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Microbial community characteristics of yellow and yellow-brown earths, two typical soils in Fanjing Mountain in southwest China

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Abstract

Although several studies have enhanced the understanding to Fanjing Mountain (Guizhou province, southwest China) from soil physiochemical parameters, stoichiometric, and endangered plants, however, there are rarely investigated to the differences in microbial communities in Fanjing Mountain. Therefore, this study mainly exhibits the difference of microbial community in the two typical soils (yellow earth and yellow-brown earth) in Fanjing Mountain as well as involves physicochemical parameters, microbial network structure and functional gene. Except for available phosphorus, cobalt and potassium, there are no significant differences between most physicochemical parameters in yellow earth and yellow-brown earth. Linear discriminant analysis effect size confirms that there are the significant differences at various levels of bacterial and fungal communities in the two typical soils, with 14 and 13 differential indicator species, respectively. Community similarity, mantel and redundancy analysis also demonstrates that pH is an important factor affecting bacterial and fungus communities in the two typical soils. Co-occurrence network of bacteria and fungus exhibits that the synergistic effect between microbial community is higher than the competitive effect. Functional gene expressions, including hydrocarbon_degradation, intracellular parasites, methylotrophy, methanotrophy, nitrogen_fixation, fermentation, in yellow earth are higher than of in yellow-brown earth. The proportion of symbiotoph and saprotroph dominates in the yellow earth in yellow-brown earth, respectively. Our results suggest that although there are merely the few differences between physicochemical parameters, the microbial community and functional gene vary found in the yellow earth and yellow-brown earth) in Fanjing Mountain via these discrepancies, which maybe caused by the discrepancy in pH in soil. Our study firstly emphasis the typical soil microbial community characteristics of the Fanjing Mountain forest ecosystem, providing key soil science basis for the precise protection and adaptive management of forest ecosystems in the future.

Keywords: Fanjing Mountain, microbial communities, yellow earth, yellow-brown earth, functional gene

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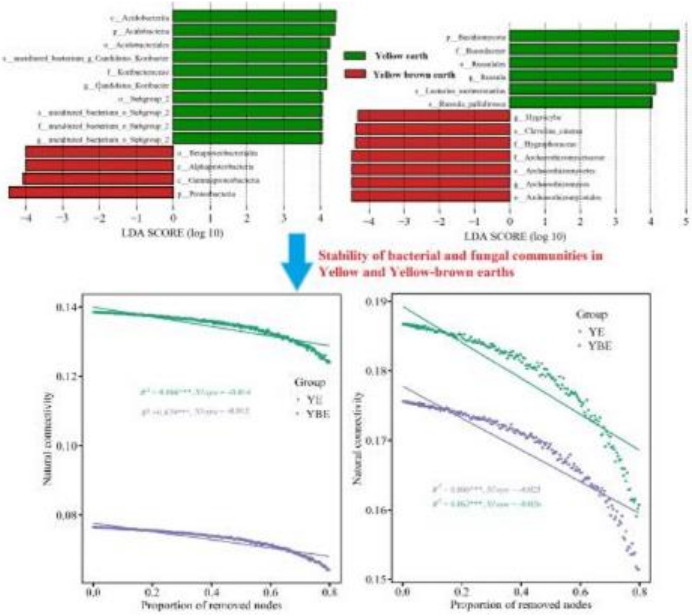
Graphical abstract



1. Introduction

Forest ecosystems are the core component of the terrestrial biosphere, and the maintenance of their structure and function depends on the succession of plant communities (Dong *et al.*, 2025). However, plants do not exist in isolation; their survival, growth, and distribution are constrained by complex underground environmental factors (Zhang *et al.*, 2025). Among these factors, soil plays a crucial role as a medium for direct interaction between plant roots and their environment. Forest soil is not a homogeneous entity, but rather a natural body with high spatial heterogeneity formed by the combined effects of parent material, climate, terrain, and biology (Chen *et al.*, 2025). This heterogeneity is directly reflected in different soil types, which exhibit significant differences in physical structure (e.g., texture and porosity), chemical properties (e.g., pH, organic matter content, and nutrient availability), and biological communities (e.g., microbial diversity), thereby forming a series of underground filters that screen and shape plant life activities (Mandah *et al.*, 2025). Numerous studies have shown that differences in soil types are key drivers of forest plant community composition, diversity, and productivity (Chen *et al.*, 2025; Zhang *et al.*, 2025). For example, sandy soil, due to its high permeability and poor ability to retain water and nutrients, generally supports only pioneer plant species that are tolerant to drought and low fertility (Zhao *et al.*, 2025). In contrast, well-developed loam soil, characterized by favorable water, nutrient, air, and temperature conditions, often sustains climax communities with rich species diversity and complex structure (Zhao *et al.*, 2025). In addition, soil pH directly regulates plant physiological metabolism and competitive dynamics by influencing the solubility and availability of nutrients (Wu *et al.*, 2023). For instance, acidic gray soil in coniferous forests and neutral to slightly alkaline brown forest soil in broad-leaved forests support significantly different plant communities (Nikovskaya *et al.*, 2004). A more profound impact is that specific soil types indirectly regulate ecosystem nutrient cycling by establishing unique symbiotic relationships with plant roots (e.g., mycorrhizal fungi), thereby influencing forest succession dynamics and ecosystem service functions (Onet *et al.*, 2025). Although the relationship between soil and plants has become a research focus in forest ecology, studies on how different soil types systematically affect key microbial community mechanisms in specific forest ecosystems remain insufficient.

Fanjing Mountain, located in Tongren City, Guizhou Province, China, is the main peak of the Wuling Mountains, with Fenghuang Mountain as its highest peak (2,572 m) (Wu *et al.*, 2023). In 2018, it was designated as a UNESCO World Heritage Site due to its role as a critical habitat for endangered flora and fauna, as well as its outstanding natural beauty and unique geological features (Wu *et al.*, 2023). The ancient metamorphic rock dome landform is preponderance in Fanjing Mountain, while karst landforms are embedded and distributed in its surroundings. Several studies have been conducted in this region. Xiao *et al.* (2024) reported that soil aggregate stability is highest at mid-elevations (1,500–1,800 m) on Fanjing Mountain, with soil organic carbon being the most influential factor, accounting for 76.3% of the variation in stability. This finding is significant for understanding soil erosion resistance and nutrient retention capacity. Zhang *et al.* (2018) collected 13 representative soil profiles across different elevations in the Fanjing Mountain area and analyzed vertical variations in soil formation environment and weathering intensity. They identified key diagnostic horizons and characteristics, and classified the soils according to the Chinese Soil Taxonomy. The results indicated that with increasing altitude, soil temperature shifts from thermic to mesic, and soil moisture transitions from humid to udic. Soil weathering in the area is generally weak, with an abundance of 2:1-type clay minerals. Desilication, iron enrichment, and aluminization are all at moderate to low levels. Guo *et al*. (2025) examined eight 1-hectare forest plots and found that soil bacterial alpha diversity decreased with elevation, whereas fungal alpha diversity peaked at 1,000 m. Leaf phosphorus content was identified as a key driver of microbial diversity, while leaf nitrogen and carbon content influenced bacterial and fungal beta diversity, respectively. This study highlights the central role of plant functional traits in maintaining microbial diversity in mountain ecosystems. Zhang and Zhang (1980) described a distinct vertical zonation of soil types on Fanjing Mountain: yellow-red earth is distributed below 500 m, yellow earth from 500-1,400 m, yellow-brown earth from 1,400-2,000m, and alpine shrub-meadow soil above 2,000 m. Surface soil organic matter content is generally high and varies significantly with vegetation type. While previous research on Fanjing Mountain has focused on soil physicochemical properties, stoichiometry, and endangered plants, the differences in microbial communities across these distinct soil types have not yet been thoroughly investigated.

