

1 **Title:** Seasonal Change of Microbial Diversity and Its Relation with Soil Chemical
2 Properties in Orchard

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14

15 **Abstract**

16 This study aimed to determine the microbial diversity of different soil depths (0-5 and 5-20 cm) in a subtropical
17 orchard during different seasons (i.e., Spring, Summer and Autumn) for enrich the knowledgements on micorbes
18 roles in orchard ecosystem balance. In tracking experiments conducted in an orchard (established in 1996), the
19 phospholipid fatty acid (PLFA) biomarker method was employed to know soil microbial system. Total PLFAs
20 concentration did not vary significantly between soil depths but changed between seasons. It peaked in the
21 summer at $258.97 \pm 23.48 \mu\text{g g}^{-1}$ soil from 0-5 cm and at $270.99 \pm 58.94 \mu\text{g g}^{-1}$ soil from 5-20 cm. A total of 33
22 microbial fatty acid biomarkers were observed and identified in the sampled soil. Quantities of PLFAs for 29
23 microbe groups varied significantly between seasons, except for 15:0 iso 3OH, 15:1 iso G, 16:0 2OH, and 17:0
24 iso 3OH. The bacterial PLFAs and fungal and actinomycotic PLFAs in the orchard soil collected in Summer were
25 significantly higher than in the Spring or Autumn ($P < 0.01$). The number of soil microorganism species (Richness)
26 and the Simpson and Shannon-Wiener indexes were all the highest in summer. The total PLFAs, bacterial PLFAs,
27 fungal PLFAs, actinomycotic PLFAs, Richness, or the Simpson and Shannon-Wiener indexes were all
28 significantly negatively correlated with soil pH, total carbon (TOC), total nitrogen (TN) and cation-exchange
29 capacity (CEC) ($P < 0.05$).

30 **Keywords:** phospholipid fatty acid (PLFA); red soil; soil microorganisms; subtropics

31 **Introduction**

32 The orchard ecosystem is important for fruit production and carbon sequestration, biodiversity decreases [1] and
33 soil erosion [2], and pollution [3,4]. Hence, maintaining a balanced orchard ecosystem is essential. Soil microbes
34 are essential for the functioning of terrestrial ecosystems because they play a unique and indispensable role in
35 ecosystem balance [5].

36 Soil microbial community change by soil quality evolution because of long-term management. The interaction
37 between microbes and soil quality is very complex. It is reflected in effects on microbial diversity of chemical
38 properties change [6-11]. Spatial and temporal distribution of microbial community have some value information
39 to explain the interaction [12-18]. However, few clear information had be found by observation on spatial and
40 temporal distribution of microbial community in subtropical orchard.

41 Thus, we hypothesized that height seasonal temperature and moisture variation and vertical soil chemical
42 properties change would lead to obvious differences in spatial and temporal distribution of microbial community in
43 subtropical orchard. To demonstrate seasonal and vertical changes in microbial diversity and the links between
44 soil microbial diversity and soil chemical properties in a subtropical orchard, PLFA was employed to monitor
45 microorganism quantity and diversity in orchard soils under different seasons in the hilly red soil of the subtropical
46 zone in southern China. The observations of this study regarding ecological parameters of orchard soil
47 microorganisms can provide a scientific basis for further studies and management strategies.

48 **Materials and methods**

49 **2.1. Experiment Area**

50 The experimental area was located at the Yuchi Village Experimental Station, Xicheng Township, Youxi County,
51 Fujian Province, southeast China (26° 25' N, 117°57' E). The area has a subtropical humid monsoon climate with
52 an actual annual sunshine time of 1781.7 h (accounting for 40% of the available annual sunshine hours); an
53 annual precipitation of 1,284 mm (Fig. 1); an annual average temperature of 19.2°C; an average temperature in
54 July of 26.6°-28.9°C and in January of 8.0°-12.0°C; and a frost-free period of more than 312 d. As an peach
55 orchard water and soil conservation monitoring system, the experimental station was established in 1996 with an

56 altitude of 150 m and a slope of 15° facing south-southeast. The soil was a Quaternary age red soil with a clay
57 soil texture [19]. The experimental field was originally the secondary shrub-barren hill, and the constructive plant
58 species were *Dicranopteris dichotoma* Bernh, *Miscanthus floridulus* War ex Schum, and *M. sinensis* Anderss.
59 The surrounding vegetation was mainly coniferous and coniferous-deciduous-bamboo mixed stands with
60 constructive species of *Pinus massoniana* Lamb and *Cunninghamia lanceolata* Hook and a grove of
61 *Phyllostachys heterocycla* cv. Pubescens. The station was initially established for fixed soil erosion monitoring.

62 2.2. Soil sampling

63 Spring, Summer and Autumn as main treatments had been settled for seasonal factors. On April 27, August 22,
64 and November 4, 2010, at 3 days (d) after raining to keep soil moisture at the same level, soils were sampled
65 from three random spots in the non-fertilizing zones of the area surrounding the average tree were collected from
66 the soil depths of 0-5 and 5-20 cm. The soil temperature before sampling was listed in Table 1, with average
67 temperature in Spring of 21.3°-22.0°C, Summer of 27.0°-28.0°C and Autumn of 18.0°-20.2°C. The air moisture
68 tested in the same time was 82% for Spring, 86% for Summer, and 82.6% for Autumn. After collection, the soils
69 from the same soil layer were mixed well in the field, sealed in bags, and immediately brought to the laboratory for
70 measurement or stored in a -80°C freezer for soil microbial analysis. Other mixed soil samples were brought to
71 the laboratory for water content test and air-dried for basic chemical properties analysis.

72 2.3. Chemical Analysis

73 Soil pH was measured in deionized water (1:5, soil:water). The total organic carbon (TOC) and total nitrogen (TN)
74 were determined by potassium dichromate [20] and Kjeldahl digestion-distillation [21]. Exchangeable cations (K⁺,
75 Na⁺, Mg²⁺ and Ca²⁺) were extracted by CH₃COONH₄ solution (pH = 7.0) [22], and analyzed using atomic
76 absorption spectrophotometry (AA-6800, Shimadzu Corp., Kyoto, Japan). Soil samples was described in
77 experimental section and conducted in triplicate.

78 2.4. Extraction and determination of microbial PLFAs

79 Four steps followed for soil PLFA extraction: 1). Five grams of soil was placed in a centrifuge tube. Then, 15 mL
80 of a 0.2 M KOH (Sinopharm Chemical Reagent Co., Ltd., Shanghai, China) and methanol (Fisher Scientific

81 Worldwide (Shanghai) Co., Ltd., Shanghai, China) solution was added before tightening the cap. The centrifuge
82 tube was shaken for 5 min at 100 rpm. After shaking, the tube was incubated in a CU600 thermostat water bath
83 for 5 min at 37°C. This procedure was repeated five times to help release the fatty acids from the soil sample. 2).
84 Then, the tube was opened, and 3 mL of 1.0 M acetic acid (Sinopharm Chemical Reagent Co., Ltd) solution was
85 added to decrease the pH of the reaction. 3). After adding 10 mL of n-hexane (Merck Co., Darmstadt, German)
86 and mixing well, the tubes were centrifuged in an N00077 centrifuge for 15 min using the following settings: rotor:
87 #12,150; speed: 2000 rpm; time: 15 min; and temperature: 4°C. After centrifugation, the supernatant n-hexane
88 was transferred to a clean flask and air-dried under a fan. 4). The air-dried sample was re-suspended in 0.5 mL of
89 a mixture of n-hexane:methyl-tert-butyl ether (Tedia Co., Inc., Fairfield, OH) (1:1, v/v) for 3-5 min and transferred
90 to gas chromatography (GC) vials for PLFA determination.

