

Soil microbial community and physicochemical properties together drive soil organic carbon in *Cunninghamia lanceolata* plantations of different stand ages

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Carbon sequestration in forest soil is critical for reducing atmospheric greenhouse gas concentrations and slowing down global warming. However, little is known about the difference in soil organic carbon (SOC) among different stand ages and the relative importance of biotic and abiotic variations such as soil microbial community and soil physicochemical properties in the regulation of SOC in forests. In the present study, we measured the SOC of the topsoil (0-10 cm) in Chinese subtropical *Cunninghamia lanceolata* plantations of three different stand ages (young plantation of 6 years, middle-aged plantation of 12 years, and mature plantation of 25 years). We further measured microbial community composition by phospholipid fatty acid (PLFA) analysis and soil organic carbon physical fractions by wet sieving and density floating as well as other physicochemical properties. The effects of the main impact factors on SOC were investigated. The results showed that: The middle-aged plantation had significantly higher SOC (10.63 g kg^{-1}) than the young plantation (5.33 g kg^{-1}), and that of the mature plantation (7.83 g kg^{-1}) was in between. Besides, the soil total PLFAs and all the functional groups (i.e. bacteria, fungi, actinomycetes, Gram-positive bacteria, and Gram-negative bacteria) of PLFAs were significantly higher in the middle-aged plantation than in the young plantation and the mature plantation. Soil physicochemical properties, including physical fractions, differed among plantations of the three stand ages. Notably, the proportion of organic carbon protected within microaggregates was significantly higher in the middle-aged plantation (40.4%) than those in the young plantation (29.2%) and the mature plantation (27.8%), indicating that the middle-aged *Cunninghamia lanceolata* plantation had stronger soil organic carbon stability. Both soil microbial community and physicochemical properties exerted dominant effects on SOC and jointly explained 82.7% of the variance of SOC among different stand ages. Among them, total and all the functional groups of PLFAs, nitrate nitrogen, total nitrogen, and organic carbon protected

within microaggregates had a significant positive correlation with SOC. These results highlight the important role of soil biotic and abiotic factors in shaping the contents of SOC in forests of different stand ages. This study provides a theoretical basis for forestry management and forest carbon cycling models.

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22 **Abstract**

23 Carbon sequestration in forest soil is critical for reducing atmospheric greenhouse gas
24 concentrations and slowing down global warming. However, little is known about the difference
25 in soil organic carbon (SOC) among different stand ages and the relative importance of biotic
26 and abiotic variations such as soil microbial community and soil physicochemical properties in
27 the regulation of SOC in forests. In the present study, we measured the SOC of the topsoil (0-10
28 cm) in Chinese subtropical *Cunninghamia lanceolata* plantations of three different stand ages
29 (young plantation of 6 years, middle-aged plantation of 12 years, and mature plantation of 25
30 years). We further measured microbial community composition by phospholipid fatty acid
31 (PLFA) analysis and soil organic carbon physical fractions by wet sieving and density floating as
32 well as other physicochemical properties. The effects of the main impact factors on SOC were
33 investigated. The results showed that: The middle-aged plantation had significantly higher SOC
34 (10.63 g kg^{-1}) than the young plantation (5.33 g kg^{-1}), and that of the mature plantation (7.83 g
35 kg^{-1}) was in between. Besides, the soil total PLFAs and all the functional groups (i.e. bacteria,
36 fungi, actinomycetes, Gram-positive bacteria, and Gram-negative bacteria) of PLFAs were
37 significantly higher in the middle-aged plantation than in the young plantation and the mature
38 plantation. Soil physicochemical properties, including physical fractions, differed among
39 plantations of the three stand ages. Notably, the proportion of organic carbon protected within
40 microaggregates was significantly higher in the middle-aged plantation (40.4%) than those in the
41 young plantation (29.2%) and the mature plantation (27.8%), indicating that the middle-aged

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44 jointly explained 82.7% of the variance of SOC among different stand ages. Among them, total
45 and all the functional groups of PLFAs, nitrate nitrogen, total nitrogen, and organic carbon
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47 highlight the important role of soil biotic and abiotic factors in shaping the contents of SOC in
48 forests of different stand ages. This study provides a theoretical basis for forestry management
49 and forest carbon cycling models.

50 **Keywords** *Cunninghamia lanceolata* plantation; stand age; SOC; microbial community;
51 physicochemical properties; soil organic matter fractions

52 **1 Introduction**

53 Global warming caused by greenhouse gas enrichment is changing the structure, functions
54 and some key ecological processes of the terrestrial ecosystem (*Jones et al., 2009*), thus has
55 become the focus of global change research (*Peters et al., 2013*). The global forest, with a
56 coverage area of 4.0×10^9 hectares, is the main carbon pool of terrestrial ecosystems (*Pan et al.,*
57 *2011*), and plays an important role in regulating the global carbon cycle and climate change (*He,*
58 *2012*). Afforestation and plantation management are the main ways to increase forest cover,
59 thereby fixing more CO₂ from the atmosphere and slowing down global warming. Plantation
60 management, such as harvesting and forest fires, could create plantations of different stand ages.
61 Stand age and corresponding biomass were found to be the most important factors in determining

62 the net primary production (NPP) of forest plantations (*Michaletz et al., 2014*). What's more, soil
63 organic carbon (SOC) content (*Hou et al., 2019*) and its decomposition (*Wu et al., 2020b*) were
64 also found to vary with stand age. How does soil organic carbon in subtropical plantations varies
65 with stand age and what are the main drivers need more research.