Yellow earth and yellow-brown earth are typical soil types in Fanjing Mountain. Yellow earth supports typical subtropical evergreen broad-leaved forests (Adams & Norton, 1991), while yellow-brown earth sustains evergreen and deciduous broad-leaved mixed forests (e.g., Davidia involucrata and Fagus longipetiolata) or coniferous and broad-leaved mixed forests (Stewart *et al*., 1993). To date, no studies have reported the influence of these typical soil types on microbial communities in Fanjing Mountain. Given the importance of microbial communities for plant growth and ecological conservation in this region, this study selects two typical soils—yellow earth and yellow-brown earth—in Fanjing Mountain to investigate their effects on soil microbial community structure. The main objective of this study is to (1) investigate the physicochemical properties of two typical soils (yellow earth and yellow-brown earth) in Fanjing Mountain; (2) reveal the impact of environmental factors on the microbial α diversity and community structure of two typical soils in Fanjing Mountain; (3) clarify the stability of bacterial and fungal network structures and corresponding functional gene predictions in two typical soils in Fanjing Mountain. The aim of this study is to systematically analyze the typical soil microbial community characteristics of the Fanjing Mountain forest ecosystem, providing key soil science basis for the precise protection and adaptive management of mountain forest ecosystems in the future.

2. Materials and methods

2.1. Study area

Fanjing Mountain is located at the junction of Jiangkou County, Yinjiang County, and Songtao County in Tongren City, Guizhou Province. It is the main peak of the Wuling Mountains, with geographic coordinates of 27°49'50" N - 28°1'30" N and 108°45'55"E -108°48'30" E. The total area is approximately 567 km^2, with a heritage site area of 402.75 km^2 and a buffer zone area of 372.39 km^2. With an altitude of 2572 m, it is the first peak on the slope from the Yunnan-Guizhou Plateau to the hills in western Hunan, with a relative height of 2000 m. The climate belongs to subtropical humid monsoon climate, with an annual average temperature of 6 to 17 ℃. The annual precipitation is 1100-2600 mm, relative humidity is over 80% and forest coverage is 97%. The low altitude (<500m) is dominated by evergreen broad-leaved forests, medium altitude (500-1400 m) are evergreen deciduous mixed forests, and subalpine altitude (>2000 m) mainly develop shrub meadows. The plant diversity is higher, including first-class protected plants such as *Davidia involucrata*, *Taxus wallichiana*, and *Abies fabri*, as well as 4395 species of plants and 2767 species of animals. The coexistence of evergreen and deciduous components forms the characteristic of "Oriental Deciduous Forest Biogeography Province", with 16302 hm^2 of evergreen forest and 16464 hm^2 of deciduous forest coexisting, reflecting the combined influence of subtropical monsoon and terrain (Wu *et al*. 2023). It is the only habitat for rare species such as Guizhou snub nosed monkey and *Fanjingshan fir.* National first-class protected animals in Fanjing Mountain include Guizhou snub nosed monkey, clouded leopard, pangolin, forest musk deer, white necked pheasant, etc. The second-class protected animals include giant salamanders, red bellied pheasants, Asian black bears, etc. According to the international grading standards and previous published literature, the soil in Fanjing Mountain was classed to light clay (Wu et al. 2023).

2.2. Soil sample collection and chemical analysis

This study used 7 yellow earth plots, e.g., LQS (27.85 N, 108.76 E, S1), LXP (27.83 N, 108.75 E, S2), HGS (27.91 N, 108.63 E, S3), XD31 (27.91 N, 108.64 E, S4), HXP (27.90 N, 108.70 E, S5), XD33 (27.91 N, 108.65 E, S6), DMS (27.90 N, 108.65 E, S7) and 7 yellow-brown earth, e.g., MXLB (27.91 N, 108.65 E, S8), SD (27.91 N, 108.69 E, S9), MXLA (27.91 N, 108.65 E, S10),YA (27.90 N, 108.70 E, S11) and YYDJ (27.92 N, 108.69 E, S12), LCDA (27.93 N, 108.70 E, S13) and LCDB (27.92 N, 108.69 E, S14) (**Figure 1**) (Yang *et al*. 2026). Surface soil samples were taken from each plot using the five-point sampling method. After removing stones, plant roots, and other impurities from the mixed composite soil, they were placed in plastic sealed bags. 5g of soil was immediately taken out and placed in sterile centrifuge tubes for soil amplicon sequencing. Then, it was placed in an insulated box (with an ice box inside) and brought back to the laboratory within 48 h. The soil sample was stored in a - 80 ℃ freezer for future use, and the remaining soil will be brought back to the laboratory for the determination of physicochemical indicators in soil. The moisture content (MC) in soil is determined using the aluminum box drying method. Fresh soil samples (approximately 10 g) are loaded into aluminum boxes of known weight and dried in a 105℃ oven to a constant weight for weighing and calculating the soil moisture content. The soil pH value is measured using a pH meter. Soil available phosphorus (AP) was determined using the dual acid leaching molybdenum antimony colorimetric method. Soil available potassium (AK) was determined by ammonium acetate extraction flame photometry method. Soil organic carbon (SOC) was determined using the potassium dichromate oxidation external heating method. Total phosphorous (TP) in the soil was determined using the $HClO_4$-H_2SO_4 method, and the sample was digested and decomposed, filtered (0.45 μm), and measured using the continuous flow analyzer. Ca, Co, Fe, K, Pb, and Zn in soil were extracted using HNO_3-HCl-HF (2:2:1) microwave digestion method, and their total amounts in the digested samples were determined using inductively coupled plasma mass spectrometry (ICP-MS, Thermo Fisher Scientific, USA).

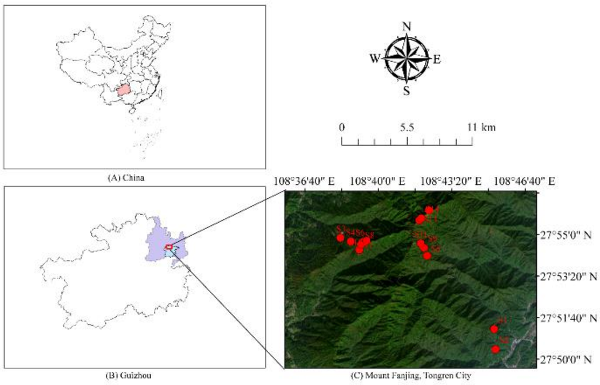


Figure 1. The collecting samples of yellow earth and yellow-brown earth in Fanjing Mountain (Yang *et al.* 2026)

2.3. Soil DNA extraction, PCR amplification, and sequencing

The bacterial and fungus in soil was identified using high-throughput sequencing, of which 16S rRNA gene and ITS were used to determine bacterial and fungus, respectively. In this study, E.Z.N.A.R soil DNA kit was used to extract soil bacterial DNA, and its quality and concentration were detected by 1% agarose gel electrophoresis and NanoDrop2000. Subsequently, for the V3-V4 region of the bacterial 16S rRNA gene, the upstream primer 341F (5 '- ACTCCTACGGGGAGGCAGCAG-3') and the downstream primer 806R (5 '-GGACTACHVGGGTWTCTAAT-3') carrying the Barcode sequence were used for PCR amplification (Liu *et al.* 2016), the amplified product was recovered by 2% agarose gel electrophoresis and purified with the AxyPrep DNA Gel Extraction Kit. Construct a sequencing library using the NEXTFLEX Rapid DNA Seq Kit and sequence it using the Miseq PE250 platform from Lumina Corporation. The sequencing data was subjected to fastp quality control and FLASH sequence concatenation. UPARSE software was used to perform OTU clustering with 97% similarity and eliminate chimeras. To reduce the impact of sequencing depth, all sample sequences were flattened to 20000, with an average sequence coverage of 99.09%. RDP classifier was compared with Silva database for species taxonomy annotation, and PICRUSt2 was used for 16S functional prediction. The phylogenetic tree of soil bacterial in Fanjing Mountain was showed in **Figure 2A**.

The soil fungal DNA was extracted by Hi Pure Soil DNA Kits kit, and the DNA quality was evaluated by Nano Drop ultra micro spectrophotometer and agarose gel electrophoresis technology. Then, using diluted genomic DNA as a template, specific primers with unique barcodes were designed for PCR amplification of the target region of ITS. The amplification process included pre denaturation, 12 cycles of denaturation, annealing, and extension steps. The amplified PCR products were purified using AMPure XP Beams and library quantification was performed using ABI StepOnePlus RealTime PCR System (Guo *et al.* 2017). Finally, according to the PE250 mode of Illumina Novaseq 6000, the quantified libraries were mixed and loaded onto a sequencer for high-throughput sequencing and subsequent bioinformatics analysis. The phylogenetic tree of soil fungus in Fanjing Mountain was showed in **Figure 2B**.