91 Microbial PLFAs were determined using the Sherlock Microbial Identification System Sherlock MIS 4.5 (MIDI
92 Inc., Newark, DE), including a 6890N Gas Chromatograph (GC) system (Agilent Technologies Inc., Palo Alto, CA),
93 automatic injection devices, quartz capillary column, and flame ionization detector. The standard phospholipid
94 fatty acid methyl ester (MIDI, Inc.) mixture and extracted samples were analyzed under the following
95 chromatographic conditions: the temperature increment was controlled by the second-order program, with an
96 initial temperature of 170°C that increased to 260°C at 5°C min⁻¹ and then to 310°C at 40°C min⁻¹ and maintained
97 at 310°C for 90 sec; vaporization chamber temperature: 250°C; detector temperature: 300°C; carrier gas: H₂ (2
98 mL min⁻¹); blowing gas: N₂ (30 mL min⁻¹); pre-column pressure: 68.95 kPa; injection volume: 1 µL; injection split
99 ratio: 100:1; and ionization mode: electron ionization (EI).

100 2.5. Calculation of Microbial Diversity

101 Known concentrations of 19:0 (nonadecanoic methyl ester) were added as internal standards and used to convert
102 the retention-time peak areas to nanomoles per gram (nmol g⁻¹) of soil (absolute abundance) and mole percent
103 (mol %) (proportional abundance) of lipids. The absolute and proportional abundances of specific microbial
104 groups were calculated by a summation of diagnostic lipid markers. The sum of 16:1 ω_{9c} (PLFAs configuration
105 type), 18:1 ω_{9c} and 18:3 ω_{6c} (6, 9, 12) was used to indicate fungi. The sum of 17:0 10 methyl and 18:0 10 methyl
106 18:1 ω_{9c} and 18:3 ω_{6c} (6, 9, 12) was used to indicate actinomycetes. The sum of 12:0, 14:0, 14:0 anteiso, 14:0
107 iso, 15:0 2OH, 15:0 3OH, 15:0 anteiso, 15:0 iso, 15:0 iso 3OH, 15:1 iso G, 16:0, 16:0 10 methyl, 16:0 2OH, 16:0

108 anteiso, 16:0 iso, 16:1 ω 5c, 17:0 anteiso, 17:0 cyclo, 17:0 iso, 17:0 iso 3OH, 17:1 ω 8c, 18:0, 18:0 iso, 18:1 ω 7c,
109 18:1 ω 7c 11 methyl, 18:3 ω 6c (6,9,12), 19:0 cyclo ω 8c, 19:0 iso, and 20:0 was used to indicate bacteria [23].

110 The number of species (Richness), Simpson diversity, Shannon-Wiener diversity and Alatalo evenness were
111 used to calculate the ecological parameters of the microbial fatty acid biomarkers. The calculation equations are
112 expressed as follows:

113 The Simpson diversity index was calculated according to $D = 1 - \sum Pi^2$ (1);

114 The Shannon-Wiener diversity index was calculated according to $H = -\sum Pi \cdot \ln(Pi)$ (2)

115 The Alatalo evenness index was calculated according to $J = [1/\sum (Pi^2) - 1] / [\exp(H) - 1]$ (3)

116 where $Pi = Ni/N$; Ni is the content of the i^{th} kind of phospholipid fatty acid (PLFA); and N is the total PLFA
117 content.

118 2.6. Statistical Analysis

119 An one-way ANOVA followed by least significant difference (LSD) multiple comparison test was used to establish
120 significant differences among the means of soil properties, microbial community indicators (Bacterial PLFAs,
121 Fungal PLFAs, Actinomycotic PLFAs, and B/F ratio of PLFAs), and microbial diversity indicators (Richness,
122 Simpson index, Shannon-Wiener index and Alatalo index) in different seasons. A two-way analysis was used to
123 establish significant differences in the total PLFA and individual PLFA variance between seasons and soil depths.
124 A Spearman coefficient analysis was used to measure the correlation between soil properties and microbial
125 indicators. A principle component analysis was used to measure the microbial community change between
126 different seasons and soil depths. These analyses all used SPSS software version 17.0.

127 Results

128 3.1. Soil Chemical Properties of Different Seasons in the Trial Orchard

129 The soils could be classified as clay, thermal and Typic Hapludult [24]. Principle chemical properties of the soil
130 samples collected in the Spring, Summer and Autumn in the 0-5 and 5-20 cm depths are presented in Table 2.

131 Acidic soil pH (0-5 cm: 4.46; 5-20 cm: 4.38), total organic carbon (TOC) (0-5 cm: 12.32 g kg⁻¹; 5-20 cm: 10.25 g
132 kg⁻¹), total nitrogen (TN) (0-5 cm: 1.14 g kg⁻¹; 5-20 cm: 0.86 g kg⁻¹), and cation-exchange capacity (CEC) (0-5 cm:
133 4.95 cmol(+) kg⁻¹; 5-20 cm: 5.34 cmol(+) kg⁻¹) were the lowest in the Summer samples, with significant differences
134 ($P < 0.05$). However, the exchangeable K⁺ (0-5 cm: 141.79 g kg⁻¹; 5-20 cm: 99.22 g kg⁻¹) and Na⁺ (0-5 cm:
135 30.67 g kg⁻¹; 5-20 cm: 43.80 g kg⁻¹) were significantly higher than in the other seasons. Furthermore, the ratio of
136 total organic carbon to total nitrogen (C/N ratio) in soil varied significantly between seasons, with the highest
137 value in the Spring (0-5 cm: 15.81; 5-20 cm: 12.85), the middle value in the Summer (0-5 cm: 10.76; 5-20 cm:
138 11.88), and the lowest value in the Autumn (0-5 cm: 5.90; 5-20 cm: 9.04) ($P < 0.05$). No significant difference
139 was detected between seasons in exchangeable Mg²⁺ or Ca²⁺ ($P > 0.05$).

