1 **Microbial community characteristics of yellow and yellow-brown earths, two**

2 **typical soils in Fanjing Mountain in southwest China**

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16 **Abstract:** Although several studies have enhanced the understanding to Fanjing

17 Mountain (Guizhou province, southwest China) from soil physiochemical parameters,

18 stoichiometric, and endangered plants, however, there are rarely investigated to the

19 differences in microbial communities in Fanjing Mountain. Therefore, this study

20 mainly exhibits the difference of microbial community in the two typical soils (yellow

21 earth and yellow-brown earth) in Fanjing Mountain as well as involves

22 physicochemical parameters, microbial network structure and functional gene. Except

23 for available phosphorus, cobalt and potassium, there are no significant differences

24 between most physicochemical parameters in yellow earth and yellow-brown earth.

25 Linear discriminant analysis effect size confirms that there are the significant

26 differences at various levels of bacterial and fungal communities in the two typical soils,

27 with 14 and 13 differential indicator species, respectively. Community similarity,

28 mantel and redundancy analysis also demonstrates that pH is an important factor

29 affecting bacterial and fungus communities in the two typical soils. Co-occurrence

30 network of bacteria and fungus exhibits that the synergistic effect between microbial

31 community is higher than the competitive effect. Functional gene expressions,

32 including hydrocarbon_degradation, intracellular parasites, methylotrophy,

33 methanotrophy, nitrogen_fixation, fermentation, in yellow earth are higher than of in

34 yellow-brown earth. The proportion of symbiotoph and saprotroph dominates in the

35 yellow earth in yellow-brown earth, respectively. Our results suggest that although there

36 are merely the few differences between physicochemical parameters, the microbial

37 community and functional gene vary found in the yellow earth and yellow-brown earth)

38 in Fanjing Mountain via these discrepancies, which maybe caused by the discrepancy

39 in pH in soil. Our study firstly emphasis the typical soil microbial community

40 characteristics of the Fanjing Mountain forest ecosystem, providing key soil science

41 basis for the precise protection and adaptive management of forest ecosystems in the

42 future.

43 **Keywords:** Fanjing Mountain, microbial communities, yellow earth, yellow-brown

44 earth, functional gene

45

46 **1. Introduction**

47   Forest ecosystems are the core component of the terrestrial biosphere, and the

48 maintenance of their structure and function depends on the succession of plant

49 communities (Dong *et al*., 2025). However, plants do not exist in isolation; their

50 survival, growth, and distribution are constrained by complex underground

51 environmental factors (Zhang *et al*., 2025). Among these factors, soil plays a crucial

52 role as a medium for direct interaction between plant roots and their environment.

53 Forest soil is not a homogeneous entity, but rather a natural body with high spatial

54 heterogeneity formed by the combined effects of parent material, climate, terrain, and

55 biology (Chen *et al*., 2025). This heterogeneity is directly reflected in different soil

56 types, which exhibit significant differences in physical structure (e.g., texture and

57 porosity), chemical properties (e.g., pH, organic matter content, and nutrient

58 availability), and biological communities (e.g., microbial diversity), thereby forming a

59 series of underground filters that screen and shape plant life activities (Mandah *et al*.,

60 2025). Numerous studies have shown that differences in soil types are key drivers of

61 forest plant community composition, diversity, and productivity (Chen *et al*., 2025;

62 Zhang *et al*., 2025). For example, sandy soil, due to its high permeability and poor

63 ability to retain water and nutrients, generally supports only pioneer plant species that

64 are tolerant to drought and low fertility (Zhao *et al*., 2025). In contrast, well-developed

65 loam soil, characterized by favorable water, nutrient, air, and temperature conditions,

66 often sustains climax communities with rich species diversity and complex structure

67 (Zhao *et al.*, 2025). In addition, soil pH directly regulates plant physiological

68 metabolism and competitive dynamics by influencing the solubility and availability of

69 nutrients (Wu *et al.*, 2023). For instance, acidic gray soil in coniferous forests and

70 neutral to slightly alkaline brown forest soil in broad-leaved forests support

71 significantly different plant communities (Nikovskaya *et al.*, 2004). A more profound

72 impact is that specific soil types indirectly regulate ecosystem nutrient cycling by

73 establishing unique symbiotic relationships with plant roots (e.g., mycorrhizal fungi),

74 thereby influencing forest succession dynamics and ecosystem service functions (Onet

75 *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 1,400–2,000 m, 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

126 Fanjing Mountain forest ecosystem, providing key soil science basis for the precise

127 protection and adaptive management of mountain forest ecosystems in the future.

128 **2. Materials and methods**

129 2.1 Study area

130 Fanjing Mountain is located at the junction of Jiangkou County, Yinjiang County,

131 and Songtao County in Tongren City, Guizhou Province. It is the main peak of the

132 Wuling Mountains, with geographic coordinates of 27°49'50" N -28°1'30" N and

133 108°45'55"E -108°48'30" E. The total area is approximately 567 km^2, with a heritage

134 site area of 402.75 km^2 and a buffer zone area of 372.39 km^2. With an altitude of 2572

135 m, it is the first peak on the slope from the Yunnan-Guizhou Plateau to the hills in

136 western Hunan, with a relative height of 2000 m. The climate belongs to subtropical

137 humid monsoon climate, with an annual average temperature of 6 to 17 ℃. The annual

138 precipitation is 1100-2600 mm, relative humidity is over 80% and forest coverage is

139 97%. The low altitude (<500m) is dominated by evergreen broad-leaved forests,

140 medium altitude (500-1400 m) are evergreen deciduous mixed forests, and subalpine

141 altitude (>2000 m) mainly develop shrub meadows. The plant diversity is higher,

142 including first-class protected plants such as *Davidia involucrata*, *Taxus wallichiana*,

143 and *Abies fabri*, as well as 4395 species of plants and 2767 species of animals. The

144 coexistence of evergreen and deciduous components forms the characteristic of

145 "Oriental Deciduous Forest Biogeography Province", with 16302 hm² of evergreen

146 forest and 16464 hm² of deciduous forest coexisting, reflecting the combined influence

147 of subtropical monsoon and terrain (Wu *et al*. 2023). It is the only habitat for rare

148 species such as Guizhou snub nosed monkey and *Fanjingshan fir*. National first-class

149 protected animals in Fanjing Mountain include Guizhou snub nosed monkey, clouded

150 leopard, pangolin, forest musk deer, white necked pheasant, etc. The second-class

151 protected animals include giant salamanders, red bellied pheasants, Asian black bears,

152 etc. According to the international grading standards and previous published literature,

153 the soil in Fanjing Mountain was classed to light clay (Wu et al. 2023).

154 2.2 Soil sample collection and chemical analysis

155   This study used 7 yellow earth plots, e.g., LQS (27.85 N, 108.76 E, S1), LXP

156 (27.83 N, 108.75 E, S2), HGS (27.91 N, 108.63 E, S3), XD31 (27.91 N, 108.64 E, S4),

157 HXP (27.90 N, 108.70 E, S5), XD33 (27.91 N, 108.65 E, S6), DMS (27.90 N, 108.65

158 E, S7) and 7 yellow-brown earth, e.g., MXLB (27.91 N, 108.65 E, S8), SD (27.91 N,

159 108.69 E, S9), MXLA (27.91 N, 108.65 E, S10),YA (27.90 N, 108.70 E, S11) and YYDJ

160 (27.92 N, 108.69 E, S12), LCDA (27.93 N, 108.70 E, S13) and LCDB (27.92 N, 108.69

161 E, S14) (**Figure 1**) (Yang *et al*. 2026). Surface soil samples were taken from each plot

162 using the five-point sampling method. After removing stones, plant roots, and other

163 impurities from the mixed composite soil, they were placed in plastic sealed bags. 5g

164 of soil was immediately taken out and placed in sterile centrifuge tubes for soil

165 amplicon sequencing. Then, it was placed in an insulated box (with an ice box inside)

166 and brought back to the laboratory within 48 h. The soil sample was stored in a - 80 ℃

167 freezer for future use, and the remaining soil will be brought back to the laboratory for

168 the determination of physicochemical indicators in soil. The moisture content (MC) in

169 soil is determined using the aluminum box drying method. Fresh soil samples

170 (approximately 10 g) are loaded into aluminum boxes of known weight and dried in a

171 105 ℃ oven to a constant weight for weighing and calculating the soil moisture content.

172 The soil pH value is measured using a pH meter. Soil available phosphorus (AP) was

173 determined using the dual acid leaching molybdenum antimony colorimetric method.