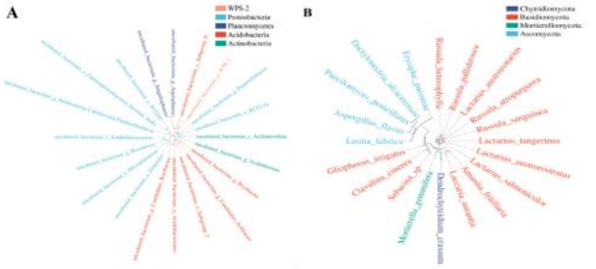


Figure 2 Phylogenetic tree of soil bacterial (A) and fungus (B) in Fanjing Mountain

2.4. Statistical analysis

Excel 2021 was use for data organization, SPSS (27.0) and R4.3.1 were use for data statistical analysis, and Origin 2022 and R4.3.1 were used for plotting. One way ANOVA is used to test the differences in soil physical and chemical properties and microbial α diversity among different treatments. All ANOVA required the normal distribution and homogeneity of variance tests. The least significant difference test is performed if the variance is homogeneous. The Dunnett T3 test was used if the variance is non-homogeneous. The construction of bacterial networks is based on the molecular ecological network analysis method of Random Matrix Theory (RMT) (http:/lieg4. rccc. ou. edu/mena/). In most cases, only nodes detected in half or more of the total sample are reserved for subsequent network construction. In constructing a network, when selecting the interrelationships between bacterial species at the OTU level, it is necessary to satisfy spearman correlation with $|r^2| > 0.8$ and $P < 0.05$ between species. Baimaike Cloud Platform (https://international.biocloud.net）was using to visualize the co-occurrence network of soil fungi and bacteria. Redundancy analysis (RDA) was conducted using R language's "Ape", "vegan", "psyche", and "reshape2" pack ages to explore the relationship between physicochemical parameters and dominant phyla of bacterial and fungal in soil.

Table 1. Physicochemical parameters of yellow earth and yellow-brown earth.

Parameters	**Yellow earth**						
	DMS	**HGS**	**HXP**	**LQS**	**LXP**	**XD31**	**XD33**
AK(mg/kg)	104.02±21.56	127.97±16.23	79.37±20.14	102.28±28.14	50.01±14.26	113.33±48.22	100.15±3.63
AP(mg/kg)	78.58±9.74	63.12±9.57	73.3±30.51	63.48±11.94	35.4±4.74	89.32±17.86	87.12±13.37
Ca(mg/kg)	601.93±184.2	1072.97±631.4	1016.97±185.57	753.83±683.05	358.53±211.49	813.63±228.8	982.67±224.93
Co(mg/kg)	7.29±1.33	11.64±2.2	12.37±8.55	11.21±1.38	11.68±0.92	13.96±6.00	5.89±1.12
Fe(g/kg)	18.04±5.14	21.71±2.67	34.61±13.34	22.24±4.87	20.81±0.84	25.21±5.86	16.7±3.31
K(g/kg)	2±0.23	4.5±0.29	2.74±1.42	2.79±1.52	4.76±0.37	4.13±0.87	2.72±0.48
MC	64.09±2.32	56.47±3.59	45.64±7.09	51.5±6.43	39.97±2.47	51.62±4.41	65.2±6.07
P(mg/kg)	310.63±13.66	327.17±26.56	490.13±93.14	380±16.87	271.53±23.71	520.93±81.78	523.37±22.01
Pb(mg/kg)	52.79±12.01	49.97±6.45	72.25±33.41	28.76±2.18	27.28±5.28	38.6±4.42	52.28±7.24
pH	4.01±0.08	4.03±0.74	3.86±0.38	4.65±0.23	4.51±0.19	4.38±0.09	3.75±0.49
SOC (g/kg)	276.45±21.5	170.16±37.46	236.91±136.24	195.81±32.76	46.43±7.6	204.99±27.38	288.92±38.28
Zn(mg/kg)	115.74±58.53	449.27±222.04	1267.6±349.93	427.93±193.1	358.13±177.28	341.93±99.48	225.3±40.44
Parameters	**Yellow-brown earth**						
	LCDA	**LCDB**	**MXLA**	**MXLB**	**SD**	**YA**	**YYDJ**
AK(mg/kg)	84.44±5.62	101.42±10.76	130.39±56.75	98.48±31.31	94.19±20.55	79.91±14.11	88.6±11.74
AP(mg/kg)	91.35±14.47	89.56±22.36	106.57±16.8	106.64±49.17	145.97±14.67	98.21±16.33	114.77±10.01
Ca(mg/kg)	155.97±104.03	416.17±232.13	1549.77±803.82	1042.53±278.72	292.23±169.83	892.54±1028.45	157.5±141.78
Co(mg/kg)	5.43±0.28	6.35±0.38	3.99±1.75	15.4±6.16	6.09±0.88	7.78±2.8	7.05±1.37
Fe(g/kg)	12.34±2.86	15.47±3.81	9.2±4.17	31.96±7.1	20.72±3.01	22.06±8.97	12.07±1.81
K (g/kg)	7.56±1.05	8.86±0.65	2.17±1.3	3.87±0.57	1.5±0.18	5.44±0.94	13.42±1.18
MC	46.45±6.09	53.34±4.79	69.45±11.34	46.45±6.09	51.62±4.41	51.62±4.41	53.01±0.66
P (mg/kg)	294.17±32.48	391.63±90.07	487.43±52.53	709.43±48.37	491.77±45.14	499.63±122.33	330.53±45.28
Pb (mg/kg)	30.48±4.21	31.9±9.43	61.29±13.71	50.46±7.7	51.74±7.13	36.38±6.32	27.56±4.86
pH	3.95±0.15	4.04±0.25	3.75±0.31	4.33±0.76	3.58±0.12	3.85±0.15	4.01±0.04
SOC (g/kg)	128.13±20.16	141±10.71	380.08±49.85	218.17±47.98	310.17±39.2	174.13±63.5	74.9±5.98
Zn (mg/kg)	470.63±113.44	1561.33±435.53	207.49±105.78	3069.9±3921	147.09±101.22	513.5±193.55	149.7±50.7

*(**Note:** Different superscript letters in each row represent significant differences between different treatments (ANOVA, $p < 0.05$)*

3. Results

3.1. Physicochemical parameters of yellow earth and yellow-brown earth

There is no significant difference in AK content between yellow earth and yellow-brown earth (**Figure 3**). The AK content in the surface soil of the yellow earth in the study area varies between 35 mg/kg and 172.2 mg/kg, with an average of 96.73 mg/kg (**Table 1**). Among them, XD31 and XD33 have higher AP content, which are 89.32 ± 17.86 and 87.12 ± 13.37 mg/kg, respectively. The content of AK in yellow-brown earth ranges from 54.88 to 191.7, with an average of 96.78 mg/kg. Among them, MXLA has the highest AK content, which is 130.39 ± 56.75 mg/kg. There is a significant difference in AP content between yellow earth and yellow-brown earth, with contents of 70.04 ± 23.35 mg/kg and 107.58 ± 29.75 mg/kg, respectively. The maximum AP content was 89.32 ± 17.86 mg/kg (XD31) and 145.97 ± 14.67 mg/kg in yellow earth and yellow-brown earth, respectively. There was no significant difference in Ca content between yellow earth and yellow-brown earth, with values of 800.08 ± 458.67 mg/kg and 643.81 ± 715.81 mg/kg, respectively. There is a significant difference in Co content between yellow earth and yellow-brown earth, with contents of 10.58 ± 4.93 mg/kg and 7.44 ± 4.38 mg/kg, respectively. XD31 and MXLB have high concentrations in yellow earth and yellow-brown earth, with concentrations of 13.96 ± 6 and 15.4 ± 6.16 mg/kg, respectively. There was no significant difference in Fe content between yellow earth and yellow-brown earth, with values of 22.76.08 ± 8.38 g/kg and 17.69 ± 8.88 g/kg, respectively. There is a significant difference in K content between yellow earth and yellow-brown earth, with the highest K content in LXP (4.76 ± 0.37 g/kg) in yellow earth and the highest K content in XD33 (13.42 ± 1.18 g/kg) in yellow earth. The variation of K content is greater in yellow-brown earth. There is a significant difference in MC content between yellow earth and yellow-brown earth, with values of 53.50 ± 9.88% g and 53.13 ± 9.45%, respectively, and their variability is also relatively small. There is no significant difference in P content between yellow earth and yellow-brown earth, with values of 403.40 ± 110.63 mg/kg and 457.8 ± 145.30 mg/kg, respectively. There is no significant difference in Pb content between yellow earth and yellow-brown earth, with values of 45.99.40 ± 20.35 mg/kg and 41.40 ± 14.54 mg/kg, respectively. There is no significant difference in pH between yellow earth and yellow-brown earth. The pH contents of the surface soil in the yellow earth of the research area vary between 3.07 and 4.97, with an average value of 4.17 mg/kg. Among them, the pH value of XD33 (3.75 ± 0.49) is the lowest in the yellow earth. The pH of the surface soil of yellow-brown earth is 3.93 ± 0.40, with a minimum value of 3.58 ± 0.12. There is no significant difference in SOC content between the two soils, which are 202.81 ± 95.13 g/kg and 203.80 ± 107.35 g/kg in yellow earth and yellow-brown earth, respectively. Although there is no significant difference in Zn content between yellow earth and yellow-brown earth, the Zn contents in yellow-brown earth (874.25 ± 1801.69 mg/kg) are significantly higher than that in yellow earth (455.13 ± 397.59 mg/kg). Overall, merely the contents of AP, Co, and K in yellow earth and yellow-brown earth show the significant differences, while there are no significant differences between most physicochemical parameters.