140 No significant difference of pH, TOC, C/N ratio, CEC, exchangeable Mg²⁺ or Ca²⁺ was found between soil
141 depths.

142 3.2. PLFAs of Total Microbial, Bacteria, Fungi and Actinomycotic of Different Seasons

143 The total microbial PLFAs peaked in the Summer in both the 0-5 and 5-20 cm soil depths (0-5 cm: 258.97 µg g⁻¹
144 soil, $P < 0.01$; 5-20 cm: 270.99 µg g⁻¹ soil, $P < 0.01$). The results of the two-way analysis demonstrated that
145 the total microbial PLFAs were significantly different between seasons ($P < 0.001$). The quantities of bacterial,
146 fungal and actinomycotic PLFAs in the orchard soil increased significantly in the Summer compared to those in
147 the Spring and Autumn in the 0-5 and 5-20 cm soil depths ($P < 0.01$). In the 0-5 cm soil depth, the peak values
148 of bacterial PLFAs, fungal PLFAs and actinomycotic PLFAs were 216.05, 33.94 and 8.96 µg g⁻¹ soil, respectively.
149 For the 5-20 cm soil depth, bacterial PLFAs, fungal PLFAs and actinomycotic PLFAs summit to 230.00, 31.15 and
150 9.83 µg g⁻¹ soil, respectively (Table 3). Microbial PLFAs contents (µg g⁻¹ soil) of different seasons sampled at 0-5
151 and 5-20 cm soil depths in orchard is shown in Table 4. Two-way analysis of variance for the effects of seasons
152 (Spring, Summer, Autumn) and soil depths (0-5 cm, 5-20 cm) on microbial PLFAs contents are demonstrated on
153 Table 5. Quantities of PLFAs for 29 microbe groups varied significantly between seasons, except for 15:0 iso
154 3OH, 15:1 iso G, 16:0 2OH, and 17:0 iso 3OH.

155 3.3. Microbial Diversity Change between Seasons in the Trial Orchard

156 The microbial diversity analysis of the orchard soil showed that the Richness (number of microbial species) was in
157 the range of 18 to 31, and the Simpson index, Shannon-Wiener index and Alatalo index were 0.76 to 0.93, 3.16 to
158 3.97 and 0.59 to 0.76, respectively (Fig. 2). The microbial diversities of the orchard soil in different seasons varied.
159 In the 0-5 cm soil depth, the Richness and the Simpson, Shannon-Wiener and Alatalo indexes peaked in the
160 Summer, with values of 30.0, 0.92, 3.91 and 0.65, respectively. The Simpson and Shannon-Wiener indexes in the
161 Summer were significantly different from those in the Spring and Autumn ($P < 0.05$). A significantly difference in
162 Richness was been found between the Summer and Spring. No significant difference in the Alatalo index
163 between seasons was found ($P > 0.05$). In the 5-20 cm soil layer, the highest values of Richness and the
164 Simpson and Shannon-Wiener index were still been found in the Summer, with values of 29.2, 0.92 and 3.81,
165 respectively. The Richness and the Simpson index of the soil microbes in the Summer were significantly higher
166 than those in the Spring ($P < 0.05$). There was no significant difference in the Shannon-Wiener index. However,
167 the Alatalo index of the soil microbes in the Autumn (0.76) was significantly higher than that in the Spring (0.62) (P
168 < 0.05). Overall, the microbial diversity of the orchard soil in the Summer was higher than in the Spring and
169 Autumn.

170 3.4. Correlation between Microbial Communities and Soil Properties

171 The correlation analysis was carried out between the soil properties (pH, TOC, TN, C/N ratio, CEC, and
172 exchangeable K^+ , Na^+ , Mg^{2+} and Ca^{2+}), microbial quantities (total PLFAs, bacterial PLFAs, fungal PLFAs,
173 actinomycotic PLFAs, B/F ratio) and microbial diversities (Richness, the Simpson, Shannon-Wiener and Alatalo
174 indexes). The results showed that the microbial quantities (total PLFAs, bacterial PLFAs, fungal PLFAs, and
175 actinomycotic PLFAs) were significantly negatively correlated with the pH, TOC, TN and CEC, with Spearman
176 correlation coefficients of -0.530 to -0.618 ($P < 0.01$), -0.572 to -0.642 ($P < 0.01$), -0.401 to -0.422 ($P < 0.05$) and
177 -0.791 to -0.831 ($P < 0.01$), respectively (Table 5). The microbial diversity (Richness, and the Simpson and
178 Shannon-Wiener indexes) was significantly negatively correlated with the pH, TOC, TN and CEC, with Spearman
179 correlation coefficients of -0.460 to -0.753 ($P < 0.05$), -0.419 to -0.707 ($P < 0.05$), -0.450 to -0.526 ($P < 0.05$), and
180 -0.446 to -0.722 ($P < 0.05$), respectively (Table 6).

181 Discussion

182 4.1. Microbial Population Variation of Soil Ecosystem Among Seasons

183 Usually, microbial population varies by moisture and temperature change among seasons. However, whether this
184 change could be found easily depend on how long the suitable season last and how hard the extreme water and
185 temperature condition affect on soil microorganisms. In subtropical mountain area, the soil was utilized as
186 planting peach, obvious microbial change was confirmed in this article. And, principal component 1 explained
187 46.8 % of the variation in the soil microbial community (Fig. 3). The total, bacterial, fungal, and actinomycotic
188 PLFAs, the B/F ratio, and the Richness were the main drivers of principal component 1 (Table S1). The
189 remarkable change in microbial community was related to the peak soil microorganism growth in the Summer
190 because of comfortable temperature and rainfall.

191 Principal component 2 explained 26.5 % of the variation in the soil microbial community (Fig. 3). The Simpson
192 index and Shannon-Wiener index were its major drivers (Table S1). This could be explained by the
193 microorganism propagating well and maintaining a good balance in the Summer in the tested orchard soil system.

194 The results of our study are consistent with the results of Zhu et al. [14] in an evergreen broadleaf forest and
195 Qi et al. [15] in a bamboo grove in the subtropical climate zone. An investigation of an orchard [13], grassland [12]
196 and forest [17] in the temperate monsoon climate zone was reported similar trends. However, unlike our results,
197 Shi et al. [16] observed seasonal variations characterized by low values for most of the microbial biomass (C, N,
198 and P), enzyme activities and PLFAs in the Summer in southwestern Quebec, Canada. This difference is related
199 to the particularly dry climate (drier than the long-term average of the season) with a significantly lower moisture
200 content than in the Spring and Autumn. It is well documented that temperature and moisture are the main factors
201 related to microbial abundance and distribution.

202 4.2. Relationship between Soil Physicochemical Properties and Microbial Communities

203 The reported relationship between soil physicochemical properties and microbial communities varies among
204 studies. In this study, in the view of distribution among seasons and soil depths, the total PLFAs, bacterial PLFAs,
205 fungal PLFAs, actinomycotic PLFAs, number of species (Richness), Simpson and Shannon-Wiener diversity
206 indexes were significantly negatively correlated with the soil TOC, TN and CEC. In the Summer, of most soil
207 microbes experienced rapid growth, and a significant decrease in the soil pH, TOC, TN, and CEC was found

208 (Table 1). Liu et al. [18] also found the microbial dominance index and Shannon-Wiener index to be negatively
209 related to soil NH_4^+ -N and NO_3^- -N in an apple system by observation on different growing periods. However, in the
210 view of change by utilization, Yao et al. [6] illustrated microbial biomass C, basal respiration and total PLFA to be
211 highly correlated with organic C and TN on red soil orchard ecosystem. In some ecosystem soil microbes grew
212 rapidly with energy and nutrition consumption [25, 26]. It is clearly suggested that the propagation and growth of
213 soil microorganisms from Spring to Summer require energy from TOC and nutrition from N in an subtropical
214 orchard system. Microbes mainly act as “consumers” could be well documented.