66 It is worth noting that SOC could be partly protected from decomposition by being
67 encapsulated in aggregates or adsorbed by minerals (*Krull et al., 2003*). Therefore, according to
68 the stability and turnover time, SOC could be divided into different components, including
69 mineral-associated organic carbon (SC), organic carbon protected within microaggregates (SA),
70 and particulate organic matter (POM) (*Mitchell et al., 2018*). However, most studies about SOC
71 in forests focused on its total content (*Guan et al., 2019; Thom et al., 2019*) and there is still a
72 lack of studies about SOC fractions. We assume that the ratio of different components of SOC as
73 well as other soil physicochemical properties will affect SOC storage. Soil microbes are an
74 important part of the soil ecosystem, affecting soil fertility, nutrients, and carbon cycling
75 processes (*Soong et al., 2020*). Plantations of different stand ages have diverse NPP
76 (*Anderson-Teixeira et al., 2016*), litter, and root exudates (*Wu et al., 2020a*), which could
77 directly lead to microbial differences. Previous studies have found that microbial community
78 composition plays an important role in the formation and persistence of soil organic matter
79 (*Condrón et al., 2010*). Therefore, we assume that microbial community is one of the most
80 important drivers of SOC among plantations of different stand ages.

81 There is a large area of artificial forests in China. *Cunninghamia lanceolata* is an excellent
82 fast-growing native species, which is not susceptible to pests and diseases and is widely used in

83 commercial wood. *Cunninghamia lanceolata* has the largest planting area (8.5×10^6 hm²) among
84 China's artificial forests and it accounts for 21.4% of the total forest area in China based on the
85 seventh national forest inventory statistics. In this study, we compared SOC in *Cunninghamia*
86 *lanceolata* plantations of three different stand ages (young plantation of 6 years, middle-aged
87 plantation of 12 years, and mature plantation of 25 years) in subtropical China. To explore the
88 key determinant of SOC, we further detected microbial community composition, SOC physical
89 fractions, and other physicochemical properties. We then conducted variation partitioning
90 analysis (VPA) to quantify the relative contribution of microbial community and
91 physicochemical properties to the variations of SOC among different stand ages. The results will
92 reveal patterns and drivers of SOC in different developmental stages of *Cunninghamia*
93 *lanceolata* plantations and provide a theoretical basis for the scientific management of the
94 artificial forest.

95 **2 Materials & Methods**

96 **2.1. Study site and soil sample collection**

97 Our study was conducted at Gaojingmiao Forest Farm (31°00'59"N, 119°12'08"E) in
98 Langxi County, Xuancheng City, Anhui Province, China. Gaojingmiao Forest Farm is a state-
99 owned forest farm, covering an area of 10.37 km², with large areas of *Pinus massoniana*, *Pinus*
100 *elliottii*, and *Cunninghamia lanceolata*. This forest farm is located in the southeast of Anhui
101 Province and has a humid subtropical monsoon climate with four distinct seasons and sufficient

102 sunlight. The mean annual temperature in this area is 15.9°C, and the coldest and warmest
103 months are January (with a mean temperature of 2.7°C) and July (with a mean temperature of
104 28.1°C), respectively. The region receives an average total annual precipitation of 1294.4 mm
105 mostly occurring in summer. The area has 1784 h of sunshine and 228 days of Frost-free period
106 per year. The soil is acidic yellow-red soil.

107 In December 2018, *Cunninghamia lanceolata* plantations of three stand ages (young
108 plantation of 6 years, middle-aged plantation of 12 years, and mature plantation of 25 years) with
109 basically the same site conditions (30-50 m above sea level, slope less than 30°) were selected as
110 the sample blocks. Three plots (10 m×10 m) were randomly set in each of the stand ages of
111 *Cunninghamia lanceolata* plantation. Five soil cores were randomly collected from the 0-10 cm
112 soil layer in each plot using a corer 6 cm in diameter. These five soil cores were then combined
113 and mixed thoroughly as one sample for each plot. The individual soil samples of each plot were
114 collected in plastic bags and placed in a cooler in the field, then transported to the laboratory for
115 further analysis.

116 After visible plant residues and stones were removed, each soil sample was divided into two
117 subsamples. One subsample was used to determine pH, soil organic carbon (SOC), and total
118 nitrogen (TN) content after air-dried; one subsample was stored at -20°C and used to determine
119 microbial community composition, ammonium nitrogen (NH₄⁺-N), nitrate nitrogen (NO₃⁻-N),
120 and dissolved organic carbon (DOC) (Yuan *et al.*, 2020). Cylinders were used to obtain 4
121 undisturbed soil cores from the 0-10 cm profile of each plot. One of these soil cores was used to
122 determine soil bulk density (BD) and soil water content (SWC), while the other three of them

123 were used to determine SOC physical fractions. The three soil cores used to determine SOC
124 fractions were gently broken apart along the natural breakpoints and passed through a 2 mm
125 sieve to remove visible organic debris and stones, and then air-dried for further analysis
126 (*Mitchell et al., 2018*).

127 **2.2. Soil physicochemical properties analysis**

128 Both SOC and TN were measured using a C/N analyzer (Elementar, Vario Max CN,
129 Germany) with a combustion temperature of 900 °C. Soil samples collected with cylinders were
130 oven-dried to calculate BD and SWC according to the volume of the cylinder and the soil weight
131 before and after drying. Soil pH was measured at a soil: water ratio of 1:2.5 using a pH meter
132 (Mettler Toledo, Greifensee, Switzerland). Soil NH₄⁺-N and NO₃⁻-N were extracted from 20 g of
133 fresh soil with 1 mol L⁻¹ KCl (soil: extract, 1:5) and analyzed using a flow-injection
134 autoanalyzer ((CFA)-AA3, SEAL, Germany). Soil DOC was extracted using deionized water
135 (soil: extract = 1:5) and analyzed using a TOC analyzer (Elementar, Vario TOC cube, Hanau,
136 Germany).