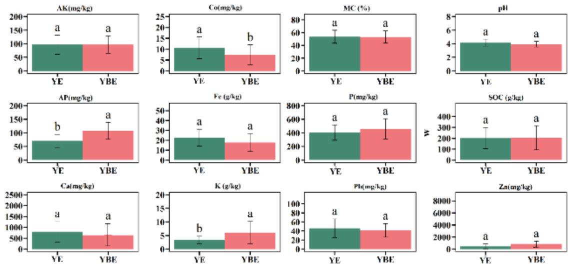


Figure 3. The significant difference of physicochemical parameters of yellow earth and yellow-brown earth (**Note:** Different superscript letters in each row represent significant differences between different treatments (ANOVA, $p < 0.05$); YE and YBE represent yellow earth and yellow-brown earth, respectively.)

3.2. The microbial community structure of yellow earth and yellow-brown earth at the phylum level

In bacteria, there is a significant difference in Shannon index and Simpson index between yellow earth and yellow-brown earth, while there is no significant difference in α diversity index of other bacteria (**Figure 4**). However, the values of bacterial diversity index in yellow earth are slightly higher than that in yellow-brown earth. The values of Shannon indices in yellow earth and yellow-brown earth are 8.31 ± 0.25 and 8.03 ± 0.32, respectively, while the values of Simpson indices in yellow earth and yellow-brown earth are 0.992 ± 0.002 and 0.988 ± 0.005, respectively. In fungi, there is a significant difference in the PDw_hole tree index between yellow earth and yellow-brown earth, with values of 86.73 ± 5.94 and 90.82 ± 6.64, respectively. There is no significant difference in other α diversity indices of fungi between yellow earth and yellow-brown earth, such as ACE, Chao1, Feature, Shannon, Simpson, Conveage indices, while the fungal diversity indices of yellow earth are slightly lower than those of yellow-brown earth. The bacteria at the phylum level of yellow earth and yellow brown earth mainly include Acidobacteria, Proteobacteria, Planctomycetes, Actinobacteria, Verrucomicrobia, WPS-2, Chloroflexi, Gemmatimonadetes, Bacteroidetes, Patescibacteria Composition, among which Acidobacteria and Proteobacteria are the main phyla of bacterial (**Figure 5A and C**). Specifically, Acidobacteria (40.4%) and Proteobacteria (36.4%) have a higher proportion in yellow earth, while Acidobacteria (45.5%) has a much higher proportion than Proteobacteria (30.6%) in yellow-brown earth. The variability of Acidobacteria and Proteobacteria is higher in yellow-brown earth than in yellow earth. The fungi at the phylum level of yellow earth and yellow-brown earth mainly include Ascomycota, Basidiomycota, Chytridiomycota, Glomeromycota, Mortierellomycota, Olpidiomycota, Rozellomycota, Zoopagomycota, Ascomycota and Basidiomycota have a higher proportion among them (**Figure 5B and D**). The proportion of Basidiomycota (57.4%) in yellow earth is much higher than that of Ascomycota (32.9%), while the proportion of Ascomycota (42.8%) and Basidiomycota (43.7%) in yellow-brown earth is very close. Overall, although the bacteria and bacterial composition of the two typical soils in Fanjing Mountain are basically the same, the proportion of bacteria and fungi differs significantly between the two typical soils. Acidobacteria and Proteobacteria are the main phyla of bacterial in yellow earth, while Acidobacteria is the main phyla of bacterial in yellow-brown earth. Ascomycota and Basidiomycota are the main phyla of fungal in yellow loam soil, while Basidiomycota is the main phyla of fungal in yellow earth.

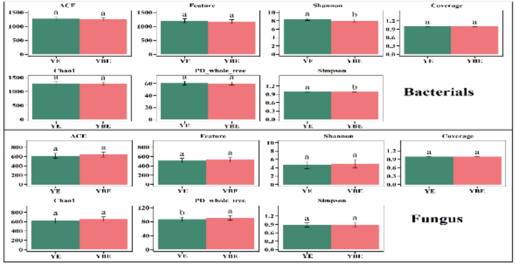


Figure 4. The significant difference of physicochemical parameters of yellow earth and yellow-brown earth (**Note:** Different superscript letters in each row represent significant differences between different treatments (ANOVA, $p < 0.05$); YE and YBE represent yellow earth and yellow-brown earth, respectively.)

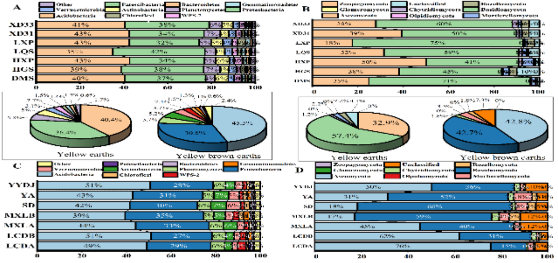


Figure 5. Community structure of yellow earth in bacterial (A) and fungus (C) and yellow-brown earth in bacterial (B) and fungus (D) at the phylum level. (**Note:** YE and YBE represent yellow earth and yellow-brown earth, respectively.)

3.3. LEfSe analysis of microbial communities and effect of physicochemical indicators on microbial communities

LEfSe analysis can identify species with significant differences between yellow earth and yellow-brown earth (**Figure 6**). The bacterial and fungal communities show significant differences at various levels (phylum, class, order, family, genus) between the two typical soils, with 14 and 13 species, respectively ($LDA > 4$, $P < 0.05$). Specifically, bacterial communities in two typical soils consist of 2 phyla (p-Acidobacteria and p-Proteobacteria), 3 classes (c_Acidobacteria, c_Alphaproteobacteria, and c_Gamnaproteobacteria), 3 orders (o-Acidobacteriales, o-Subgroup_2, and o-Metaproteobacteriales), 2 families (f_Koribacteraceae and f_unctltured_bacterioum_o_Subgroup_2), and 2 genera (d_Candidatus_Koribacter and d_uncultured bacteria o Subgroup 2) and 2 species (s __uncultured_bacterium_g_Candidatus_Koribacter and f_uncultured_bacverium_o_Subgroup_2) (**Figure 6A**). The fungal community in two typical soils consists of 1 phylum (p_Basidiomycota), 1 Class (c_Archaeorhizomyeetes), 2 orders (o'Russulales and o'Archaeorhizomyeetes), 3 families (f_Russulaceae, f_Hygrophoraceae and f_Archaeorhizomyetaceae), 3 genera (d_Russula, d_Hygrdcybe and d_Archaeorhizomyces), and 3 species (s_Lactarius austrozonarius, s_Russula pallidirosea and s_Clavulina_cinerea) (**Figure 6B**). This means that there is a significant difference in the bacterial and fungal communities between the two typical soils, with the higher differences of bacterial occurring in yellow earth. **Figure 7** exhibits the effect of soil physicochemical parameters on bacterial community similarity. The larger the absolute value of the slope is, the greater the influence of this factor is. For all physicochemical parameters, the absolute values of pH slope (-0.10555 in yellow earth and -0.14962 in yellow-brown earth) are significantly greater than other indicators, indicating that pH has the greatest impact on the bacterial communities of the two typical soils in Fanjing Mountain. Similar patterns have also been found in fungi, where the absolute values of pH slope (-0.05956 in yellow earth and -0.13697 in yellow-brown earth) are significantly higher than other indicators (**Figure 8**). pH is an important factor affecting fungal communities in the two typical soils of Mount Fanjing. In addition, the slope of pH in bacteria and fungi is greater in yellow-brown earth than in yellow earth, indicating that pH has a greater impact on the microbial community in yellow-brown earth in comparison with yellow earth.