215 **Conclusions**

216 In subtropical orchards, the temperature and humidity in the Summer are conducive to the growth of soil
217 microorganisms. PLFA analysis showed that the quantity of soil microbes in the soil samples collected in the
218 Summer was significantly higher than in the Spring and Autumn. The Simpson and Shannon-Wiener indices also
219 both peaked in the Summer sample collections. The total PLFAs, bacterial PLFAs, fungal PLFAs, actinomycotic
220 PLFAs, Richness, and the Simpson and Shannon-Wiener indexes were significantly negatively correlated with
221 seasonal changes in the soil pH, TOC, TN and CEC.

222 The function of microbial community in the translation and accumulation of soil nutrition from Summer to
223 Autumn should be studied further. The changes in functional flora (including Archaea) in the soil microorganisms
224 resulting from different orchard management strategies merit further investigations, and the relationships between
225 the flora change and the orchard litter, soil organic matter (SOM), soil C/N ratio, ammonia N, nitrate N, pH, soil
226 respiration, and other parameters should be merited further studied.

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234 **Funding acquisition:** BW XL.

235 **Project administration:** BW.

236 **Investigation:** XL.

237 **Chemical Analysis:** XL.

238 **Determination of microbial PLFAs:** GH.

239 **Statistical Analysis:** XL.

240 **Writing-original draft:** XL.

241 **Writing-review & editing:** MW BW.

242 **References**

- 243 1. Simon S, Bouvier JC, Debras JF, Sauphanor B. Biodiversity and pest management in orchard systems. A
244 review. *Agron. Sustainable Dev.* 2010; **30**: 139-152.
- 245 2. Labrière N, Locatelli B, Laumonier Y, Freycon V, Bernoux M. Soil erosion in the humid tropics: A systematic
246 quantitative review. *Agric. Ecosyst. Environ.* 2015; **203**: 127-139.
- 247 3. Rowlings DW, Grace PR, Scheer C, Kiese R. Influence of nitrogen fertiliser application and timing on
248 greenhouse gas emissions from a lychee (*Litchi chinensis*) orchard in humid subtropical Australia. *Agric.*
249 *Ecosyst. Environ.* 2013; **179**: 168-178.
- 250 4. Cai MF, McBride MB, Li KM. Bioaccessibility of Ba, Cu, Pb, and Zn in urban garden and orchard soils.
251 *Environ. Pollut.* 2016; **208**: 145-152.
- 252 5. Young IM, Crawford JW. Interactions and self-organization in the soil-microbe complex. *Science (New*
253 *series)*, 2004; **304**: 1634-1637.
- 254 6. Yao H, He Z, Wilson MJ, Campbell CD. Microbial biomass and community structure in a sequence of soils
255 with increasing fertility and changing land use. *Microb. Ecol.* 2000; **40**: 223-237.

- 256 7. Li R, Khafipour E, Krause DO, Entz MH, de Kievit TR. Pyrosequencing reveals the influence of organic and
257 conventional farming systems on bacterial communities. PLoS One; 2012; **7**, e51897.
- 258 8. Mercier A, Dictor MC, Harris-Hellal J, Breeze D, Mouvet C. Distinct bacterial community structure of 3
259 tropical volcanic soils from banana plantations contaminated with chlordecone in Guadeloupe (French West
260 Indies). Chemosphere. 2013; **92**: 787-794.
- 261 9. Joa JH, Weon YH, Hyun HN, Jeun YC, Koh SW. Effect of long-term different fertilization on bacterial
262 community structures and diversity in citrus orchard soil of volcanic ash. J. Microbiol. 2014; **52**: 995-1001.
- 263 10. Yang DW, Zhang MK. Effects of land-use conversion from paddy field to orchard farm on soil microbial
264 genetic diversity and community structure. Eur. J. Soil Biol. 2014; **64**: 30-39.
- 265 11. Gilbert JA, Field D, Swift P, Thomas S, Cummings D, Temperton B, Weynberg K, Huse S, Hughes M, Joint I,
266 Somerfield PJ, Mühling M, Rodriguez-Valera F. The taxonomic and functional diversity of microbes at a
267 temperate voastal site: a 'Multi-Omic' study of seasonal and diel temporal variation. PloS One. 2010; **5**: 1-17.
- 268 12. Bardgett RD, Lovell RD, Hobbs PJ, Jarvis SC. Seasonal changes in soil microbial communities along a
269 fertility gradient of temperate grasslands. Soil Biol. Biochem. 1999; **31**: 1021-1030.
- 270 13. Shishido M, Sakamoto K, Yokoyama H, Momma N, Miyashita S. Changes in microbial communities in an
271 apple orchard and its adjacent bush soil in response to season, land-use, and violet root rot infestation. Soil
272 Biol. Biochem. 2008; **40**: 1460-1473.
- 273 14. Zhu WZ, Cai XH, Liu XL, Wang JX, Cheng JX, Cheng S, Zhang XY, Li DY, Li MH. Soil microbial population
274 dynamics along a chronosequence of moist evergreen broad-leaved forest succession in southwestern
275 China. J. Mount. Sci. 2010; **7**: 327-338.
- 276 15. Qi LH, Ai WS, Fan SH, Du MY, Meng Y, Mao C. Soil microbial biomass carbon dynamics of *Phyllostachys*
277 *edulis* forests under different managing patterns in the hilly region of central Hunan, southern China. J.
278 Nanjing Forest Univ. 2013; **37**: 45-48 (in Chinese with English abstract).
- 279 16. Shi Y, Lalande R, Hamel C, Ziadi N, Gagnon B, Hu Z. Seasonal variation of microbial biomass, activity, and
280 community structure in soil under different tillage and phosphorus management practices. Biol. Fert. Soils.
281 2013; **49**: 803-818.

