei Wu and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

**Funding** The authors acknowledge the support of the National Natural Science Foundation(41563011), Guizhou Provincial Science and Technology Plan Project (Qiankehe foundation [2020] 1Y190), Natural Science Project of Guizhou Provincial Department of Education (Qianjiaohe KY Zi [2017] 151),Cultivation project of Guizhou University (Guizhou University Cultivation [2020]61).

**Data Availability** The datasets used or analysed during the current study are available from the corresponding author on reasonable request.

**Declarations**

**Ethics Approval** This article does not contain any studies with human participants or animals performed by any of the authors.

**Consent to Participate** All authors agree to participate.

**Consent for Publication** All authors have read and agreed to the published version of the manuscript.

**Competing Interests** The authors declare no competing interests.

## References

Amundson, R. (2001). The carbon budget in soils. *Annual Review of Earth & Planetary Sciences, 29*, 535–562.

Averill, C., & Waring, B. (2018). Nitrogen limitation of decomposition and decay: how can it occur? *Global Change Biology, 24*, 1417–1427.

Barré, P., Durand, H., Chenu, C., Meunier, P., Montagne, D., Castel, G., Billiou, D., Soucémarianadin, L. & Cécillon, L. (2017). Geological control of soil organic carbon and nitrogen stocks at the landscape scale. *Geoderma, 285*, 50–56.

Bimüller, C., Kreyling, O., Kölbl, A., Lützow, M. V., & Kögel-Knabner, I. (2016). Carbon and nitrogen mineralization in hierarchically structured aggregates of different size. *Soil & Tillage Research, 160*, 23–33.

Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J., & Holmes, S. P. (2016). DADA2: High-resolution sample inference from Illumina amplicon data. *Nat Methods, 13*, 581–583.

Chen, M. D., & Cui, X. Y. (2022). Mechanisms and influencing factors of soil organic carbon sequestration by minerals. *Chinese Journal of Eco-Agriculture, 30*, 175–183.

Cui, Y. X., Wang, X., Zhang, X. C., Ju, W. L., & Fang, L. C. (2020). Soil moisture mediates microbial carbon and phosphorus metabolism during vegetation succession in a semiarid region. *Soil Biology and Biochemistry, 147*, 107814.

Davinic, M., Fultz, L. M., Acosta-Martinez, V., Calderón, F. J., Cox, S. B., Dowd, S. E., Allen, V. G., Zak, J. C., & Moore-Kucera, J. (2012). Pyrosequencing and mid-infrared spectroscopy reveal distinct aggregate stratification of soil bacterial communities and organic matter composition. *Soil Biology & Biochemistry, 46*, 63–72.

DeSantis, T. Z., Hugenholtz, P., Larsen, N., Rojas, M., Brodie, E. L., Keller, K., Huber, T., Dalevi, D., Hu, P., & Andersen, G. L. (2006). Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. *Applied and Environment Microbiology, 72*, 5069–5072.

Du, K., Chen, Y., Ji, J., Li, H., Long, X., & Chen, J. (2012). Characteristics of clay minerals and CO2 consumption rates of weathering profiles from Cenozoic Basalts in Eastern China. *Geological Journal of China Universities, 18*, 256–272.

Eusterhues, K., Rumpel, C., Kleber, M., & Kögel-Knabner, I. (2003). Stabilisation of soil organic matter by interactions with minerals as revealed by mineral dissolution and oxidative degradation. *Organic Geochemistry, 34*, 1591–1600.

Fan, W. (2022). Effects of different maize straw return methods on organic carbon fraction and microbial diversity in Chernozem. *Jilin Agricultural University, 03*, 1–2.

Fomina, M., & Skorochod, I. (2020). Microbial interaction with clay minerals and its environmental and biotechnological implications. *Minerals, 10*, 1–10.

Fu, R. D., Li, D. J., Hu, P. L., Duan, P. P., & Zhang, Y. L. (2023). Effects of lithology on forest soil organic carbon mineralization. *Chinese Journal of Ecology, 43*(04), 1000–1007.

Gao, X. X., Dong, S. K., Xu, Y., Li, Y., Li, S., Wu, S. G., Shen, H., Liu, S. L., & Fry, E. L. (2021). Revegetation significantly increased the bacterial-fungal interactions in different successional stages of alpine grasslands on the Qinghai-Tibetan Plateau. *CATENA, 205*, 105385.

Hu, L., Li, Q., Yan, J. H., Liu, C., & Zhong, J. X. (2022). Vegetation restoration facilitates belowground microbial network complexity and recalcitrant soil organic carbon storage in southwest China karst region. *Science of the Total Environment, 820*, 153137.