174 Soil available potassium (AK) was determined by ammonium acetate extraction flame

175 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).
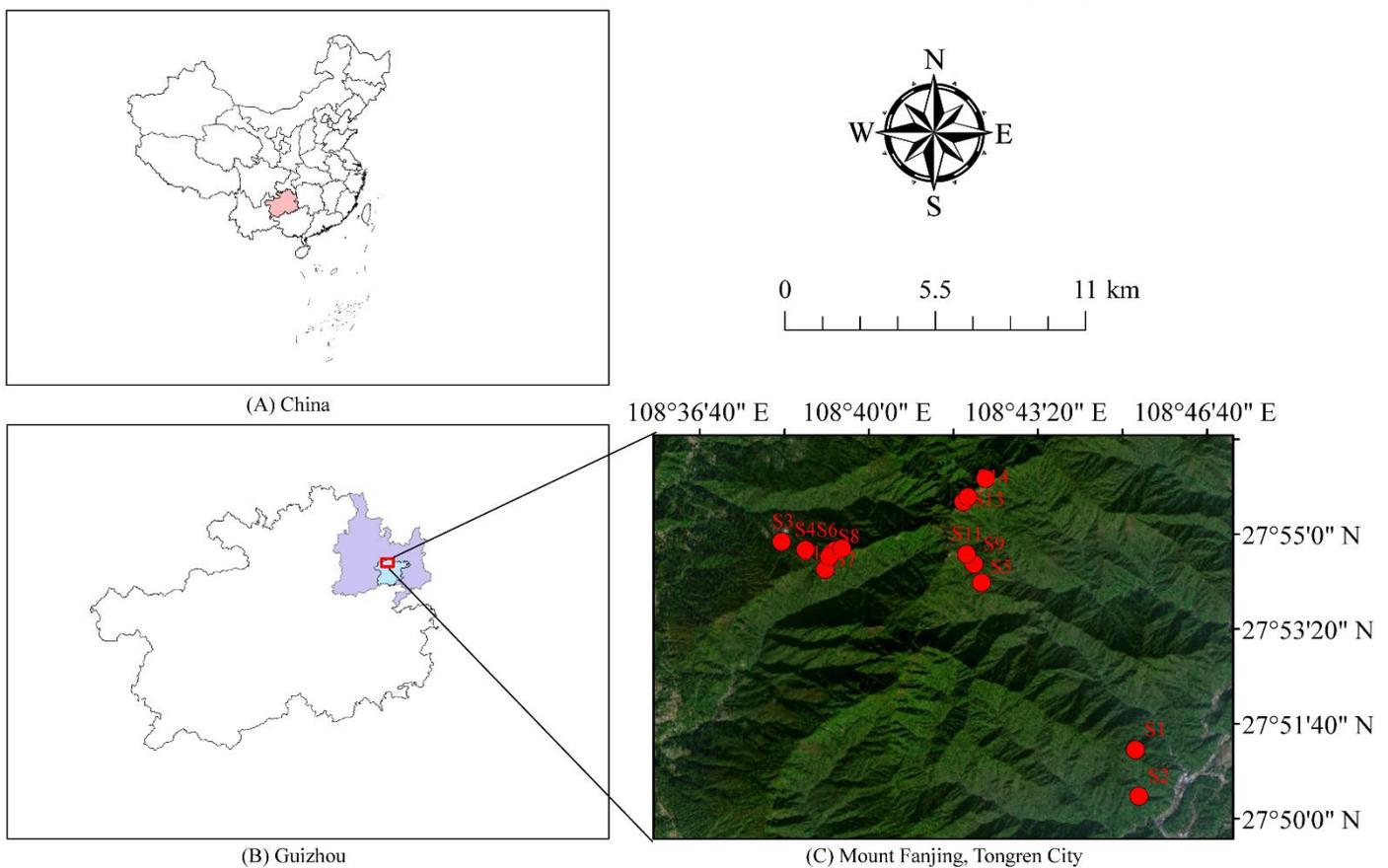
Figure 1. The collecting samples of yellow earth and yellow-brown earth in Fanjing Mountain (Yang *et al*. 2026)

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,

188 respectively. In this study, E.Z.N.A.R soil DNA kit was used to extract soil bacterial

189 DNA, and its quality and concentration were detected by 1% agarose gel

190 electrophoresis and NanoDrop2000. Subsequently, for the V3-V4 region of the

191 bacterial 16S rRNA gene, the upstream primer 341F (5 '-

192 ACTCCTACGGGGAGGCAGCAG-3') and the downstream primer 806R (5 '-

193 GGACTACHVGGGTWTCTAAT-3') carrying the Barcode sequence were used for

194 PCR amplification (Liu *et al*. 2016), the amplified product was recovered by 2%

195 agarose gel electrophoresis and purified with the AxyPrep DNA Gel Extraction Kit.

196 Construct a sequencing library using the NEXTFLEX Rapid DNA Seq Kit and

197 sequence it using the Miseq PE250 platform from Lumina Corporation. The sequencing

198 data was subjected to fastp quality control and FLASH sequence concatenation.

199 UPARSE software was used to perform OTU clustering with 97% similarity and

200 eliminate chimeras. To reduce the impact of sequencing depth, all sample sequences

201 were flattened to 20000, with an average sequence coverage of 99.09%. RDP classifier

202 was compared with Silva database for species taxonomy annotation, and PICRUSt2

203 was used for 16S functional prediction. The phylogenetic tree of soil bacterial in

204 Fanjing Mountain was showed in **Figure 2A**.

205 The soil fungal DNA was extracted by Hi Pure Soil DNA Kits kit, and the DNA

206 quality was evaluated by Nano Drop ultra micro spectrophotometer and agarose gel

207 electrophoresis technology. Then, using diluted genomic DNA as a template, specific

208 primers with unique barcodes were designed for PCR amplification of the target region

209 of ITS. The amplification process included pre denaturation, 12 cycles of denaturation,

210 annealing, and extension steps. The amplified PCR products were purified using

211 AMPure XP Beams and library quantification was performed using ABI StepOnePlus

212 RealTime PCR System (Guo *et al*. 2017). Finally, according to the PE250 mode of

213 Illumina Novaseq 6000, the quantified libraries were mixed and loaded onto a

214 sequencer for high-throughput sequencing and subsequent bioinformatics analysis. The

215 phylogenetic tree of soil fungus in Fanjing Mountain was showed in **Figure 2B**.

216

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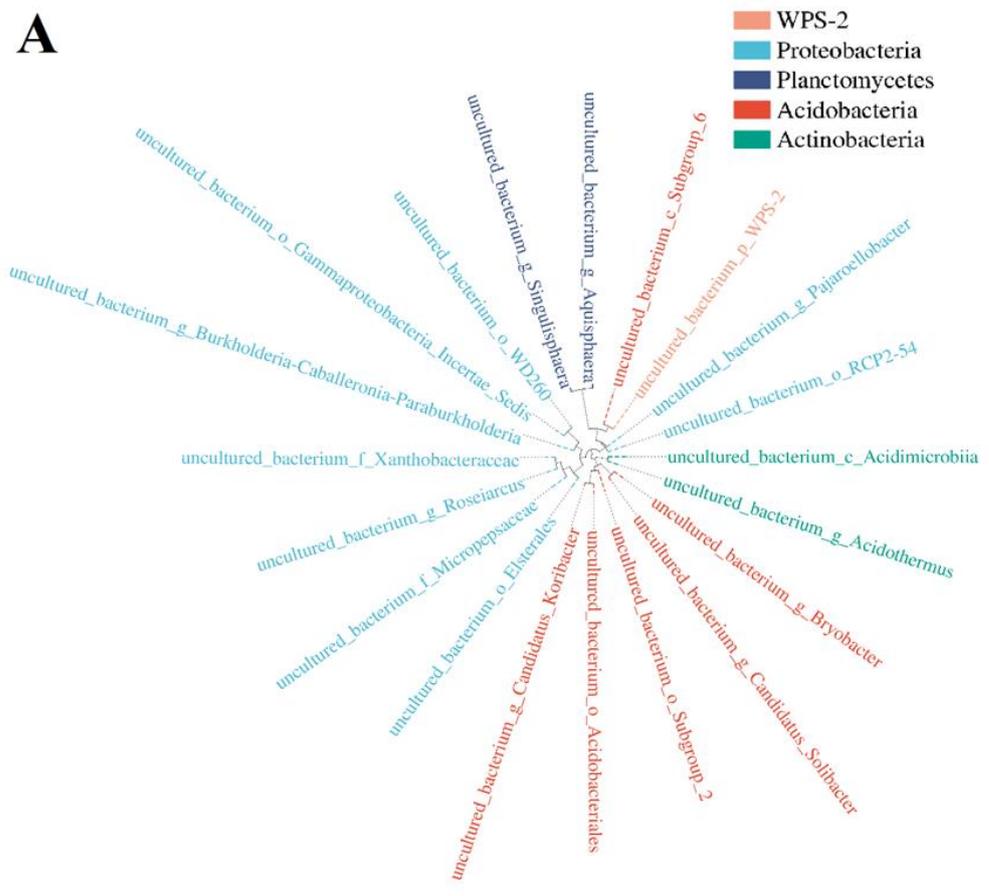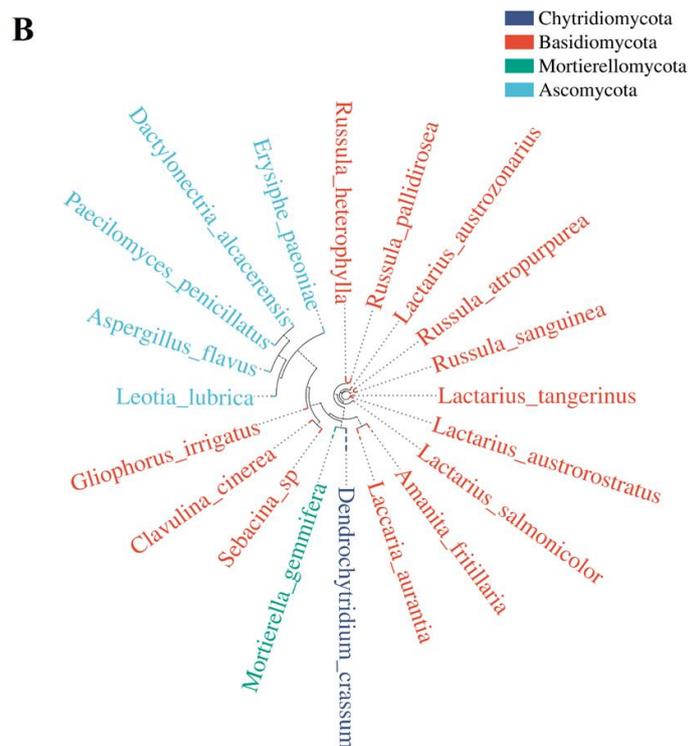
Figure 2 Phylogenetic tree of soil bacterial (A) and fungus (B) in Fanjing Mountain

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.

232 Baimaike Cloud Platform (https://international.biocloud.net）was using to visualize the

233 co-occurrence network of soil fungi and bacteria. Redundancy analysis (RDA) was

234 conducted using R language's "Ape", "vegan", "psyche", and "reshape2" pack ages to

235 explore the relationship between physicochemical parameters and dominant phyla of

236 bacterial and fungal in soil.