- 282 17. Kim CS, Nam JW, Jo JW, Kim SY, Han JG, Hyun MW, Sung GH, Han SK. Studies on seasonal dynamics of
283 soil-higher fungal communities in Mongolian oak-dominant Gwangneung forest in Korea. *J. Microbiol.* 2016;
284 **54**: 14-22.
- 285 18. Liu LZ, Qin SJ, Lu DG, Wang BY, Yang ZY. Variation of potential nitrification and ammonia-oxidizing
286 bacterial community with plant-growing period in apple orchard soil. *J. Integr. Agric.* 2014; **13**: 415-425.
- 287 19. Zhuan WM. Map of Fujian Province. Fuzhou: Fujian provincial map and atlas publishing house; 2008.
- 288 20. Nelson DW, Sommers LE. Total carbon, organic carbon and organic matter. In Page AL, Miller RH. and
289 Keeney DR. editors. *Methods of Soil Analysis*. Madison WI: Soil Sci. Soc. Am. 1982; 539-577.
- 290 21. Bremner JM, Mulvaney CS. Total nitrogen. In: Page AL, Miller RH, Keeney DR, editors. *Methods of Soil*
291 *Analysis*. Madison WI: Soil Sci. Soc. Am.; 1982.
- 292 22. Jackson ML. *Soil Chemical Analysis*. Published by Author, 2nd ed. Madison WI; 1979.
- 293 23. Zhu YJ, Hu GP, Liu B, Xie HA, Zheng XF, Zhang JF. Using phospholipid fatty acid technique to analysis the
294 rhizosphere specific microbial community of seven hybrid rice cultivars. *J. Integr. Agric.* 2012; **11**:
295 1817-1827.
- 296 24. Soil Survey Staff. *Keys to Soil Taxonomy*. 11th ed. Washington, DC: USDA-Natural Resources Conservation
297 Service; 2010.
- 298 25. Huang PM, Wang MK, Chiu CY. Soil mineral-organic matter-microbe interactions: impacts on
299 biogeochemical processes and biodiversity in soils. *Pedobiologia*. 2005; **49**: 609-635.
- 300 26. Huang PM, Wang SL, Tzou YM, Huang YB , Weng BQ, Zhuang SY, Wang MK. Physicochemical and
301 biological interfacial interactions: impacts on soil ecosystem and biodiversity. *Environ. Earth. Sci.* 2013; **28**:
302 2199-2209.

303

304 **Table 1**
305 Soil temperature and air moisture at different sampling stages in orchard

Item	Spring	Summer	Autumn
Soil temperature (°C)			
0 cm	21.3	27.5	18.0
5 cm	22.0	27.7	19.0
10 cm	21.5	28.0	19.5
15 cm	21.7	27.3	20.2
20 cm	21.4	27.0	19.7
Air relative moisture (%)	82.0	86.0	82.6

306 Soil temperature and air moisture was the average of two weeks data before sampling that was on April 27 for
307 Spring, on August 22 for Summer and on November 4 for Autumn.
308

309

Table 2

310

Chemical characteristics of soil sampling in different seasons at 0-5 and 5-20 cm soil depths in orchard

Item	Spring	Summer	Autumn
0-5 cm			
pH	4.87±0.06 a (5)	4.46±0.08 b (5)	4.95±0.04 a (5)
TOC (g kg ⁻¹)	20.90±1.07 a	12.32±1.53 b	20.92±1.17 a
TN (g kg ⁻¹)	1.46±0.24 bc	1.14±0.08 c	3.95±0.75 a
C/N ratio	15.81±3.30 a	10.76±0.93 b	5.90±1.18 c
CEC (cmol(+) kg ⁻¹)	9.42±0.26 a	4.95±0.29 c	7.09±0.25 b
Exchangeable K ⁺ (mg kg ⁻¹)	124.00±15.64 a	141.79±30.11 a	99.67±13.16 b
Exchangeable Na ⁺ (mg kg ⁻¹)	17.75±0.62 b	30.67±3.61 a	14.09±1.13 b
Exchangeable Mg ²⁺ (mg kg ⁻¹)	30.14±3.83 a	28.41±7.56 a	24.80±2.79 a
Exchangeable Ca ²⁺ (mg kg ⁻¹)	163.98±20.25 a	122.72±20.74 a	192.83±33.25 a
5-20 cm			
pH	4.81±0.06 a (5)	4.38±0.07 b (5)	4.83±0.08 a (5)
TOC (g kg ⁻¹)	19.15±0.92 a	10.25±0.89 b	18.78±0.67 a
TN (g kg ⁻¹)	1.61±0.14 ab	0.86±0.06 b	2.20±0.25 a
C/N ratio	12.85±0.81 ab	11.88±0.55 b	9.04±1.10 bc
CEC (cmol(+) kg ⁻¹)	9.29±0.56 a	5.34±0.39 c	6.87±0.18 b
Exchangeable K ⁺ (mg kg ⁻¹)	62.85±7.54 ab	99.22±12.24 a	55.95±7.85 ab
Exchangeable Na ⁺ (mg kg ⁻¹)	15.22±1.26 b	43.80±5.91 a	10.21±0.85 b
Exchangeable Mg ²⁺ (mg kg ⁻¹)	22.71±6.17 a	34.47±8.80 a	20.05±4.82 a
Exchangeable Ca ²⁺ (mg kg ⁻¹)	121.38±22.12 a	117.97±51.79 a	164.97±18.31 a

311

TOC = total organic carbon, TN = total nitrogen, CEC = cation exchange capacity, C/N ratio = ratio of total organic carbon to total nitrogen. Values followed by the same letter (s) in a low are not significantly different at $P < 0.05$ using LSD post hoc tests. Case number is shown in parentheses

312

313

314

315 **Table 3**
 316 Contents of total PLFAs, bacterial PLFAs, fungal PLFA, actinomycetrical PLFAs, and the ratio of bacterial to fungal
 317 of soils sampling on different seasons at 0-5 and 5-20 cm depths in orchard

Item	Spring	Summer	Autumn
0-5 cm			
Total PLFAs ($\mu\text{g g}^{-1}$ soil)	14.07 \pm 8.23 c B (4)	258.97 \pm 23.48 a A (5)	99.93 \pm 18.62 b B (4)
Bacterial PLFAs ($\mu\text{g g}^{-1}$ soil)	11.46 \pm 6.75 b B	216.05 \pm 20.44 a A	79.79 \pm 14.56 b B
Fungal PLFAs ($\mu\text{g g}^{-1}$ soil)	2.27 \pm 1.23 c B	33.94 \pm 3.96 a A	16.09 \pm 3.64 b B
Actinomycetrical PLFAs ($\mu\text{g g}^{-1}$ soil)	0.34 \pm 0.26 b B	8.96 \pm 0.81 a A	4.05 \pm 1.00 b B
B/F ratio	4.79 \pm 0.29 a A	6.37 \pm 0.61 a A	5.15 \pm 0.60 a A
5-20 cm			
Total PLFAs ($\mu\text{g g}^{-1}$ soil)	10.63 \pm 1.58 b B (5)	270.99 \pm 58.94 a A (5)	51.28 \pm 7.17 b B (5)
Bacterial PLFA ($\mu\text{g g}^{-1}$ soil)	8.66 \pm 1.29 b B	230.00 \pm 50.36 a A	44.60 \pm 6.05 b B
Fungal PLFA ($\mu\text{g g}^{-1}$ soil)	1.71 \pm 0.32 c B	31.15 \pm 6.26 a A	5.37 \pm 0.83 bc B
Actinomycetrical PLFA ($\mu\text{g g}^{-1}$ soil)	0.24 \pm 0.05 b B	9.83 \pm 2.45 a A	1.30 \pm 0.60 b B
B/F ratio	5.33 \pm 0.59 b B	7.38 \pm 0.24 a AB	8.70 \pm 1.07 a A