Islam, K. R., Weil, R. R., Mulchi, C. L., & Glenn, S. D. (1997). Freeze-dried soil extraction method for the measurement of microbial biomass C. *Biology and Fertility of Soils, 24*, 205–210.

Kõljalg, U., Nilsson, R. H., Abarenkov, K., Tedersoo, L., Taylor, A. F., Bahram, M., Bates, S. T., Bruns, T. D., Bengtsson-Palme, J., Callaghan, T. M., Douglas, B., Drenkhan, T., Eberhardt, U., Dueñas, M., Grebenc, T., Griffith, G. W., Hartmann, M., Kirk, P. M., Kohout, P., … Larsson, K. H. (2013). Towards a unified paradigm for sequence-based identification of fungi. *Molecular Ecology, 22*, 5271–5277.

Lehmann, J., & Kleber, M. (2015). The contentious nature of soil organic matter. *Nature, 528*, 60–68.

Li, Q., Hu, Q. J., Zhang, C. L., Muller, W. E. G., Schroeder, H. C., Li, Z. Y., Zhang, Y., Liu, C., & Jin, Z. J. (2015).

The effect of toxicity of heavy metals contained in tailing sands on the organic carbon metabolic activity of soil microorganisms from different land use types in the karst region. *Environmental Earth Sciences, 74*, 6747–6756.

Liang, B., Zhou, J. B., & Yang, X. Y. (2010). Changes of soil microbial biomass carbon and nitrogen, and mineral nitrogen after a long-term different fertilization. *Plant Nutrition and Fertilizer Science, 16*, 321–326.

Ma, T., Zhu, S., Wang, Z., Chen, D., Dai, G., Feng, B., Su, X., Hu, H., Li, K., Han, W., Liang, C., Bai, Y., & Feng, X. (2018). Divergent accumulation of microbial necromass and plant lignin components in grassland soils. *Nature Communications, 9*, 3480.

Mao, X. L. (2021). Accumulation characterisitcs and stabilization mechinisms of organic carbon in soils developed from different parent materials in subtropical regions. *Zhejiang University, 01*, 1–96.

McNally, S. R., Beare, M. H., Curtin, D., Meenken, E. D., Kelliher, F. M., Calvelo Pereira, R., Shen, Q., & Baldock, J. (2017). Soil carbon sequestration potential of permanent pasture and continuous cropping soils in New Zealand. *Global Change Biology, 23*, 4544–4555.

Mouvenchery, Y. K., Kuerík, J., Diehl, D., & Schaumann, G. E. (2012). Cation-mediated cross-linking in natural organic matter: a review. *Reviews in Environmental Science and Bio/technology, 11*, 41–54.

Qiu, J. M., Cao, J. H., Lan, G. Y., Liang, Y. M., & Li, Q. (2020). The influence of land use patterns on soil bacterial community structure in the Karst Graben Basin of Yunnan Province. *China. Forests, 11*, 51.

Qu, Z. L., Liu, B., Ma, Y., Xu, J., & Sun, H. (2020). The response of the soil bacterial community and function to forest succession caused by forest disease. *Functional Ecology, 34*, 2548–2559.

Rashid, M. I., Mujawar, L. H., Shahzad, T., Almeelbi, T., Ismail, I. M., & Oves, M. (2016). Bacteria and fungi can contribute to nutrients bioavailability and aggregate formation in degraded soils. *Microbiological Research, 183*, 26–41.

Schmidt, M. W., Torn, M. S., Abiven, S., Dittmar, T., Guggenberger, G., Janssens, I. A., Kleber, M., Kögel-Knabner, I., Lehmann, J., Manning, D. A., Nannipieri, P., Rasse, D. P., Weiner, S., & Trumbore, S. E. (2011). Persistence of soil organic matter as an ecosystem property. *Nature, 478*, 49–56.

Stockmann, U., Adams, M. A., Crawford, J. W., Field, D. J., Henakaarchchi, N., Jenkins, M., Minasny, B., Mcbratney, A. B., Remy, V. D., & Courcelles, D. (2013). Agriculture, ecosystems and environment the knowns, known unknowns and unknowns of sequestration of soil organic carbon. *Agriculture, Ecosystems & Environment, 164*, 80–99.

Sun, Y. F., Sun, M. L., Chen, G. W., Chen, X., Li, B. G., & Wang, G. (2021). Aggregate sizes regulate the microbial community patterns in sandy soil profile. *Soil Ecology Letters, 3*, 313–327.