237

238 **3. Results**

239 3.1 Physicochemical parameters of yellow earth and yellow-brown earth

240 There is no significant difference in AK content between yellow earth and yellow-

241 brown earth (**Figure 3**). The AK content in the surface soil of the yellow earth in the

242 study area varies between 35 mg/kg and 172.2 mg/kg, with an average of 96.73 mg/kg

243 (**Table 1**). Among them, XD31 and XD33 have higher AP content, which are $89.32 \pm$

244 17.86 and 87.12 ± 13.37 mg/kg, respectively. The content of AK in yellow-brown earth

245 ranges from 54.88 to 191.7, with average of 96.78 mg/kg. Among them, MXLA has

246 the highest AK content, which is 130.39 ± 56.75 mg/kg. There is a significant difference

247 in AP content between yellow earth and yellow-brown earth, with contents of $70.04 \pm$

248 23.35 mg/kg and 107.58 ± 29.75 mg/kg, respectively. The maximum AP content was

249 89.32 ± 17.86 mg/kg (XD31) and 145.97 ± 14.67 mg/kg in yellow earth and yellow-

250 brown earth, respectively. There was no significant difference in Ca content between

251 yellow earth and yellow-brown earth, with values of 800.08 ± 458.67 mg/kg and 643.81

252 ± 715.81 mg/kg, respectively. There is a significant difference in Co content between

253 yellow earth and yellow-brown earth, with contents of 10.58 ± 4.93 mg/kg and $7.44 \pm$

254 4.38 mg/kg, respectively. XD31 and MXLB have high concentrations in yellow earth

255 and yellow-brown earth, with concentrations of 13.96 ± 6 and 15.4 ± 6.16 mg/kg,

256 respectively. There was no significant difference in Fe content between yellow earth

257 and yellow-brown earth, with values of 22.76.08 ± 8.38 g/kg and 17.69 ± 8.88 g/kg,

258 respectively. There is a significant difference in K content between yellow earth and

259 yellow-brown earth, with the highest K content in LXP (4.76 ± 0.37 g/kg) in yellow

260 earth and the highest K content in XD33 (13.42 ± 1.18 g/kg) in yellow earth. The

261 variation of K content is greater in yellow-brown earth. There is a significant difference

262 in MC content between yellow earth and yellow-brown earth, with values of 53.50 ±

263 9.88% g and 53.13 ± 9.45%, respectively, and their variability is also relatively small.

264 There is no significant difference in P content between yellow earth and yellow-brown

265 earth, with values of 403.40 ± 110.63 mg/kg and 457.8 ± 145.30 mg/kg, respectively.

266 There is no significant difference in Pb content between yellow earth and yellow-brown

267 earth, with values of 45.99.40 ± 20.35 mg/kg and 41.40 ± 14.54 mg/kg, respectively.

268 There is no significant difference in pH between yellow earth and yellow-brown earth.

269 The pH contents of the surface soil in the yellow earth of the research area vary between

270 3.07 and 4.97, with an average value of 4.17 mg/kg. Among them, the pH value of

271 XD33 (3.75 ± 0.49) is the lowest in the yellow earth. The pH of the surface soil of

272 yellow-brown earth is 3.93 ± 0.40, with a minimum value of 3.58 ± 0.12. There is no

273 significant difference in SOC content between the two soils, which are 202.81 ± 95.13

274 g/kg and 203.80 ± 107.35 g/kg in yellow earth and yellow-brown earth, respectively.

275 Although there is no significant difference in Zn content between yellow earth and

276 yellow-brown earth, the Zn contents in yellow-brown earth (874.25 ± 1801.69 mg/kg)

277 are significantly higher than that in yellow earth (455.13 ± 397.59 mg/kg). Overall,

278 merely the contents of AP, Co, and K in yellow earth and yellow-brown earth show the

279 significant differences, while there are no significant differences between most

280 physicochemical parameters.

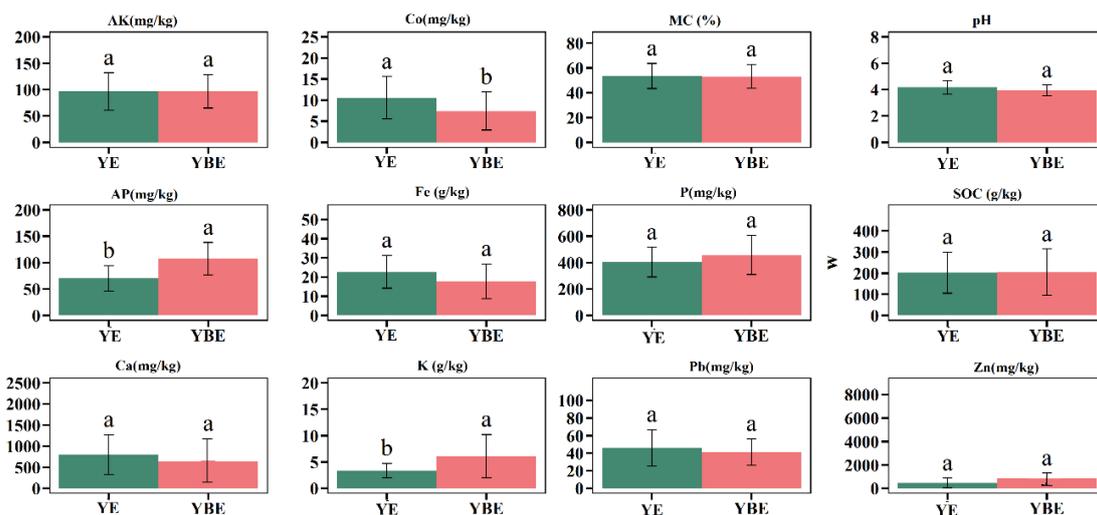281   **Table 1**. Physicochemical parameters of yellow earth and yellow-brown earth

Parameters	Yellow earth					
	DMS	HGS	HXP	LQS	LXP	XD31
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
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
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
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
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
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
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
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
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
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
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
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

Parameters	Yellow-brown earth					
	LCDA	LCDB	MXLA	MXLB	SD	YA
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
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
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
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
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
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
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
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
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

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
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
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

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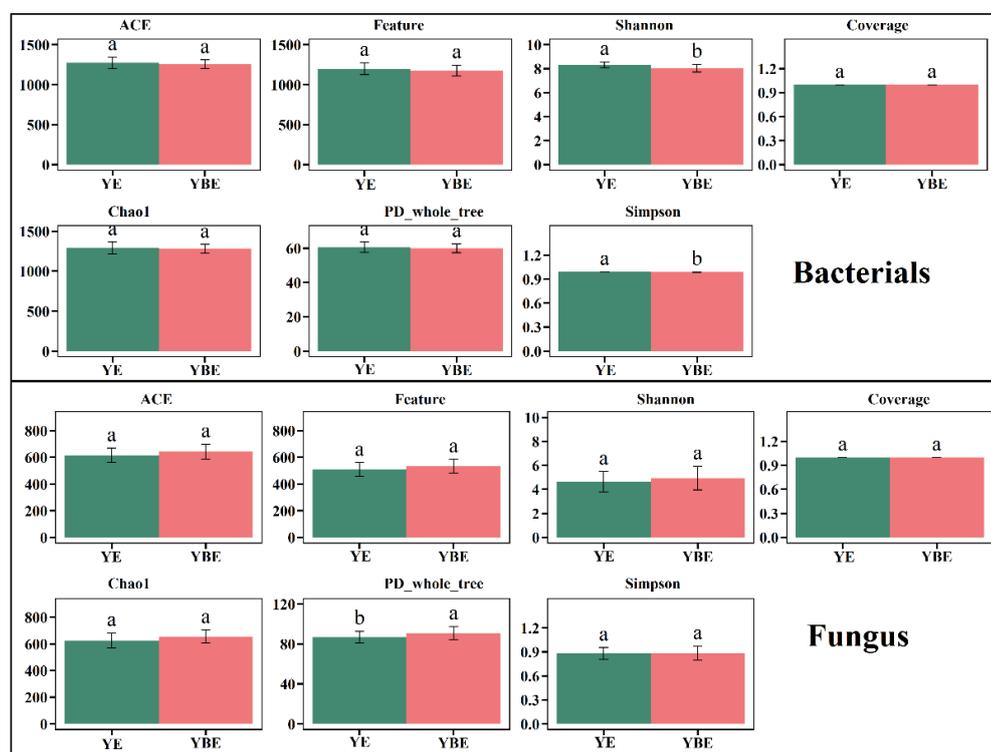

Figure 3. The significant difference of physicochemical parameters of yellow earth and yellow-brown earth (**Note:** Different superscript letters in each row represent significant differences between different treatments (ANOVA, p < 0.05); YE and YBE represent yellow earth and yellow-brown earth, respectively.)

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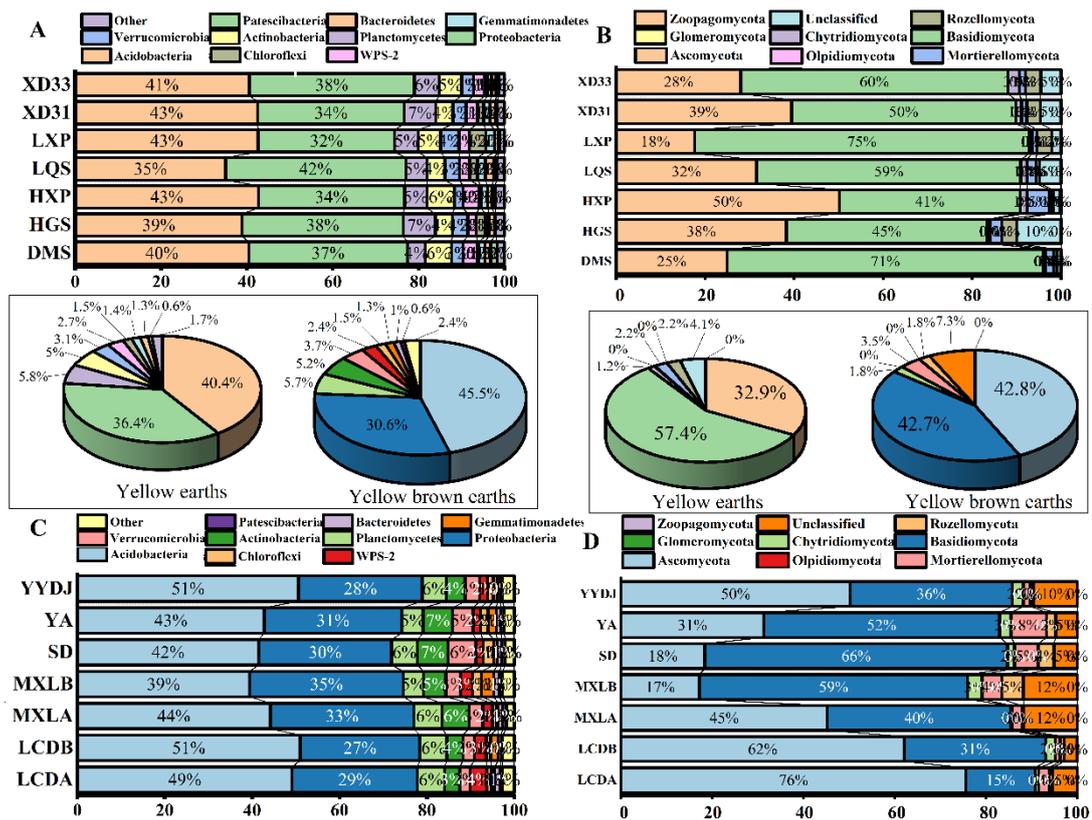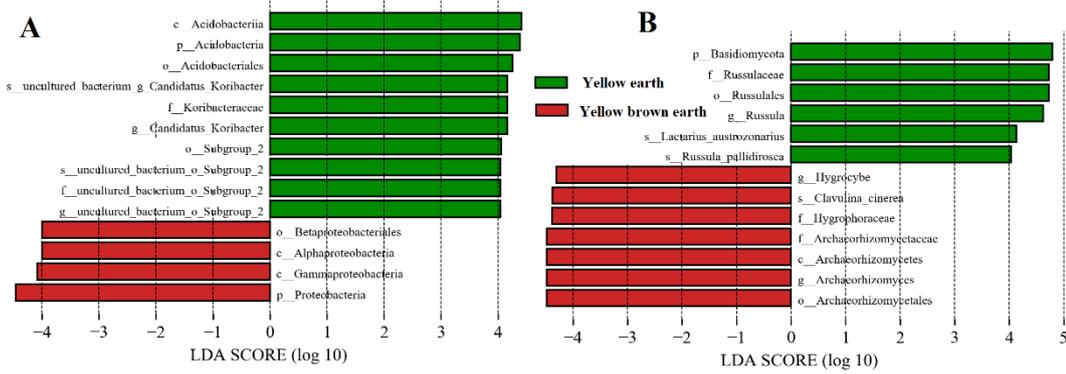
Figure 5. Community structure of yellow earth in bacterial (A) and fungus (C) and yellow-brown earth in bacterial (B) and fungus (D) at the phylum level. (**Note:** YE and YBE represent yellow earth and yellow-brown earth, respectively.)