318 Mean \pm standard error. the values followed by the same lowercase and capital letter (s) in a column are not
 319 significantly different at $P < 0.05$ and $P < 0.01$ using LSD post hoc tests, respectively. Case number is shown
 320 in parentheses, 1 case was missed for Spring and Autumn at 0-5 cm depth respectively.
 321

322

Table 4

323

Microbial PLFAs contents ($\mu\text{g g}^{-1}$ soil) of different seasons sampled at 0-5 and 5-20 cm soil depths in orchard

Fatty acid configuration	0-5 cm			5-20 cm		
	Spring (4)	Summer (5)	Autumn (4)	Spring (5)	Summer (5)	Autumn (5)
12:0	0.05±0.04	2.67±0.44	0.65±0.17	0.00±0.00	1.68±1.03	0.23±0.14
14:0	0.19±0.10	4.89±0.54	1.43±0.26	0.16±0.03	5.15±1.06	0.76±0.06
14:0 anteiso	0.04±0.04	0.00±0.00	0.15±0.15	0.03±0.03	0.00±0.00	0.68±0.23
14:0 iso	0.03±0.03	1.72±0.20	0.38±0.09	0.01±0.01	1.70±0.41	0.05±0.05
15:0 2OH	0.06±0.06	0.37 ±0.18	0.00±0.00	0.01±0.01	0.46±0.19	0.00± 0.00
15:0 3OH	0.19±0.14	3.99±0.88	1.14±0.37	0.18±0.04	4.33±0.86	0.61±0.30
15:0 anteiso	0.40±0.15	9.07±1.17	3.22±0.68	0.43±0.08	9.25±1.85	2.13±0.23
15:0 iso	0.58±0.38	15.08±0.91	5.44±1.15	0.22±0.07	13.97±5.74	2.74±0.86
15:0 iso 3OH	0.02±0.02	0.00±0.00	0.00±0.00	0.07±0.04	0.00±0.00	0.00±0.00
15:1 iso G	0.04±0.03	0.00±0.00	0.15±0.11	0.94±0.84	13.96±13.96	2.29±2.25
16:0	3.85±2.34	56.42±4.23	23.36±3.44	2.14±0.45	48.29±14.45	9.61±2.13
16:0 10 methyl	0.68±0.36	16.04±1.90	5.92±1.22	0.47±0.07	17.58±3.72	3.54±0.82
16:0 2OH	0.00±0.00	0.00±0.00	0.00±0.00	0.01±0.01	0.00±0.00	0.00±0.00
16:0 anteiso	0.24±0.04	4.01±1.50	1.30±0.24	0.37±0.07	2.49±0.36	0.92±0.17
16:0 iso	0.64±0.40	17.89±2.61	6.09±1.33	0.38±0.06	18.19±3.91	3.70±0.64
16:1 ω9c	0.00±0.00	1.86±0.57	2.76±0.61	0.00±0.00	1.14±0.41	0.00±0.00
16:1 ω5c	1.13±0.88	7.33±0.77	0.00±0.00	0.52±0.17	7.86±2.04	1.22±0.19
17:0 10 methyl	0.14±0.11	3.22±0.26	1.33±0.28	0.08±0.02	3.89±0.76	0.59±0.20
17:0 anteiso	0.46±0.14	8.94±1.36	3.06±0.64	0.52 ±0.11	8.70±1.52	1.78±0.17
17:0 cyclo	0.09±0.07	4.38±0.77	1.04±0.29	0.08±0.01	4.31±0.77	0.52±0.15
17:0 iso	0.48 ±0.25	17.13±2.33	5.35±1.21	0.33±0.05	18.53±3.27	3.42±0.28
17:0 iso 3OH	0.00±0.00	0.00±0.00	0.00±0.00	0.12±0.07	0.00±0.00	0.00±0.00
17:1 ω8c	0.08±0.08	2.23±0.49	0.40±0.18	0.02±0.02	1.73±0.50	0.00±0.00
18:0	0.70±0.35	12.99±1.20	5.89±1.07	0.66±0.13	13.39±2.69	3.19±0.37
18:0 iso	0.03±0.03	2.24±0.24	0.47±0.27	0.03±0.02	2.73±0.52	0.20±0.13
18:0 10 methyl	0.20±0.15	5.75±0.58	2.72±0.76	0.16±0.04	5.79±1.72	0.70±0.43
18:1 ω9c	1.93±1.06	28.87±3.45	14.79±3.42	1.44±0.30	27.09±5.88	4.57±0.74
18:1 ω7c	0.53±0.34	7.86±0.86	3.28±0.56	0.38±0.15	8.90±2.45	1.55±0.28
18:1 ω7c 11 methyl	0.08±0.08	1.66±0.14	0.58±0.42	0.00±0.00	1.56±0.48	0.00±0.00
18:3 ω6c (6,9,12)	0.33±0.17	3.21±0.80	1.30±0.23	0.28±0.03	3.06±0.40	0.79±0.24
19:0 cyclo ω8c	0.65±0.38	15.95±0.72	6.39±1.43	0.43±0.06	22.14±5.22	4.83±0.84
19:0 iso	0.01±0.01	0.53±0.32	0.00±0.00	0.01±0.01	0.44±0.14	0.00±0.00
20:0	0.20±0.10	2.67±0.10	1.34±0.24	0.16±0.04	2.66±0.62	0.63±0.12

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Case number is shown in parentheses. Mean±standard error.

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Table 5

Two-way analysis of variance for the effects of seasons (Spring, Summer, Autumn) and soil depths (0-5 cm, 5-20 cm) on microbial PLFAs contents

Fatty acid configuration	Microbial group	Season	Soil depth	r^2
12:0	Gram-negative bacteria	***a	n.s.	0.522
14:0	Gram-negative bacteria	**	n.s.	0.815
14:0 anteiso	Gram-positive bacteria	**	n.s.	0.554
14:0 iso	Gram-positive bacteria	***	n.s.	0.795
15:0 2OH	Gram-negative bacteria	**	n.s.	0.425
15:0 3OH	Gram-negative bacteria	***	n.s.	0.723
15:0 anteiso	Gram-positive bacteria	***	n.s.	0.796
15:0 iso	Gram-positive bacteria	***	n.s.	0.599
15:0 iso 3OH	Gram-negative bacteria	n.s.	n.s.	0.297
15:1 iso G	Bacteria	n.s.	n.s.	0.155
16:0	Bacteria	***	n.s.	0.733
16:0 10 methyl	Sulfate-reducing bacteria	***	n.s.	0.785
16:0 2OH	<i>Ralstonia</i> spp.	n.s.	n.s.	0.170
16:0 anteiso	Gram-positive bacteria	**	n.s.	0.508
16:0 iso	Gram-positive bacteria	***	n.s.	0.774
16:1 ω9c	Fungi	***	n.s.	0.704
16:1 ω5c	Methane-oxidizing bacteria	***	n.s.	0.613
17:0 10 methyl	Actinomycetes	***	n.s.	0.814
17:0 anteiso	Gram-positive bacteria	***	n.s.	0.806
17:0 cyclo	Gram-negative bacteria	***	n.s.	0.801
17:0 iso	Gram-positive bacteria	***	n.s.	0.806
17:0 iso 3OH	Gram-negative bacteria	n.s.	n.s.	0.352
17:1 ω8c	Gram-negative bacteria	***	n.s.	0.693
18:0	<i>Hydrogenobacter</i>	***	n.s.	0.808
18:0 iso	Gram-positive bacteria	***	n.s.	0.821
18:0 10 methyl	Actinomycetes	***	n.s.	0.691
18:1 ω9c	Fungi	***	n.s.	0.775
18:1 ω7c	<i>Pseudomonas</i> spp.	***	n.s.	0.705
18:1 ω7c 11 methyl	<i>Cellulomonas</i> spp.	***	n.s.	0.670
18:3 ω6c (6,9,12)	Fungi	***	n.s.	0.700
19:0 cyclo ω8c	<i>Burkholderia</i>	***	n.s.	0.758
19:0 iso	Bacteria in general	**	n.s.	0.375
20:0	Bacteria in general	***	n.s.	0.782