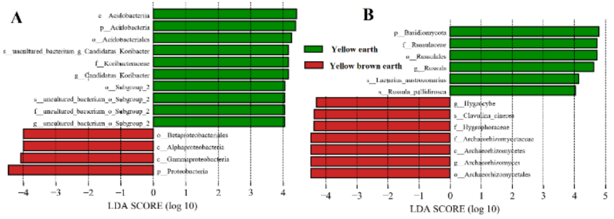


Figure 6. LEfSe analysis of bacterial (A) and fungus (B) in yellow earth and yellow-brown earth

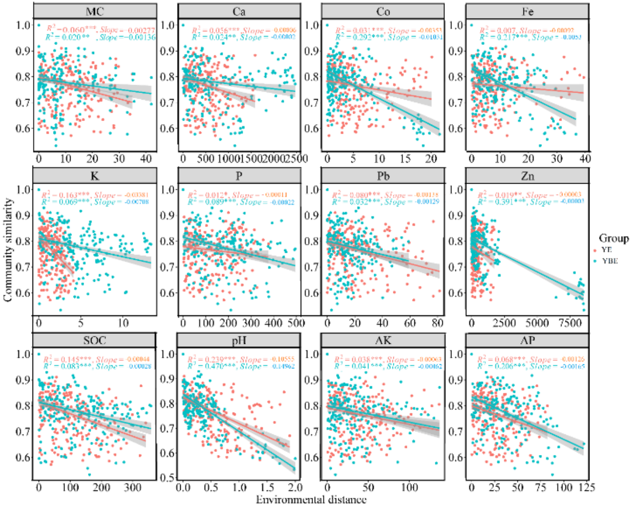


Figure 7. Effect of physicochemical parameters on bacterial community similarity in soil. (**Note:** YE and YBE represent yellow earth and yellow-brown earth, respectively.)

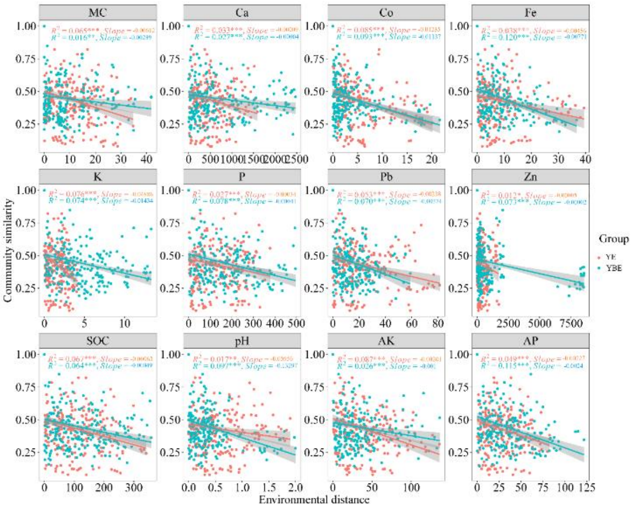


Figure 8. Effect of physicochemical parameters on fungus community similarity in soil. (**Note:** YE and YBE represent yellow earth and yellow-brown earth, respectively.)

3.4. Microbial network structures and resistance testing in yellow earth and yellow-brown earth

In the co-occurrence network of bacteria in the yellow earth of Fanjing Mountain, Acidobacteria and Proteobacteria occupy more nodes, followed by Verrucomicobia and Actinobacteria. In network related relationships, 38% and 62% of species relationships are negatively and positively correlated, respectively, indicating that the synergistic effect between bacterial is higher than the competitive effect (**Figure 9A**). In the co-occurrence network of bacteria in the yellow-brown earth of Fanjing Mountain, Acidobacteria and Proteobacteria occupy more nodes, followed by WPS-2, Actinobacteria, Gemmatimonasides, and Actinobacteria. In the network related relationships, 47% and 53% of species relationships are negatively and positively correlated, respectively, indicating that the synergistic effect between bacterial is slightly higher than the competitive effect (**Figure 9B**). In the bacterial networks of yellow earth and yellow-brown earth, the difference of nodes number, edges number, average degree, average path length, graph diameter, graph density, clustering coefficient, betweenness centralization, degree centralization and modularity are few, while the value of graph diameter in yellow earth is greater than that in yellow-brown earth (**Table 2**). In the co-occurrence network of fungi in the yellow earth and yellow-brown earth of Fanjing Mountain, Ascomycota and Basidiomycota occupy more nodes, with the highest proportion of positive correlations between species, indicating that the two typical soil fungus mainly cooperate with each other (**Figure 9C and 9D**). Some key parameters in the yellow earth fungal network diagram, such as node number, average path length, graph diameter, and modularity, are greater than those in the yellow-brown earth fungal network diagram. Natural connectivity is a global metric based on network graphs, which measures the redundancy and connectivity of a network by calculating the average of all its eigenvalues. The higher the natural connectivity is, the more redundant the connection paths between species within the microbial network is. The network is more stable when facing external disturbances such as environmental changes and species extinction, making it less likely to collapse. There is no significant difference in the natural connectivity of bacterial and fungal networks between yellow earth and yellow-brown earth (**Figure 10**). The microbial networks in the two typical soils are relatively stable when facing environmental changes, while bacteria are more sensitive than fungi when facing environmental pressures.

Table 2. The topological structure of bacterial and fungus in yellow earth and yellow-brown earth

Topological parameters	Bacterial		Fungus	
	YE	YBE	YE	YBE
Nodes number	37	35	45	33
Edges number	100	100	42	79
Average degree	5.41	5.71	1.87	4.79
Average path length	3.18	2.52	1.33	1.08
Graph diameter	20.61	11.28	8.96	5.35
Graph density	0.15	0.17	0.04	0.15
Clustering coefficient	0.58	0.61	0.75	0.99
Betweenness centralization	0.26	0.31	0.01	0.01
Degree centralization	0.27	0.24	0.05	0.16
Modularity	0.30	0.30	0.89	0.49

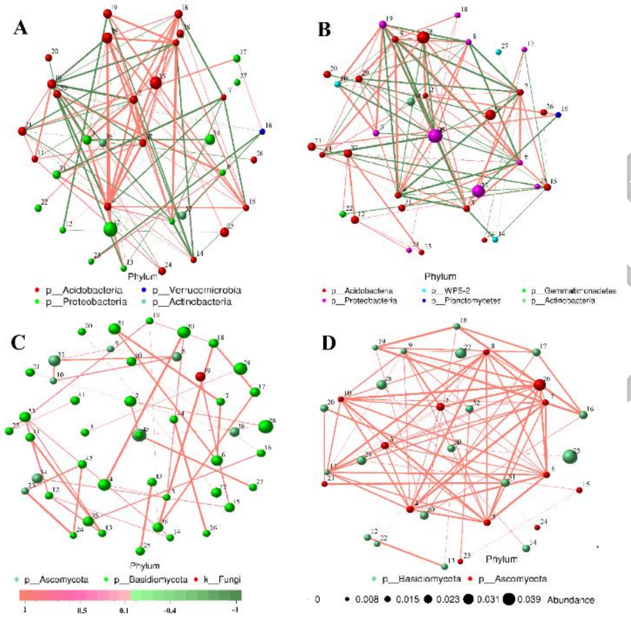


Figure 9. Co-occurrence network of bacteria in the yellow earth (A) and yellow-brown earth (B), and of bacteria in the yellow earth (C) and yellow-brown earth (D) of Fanjing Mountain

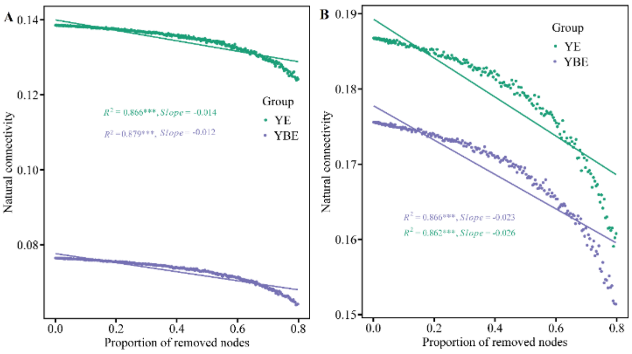


Figure 10. Natural connectivity of bacteria (A) and of fungus (B) in the yellow earth and yellow-brown earth of Fanjing Mountain (**Note:** YE and YBE represent yellow earth and yellow-brown earth, respectively.)