137 Wet sieving and density flotation methods were used to detect SOC fractions (*Mitchell et al.,*
138 *2018*). First, soil samples were dispersed by low-energy sonication. Briefly, add 30 g of air-dried
139 soil into 150 mL water and then put them into an ultrasonic treatment (KQ5200DE, Kunshan
140 Ultrasound Instrument Co., Ltd., China) with the output energy of 22 J ml⁻¹. The
141 macroaggregates were disrupted in this step and only the more stable microaggregates were left.
142 Secondly, the dispersed suspension was then wet sieved over a 53 µm aperture sieve several

143 times until the rinsing water was clear. Soil samples were separated into two parts in this step:
144 the fraction $> 53 \mu\text{m}$ which was left on the sieve and the fraction $< 53 \mu\text{m}$ which passed through
145 the sieve and remained in suspension. The fraction $> 53 \mu\text{m}$ was rinsed repeatedly with deionized
146 water, dried in the oven at 40°C , and weighed. Thirdly, density flotation was conducted to
147 separate the fraction $> 53 \mu\text{m}$ from the second step into organic carbon protected within
148 microaggregates (SA) and particulate organic matter (POM). The fraction $> 53 \mu\text{m}$ from the
149 second step was stirred with sodium polytungstate (SPT) at a density of 1.8 g cm^{-3} and then
150 centrifuged at $1000g$ for 15 min . The light part was POM, which could be decanted and then
151 washed with deionized water to remove all SPT, dried at 40°C , and weighed. The heavy part was
152 also dried at 40°C and weighed as SA. At last, the fraction $< 53 \mu\text{m}$ from the second step was
153 filtered through a $0.45 \mu\text{m}$ aperture nylon mesh, and the material $> 0.45 \mu\text{m}$ was dried at 40°C
154 and weighed as mineral-associated organic carbon (SC).

155 **2.3. Phospholipid fatty acid (PLFA) analysis**

156 The PLFA contents of the samples were analyzed using the method described by *Bååth and*
157 *Anderson (2003)*. Briefly, lipids were extracted from freeze-dried soil (8 g) in a single-phase
158 mixture of chloroform:methanol:phosphate buffer ($1:2:0.5$). After extraction, the lipids were
159 separated into neutral lipids, glycolipids, and polar lipids (phospholipids) on a silicic acid
160 column. The samples were analyzed using a Thermo ISQ gas chromatography-mass
161 spectroscopy system (TRACE GC Ultra ISQ). The concentrations of the individual compounds
162 were obtained by comparing the peaks with an internal standard (nonadecanoic acid methyl ester

163 19:0). The fatty-acid signatures 15:0, i15:0, a15:0, i16:0, 16:1 ω 7c, 17:0, i17:0, cy17:0 and
164 cy19:0 were used as bacterial biomarkers (B). The fatty acids 18:2 ω 6 and 18:1 ω 9c were used as
165 fungal indicators (F) and 10Me16:0 and 10Me18:0 were used as indicators for the actinomycetes
166 (ACT). The fatty acids i15:0, a15:0, i16:0, and i17:0 were used to represent Gram-positive
167 bacteria (G⁺), while 16:1 ω 7c, cy17:0, and cy19:0 were used to represent Gram-negative bacteria
168 (G⁻). The total PLFAs (TPLFA) were the sum of bacterial, fungal, and actinomyces PLFA
169 biomarkers.

170 **2.4. Statistical analysis**

171 A one-way ANOVA was performed to identify significant differences in SOC, soil
172 physicochemical properties, and PLFAs among the three stand ages. A principal components
173 analysis (PCA) was used to analyze soil microbial community structure. The Pearson correlation
174 method was used to analyze the correlation between SOC and some important physicochemical
175 properties and PLFAs. One-way ANOVA and Pearson correlation analysis was performed using
176 SPSS 19.0 (SPSS Inc., Chicago, USA). PCA was conducted with CANOCO for Windows 4.5.
177 Other figures were generated using the Origin 9.5 package (Origin Lab Corporation,
178 Northampton, USA). $P < 0.05$ was considered to be statistically significant. Mean \pm standard
179 deviation was shown in tables and figures.

180 Variation partitioning analysis (VPA) was conducted to quantify the relative importance of
181 soil microbial community and soil physicochemical properties to the variations of SOC among
182 *Cunninghamia lanceolata* plantations of different stand ages. To avoid collinearity, variables

183 with a large variance inflation factor (VIF) were removed in order until the VIF of the retained
184 variables does not exceed 10. Next, principal component analysis was performed on microbial
185 variables and physicochemical variables respectively (the first 2 principal components were
186 retained). Then VPA was employed to quantify their explanation for the variations of SOC
187 among different stand ages. VPA was conducted in R 4.0.2 (*R Core Team, 2020*) and the vegan
188 package (*Oksanen, et al. 2020*).

189 **3 Results**

190 **3.1 Soil organic carbon content**

191 Soil organic carbon content exhibited large variability among different stand ages (Fig. 1).
192 The middle-aged plantation had the highest SOC (10.63 g kg⁻¹) followed by the mature
193 plantation (7.83 g kg⁻¹), and the young plantation had the lowest SOC (5.33 g kg⁻¹). Soil organic
194 carbon content of the middle-aged plantation was 99.4% and 35.8% higher than those of the
195 young and the mature plantation, respectively. The difference in SOC between the middle-aged
196 and the young plantations was significant.

197 **3.2 Soil physicochemical properties**

198 Soil physicochemical properties of the *Cunninghamia lanceolata* plantations varied among
199 different stand ages (Table 1). The middle-aged plantation had the highest pH, SWC and TN.
200 The mature plantation had a significantly higher NH₄⁺-N content than the other stand ages. Soil

201 BD, C/N, NO_3^- -N, and DOC showed no significant difference among the three stand ages.

202 Soil organic carbon fractions were different among *Cunninghamia lanceolata* plantations of
203 different stand ages (Fig. 2). The proportion of SA was significantly higher in the soil of the
204 middle-aged plantation (40.4%) than those of the young (29.2%) and the mature (27.8%)
205 plantation. The other two fractions, SC and POM, showed no significant difference among the
206 three stand ages.