Tonneijck, F. H., Jansen, B., Nierop, K. G. J., Verstraten, J. M., & Lange, L. D. (2010). Towards understanding of carbon stocks and stabilization in volcanic ash soils in natural Andean ecosystems of northern Ecuador. *European Journal of Soil Science, 61*, 392–405.

Vestin, J. L. K., Nambu, K., van Hees, P. A. W., Bylund, D., & Lundström, U. S. (2006).The influence of alkaline and non-alkaline parent material on soil chemistry. *Geoderma 135*, 97–106.

Wang, Q. S., Luo, J., Cai, L. M., Mu, G. Z., Wang, H. Z., Jiang, H. H., Wang, S., & He, M. H. (2018). Distribution of soil selenium and its influential factors in Jiexi County, Guangdong Province. *Soils, 50*, 1126–1133.

Whittaker, R. H. (1960). Vegetation of the Siskiyou Mountains Oregon and California. *Ecological Monographs, 30*, 279–338.

Whittaker, R. H. (1972). Evolution and measurement of tree species diversity. *Taxon, 01*, 213–251.

Whittinghill, K. A., & Hobbie, S. E. (2012). Effects of pH and calcium on soil organic matter dynamics in Alaskan tundra. *Biogeochemistry, 111*, 569–581.

Witt, C., Gaunt, J. L., Galicia, C. C., Ottow, J. C. G., Neue, H. U. J. B., & Soils, F. O. (2000). A rapid chloroform-fumigation extraction method for measuring soil microbial biomass carbon and nitrogen in flooded rice soils. *Biology and Fertility of Soils, 30*, 510–519.

Wu, D., Feng, Y., Tao, Z., Deng, H., Zhong, Q., Song, W., He, Y., Wang, Z., & Ding, J. (2023). Topsoil carbon storage and its driving factors in the lower reaches of the Yalong River. *Quaternary Sciences, 43*, 368–380.

Xiong, X., Xing, Y., He, J., Wang, L., Shen, Z., Chen, W., & Huang, Q. (2021). Keystone species determine the "selection mechanism" of multispecies biofilms for bacteria from soil aggregates. *Science of the Total Environment, 773*, 145069.

Yan, B. S., Sun, L. P., Li, J. J., Liang, C. Q., Wei, F. R., Xue, S., & Wang, G. L. (2020). Change in composition and potential functional genes of soil bacterial and fungal communities with secondary succession in Quercus liaotungensis forests of the Loess Plateau, Western China. *Geoderma, 364*, 114199.

Yang, Y., Yanxing, D., Baorong, W., Zhijing, X., Zhaolong, Z., Yimei, H., Yunqiang, W., & Shaoshan, A. (2023). Advances in soil organic carbon sequestration mechanisms on the Chinese Loess Plateau. *43*, 509–522.

Yu, X. J., Chen, Q., Shi, W. C., Gao, Z., Sun, X., Dong, J. J., Li, J., Wang, H. T., Gao, J. G., Liu, Z. G., & Zhang, M. (2022). Interactions between phosphorus availability and microbes in a wheat–maize double cropping system: a reduced fertilization scheme. *Journal of Integrative Agriculture, 21*(3), 840–854.

Zeng, X. M., Feng, J., Yu, D. L., Wen, S. H., Zhang, Q., Huang, Q., Delgado-Baquerizo, M., & Liu, Y. R. (2022). Local temperature increases reduce soil microbial residues and carbon stocks. *Global Change Biology, 28*, 6433–6445.

Zhang, C., Li, J., Wang, J., Liu, G. B., Wang, G. L., Guo, L., & Peng, S. Z. (2019). Decreased temporary turnover of bacterial communities along soil depth gradient during a 35-year grazing exclusion period in a semiarid grassland. *Geoderma, 351*, 49–58.

Zhang, T., Wang, L., Zhang, D., & Don, H. (2020). Effects of soil management measures and environmental factors on soil microorganisms in farmland. *Journal of Northern Agriculture, 48*, 87–92.

Zhao, C. M., Wang, W. B., Zhang, Y. F., Xue, X. X., Luo, X. H., Luo, L. Y., & Wu, X. P. (2021). Characterization of soil microbial community structure among different parent materials in rubber plantation. *Journal of Southern Agriculture, 52*, 1869–1876.

Zheng, J. Y. (2022). Soil organic carbon distribution in soil aggregates and its microbial influencing mechanisms in orchards of different age. *Huazhong Agricultural University, 03*, 1–61.

Zhu, T. Q., Herath, S., Newton, P., Hou, F. J., & Bowatte, S. (2021). Distribution of physiochemically defined soil organic carbon pools and their relationship to the soil microbial community in grasslands. *Pedobiologia, 84*, 1.