329 *, **and *** indicate significant differences in that row at $P < 0.05, 0.01, 0.001$, respectively. Not significant
330 results are labelled n.s. ($P > 0.05$).
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Table 6

Spearman correlation coefficients matrix for microbial community variations and chemical properties in orchard soils

Item	pH	TOC	TN	C/N ratio	CEC	Exchangeable			
						K ⁺	Na ⁺	Mg ²⁺	Ca ²⁺
Total PLFAs	-0.614**	-0.617**	-0.401*	-0.302	-0.817**	0.284	0.493**	0.119	-0.177
Bacterial PLFAs	-0.618**	-0.642**	-0.422*	-0.317	-0.831**	0.296	0.485**	0.141	-0.160
Fungal PLFAs	-0.530**	-0.572**	-0.401*	-0.313	-0.791**	0.390*	0.482**	0.229	-0.074
Actinomycetial PLFAs	-0.593**	-0.555**	-0.434*	-0.248	-0.744**	0.320	0.525**	0.150	-0.165
B/F ratio	-0.517**	-0.565**	-0.354	-0.119	-0.595**	-0.259	0.131	-0.189	-0.263
Richness	-0.460*	-0.419*	-0.526**	0.051	-0.446*	0.403*	0.622**	0.332	-0.085
Simpson diversity	-0.753**	-0.707**	-0.498**	-0.159	-0.722**	0.132	0.517**	-0.012	-0.328
Shanon-Wiener diversity	-0.602**	-0.446*	-0.450*	0.007	-0.556**	0.330	0.504**	0.090	-0.380*
Alatalo evenness	-0.054	0.096	0.215	-0.062	0.028	-0.176	-0.252	-0.203	-0.092

335 FLFA = phospholipid fatty acid, B/F ratio = ratio of bacterial to fungal PLFA, TOC = total organic carbon, TN =
336 total nitrogen, CEC = cation exchange capacity, C/N ratio = ratio of total organic carbon to total nitrogen.

337 *, ** indicate spearman coefficient significant differences at $P < 0.05, 0.01$, respectively ($n = 28$).

338

Figure Captions

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342 Fig. 1. Monthly dynamics of precipitation (A), average air temperature (B), and extremes air temperature (C) at
343 the trail location from 1997 to 2010. Annul precipitation is shown in parentheses (A).

344

345

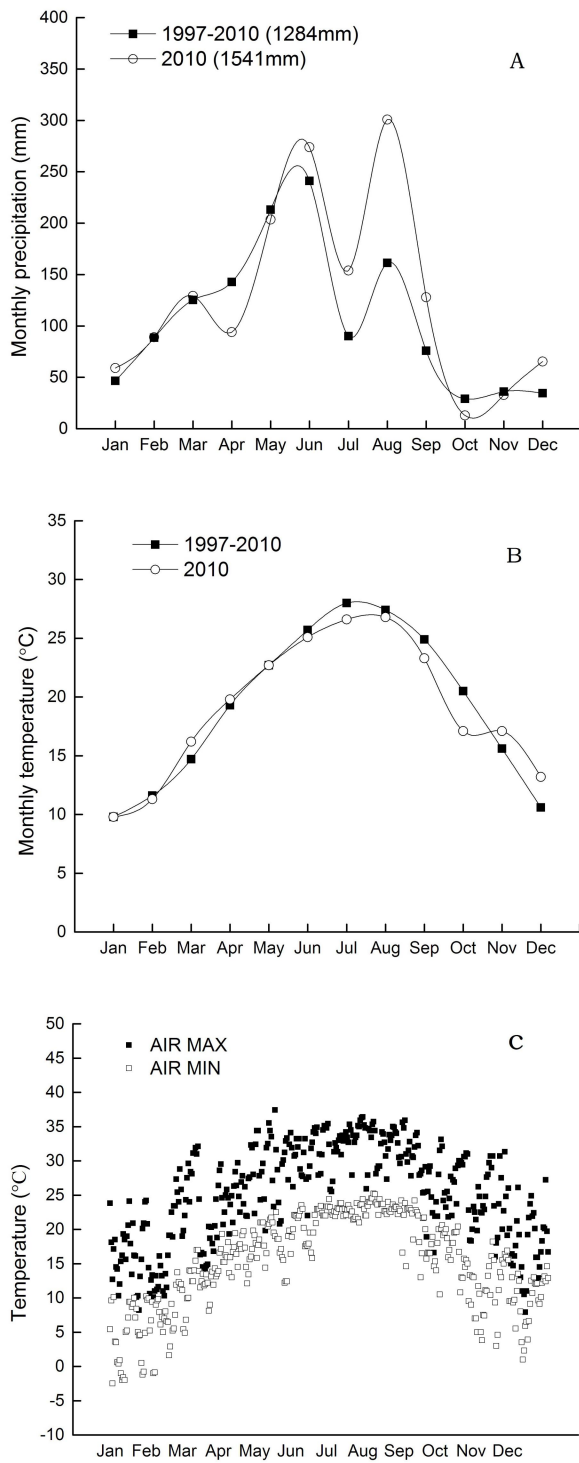
346 Fig. 2. Microbial diversity of Richness (A) Simpson index (B), Shannon-Wiener index (C), and Alatalo index (D) in
347 orchard soil of 0-5 and 5-20 cm s at different seasons. Bars with the same letter (s) are not significantly
348 differences between seasons for each depth at $P < 0.05$ using LSD post hoc tests.