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

344 f_unctltured_bacterioum_o_Subgroup_2), and 2 genera (d_Candidatus_Koribacter and

345 d_uncultured   bacteria   o   Subgroup   2)   and   2   species   (s

346 __uncultured_bacterium_g_Candidatus_Koribacter   and

347 f_uncultured_bacverium_o_Subgroup_2) (**Figure 6A**).   The fungal community in two

348 typical   soils   consists   of   1   phylum   (p_Basidiomycota),   1   Class

349 (c_Archaeorhizomyeetes), 2 orders (o'Russulales and o'Archaeorhizomyeetes), 3

350 families (f_Russulaceae, f_Hygrophoraceae and f_Archaeorhizomyetaceae), 3 genera

351 (d_Russula, d_Hygrdcybe and d_Archaeorhizomyces), and 3 species (s_Lactarius

352 austrozonarius, s_Russula pallidirosea and s_Clavulina_cinerea) (**Figure 6B**). This

353 means that there is a significant difference in the bacterial and fungal communities

354 between the two typical soils, with the higher differences of bacterial occurring in

355 yellow earth. **Figure 7** exhibits the effect of soil physicochemical parameters on

356 bacterial community similarity. The larger the absolute value of the slope is, the greater

357 the influence of this factor is. For all physicochemical parameters, the absolute values

358 of pH slope (-0.10555 in yellow earth and -0.14962 in yellow-brown earth) are

359 significantly greater than other indicators, indicating that pH has the greatest impact on

360 the bacterial communities of the two typical soils in Fanjing Mountain. Similar patterns

361 have also been found in fungi, where the absolute values of pH slope (-0.05956 in

362 yellow earth and -0.13697 in yellow-brown earth) are significantly higher than other

363 indicators (**Figure 8**). pH is an important factor affecting fungal communities in the

364 two typical soils of Mount Fanjing. In addition, the slope of pH in bacteria and fungi is

365 greater in yellow-brown earth than in yellow earth, indicating that pH has a greater

366 impact on the microbial community in yellow-brown earth in comparison with yellow

367 earth.

368

A
- c__Acidobacteriia
- p__Acidobacteria
- o__Acidobacteriales
- s__uncultured_bacterium_g_Candidatus_Koribacter
- f__Koribacteraceae
- g__Candidatus_Koribacter
- o__Subgroup_2
- s__uncultured_bacterium_o_Subgroup_2
- f__uncultured_bacterium_o_Subgroup_2
- g__uncultured_bacterium_o_Subgroup_2
- o__Betaproteobacteriales
- c__Alphaproteobacteria
- c__Gammaproteobacteria
- p__Proteobacteria

B
- p__Basidiomycota
- f__Russulaceae
- o__Russulales
- g__Russula
- s__Lactarius_austrozonarius
- s__Russula_pallidirosca
- g__Hygrocybe
- s__Clavulina_cinerea
- f__Hygrophoraceae
- f__Archaeorhizomycetaceae
- c__Archaeorhizomycetes
- g__Archaeorhizomyces
- o__Archaeorhizomycetales

Yellow earth
Yellow brown earth

LDA SCORE (log 10)

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

370 brown earth
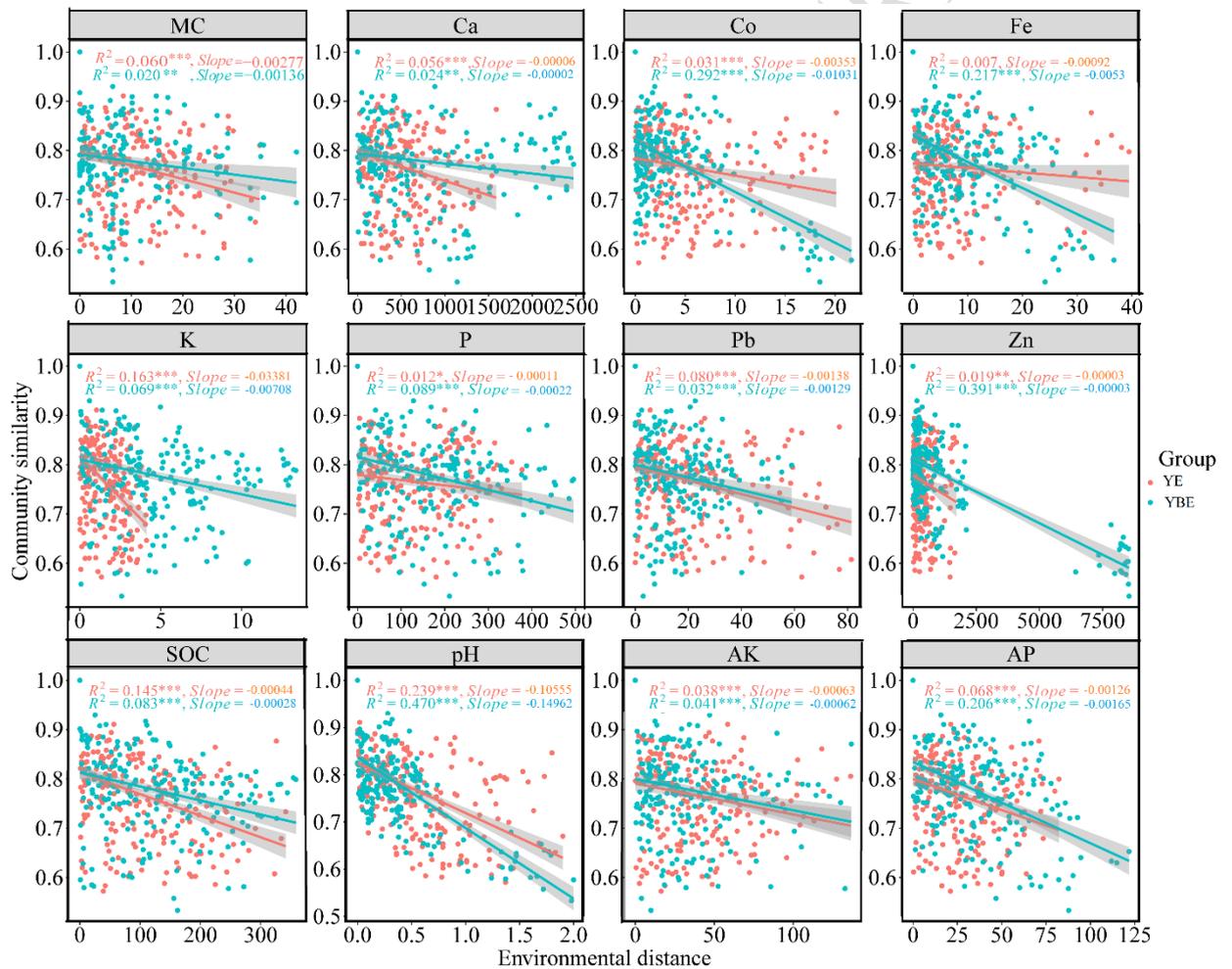
371

372 **Figure 7.** Effect of physicochemical parameters on bacterial community similarity in

373 soil. (**Note:** YE and YBE represent yellow earth and yellow-brown earth, respectively.)