207 3.3 Soil microbial community

208 Soil PLFAs showed significant differences among different stand ages (Fig. 3). The middle-
209 aged plantation had significantly higher soil total PLFAs, bacterial PLFAs, fungal PLFAs,
210 actinobacterial PLFAs, Gram-positive and Gram-negative bacterial PLFAs than the young
211 plantation and the mature plantation (Fig. 3a). Soil total PLFAs of the middle-aged plantation
212 were $30.23 \text{ nmol g}^{-1}$, while those of the young plantation and the mature plantation were 72.5%
213 and 60.3% lower than the middle-aged plantation. The ratio of F/B and the ratio of G^+/G^-
214 showed no significant difference among stand ages (Fig. 3b). Principal components analysis
215 (PCA) also confirmed that soil microbial community composition was different among the three
216 stand ages and 94% of the variance was explained by the first component of the PCA (Fig. 4).
217 The soil PLFAs of the middle-aged plantation were separated from those of the other two stand
218 ages along with the first principal component.

219 3.4 Associations of SOC with the microbial community and physicochemical properties

220 The results of VPA showed that the soil microbial community and physicochemical
221 properties explained 82.7% of the variance in SOC of different stand ages (Fig. 5). Pearson
222 correlation analysis also showed that some of the microbial and physicochemical factors were
223 significantly correlated with SOC (Table 2). Among the microbial factors, TPLFA, B, F, ACT,
224 G⁺, and G⁻ were positively correlated with SOC while F/B was negatively correlated with SOC.
225 Among the physicochemical properties, TN, NO₃⁻-N, and SA were positively correlated with
226 SOC.

227 4 Discussion

228 The SOC concentrations in this study (ranged from 5.33 to 10.63 g kg⁻¹, Fig. 1) were lower
229 than those measured in some other subtropical *Cunninghamia lanceolata* plantations, which
230 ranged from 18 to 25 g kg⁻¹ (Chen *et al.*, 2013; Song *et al.*, 2017). The possible reason for the
231 lower SOC in our study is that the plantations here were converted from farmland decades ago,
232 and the SOC of farmlands is generally lower than that of forest plantations (Xie *et al.*, 2007).
233 This implies that the forest plantations in this study area still have large carbon sequestration
234 potential with proper management.

235 The middle-aged *Cunninghamia lanceolata* plantation had the highest SOC (Fig. 1) and the
236 highest fraction of SA (Fig. 2). Compared with the POM fraction, the SOC occluded within
237 microaggregates is more stable because microaggregates excluded microbes and enzymes from

238 pores (Yu *et al.*, 2012), indicating that the middle-aged plantation has more stable SOC. Forest
239 SOC mainly comes from above-ground litter, fine root decomposition, and root exudates
240 (Berhongaray *et al.*, 2019). Young plantations, which are in the fast-growing stage, produce little
241 litter. With the growth of the plantation age, the above-ground litterfall increased (Zheng *et al.*,
242 2019). What's more, the increasing canopy closure will also accelerate the withering of
243 understory vegetation (Verburg *et al.*, 2001), and further increase the amount of surface litter.
244 Most of the previous studies found that the mature forests had the highest SOC due to higher
245 levels of litter accumulation and lower soil respiration (Nath *et al.*, 2022, Wang *et al.*, 2019).
246 However, our study found that the SOC of mature plantations was lower than that of middle-
247 aged plantations. This may be due to inactive root activities in the mature plantations. The
248 decomposition process of litter takes a longer time, while the carbon input from root exudates to
249 soil is more rapid. A previous study conducted in subtropical China showed that middle-aged
250 *Cunninghamia lanceolata* plantations had higher underground carbon allocations than young and
251 mature plantations (Chen *et al.*, 2008). Because mature forests grow slowly and require fewer
252 nutrients, they do not need as many roots for nutrients. The higher underground carbon
253 allocations in middle-aged forests provided more organic carbon to the soil in the form of
254 exudates and dead roots. While delivering large amounts of carbon directly to the soil, root
255 exudate contains macromolecular viscose and promotes the formation of microaggregates
256 (Traoré *et al.*, 2000).

257 Soil total PLFAs and all microbial groups were highest in the middle-aged plantation (Fig.
258 3a). The possible reason is that the middle-aged plantations, had higher litter accumulation than

259 the young plantations and more root allocation than the mature plantations and this provided
260 more carbon sources for the growth and reproduction of microbes. Higher microbial biomass
261 generally corresponds to better soil structure and nutrient status (*Kang et al., 2021*). The ratio of
262 F/B could reflect ecosystem stability and soil nutritional status (*Liu et al., 2019*). The ratios of
263 F/B were all smaller than 1 (Fig. 3b), indicating the absolute dominance of bacteria. And in the
264 present study, there was no significant difference in the ratio of F/B among plantations of
265 different stand ages. The ratios of G⁺/G⁻ were all bigger than 1 (Fig. 3b). This may be due to the
266 different water requirements of G⁺ and G⁻ bacteria, the subtropical humid soil environment is
267 more suitable for the growth and reproduction of G⁺ bacteria (*Zhou et al., 2017*).