3.5. Factors driving the seasonal variation in soil microbial community composition

The bacterial community in the yellow earth of Fanjing Mountain is positively correlated with K, SOC, pH, and AP, while fungi are negatively correlated with MC, P, and Pb (**Figure 11A)**. Compared with fungal communities, bacteria have a greater impact on the physicochemical indicators of yellow earth. pH in yellow earth is significantly positively correlated with MC and SOC, and significantly negatively correlated with Co. SOC is significantly positively correlated with MC, P, and Pb, and significantly negatively correlated with Co and K. The bacterial community in the yellow-brown earth of Fanjing Mountain is significantly positively correlated with Zn, SOC, and pH, while the fungal Pb, SOC, and AK are significantly positively correlated (**Figure 11B)**. SOC in yellow earth is significantly positively correlated with Ca, P, and Pb, and significantly negatively correlated with K and pH. Overall, compared to yellow earth, fungi have a greater impact on physical and chemical indicators in yellow-brown earth. pH and SOC have a greater impact on bacteria in two typical soils in comparison with fungi.

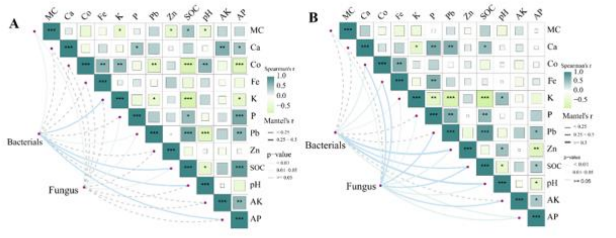


Figure 11. Relationship between microbial community and physicochemical indicators using Mantel analysis

The sum of the percentages of RDA1 and RDA2 represents the total variance of species environment relationships that can be explained by the first two axes. The higher this value is, the more reliable the information in the graph is. If the total sum is very low (< 30 %), it indicates that there are still important environmental factors that have not been measured (or there is a lot of noise). The environmental factors of the yellow earth in Fanjing Mountain have a significant impact on bacterial distribution, with RDA1 (37.96%) and RDA2 (15.06%) explaining 53.02% of the variance in species environment relationships (**Figure 12A**). pH, Zn, MC, Co, Pb have a significant impact on the bacterial community of phylum level. Among them, Acidobacteria is positively correlated with Fe, Zn, Co, P, Pb, and negatively correlated with Ca and AK. Proteobacteria is positively correlated with pH, AP, P, AK and Ca, and negatively correlated with Zn, Fe, and Co. There is little correlation between Acidobacteria and Proteobacteria. Zn, Co, Fe, Pb, Ph, and AP in yellow earth have a significant impact on bacterial communities, with RDA1 (38.54%) and RDA2 (18.93%) explaining 58.77% of the variance in species environment relationships (**Figure 12B**). Acidobacteria is negatively correlated with all physical and chemical indicators, while it is positively correlated with most physical and chemical indicators. The correlation between Acidobacteria and Proteobacteria is not significant. The environmental factors of the yellow earth in Fanjing Mountain have a relatively small impact on the distribution of fungi, with RDA1 (45.34%) and RDA2 (8.991%) explaining 54.33% of the variance in species environment relationships (**Figure 12C**). Ascomycota is positively correlated with AK, Ca, P, AP, Zn, Pb, and SOC, and negatively correlated with MC, Co, and Fe, while Basidiomycota is the opposite. Ascomycota and Basidiomycota are not correlated. The environmental factors in the yellow-brown earth of Mount Fanjing have a relatively small impact on the distribution of fungi, with RDA1 (47.92%) and RDA2 (9.295%) explaining 57.81% of the variance in species environment relationships (**Figure 12D**). In summary, Ascomycota is positively correlated with AK and MC, and negatively correlated with other physicochemical indicators, while Basidiomycota is the opposite.

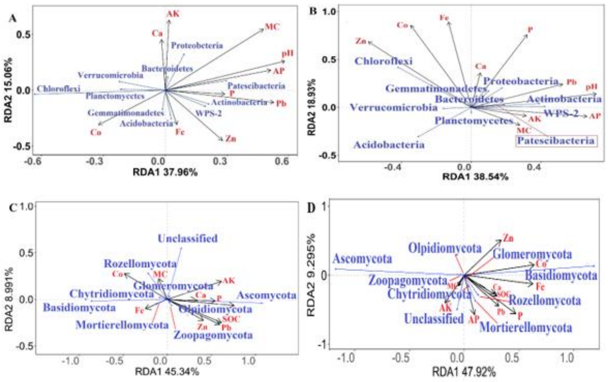


Figure 12. RDA analysis of bacterial in yellow earth（A）and yellow-brown earth (B), and fungus in yellow earth (C) and yellow-brown earth (D)

3.6. Function prediction for microbial community in yellow earth and yellow-brown earth

Based on published literature on microbial pure culture research, the taxonomic information (phylum, class, order, family, genus) of known prokaryotes (bacteria and archaea) is correlated with the ecological functions/biochemical processes that they participate in (such as nitrification, denitrification, fermentation, etc.). Functional gene expressions, including hydrocarbon_degradation, intracellular parasites, methylotrophy, methanotrophy, nitrogen_fixation, fermentation, in yellow earth are higher than of yellow-brown earth (**Figure 13A**). The expression of ureolysis in yellow-brown earth are higher than those in yellow earth. FUNGuild, based on currently published literature or authoritative website data, first divides fungi into three categories according to their nutritional methods. pathotrophs fungus obtain nutrients by damaging host cells, including phagocytic fungi phagotrophs. Symbiotic troph fungus obtains nutrients by exchanging resources with host cells. Saprotroph fungus obtains nutrients by degrading dead host cells. The proportion of symbiotoph in the yellow earth of Fanjing Mountain is higher than that in the yellow-brown earth, while the proportion of Saprotroph is higher in the yellow-brown earth (**Figure 13B**).

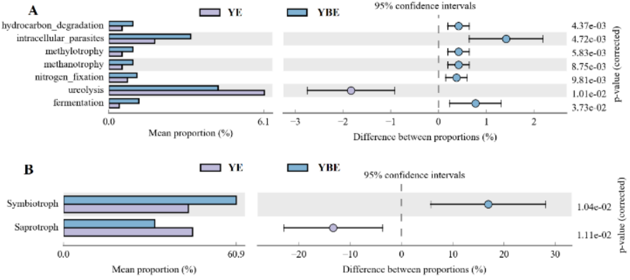


Figure 13. Function prediction for bacterial (A) and fungus (B) in yellow earth and yellow-brown earth. (**Note:** YE and YBE represent yellow earth and yellow-brown earth, respectively.)