20
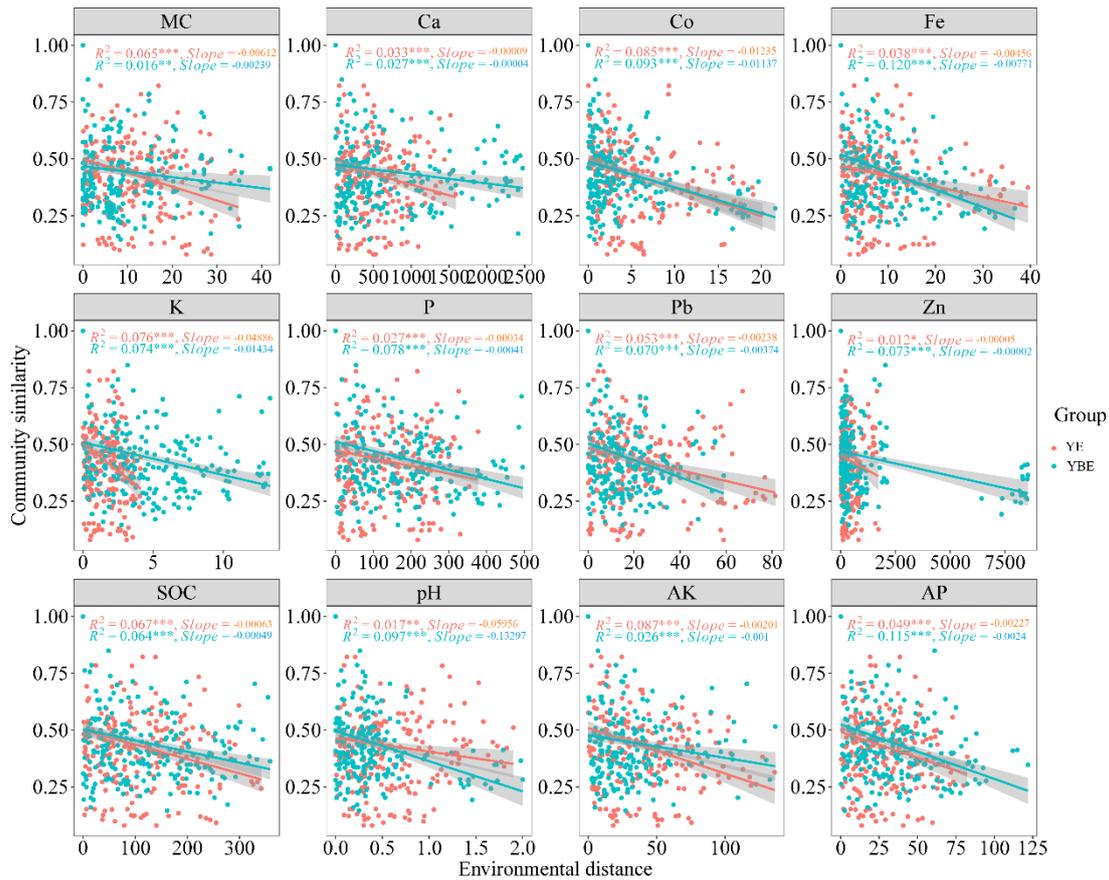
**Figure 8.** Effect of physicochemical parameters on fungus community similarity in soil.

(**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

21

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.

412
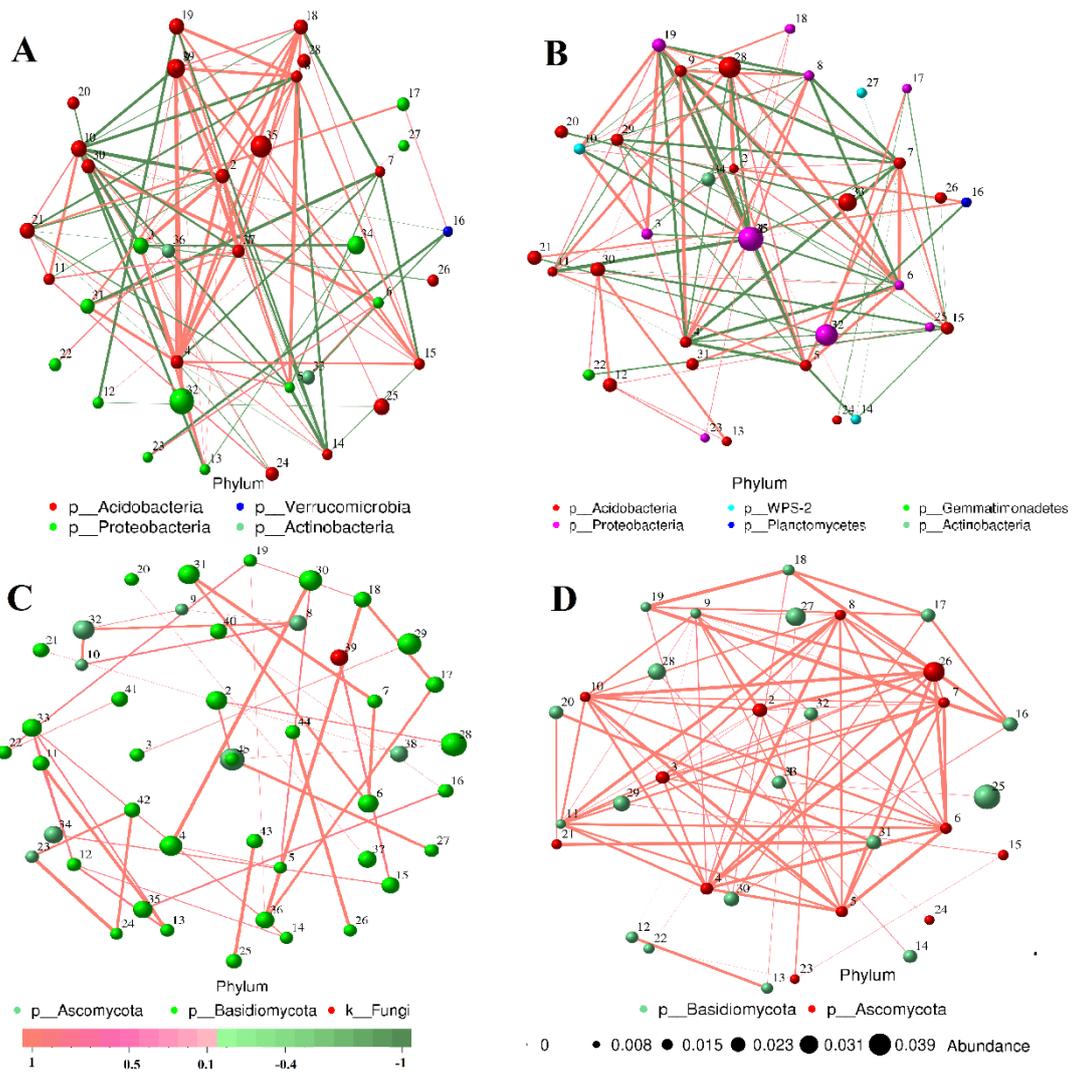
Figure 9. Co-occurrence network of bacteria in the yellow earth (A) and yellow-

brown earth (B), and of bacteria in the yellow earth (C) and yellow-brown earth (D)

of Fanjing Mountain

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

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419
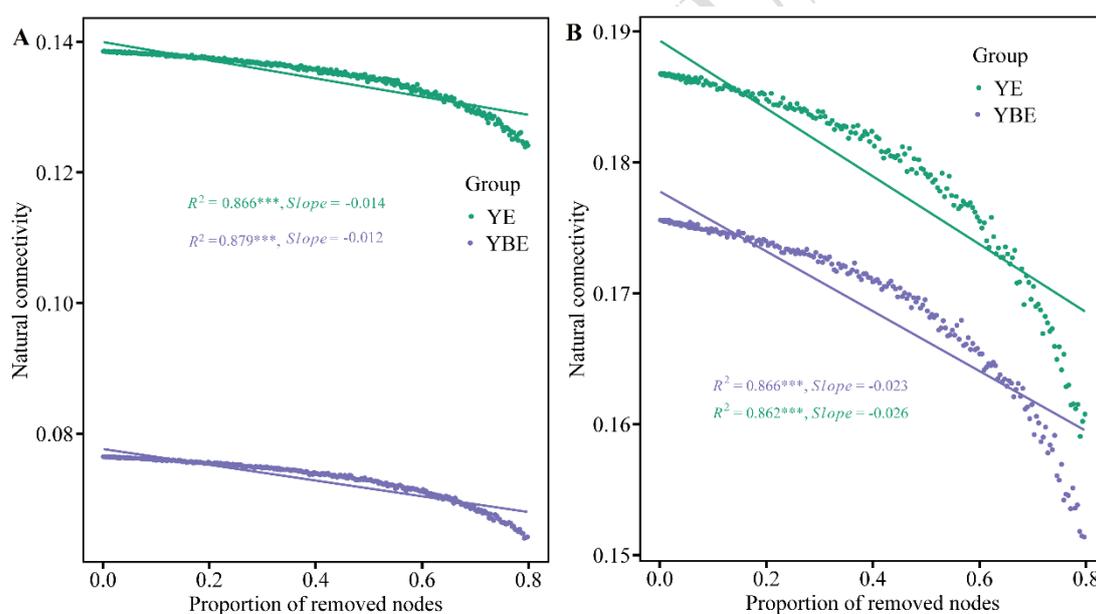
Figure 10. Natural connectivity of bacteria (A) and of fungus (B) in the yellow earth and yellow-brown earth of Fanjing Mountain (**Note:** YE and YBE represent yellow earth and yellow-brown earth, respectively.)

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.
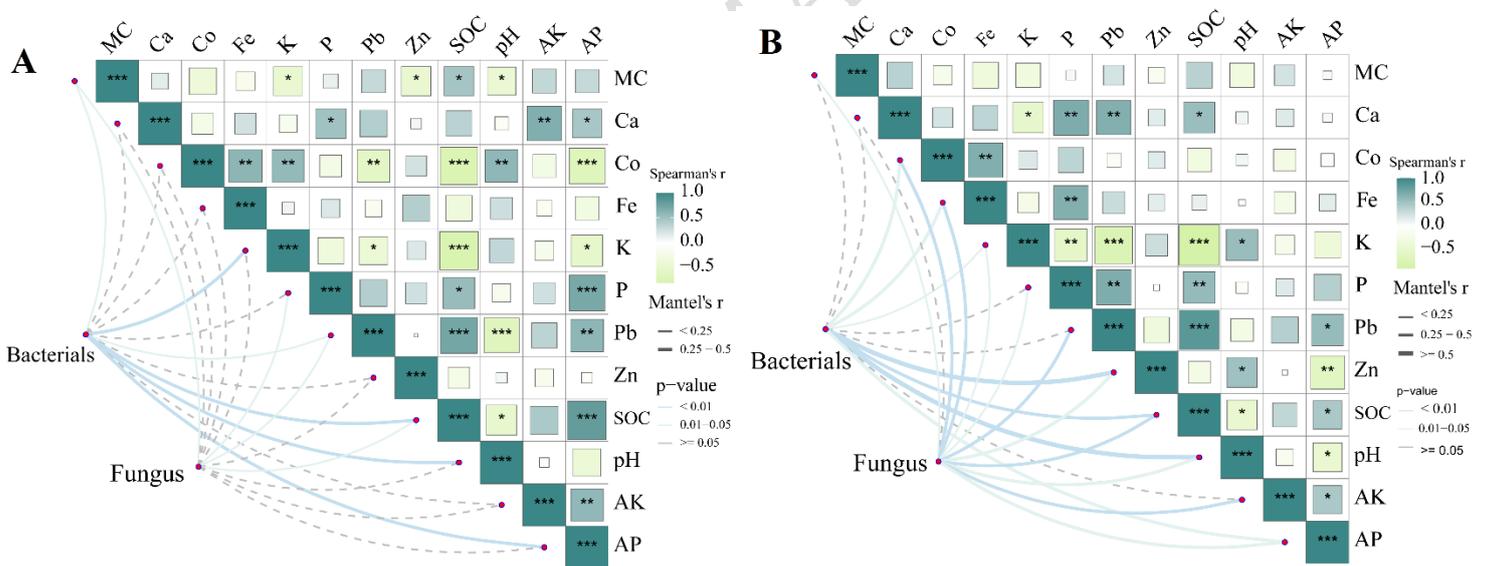

Figure 11. Relationship between microbial community and physicochemical indicators using Mantel analysis

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

25

443   very low (< 30 %), it indicates that there are still important environmental factors that

444   have not been measured (or there is a lot of noise). The environmental factors of the

445   yellow earth in Fanjing Mountain have a significant impact on bacterial distribution,

446   with RDA1 (37.96%) and RDA2 (15.06%) explaining 53.02% of the variance in species

447   environment relationships (**Figure 12A**). pH, Zn, MC, Co, Pb have a significant impact

448   on the bacterial community of phylum level. Among them, Acidobacteria is positively

449   correlated with Fe, Zn, Co, P, Pb, and negatively correlated with Ca and AK.