268 Our results illustrated the roles of soil microbial community and physicochemical properties
269 in regulating SOC across different stand ages (Fig. 5). We found that all microbial groups
270 (PLFAs) were positively correlated with SOC (Table 2). While SOC provides food sources for
271 microorganisms, soil microorganisms and their debris are important components of SOC (*Guo et*
272 *al., 2021*). The higher root exudates of middle-aged plantations provided more carbon sources
273 for the growth and reproduction of microorganisms and produced more microbial necromass C
274 to SOC. Besides, soil physicochemical properties, especially TN, NO₃⁻-N, and SA, were also
275 found to regulate SOC significantly (Table 2). The interactions between soil C and N have been
276 intensively studied as N could regulate plant photosynthesis, allocation, rhizosphere priming
277 effect, and greenhouse gas emissions (*Gärdenäs et al., 2011*). For example, *Tian et al. (2019)*
278 found that high N increased SOC mainly by decreasing CO₂ efflux. Organic carbon protected
279 within microaggregates is isolated from microorganisms and hard to be decomposed. As a result,

280 higher SA facilitates the storage of soil SOC. Unexpectedly, soil moisture, which is an important
281 factor in regulating SOC decomposition (*Meyer et al., 2018*), was insignificantly related to SOC
282 in our study (Table 2). We measured SWC only one time, and it could not be representative of
283 long-term conditions of soil moisture, which has a lasting impact on SOC decomposition. Higher
284 soil pH was found in the middle-aged plantation than in the young and mature plantation (Table
285 1). In acidic soils, lower pH suppresses the growth of microorganisms and elevated pH could
286 promote microbial biomass (*Silva-Sánchez et al., 2019*). The higher pH and higher microbial
287 biomass of middle-aged forests in this study are consistent. Although soil pH was not
288 significantly related to SOC, pH can indirectly affect SOC through the regulation of
289 microorganisms.

290 **5 Conclusions**

291 Our study detected the variation in SOC of different stand ages, which has important
292 implications for forest carbon sink function. Overall, middle-aged plantations had higher total
293 SOC and organic carbon protected within microaggregates, which indicated that the SOC
294 stability of middle-aged forests was stronger. Moreover, our study clarified that the
295 physicochemical properties and microbial communities are the two main driving factors of SOC.
296 The middle-aged plantation had significantly higher soil total PLFAs and all the functional
297 groups of PLFAs than those of the young and mature plantations, indicating that the middle-aged
298 plantation had better soil structure and nutrient status. In general, these findings jointly highlight
299 the important role of stand age and soil biotic and abiotic factors in shaping the contents of SOC

300 in subtropical *Cunninghamia lanceolata* plantations. These results will greatly improve our
301 understanding and prediction of soil carbon dynamics in forests with their development.

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306 **References**

- 307 Anderson-Teixeira, K.J., Wang, M.M., McGarvey, J.C. and LeBauer, D.S., 2016. Carbon
308 dynamics of mature and regrowth tropical forests derived from a pantropical database (T
309 rop F or C-db). *Global Change Biology*, 22(5): 1690-1709.
- 310 Bååth E., Anderson T.H., 2003. Comparison of soil fungal/bacterial ratios in a pH gradient using
311 physiological and PLFA-based techniques. *Soil Biology and Biochemistry*, 35(7): 955-
312 963.
- 313 Berhongaray, G., Cotrufo, F.M., Janssens, I.A. and Ceulemans, R., 2019. Below-ground carbon
314 inputs contribute more than above-ground inputs to soil carbon accrual in a bioenergy
315 poplar plantation. *Plant and Soil*, 434(1): 363-378.
- 316 Chen, G.S. et al., 2008. Changes in belowground carbon allocation in a Chinese fir
317 chronosequence in Fujian Province, China. *Chinese Journal of Plant Ecology*, 32(6):
318 1285.

- 319 Chen, G.S. et al., 2013. Carbon storage in a chronosequence of Chinese fir plantations in
320 southern China. *Forest Ecology and Management*, 300: 68-76.
- 321 Condrón, L., Stark, C., O’Callaghan, M., Clinton, P. and Huang, Z., 2010. The role of microbial
322 communities in the formation and decomposition of soil organic matter, *Soil*
323 *microbiology and sustainable crop production*. Springer, pp. 81-118.
- 324 Gärdenäs, A.I. et al., 2011. Knowledge gaps in soil carbon and nitrogen interactions—From
325 molecular to global scale. *Soil Biology and Biochemistry*, 43(4): 702-717.
- 326 Guan, J.H. et al., 2019. Soil organic carbon density and its driving factors in forest ecosystems
327 across a northwestern province in China. *Geoderma*, 352: 1-12.
- 328 Guo, Z. et al., 2021. Contribution of soil microbial necromass to SOC stocks during vegetation
329 recovery in a subtropical karst ecosystem. *Science of the Total Environment*, 761: 143945.
- 330 He, J., 2012. Carbon cycling of Chinese forests: From carbon storage, dynamics to models.
331 *Science China. Life Sciences*, 55(2): 188.
- 332 Hou, G., Delang, C.O., Lu, X. and Gao, L., 2019. Soil organic carbon storage varies with stand
333 ages and soil depths following afforestation. *Annals of Forest Research*, 62(2): 3-20.
- 334 Jari Oksanen, F. Guillaume Blanchet, Michael Friendly, Roeland Kindt, Pierre Legendre, Dan
335 McGlinn, Peter R. Minchin, R. B. O'Hara, Gavin L. Simpson, Peter Solymos, M. Henry
336 H. Stevens, Eduard Szoecs and Helene Wagner (2020). *vegan: Community Ecology*
337 *Package*. R package version 2.5-7. <https://CRAN.R-project.org/package=vegan>
- 338 Jones, C., Lowe, J., Liddicoat, S. and Betts, R., 2009. Committed terrestrial ecosystem changes
339 due to climate change. *Nature Geoscience*, 2(7): 484-487.