4. Discussion

Yellow earth is mainly distributed in subtropical humid climate conditions, commonly found in mountainous areas at elevations of 700-1200 m. The significant moderate desilication and aluminum rich weathering process leads to the massive leaching of base ions, making the soil being the stronger acidic (Liu *et al.* 2010). Yellow-brown earth is a soil of warm and humid deciduous broad-leaved forests in the northern subtropical region, and can also be distributed in high-altitude mountains in the central subtropical region, including 1300 to 2300 m. It is a type of transition from yellow earth to brown earth, with weak aluminum rich weathering and usually weaker acidity than yellow earth (Zhang *et al.* 2019). The pH content of the surface soil of yellow earth in this study varies between 3.07 and 4.97, with an average value of 4.17. The pH of the surface soil of yellow-brown earth is 3.93 ± 0.40. In this study, there is no significant difference in pH between yellow earth and yellow-brown earth, while the pH of yellow earth is slightly lower than that of yellow earth, which may be due to strong biological acidification. Forest vegetation, especially yellow-brown earth, is mostly composed of evergreen deciduous mixed forests. During the decomposition process of their litter (such as dead branches and fallen leaves), the massive organic acids (such as humic acid and fulvic acid) are produced and released (Zhang *et al*. 2021). The forest on yellow-brown earth is composed of rhododendrons with stronger acid production capacity, while the vegetation in yellow earth has weaker acid production capacity. This significant biological acidification may further reduce the pH value of the topsoil of yellow-brown earth (Zhao *et al*. 2021). In addition, the organic acids secreted by tree root activity and the H $^+$ released during nutrient absorption by roots to maintain charge balance can also exacerbate soil acidification. The yellow-brown earth of Fanjing Mountain is concentrated in areas with higher altitude, more abundant precipitation, and higher air humidity, and may undergo stronger weathering and leaching processes. A large amount of precipitation causes a significant leaching of neutral and acidic base ions (such as Ca^{2+}) in the soil, leading to the dominance of acidic ions (H^+ and Al^{3+}) on soil colloids, thereby exacerbating soil acidification (Lu *et al.* 2014). This is consistent with the findings of this study that the Ca content in yellow earth is lower than that in yellow earth in Fanjing Mountain. If this leaching process is stronger in the yellow-brown earth area than in the yellow earth area, it may result in a lower pH in the former. Yan *et al*. (2015) reported that the soil pH at different altitudes in Fanjing Mountain ranged from 4.02 to 6.41, and the soil exhibits weak acidity shifting to strong acidity. With the increase of altitude, nutrient content showed a certain vertical difference distribution, and the content of soil organic matter, alkali hydrolyzed nitrogen, available potassium, and available phosphorus at different depths showed a trend of first increasing and then decreasing. The comprehensive content of soil nutrients is relatively low at altitudes of 500-520 m, while nutrient content is relatively abundant at other altitudes, reaching its maximum value at altitudes of 1500-2000 m. In yellow earth and yellow-brown earth, the values are 202.81 ± 95.13 g/kg and 203.80 ± 107.35 g/kg, respectively. There is no significant difference in SOC content between the two soils, which may be due to the similarity in soil texture and bulk density. The clay content, bulk density, and moisture content of yellow earth and yellow-brown earth may be similar under the same parent material or terrain conditions, resulting in similar physical protection mechanisms for organic carbon (such as aggregate formation), thereby reducing differences (Xiao 2013). Xiao *et al*. (2024) found that in the 0-60 cm soil layer, soil aggregates were mainly composed of water stable macroaggregates larger than 0.25 mm, with an average content of 86.78%. The stability of soil aggregates along the altitude gradient is mainly influenced by soil SOC and pH values, with explanatory powers of 76.3% and 1.3%, respectively, which are the main environmental factors affecting soil aggregate stability. In this study, the microbial communities of yellow earth and yellow-brown earth are functionally similar. In forest ecosystems, the microbial communities of yellow earth and yellow-brown earth may have similar functions due to sharing similar environmental conditions, resulting in similar rates of organic carbon decomposition. Research has shown that there is no significant difference in soil respiration rate and microbial activity between yellow-brown earth and yellow earth under the same vegetation and climate conditions, resulting in similar rates of organic carbon mineralization (Jin 2019). In this study, the pH value of yellow-brown earth is relatively low, and this extremely acidic environment is sufficient to dissolve the iron oxide film. Once the outer shell is dissolved, P enclosed inside will be released, becoming AP that can be utilized by plants. Therefore, AP in yellow-brown earth is significantly higher than that in yellow earth.

Generally, Acidobacteria is the most dominant phylum in yellow earth. Especially, subgroups such as GP1 and GP3, which are particularly adapted to acidic and nutrient poor environments, can decompose recalcitrant organic matter and are the main microbial communities in the acidic environment of yellow earth. The bacterial community diversity in yellow-brown earth is usually higher than that in yellow earth. The dominant phylum of bacteria has shifted from acidophilic Acidobacteria to a more balanced situation dominated by both Proteobacteria and Acidobacteria, and the importance of Actinobacteria has also increased. In this study, Acidobacteria and Proteobacteria were the main phyla of bacterial in yellow earth and yellow-brown earth. Acidobacteria (40.4%) and Proteobacteria (36.4%) have a higher proportion in yellow earth, while Acidobacteria (45.5%) has a much higher proportion in yellow-brown earth than Proteobacteria (30.6%), and Acidobacteria and Proteobacteria are differential indicator species in yellow earth and yellow-brown earth, respectively. Wu *et al*. (2023) reported that Acidobacteria, Proteobacteria, Planktonic Bacteria, and Actinobacteria are dominant phyla in the soil layers of Fanjing Mountain. Candidatus_Koribacter is the main indicator species for rhizosphere surface soil and subsoil. Santolamazza Carbon *et al.* (2025) reported that Acidobacteria, Chloroflexi, and Proteobacteria constituted the most of the bacterial kingdom, while Ascomycota and Basidiomycota dominate the fungus community. Their study investigated for the first time the seasonal changes in soil microbial communities in the habitat of Quercus acutissima in Galicia (northwest Spain). The bacterial community was dominated by the Acinetobacter (34%) and Proteobacter (33%), with Acinetobacteraceae (12%) and Bacteroidellaceae (9%), and Escherichia coli (7%) identified as the most abundant. The fungus community was mainly composed of the Basidiomycoceae family (93%), with the Red Mushroom (46%) being the main species. Lei *et al*. (2025) investigated the co-occurrence network and function of soil microbial communities under different site index (SI-14.96, SI-15.70, and SI-16.90) and soil depths (0–20 cm, 20–40 cm, and 40–60 cm) within a mixed Chinese fir plantation. Dominant bacterial communities included Acidobacteria, Chloroflexi, and Proteobacteria, while Ascomycota and Basidiomycota dominated the fungal community. These studies are not entirely consistent with studies in other regions, which may be due to the lower pH value of yellow-brown earth. In RDA analysis, the relationship between Acidobacteria and pH values in yellow earth is not significant, while there is a clear negative correlation in yellow-brown earth. As the soil pH decreases, the relative abundance of

Acidobacteria will significantly increase. Most members of the Acidobacterium are acidophilic bacteria, meaning they grow best in low pH (acidic) environments. In addition, in strongly acidic soils (pH value < 5.0), high H^+ concentrations can cause toxicity to the cell membranes and enzyme activities of many microorganisms, inhibiting their growth. Acidobacterium adapted to this environment through its unique cellular structure and metabolic mechanism, thereby reducing competitors and becoming the absolute dominant bacterial group in acidic yellow-brown earth (Fujii *et al*. 2021). Generally, due to the strong acidity and poor fertility of yellow earth, Ascomycota often dominates, which is because Ascomycota are acid tolerant and r-strategist decomposing simple organic matter (Yang *et al.* 2020). However, in this study, the proportion of Basidiomycota (57.4%) in yellow earth is much higher than that of Ascidiomycota (32.9%), while the proportion of Ascidiomycota (42.8%) and Basidiomycota (43.7%) in yellow-brown earth is very close. Lefse analysis also indicates that Basidiomycota is a differential indicator species. The most plant communities in yellow earth are composed of Cyclobalanopsis. These tree species are typical ectomycorrhizal dependent plants, and their roots must coexist with ectomycorrhizal fungi to grow well. Although ectomycorrhizal fungi are present in both Ascomycota and Basidiomycota, many dominant ECM fungi that can form large symbiotic networks belong to the Basidiomycota (López-García *et al*. 2023). Trees produce a large amount of carbon fixing substances (sugars) through photosynthesis. This means that trees have become the carbon source supply for Basidiomycota, providing them with a huge energy advantage in this barren acidic environment. This stable and abundant input of carbon sources has led to a sharp increase in the biomass of ECM fungi (Basidiomycota), to the point where their numbers completely surpass those of saprophytic fungi (many of which belong to the Ascomycota) that primarily rely on decomposing dead branches and leaves for energy (Fernandez *et al*. 2018). Compared to yellow earth, fungus have a greater impact on physiochemical indicators in yellow-brown earth in this study. The more suitable temperature and humidity accelerate the decomposition rate of fungus, making the nutrient cycling rate of yellow-brown earth faster and the soil fertility self-sustaining ability stronger (Lustenhouwer *et al*. 2020).