450   Proteobacteria is positively correlated with pH, AP, P, AK and Ca, and negatively

451   correlated with Zn, Fe, and Co. There is little correlation between Acidobacteria and

452   Proteobacteria. Zn, Co, Fe, Pb, Ph, and AP in yellow earth have a significant impact on

453   bacterial communities, with RDA1 (38.54%) and RDA2 (18.93%) explaining 58.77%

454   of the variance in species environment relationships (**Figure 12B**). Acidobacteria is

455   negatively correlated with all physical and chemical indicators, while it is positively

456   correlated with most physical and chemical indicators. The correlation between

457   Acidobacteria and Proteobacteria is not significant. The environmental factors of the

458   yellow earth in Fanjing Mountain have a relatively small impact on the distribution of

459   fungi, with RDA1 (45.34%) and RDA2 (8.991%) explaining 54.33% of the variance in

460   species environment relationships (**Figure 12C**). Ascomycota is positively correlated

461   with AK, Ca, P, AP, Zn, Pb, and SOC, and negatively correlated with MC, Co, and Fe,

462   while Basidiomycota is the opposite. Ascomycota and Basidiomycota are not correlated.

463   The environmental factors in the yellow-brown earth of Mount Fanjing have a relatively

464   small impact on the distribution of fungi, with RDA1 (47.92%) and RDA2 (9.295%)

465   explaining 57.81% of the variance in species environment relationships (**Figure 12D**).

466   In summary, Ascomycota is positively correlated with AK and MC, and negatively

467   correlated with other physicochemical indicators, while Basidiomycota is the opposite.

468
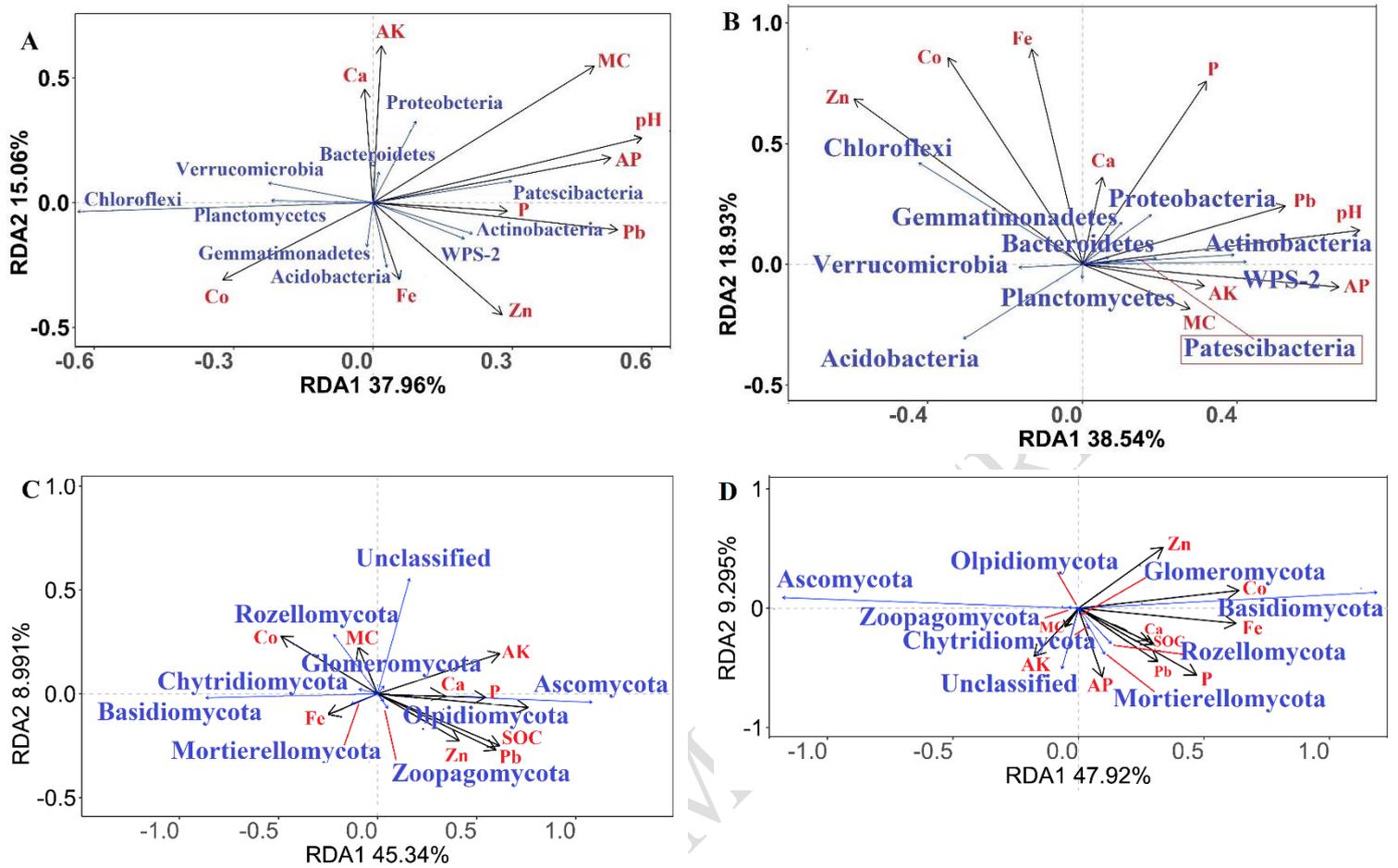
469

470 **Figure 12**. RDA analysis of bacterial in yellow earth （A） and yellow-brown earth (B),

471 and fungus in yellow earth (C) and yellow-brown earth (D)

472 3.6 Function prediction for microbial community in yellow earth and yellow-brown

473 earth

474 Based on published literature on microbial pure culture research, the taxonomic

475 information (phylum, class, order, family, genus) of known prokaryotes (bacteria and

476 archaea) is correlated with the ecological functions/biochemical processes that they

477 participate in (such as nitrification, denitrification, fermentation, etc.). Functional gene

478 expressions, including hydrocarbon_degradation, intracellular parasites, methylotrophy,

479 methanotrophy, nitrogen_fixation, fermentation, in yellow earth are higher than of

27

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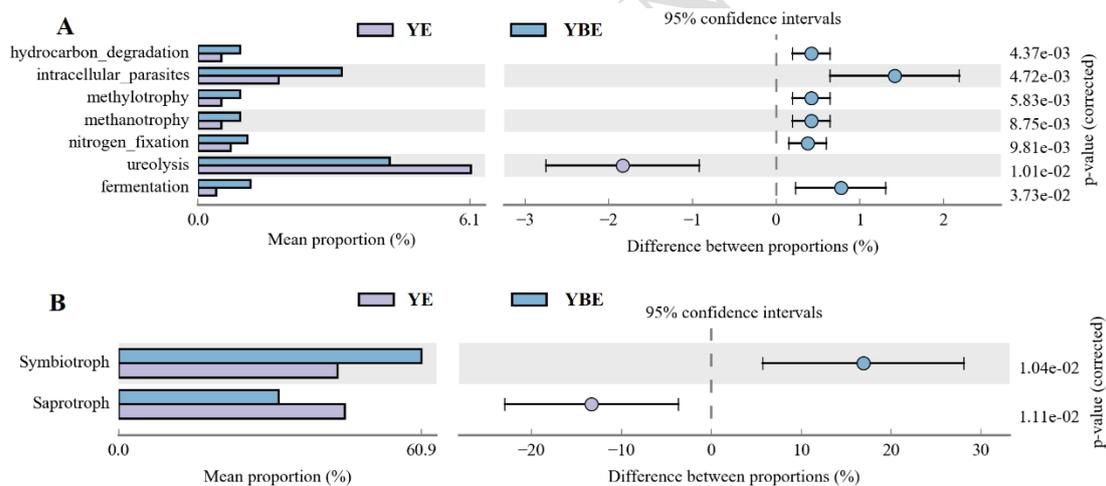
Figure 13. Function prediction for bacterial (A) and fungus (B) in yellow earth and yellow-brown earth. (**Note:** YE and YBE represent yellow earth and yellow-brown earth, respectively.)

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

524   ions (H^+ and Al^{3+}) on soil colloids, thereby exacerbating soil acidification (Lu *et al.*

525   2014). This is consistent with the findings of this study that the Ca content in yellow

526   earth is lower than that in yellow earth in Fanjing Mountain. If this leaching process is

527   stronger in the yellow-brown earth area than in the yellow earth area, it may result in a

528   lower pH in the former. Yan *et al*. (2015) reported that the soil pH at different altitudes

529   in Fanjing Mountain ranged from 4.02 to 6.41, and the soil exhibits weak acidity

530   shifting to strong acidity. With the increase of altitude, nutrient content showed a certain

531   vertical difference distribution, and the content of soil organic matter, alkali hydrolyzed

532   nitrogen, available potassium, and available phosphorus at different depths showed a

533   trend of first increasing and then decreasing. The comprehensive content of soil

534   nutrients is relatively low at altitudes of 500-520 m, while nutrient content is relatively

535   abundant at other altitudes, reaching its maximum value at altitudes of 1500-2000 m.