- 340 Kang, H., Yu, W., Dutta, S. and Gao, H., 2021. Soil microbial community composition and
341 function are closely associated with soil organic matter chemistry along a latitudinal
342 gradient. *Geoderma*, 383: 114744.
- 343 Krull, E.S., Baldock, J.A. and Skjemstad, J.O., 2003. Importance of mechanisms and processes
344 of the stabilisation of soil organic matter for modelling carbon turnover. *Functional Plant
345 Biology*, 30(2): 207-222.
- 346 Liu, M., Sui, X., Hu, Y. and Feng, F., 2019. Microbial community structure and the relationship
347 with soil carbon and nitrogen in an original Korean pine forest of Changbai Mountain,
348 China. *BMC Microbiology*, 19(1): 218.
- 349 Meyer, N., Welp, G. and Amelung, W., 2018. The temperature sensitivity (Q₁₀) of soil
350 respiration: Controlling factors and spatial prediction at regional scale based on
351 environmental soil classes. *Global Biogeochemical Cycles*, 32(2): 306-323.
- 352 Michaletz, S.T., Cheng, D., Kerkhoff, A.J. and Enquist, B.J., 2014. Convergence of terrestrial
353 plant production across global climate gradients. *Nature*, 512(7512): 39-43.
- 354 Mitchell, E. et al., 2018. Amount and incorporation of plant residue inputs modify residue
355 stabilisation dynamics in soil organic matter fractions. *Agriculture, Ecosystems &
356 Environment*, 256: 82-91.
- 357 Nath, P.C., Sileshi, G.W., Ray, P., Das, A.K., and Nath, A.J., 2022. Variations in soil properties
358 and stoichiometric ratios with stand age under agarwood monoculture and polyculture on
359 smallholder farms. *Catena*, 213: 106174.

- 360 Pan, Y. et al., 2011. A large and persistent carbon sink in the world's forests. *Science*, 333(6045):
361 988-993.
- 362 Peters, G.P. et al., 2013. The challenge to keep global warming below 2 °C. *Nature Climate*
363 *Change*, 3(1): 4-6.
- 364 R Core Team (2020). R: A language and environment for statistical computing. R Foundation for
365 Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.
- 366 Silva-Sánchez, A., Soares, M., and Rousk, J., 2019. Testing the dependence of microbial growth
367 and carbon use efficiency on nitrogen availability, pH, and organic matter quality. *Soil*
368 *Biology and Biochemistry*, 134: 25-35.
- 369 Song, X., Kimberley, M.O., Zhou, G. and Wang, H., 2017. Soil carbon dynamics in successional
370 and plantation forests in subtropical China. *Journal of Soils and Sediments*, 17(9): 2250-
371 2256.
- 372 Soong, J.L. et al., 2020. Microbial carbon limitation: the need for integrating microorganisms
373 into our understanding of ecosystem carbon cycling. *Global Change Biology*, 26(4):
374 1953-1961.
- 375 Thom, D. et al., 2019. The climate sensitivity of carbon, timber, and species richness covaries
376 with forest age in boreal–temperate North America. *Global Change Biology*, 25(7): 2446-
377 2458.
- 378 Tian, J. et al., 2019. Long-term nitrogen addition modifies microbial composition and functions
379 for slow carbon cycling and increased sequestration in tropical forest soil. *Global Change*
380 *Biology*, 25(10): 3267-3281.

- 381 Traoré, O., Groleau-Renaud, V., Plantureux, S., Tubeileh, A. and Boeuf-Tremblay, V., 2000.
382 Effect of root mucilage and modelled root exudates on soil structure. *European Journal*
383 *of Soil Science*, 51(4): 575-581.
- 384 Verburg, P., Johnson, D. and Harrison, R., 2001. Long-term nutrient cycling patterns in Douglas-
385 fir and red alder stands: a simulation study. *Forest Ecology and Management*, 145(3):
386 203-217.
- 387 Wang, Y., Liu, L., Yue, F., and Li, D., 2019. Dynamics of carbon and nitrogen storage in two
388 typical plantation ecosystems of different stand ages on the Loess Plateau of China. *PeerJ*,
389 7: e7708.
- 390 Wu, H. et al., 2020a. Soil phosphorus bioavailability and recycling increased with stand age in
391 Chinese fir plantations. *Ecosystems*, 23(5): 973-988.
- 392 Wu, X. et al., 2020b. Land use change and stand age regulate soil respiration by influencing soil
393 substrate supply and microbial community. *Geoderma*, 359: 113991.
- 394 Xie, Z. et al., 2007. Soil organic carbon stocks in China and changes from 1980s to 2000s.
395 *Global Change Biology*, 13(9): 1989-2007.
- 396 Yu, H. et al., 2012. Effects of long-term compost and fertilizer application on stability of
397 aggregate-associated organic carbon in an intensively cultivated sandy loam soil. *Biology*
398 *and Fertility of Soils*, 48(3): 325-336.
- 399 Yuan, Y., Dai, X., Fu, X., Kou, L., Luo, Y., Jiang, L., and Wang, H., 2020. Differences in the
400 rhizosphere effects among trees, shrubs and herbs in three subtropical plantations and
401 their seasonal variations. *European Journal of Soil Biology*, 100: 103218.

402 Zheng, L.T., Chen, H.Y. and Yan, E.R., 2019. Tree species diversity promotes litterfall
403 productivity through crown complementarity in subtropical forests. *Journal of Ecology*,
404 107(4): 1852-1861.

405 Zhou, W., Shen, W., Li, Y. and Hui, D., 2017. Interactive effects of temperature and moisture on
406 composition of the soil microbial community. *European Journal of Soil Science*, 68(6):
407 909-918.

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Figure 1

Soil organic carbon (SOC) content in *Cunninghamia lanceolata* plantations of three different stand ages

Different lower case letters indicated a significant difference among plantations of different stand ages at 0.05 level