In network related relationships, 38% and 62% of species relationships are negatively and positively correlated, respectively, indicating that the synergistic effect between bacterial is higher than the competitive effect. In the network related relationships, 47% and 53% of species relationships are negatively and positively correlated, respectively, indicating that the synergistic effect between bacterial is slightly higher than the competitive effect. Wu *et al*. (2023) also reported that the positive correlation was found in co-occurrence network of bacteria and fungus, which implied that cooperation dominated among bacteria and fungus of the four soil types. There is no significant difference in the natural connectivity of bacterial and fungal networks between yellow earth and yellow-brown earth, while the stability of bacterial communities in yellow earth under environmental pressure is poorer than in yellow-brown earth. This may be due to the strong acidity, high moisture content, and specific mineral composition of yellow loam soil, which collectively lead to a decrease in bacterial community diversity, imbalanced functional interactions, and weaker stability than yellow-brown earth. The acidic environment of yellow loam soil inhibits the growth of most bacteria, leading to a significant decrease in β diversity of bacterial and a convergence characteristic of the community (i.e. reduced species richness). For example, acidification can intensify the competition for resources between bacteria and eukaryotes, disrupt the original balance, weaken functional synergy, and threaten community stability (Duan *et al*. 2025). In addition, yellow earth is mainly composed of clay minerals such as vermiculite, followed by kaolinite and illite. The process of aluminum enrichment is weak, while the yellowing process is significant. The high water holding capacity and low base saturation of vermiculite may limit the effectiveness of nutrients and affect the metabolic activity of bacteria (Chai *et al*. 2025). Yellow-brown earth is composed of clay minerals including kaolinite, illite, and a small amount of montmorillonite. It has more obvious leaching and cementation, moderate aluminum enrichment and a more balanced mineral composition, which support a more complex microbial interaction network (Yang *et al*. 2023). The correlation network constructed based on 16S/ITS amplicon data is essentially an ecological niche preference similarity network. The positive correlation between the two groups may only stem from a common response to environmental factors such as pH and temperature, rather than metabolic synergy; Negative correlation may also reflect niche differentiation or sampling effects, rather than direct antagonism (Blüthgen, 2024). Siegenthaler et al. (2024) found in the synthetic microbiota that the strong antagonistic relationship confirmed by in vitro co culture (Pseudomonas inhibits other bacteria through pseudomonas) is either completely invisible or positively correlated in the in vivo correlation network. This suggests that symbiotic networks may completely mask true antagonism. Therefore, the co-occurrence network in this study is merely providing a reference to interaction between microorganism of yellow earth and yellow-brown earth.

Functional gene expressions, including hydrocarbon_degradation, intracellular parasites, methylotrophy, methanotrophy, nitrogen_fixation, fermentation, in yellow earth are higher than of yellow-brown earth. Yellow earth faces a relatively severe environment, where nutrients are firmly trapped in forms that are difficult to utilize, such as P adsorbed by iron and aluminum oxides and complex organic matter. Microorganisms need to secrete more types of acid phosphatases to desorb and obtain P. More types and potent extracellular enzymes (such as cellulase, chitinase, lignin peroxidase) need to be produced to break down extremely stubborn organic matter and extract carbon, nitrogen, and phosphorus from it. This directly leads to a richer and more diverse family of functional genes related to nutrient cycling (C, N, P, S cycles) (Wu et al. 2023). Yellow-brown earth is relatively in suitable environment, with high nutrient availability and easier decomposition of organic matter. Microorganisms can easily access resources, so there is no need to maintain a large and diverse enzyme pools (Wu et al. 2023). Their functional genes may be more focused on utilizing readily available and simple resources. This study also found that the ureolysis functional genes in forest yellow-brown earth are higher than those in yellow earth. In strong acid environments, microorganisms may rely on other more effective nitrogen acquisition pathways rather than investing in a ureolysis pathway severely inhibited by acidic environments. For example, they may be more focused on decomposing organic nitrogen (such as proteins, chitin) to directly release NH_4^+ (ammonification). Therefore, for fungus in yellow earth, maintaining high abundance of ureolysis is an uneconomical, as natural selection pressure tends to favor genes from other nitrogen acquisition strategies (Li *et al*. 2021). In the co-occurrence network of fungi in the yellow earth and yellow-brown earth of Fanjing Mountain, positive correlations between species account for the largest proportion, indicating that there is mainly a synergistic effect between the two typical soil microorganisms. The proportion of symbiotoph in the yellow earth of Fanjing Mountain is higher than that in the yellow-brown earth, while the proportion of Saprotroph is higher in the yellow-brown earth. Most plants are difficult to obtain sufficient nutrients from poor yellow earth by relying on their own root systems. Cooperating with arbuscular mycorrhizal fungi (AMF) and other symbionts, the extremely large mycelial network of fungus can help plants explore and absorb water and difficult to move nutrients in larger soil volumes (van Galen *et al.* 2025). Yuan (2019) reported the AMF in five different forest types on Mount Fanjing. AMF can form symbiotic relationships with the root systems of higher plants, helping them absorb water and nutrients. This study found that different forest types form unique AMF communities, indicating a close coevolutionary relationship between AMF and host plants, which is an important link in maintaining the stability of forest ecosystems. In yellow-brown earth, nutrients are relatively abundant, and plant roots can easily obtain nutrients on their own. The cost-effectiveness of investing in symbiotic relationships (which require many photosynthetic products) is relatively low. Therefore, saprotroph microorganisms that live freely may be more dominant, as they directly decompose soil organic matter to obtain carbon and nutrients (Fernández *et al*. 2024). For yellow earth, the harsh environment has screened out microbial communities that are good at cooperation. The proportion of symbiotic nutritional microorganisms (such as arbuscular mycorrhizal fungi, ectomycorrhizal fungi, and certain nitrogen fixing bacteria that symbiotically coexist with plants) has therefore increased. The entire microbial network may be more inclined towards a mutualistic symbiotic model. For yellow-brown earth, the superior environment, abundant resources, and more intense competition are between among microorganisms. Saprotroph and pathotroph fungus may have larger ecological niches, as they focus on rapidly decomposing organic matter or infecting hosts rather than establishing long-term stable cooperative relationships (Delgado-Baquerizo *et al.* 2020). Therefore, the high proportion of symbiotoph in yellow earth is the inevitable result of an efficient and mutually beneficial survival strategy evolved by plants and microorganisms under the dual pressures of nutritional and environmental stress. This symbiotic relationship is crucial for maintaining the functionality and productivity of the yellow earth ecosystem.

5. Conclusion

This study mainly exhibits the difference of microbial community in the two typical soils (yellow earth and yellow-brown earth) in Fanjing Mountain as well as involves physicochemical parameters, microbial network structure and functional gene. Except for AP, Co, and K, there are no significant differences between most physicochemical parameters in yellow earth and yellow-brown earth. Although the bacteria and fungi composition of the two typical soils in Fanjing Mountain are similar, the proportion of bacteria and fungi differs significantly between the two typical soils. Acidobacteria and Proteobacteria are also the main phyla of bacterial in yellow earth, while Acidobacteria dominates in yellow-brown earth. Community similarity, mantel and RDA analysis also demonstrates that pH is an important factor affecting bacterial and fungus communities in the two typical soils, and pH has a greater impact on the microbial community in yellow-brown earth in comparison with yellow earth. Co-occurrence network of bacteria and fungus exhibits that the synergistic effect between microbial community is higher than the competitive effect. Functional gene expressions, including hydrocarbon_degradation, intracellular parasites, methylotrophy, methanotrophy, nitrogen_fixation, fermentation, in yellow earth are higher than of yellow-brown earth. The proportion of symbiotoph and saprotroph dominates in the yellow earth in yellow-brown earth, respectively. Our results suggest that although there are merely the few differences between physicochemical parameters, the microbial community and functional gene vary found in the yellow earth and yellow-brown earth) in Fanjing Mountain via these discrepancies, which maybe caused by the discrepancy in pH in soil. Our study firstly emphasis the typical soil microbial community characteristics of the Fanjing Mountain forest ecosystem, providing key soil science basis for the precise protection and adaptive management of mountain forest ecosystems in the future.

Author contribution

Xianliang Wu, Jiang Hong and Xiuyuan Yang conceptualized and designed the problem. Material preparation, data collection and analysis were performed by Anding Li, Guiting Mu, Yingying Liu and Wenmin Luo. The first draft of the manuscript was prepared by

Xianliang Wu, and all other authors approved the same. The completed manuscript was checked and corrected by Xiuyuan Yang. The authors ranked according to their contributions.

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Data Availability Statement

The data used to support the findings of this study can be made available by the corresponding author upon request

Conflict of Interest

The authors declare no conflicts of interest

Consent to publish

All the authors agree to publish this paper in this journal

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