536   In yellow earth and yellow-brown earth, the values are 202.81 ± 95.13 g/kg and 203.80

537   ± 107.35 g/kg, respectively. There is no significant difference in SOC content between

538   the two soils, which may be due to the similarity in soil texture and bulk density. The

539   clay content, bulk density, and moisture content of yellow earth and yellow-brown earth

540   may be similar under the same parent material or terrain conditions, resulting in similar

541   physical protection mechanisms for organic carbon (such as aggregate formation),

542   thereby reducing differences (Xiao 2013). Xiao *et al*. (2024) found that in the 0-60 cm

543   soil layer, soil aggregates were mainly composed of water stable macroaggregates

544   larger than 0.25 mm, with an average content of 86.78%. The stability of soil aggregates

545   along the altitude gradient is mainly influenced by soil SOC and pH values, with

546   explanatory powers of 76.3% and 1.3%, respectively, which are the main environmental

547   factors affecting soil aggregate stability. In this study, the microbial communities of

548   yellow earth and yellow-brown earth are functionally similar. In forest ecosystems, the

549 microbial communities of yellow earth and yellow-brown earth may have similar

550 functions due to sharing similar environmental conditions, resulting in similar rates of

551 organic carbon decomposition. Research has shown that there is no significant

552 difference in soil respiration rate and microbial activity between yellow-brown earth

553 and yellow earth under the same vegetation and climate conditions, resulting in similar

554 rates of organic carbon mineralization (Jin 2019). In this study, the pH value of yellow-

555 brown earth is relatively low, and this extremely acidic environment is sufficient to

556 dissolve the iron oxide film. Once the outer shell is dissolved, P enclosed inside will be

557 released, becoming AP that can be utilized by plants. Therefore, AP in yellow-brown

558 earth is significantly higher than that in yellow earth.

559   Generally, Acidobacteria is the most dominant phylum in yellow earth. Especially,

560 subgroups such as GP1 and GP3, which are particularly adapted to acidic and nutrient

561 poor environments, can decompose recalcitrant organic matter and are the main

562 microbial communities in the acidic environment of yellow earth. The bacterial

563 community diversity in yellow-brown earth is usually higher than that in yellow earth.

564 The dominant phylum of bacteria has shifted from acidophilic Acidobacteria to a more

565 balanced situation dominated by both Proteobacteria and Acidobacteria, and the

566 importance of Actinobacteria has also increased. In this study, Acidobacteria and

567 Proteobacteria were the main phyla of bacterial in yellow earth and yellow-brown earth.

568 Acidobacteria (40.4%) and Proteobacteria (36.4%) have a higher proportion in yellow

569 earth, while Acidobacteria (45.5%) has a much higher proportion in yellow-brown earth

570 than Proteobacteria (30.6%), and Acidobacteria and Proteobacteria are differential

571 indicator species in yellow earth and yellow-brown earth, respectively. Wu *et al*. (2023)

572 reported that Acidobacteria, Proteobacteria, Planktonic Bacteria, and Actinobacteria are

573 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

649   aluminum enrichment and a more balanced mineral composition, which support a more

650   complex microbial interaction network (Yang *et al*. 2023). The correlation network

651   constructed based on 16S/ITS amplicon data is essentially an ecological niche

652   preference similarity network. The positive correlation between the two groups may

653   only stem from a common response to environmental factors such as pH and

654   temperature, rather than metabolic synergy; Negative correlation may also reflect niche

655   differentiation or sampling effects, rather than direct antagonism (Blüthgen, 2024).

656   Siegenthaler et al. (2024) found in the synthetic microbiota that the strong antagonistic

657   relationship confirmed by in vitro co culture (Pseudomonas inhibits other bacteria

658   through pseudomonas) is either completely invisible or positively correlated in the in

659   vivo correlation network. This suggests that symbiotic networks may completely mask

660   true antagonism. Therefore, the co-occurrence network in this study is merely providing

661   a reference to interaction between microorganism of yellow earth and yellow-brown

662   earth.

663   Functional gene expressions, including hydrocarbon_degradation, intracellular

664   parasites, methylotrophy, methanotrophy, nitrogen_fixation, fermentation, in yellow

665   earth are higher than of yellow-brown earth. Yellow earth faces a relatively severe

666   environment, where nutrients are firmly trapped in forms that are difficult to utilize,

667   such as P adsorbed by iron and aluminum oxides and complex organic matter.

668   Microorganisms need to secrete more types of acid phosphatases to desorb and obtain

669   P. More types and potent extracellular enzymes (such as cellulase, chitinase, lignin

670   peroxidase) need to be produced to break down extremely stubborn organic matter and

671   extract carbon, nitrogen, and phosphorus from it. This directly leads to a richer and

672   more diverse family of functional genes related to nutrient cycling (C, N, P, S cycles)

673   (Wu et al. 2023). Yellow-brown earth is relatively in suitable environment, with high

674 nutrient availability and easier decomposition of organic matter. Microorganisms can

675 easily access resources, so there is no need to maintain a large and diverse enzyme pools

676 (Wu et al. 2023). Their functional genes may be more focused on utilizing readily

677 available and simple resources. This study also found that the ureolysis functional genes

678 in forest yellow-brown earth are higher than those in yellow earth. In strong acid

679 environments, microorganisms may rely on other more effective nitrogen acquisition

680 pathways rather than investing in a ureolysis pathway severely inhibited by acidic

681 environments. For example, they may be more focused on decomposing organic

682 nitrogen (such as proteins, chitin) to directly release NH_4^+ (ammonification). Therefore,

683 for fungus in yellow earth, maintaining high abundance of ureolysis is an uneconomical,

684 as natural selection pressure tends to favor genes from other nitrogen acquisition

685 strategies (Li *et al*. 2021). In the co-occurrence network of fungi in the yellow earth and

686 yellow-brown earth of Fanjing Mountain, positive correlations between species account

687 for the largest proportion, indicating that there is mainly a synergistic effect between

688 the two typical soil microorganisms. The proportion of symbiotoph in the yellow earth

689 of Fanjing Mountain is higher than that in the yellow-brown earth, while the proportion

690 of Saprotroph is higher in the yellow-brown earth. Most plants are difficult to obtain

691 sufficient nutrients from poor yellow earth by relying on their own root systems.

692 Cooperating with arbuscular mycorrhizal fungi (AMF) and other symbionts, the

693 extremely large mycelial network of fungus can help plants explore and absorb water

694 and difficult to move nutrients in larger soil volumes (van Galen *et al.* 2025). Yuan

695 (2019) reported the AMF in five different forest types on Mount Fanjing. AMF can

696 form symbiotic relationships with the root systems of higher plants, helping them

697 absorb water and nutrients. This study found that different forest types form unique

698 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

724   for AP, Co, and K, there are no significant differences between most physicochemical

725   parameters in yellow earth and yellow-brown earth. Although the bacteria and fungi

726   composition of the two typical soils in Fanjing Mountain are similar, the proportion of

727   bacteria and fungi differs significantly between the two typical soils. Acidobacteria and

728   Proteobacteria are also the main phyla of bacterial in yellow earth, while Acidobacteria

729   dominates in yellow-brown earth. Community similarity, mantel and RDA analysis also

730   demonstrates that pH is an important factor affecting bacterial and fungus communities

731   in the two typical soils, and pH has a greater impact on the microbial community in

732   yellow-brown earth in comparison with yellow earth. Co-occurrence network of

733   bacteria and fungus exhibits that the synergistic effect between microbial community is

734   higher than the competitive effect. Functional gene expressions, including

735   hydrocarbon_degradation, intracellular parasites, methylotrophy, methanotrophy,

736   nitrogen_fixation, fermentation, in yellow earth are higher than of yellow-brown earth.

737   The proportion of symbiotoph and saprotroph dominates in the yellow earth in yellow-

738   brown earth, respectively. Our results suggest that although there are merely the few

739   differences between physicochemical parameters, the microbial community and

740   functional gene vary found in the yellow earth and yellow-brown earth) in Fanjing

741   Mountain via these discrepancies, which maybe caused by the discrepancy in pH in soil.

742   Our study firstly emphasis the typical soil microbial community characteristics of the

743   Fanjing Mountain forest ecosystem, providing key soil science basis for the precise

744   protection and adaptive management of mountain forest ecosystems in the future.

745

746   **Author contribution** Xianliang Wu, Jiang Hong and Xiuyuan Yang conceptualized and

747   designed the problem. Material preparation, data collection and analysis were

748   performed by Anding Li, Guiting Mu, Yingying Liu and Wenmin Luo. The first draft

749   of the manuscript was prepared by Xianliang Wu, and all other authors approved the

750   same. The completed manuscript was checked and corrected by Xiuyuan Yang. The

751   authors ranked according to their contributions.

752

761   **Data Availability Statement** The data used to support the findings of this study can be

762   made available by the corresponding author upon request

763

764   **Conflict of Interest**

765   The authors declare no conflicts of interest

766

767   **Consent to publish**

768   All the authors agree to publish this paper in this journal

769

770   **References**

771   Adams, J. A., & Norton, D. A. (1991). Soil and vegetation characteristics of some tree

772   windthrow features in a South Westland rimu forest. *Journal of the Royal Society*

773   *of New Zealand*, **21(1)**, 33–42.

774 Blüthgen, N., & Staab, M. (2024). A critical evaluation of network approaches for

775   studying species interactions. *Annual Review of Ecology, Evolution, and*

776   *Systematics*, **55**, 65–88.

777 Chai, R., Sun, X., An, S., Lin, T., Wang, H., Chen, W., & Song, Y.-F. (2025). Effect of

778   vermiculite on in-situ super-stable mineralization and amelioration on sodic

779   soil. *Environmental Technology & Innovation*, **25**, 104156.

780 Chen, Z., Bright, T. L., Wen, H., Lei, L., Zeng, L., Xiao, W., & Maltz, M. R. (2025).

781   Post-fire recovery of soil multiple properties, plant diversity, and community

782   structure of boreal forests in China. *Forests*, **16(5)**, 806.