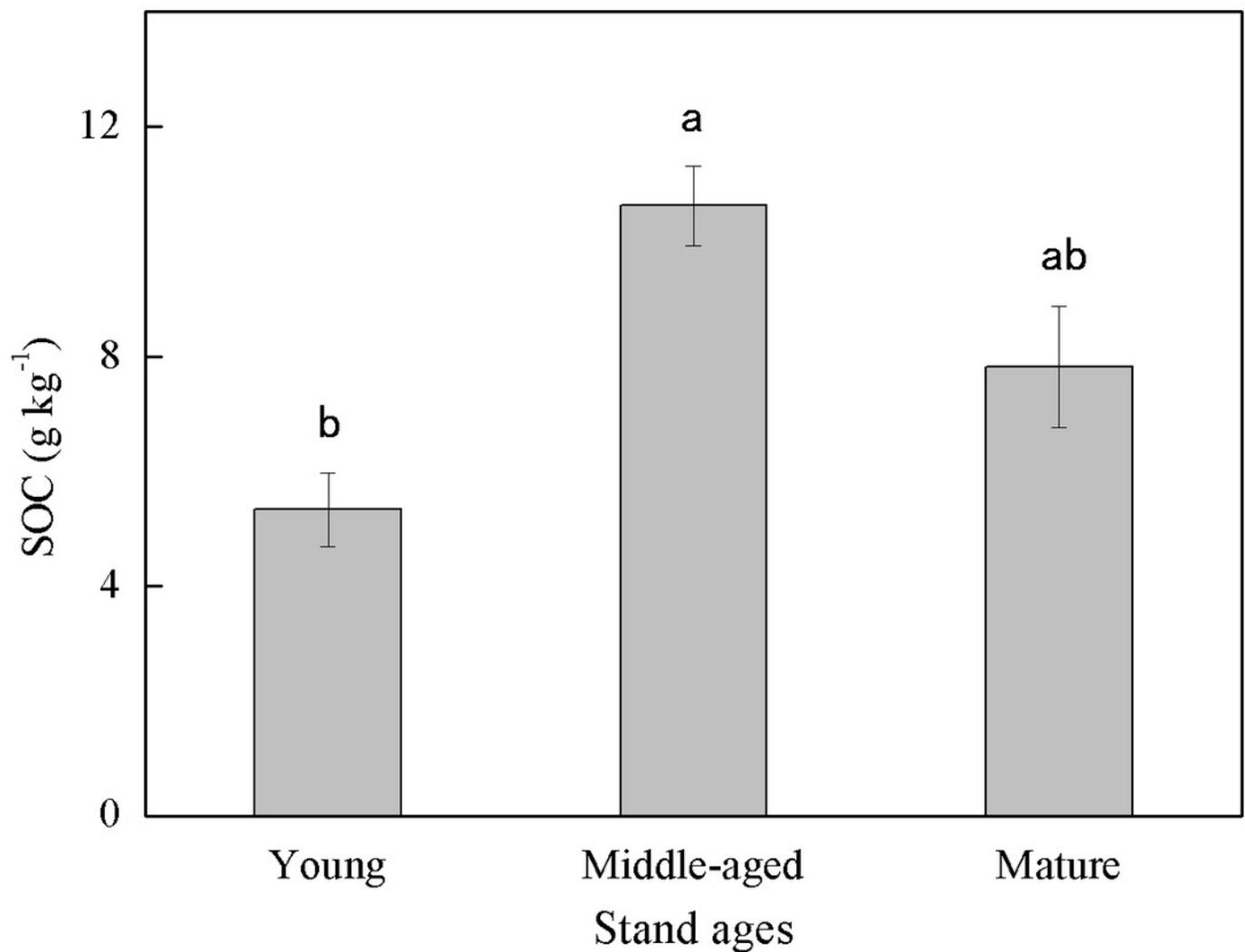


Figure 2

Soil organic carbon physical fractions in *Cunninghamia lanceolata* plantations of three different stand ages

SC, Mineral-associated organic carbon; SA, Organic carbon protected within microaggregates; POM, Particulate organic matter