349

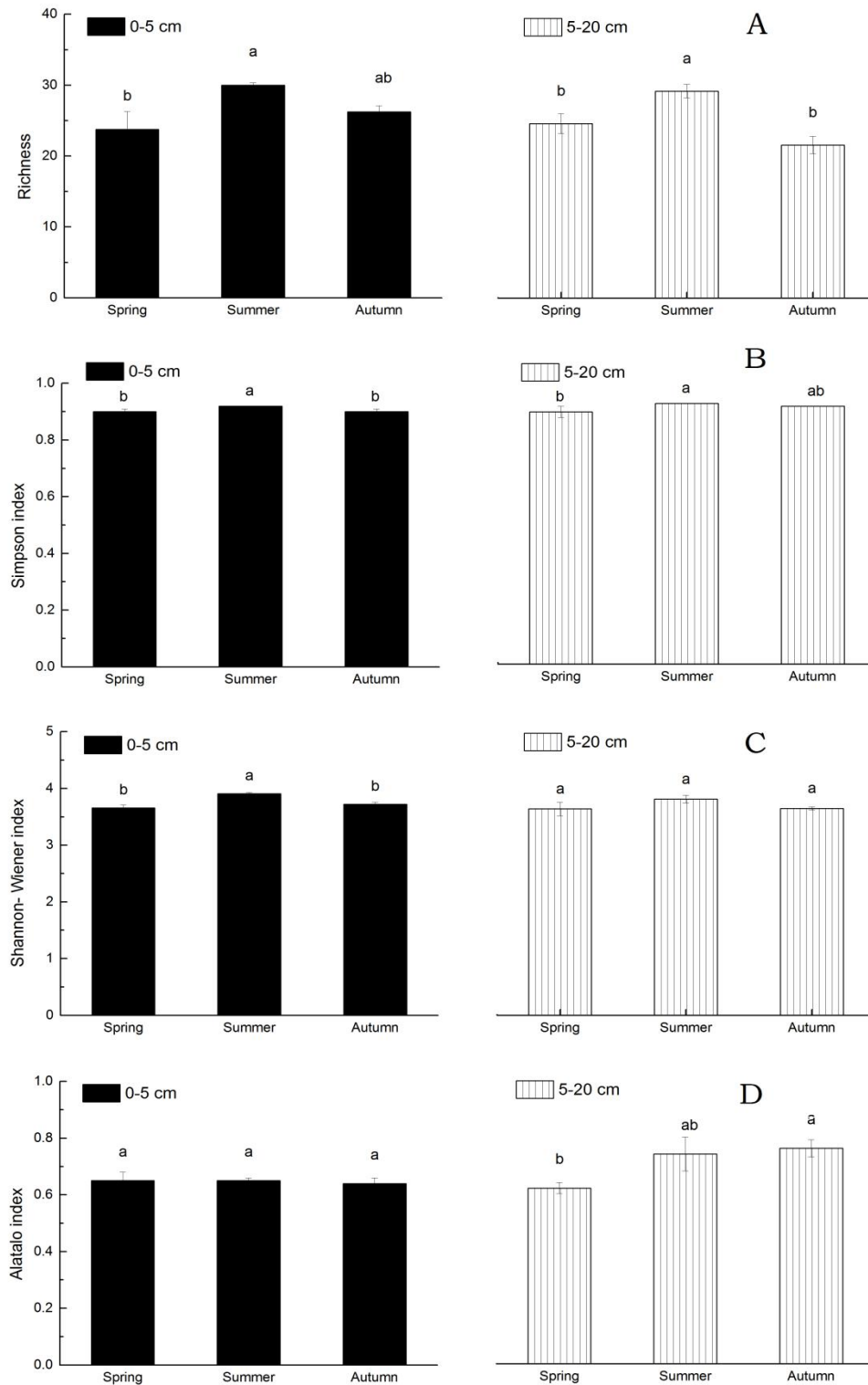
350 Fig. 3. Principal components analysis (PCA) of microbial community from orchard soil sampled at different
351 seasons and depths. Percent variance explained by each component (PC) is shown in parentheses. Error
352 bars represent standard error ($n = 28$).

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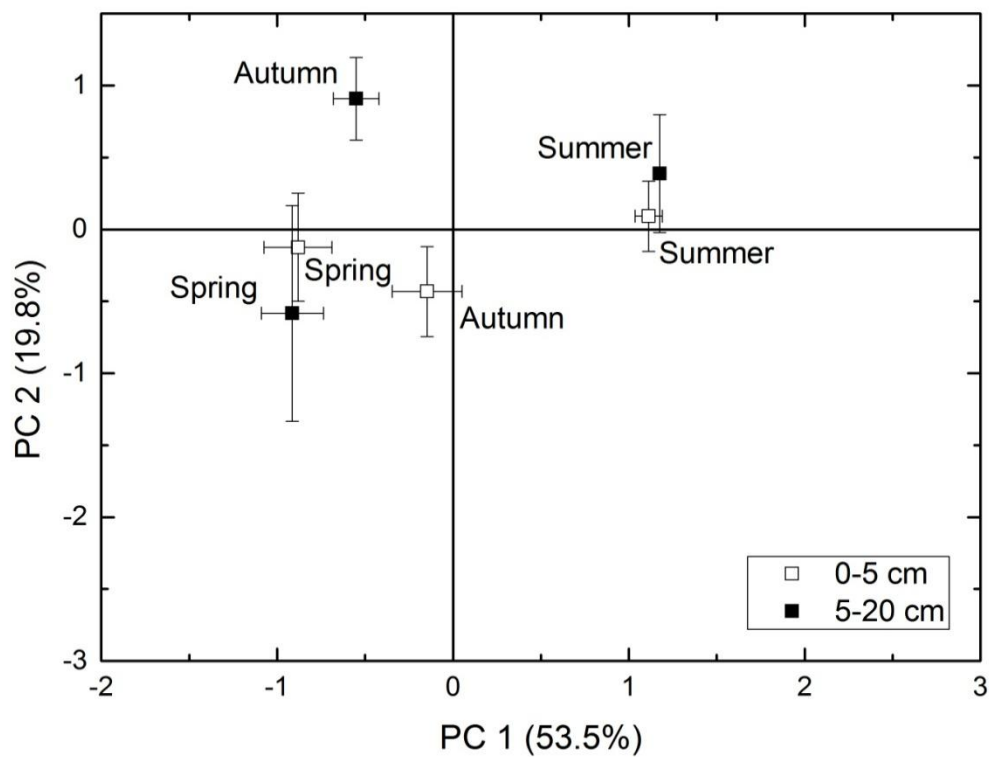


355
356 Fig. 1



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Fig. 2



361 Fig. 3
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364 Supplemental Information

365 Table S1

366 Principle component (PC) factors value and total eigenvector coefficients between PC factors and microbial
367 community indexes after varimax rotation

PC	Value	Contribution rate		Factor								
		Pr Var	Cum Var	Total Bacterial	Fungal	Actinomy	B/F ratio	Richness	Simpson	Shannon-	Alatalo	
		...%...	PLFAs.....		Indexes.....					
1	5.35	53.50	53.50	0.96	0.97	0.95	0.96	0.30	0.81	0.62	0.56	0.35
2	1.98	19.80	73.30	-0.09	-0.07	-0.14	-0.14	0.40	-0.36	0.71	0.54	0.89

368 PC= principle component, Pr Var= Principle variance, Cum Var= cumulative variance, PLFA=phospholipid fatty
369 acid, B/ F ratio =ratio of bacterial to fungal PLFA.

370 Factor loadings | x | >5% of total eigenvector coefficients after varimax rotation.