783 Delgado-Baquerizo, M., Reich, P. B., Trivedi, C. (2020). Multiple elements of soil

784   biodiversity drive ecosystem functions across biomes. *Nature Ecology &*

785   *Evolution*, **4(2)**, 210–220.

786 Dong, Z., Geng, Q., Wei, K., & Hou, L. (2025). Soil available phosphorus and pH

787   regulate the distribution of Juniperus przewalskii forest understory plant

788   community diversity along an elevation gradient. *Forest Ecology and*

789   *Management*, **580**, 122524.

790 Duan, Y., Zhang, J., Petropoulos, E., Zhao, J., Jia, R., Wu, F., Chen, Y., Wang, L., Wang,

791   X., Li, Y., & Li, Y. (2025). Soil acidification destabilizes terrestrial ecosystems via

792   decoupling soil microbiome. *Global Change Biology*, **131(4)**, e70174.

793 Fernandez, C. W., & Kennedy, P. G. (2018). The secret social lives of fungi:

794   Ectomycorrhizal fungi leverage carbon from tree hosts to outcompete saprotrophic

795   fungi. *New Phytologist*, **217**, (2), 468-471.

796 Fernández, I., & Kennedy, P. G. (2024). The decomposition imperative: The primacy

797   of saprotrophism in shaping forest soil microbial communities. *Trends in Ecology*

798   *& Evolution*, **39(2)**, 145-155.

799   Fujii, K., Hayakawa, C., & Sukartiningsih. (2021). Root exudation and biodegradation

800   of organic acids in a tropical forest soil under dipterocarp and pioneer trees. *Plant*

801   *and Soil*, **469**, 213–226.

802   Guo, M., Wu, H., Hao, G., et al. (2017). Bacillus subtilis improves immunity and

803   disease resistance in rabbits. *Frontiers in Immunology*, **8**, 354.

804   Guo, Z., Huang, X., Li, C., Ma, S., Yang, N., Li, H., Zhang, T., Wang, T., Li, S., & Su,

805   J. (2025). Altitudinal influences on soil microbial diversity: The pivotal role of

806   plant functional composition in shaping bacterial and fungal communities. *Forest*

807   *Ecology and Management*, **586**, 122728.

808   Jin, J.Y. Vertical distribution of soil organic matter and its relationship with nitrogen,

809   phosphorus and potassium content in Mountain Lu. *Hubei Agricultural Sciences*,

810   **2019**, 58, 44-46.

811   Lei, J., Z. Lv, A. Duan, C. Xiang, and J. Zhang. 2025. High Site Index Drives the Soil

812   Microbial Network Complexity and Function in Chinese Fir Mixed Plantations

813   After Near-Natural Transformation. *Land Degradation & Development* 1–17.

814   Li, T., Wang, R., Cai, J., Feng, X., Liu, H., Meng, Y., Wang, Z., & Jiang, Y. (2021).

815   Enhanced carbon acquisition and use efficiency alleviate microbial carbon relative

816   to nitrogen limitation under soil acidification. *Ecological Processes*, **10**, (1), 32.

817   Liu, C. S., Zhao, D. F., Ma, W. J., Guo, Y. D., Wang, A. J., Wang, Q. L., & Lee, D. J.

818   (2016). Denitrifying sulfide removal process on high salinity wastes in the

819   presence of Halomonas sp. *Applied Microbiology and Biotechnology*, **100(3)**,

820   1421–1426.

821   Liu, W., Tu, C., Lang, Z., Feng, J., Li, L., Wang, Q., & Liu, C. (2010). Major and Trace

822   Element Compositions of Yellow and Limestone Soils in the Karst Area of

823   Southwest China: Implications for Weathering and Soil-formation Processes.

824   *Earth and Environment*, **38(3)**, 271–279.

825   López-García, A., Müller, M. M., Pena, R., & Polle, A. (2023). Carbon allocation to the

826   fungus is driven by host tree species and fungal taxon in a temperate forest

827   ectomycorrhizal community. E*nvironmental Microbiology*, **25(11)**, 2207–2224.

828   Lu, X., Mao, Q., Gilliam, F. S., Luo, Y., & Mo, J. (2014). Nitrogen deposition

829   contributes to soil acidification in tropical ecosystems. *Global Change Biology*,

830   **20(12)**, 3790–3801

831   Lustenhouwer, N., Maynard, D. S., Bradford, M. A., Lindner, D. L., Oberle, B., Zanne,

832   A. E., & Crowther, T. W. (2020). A trait-based understanding of wood

833   decomposition by fungi. *Proceedings of the National Academy of Sciences of the*

834   *United States of America*, **117(21)**, 11551–11558.

835   Mandah, V. P., Masso, C., & Onana, A. A. (2025). Soil organic carbon and nutrient

836   content across agricultural systems in the forest-savannah transition zone of

837   Cameroon. *Soil & Tillage Research*, **248**, 106458.

838   Nikovskaya, G. N., Ul'berg, Z. R., & Borisova, E. N. (2004). Sorption-desorption of

839   copper and strontium ions by the soil: The influence of microorganisms on the

840   state of metals. *Colloid Journal*, **66(4)**, 451–455.

841   Onet, A., Grenni, P., Onet, C., Stoian, V., & Crisan, V. (2025). Forest soil microbiomes:

842   A review of key research from 2003 to 2023. *Forests*, **16(1)**, 148.

843   Parfitt, R. L., & Webb, T. H. (1984). Allophane in some South Island yellow-brown

844   shallow and stony soils and high country and upland yellow-brown earths. *New*

845   *Zealand Journal of Science*, **27(1)**, 37–40.

846   Santolamazza Carbon, S., Iglesias Bernabé, L., Benito-Rueda, E., Barreal, E., &

847   Gallego, P. P. (2025). Metabarcoding Unveils Seasonal Soil Microbiota Shifts and

848   Their Influence on Boletus edulis and Boletus reticulatus Mycelium in Quercus

849　　　robur Stands. *Microorganisms*, **13(9)**, 2196.

850　Siegenthaler, S., Agler, M. T., & Kemen, E. (2024). Strong pairwise interactions do not

851　　　drive interactions in a plant leaf associated microbial community. *ISME*

852　　　*Communications*, **5(1)**, ycae117.

853　Stewart, G. H., Basher, L. R., Burrows, L. E., Runkle, J. R., Hall, G. M. J., & Jackson,

854　　　R. J. (1993). Beech-hardwood Forest composition, landforms, and soil

855　　　relationships, North Westland, New Zealand. *Vegetatio*, **106(2)**, 111–125.

856　van Galen, L. G., Furneaux, B., Soudzilovskaia, N. A., & Crowther, T. W. (2025).

857　　　Global divergence in plant and mycorrhizal fungal diversity hotspots. *Nature*

858　　　*Communications*,**16**, 6702.

859　Wu, X., Zhang, Z., Zhang, J., Liu, Y., Luo, W., Mou, G., & Huang, X. (2023). Multiple

860　　　factors jointly lead to the lower soil microbial carbon use efficiency of *Abies*

861　　　*fanjingshanensis* in a typical subtropical forest in Southwest China. *Forests*, 14(9),

862　　　1716.

863　Xiao, S., Zhang, L., Chen, J., et al. (2024). Stability of soil aggregates and its

864　　　influencing factors at different elevations in Fanjing Mountain. *Research of Soil*

865　　　*and Water Conservation*, **31(3)**, 160–168. (In Chinese)

866　Xiao, Y.F. 2013. Soil Organic Carbon Spatial Distribution and the Analysis of the

867　　　Influencing Factors in Mangshan. Central South University of Forestry &

868　　　Technology, Hunan, Changsha, China, 1-60.

869　Yan, Q., Zhang, W., Shi, L., Lin, C., & He, T. (2015). Nutrient characteristics of forest

870　　　soil at different elevation in Fanjingshan Nature Reserve. *Guizhou Agricultural*

871　　　*Sciences*, **43(8)**, 146–150. (In Chinese)

872　Yang, X., Li, Y., Li, Y., Lu, A., Dong, H., Jin, S., & Ding, H. (2023). Microbially

873　　　induced clay weathering: Smectite-to-kaolinite transformation. *American*

874   *Mineralogist*, **108(9)**, 1637–1649.

875   Yang, X., Mu, G., Liu, Y. (2025). Spatial differentiation of metallic micronutrients in

876   soil – plant systems along an altitudinal gradient in the Fanjing Mountain,

877   Southwestern plateau of China. *Environmental Monitoring and Assessment*, **197**,

878   525.

879   Yang, Y., Cheng, H., Dou, Y., & An, S. (2020). Plant and soil traits driving soil fungal

880   community due to tree plantation on the Loess Plateau. *Science of The Total*

881   *Environment*, **708**, 134560

882   Yuan, T. 2019. Diversity Analysis of Arbuscular Mycorrhizal Fungi in the Rhizospheric

883   Soil of Five Forest Types in Fanjingshan National Nature Reserve. Guizhou,

884   Guiyang, China, 1-60.

885   Zhang, F.H. and Zhang, M. 1980. Soil types and vertical distribution characteristics of

886   Fanjing Mountain. Guizhou soil, 2, 12-20.

887   Zhang, M., & Mao, X. (2018). Genetic characteristics and taxonomic classification of

888   vertical soils in the Fanjingshan Mountain. *Chinese Journal of Soil Science*, **49(4)**,

889   757–766. (In Chinese)

890   Zhang, Q., & He, X. (2021). Low molecular weight organic acids in forest soils: A

891   review of their sources, composition, and ecological effects. *Forest Ecology and*

892   *Management*, **496**, 119441.

893   Zhang, Q., Chen, C., Chen, X., Ren, X., Zhang, Z., & Liu, W. (2019). Effects of Straw

894   Returning to Different Soil Depths on Soil Nitrogen and Microbial Biomass

895   Carbon and Nitrogen in Yellow Brown Soil. *Bulletin of Soil and Water*

896   *Conservation*, **39(2)**, 62–67.

897   Zhao, K., Hai, L., & Qin, F. (2025). Effects of micro-topography on soil nutrients and

898   plant diversity of artificial shrub forest in the Mu Us Sandy Land. *Plants*, **14(14)**,

899   2163.

900 Zhao, Y. et al. (2021). Distribution characteristics of low molecular weight organic

901   acids in soil of wild rhododendron forest. *Scientia Silvae Sinicae*,**57(8)**, 24–32.

902