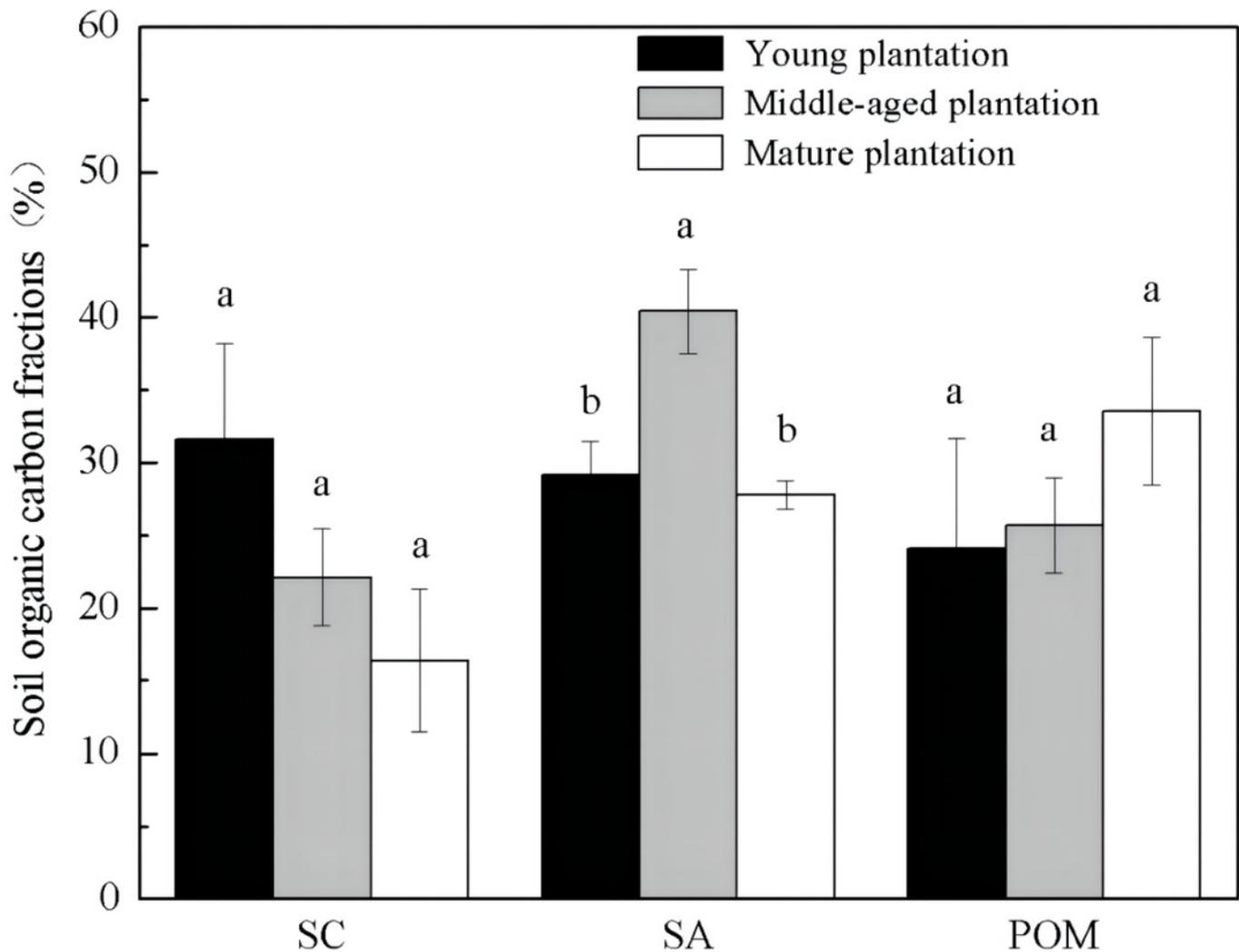


Figure 3

Soil microbial community structure in *Cunninghamia lanceolata* plantations of three different stand ages

TPLFA, Total phospholipid fatty acids; B, Bacteria; F, Fungi; ACT, Actinobacteria; G⁺, Gram-positive bacteria; G⁻, Gram-negative bacteria; F/B, Ratio of fungi to bacteria; G⁺ /G⁻, Ratio of gram-positive bacteria to gram-negative bacteria

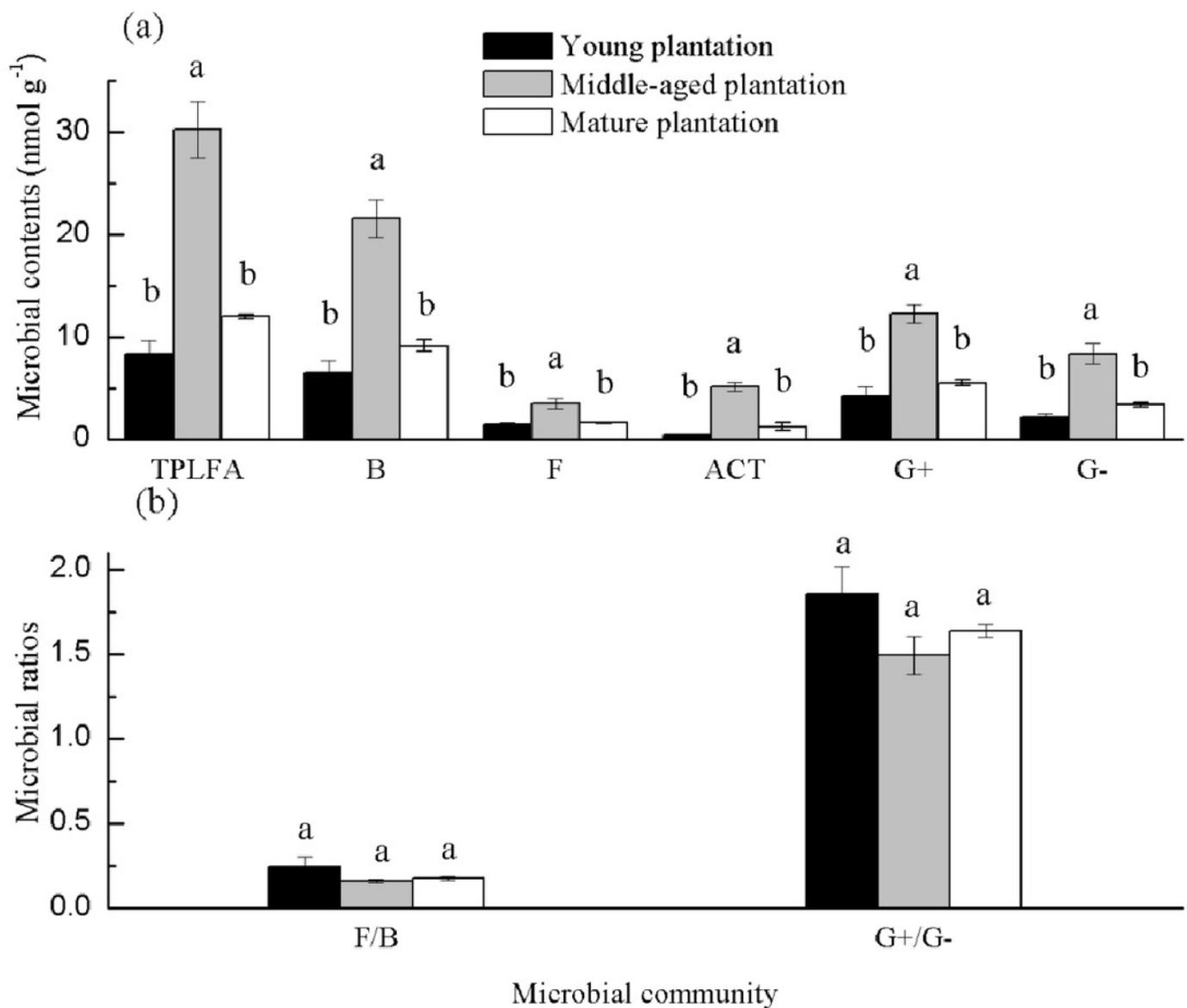


Figure 4

Principal component analysis (PCA) of soil microbial community structure in *Cunninghamia lanceolata* plantations of different ages

The red circles in the picture represent the young plantation, the blue triangles represent the middle-aged plantation, and the green stars represent the mature plantation

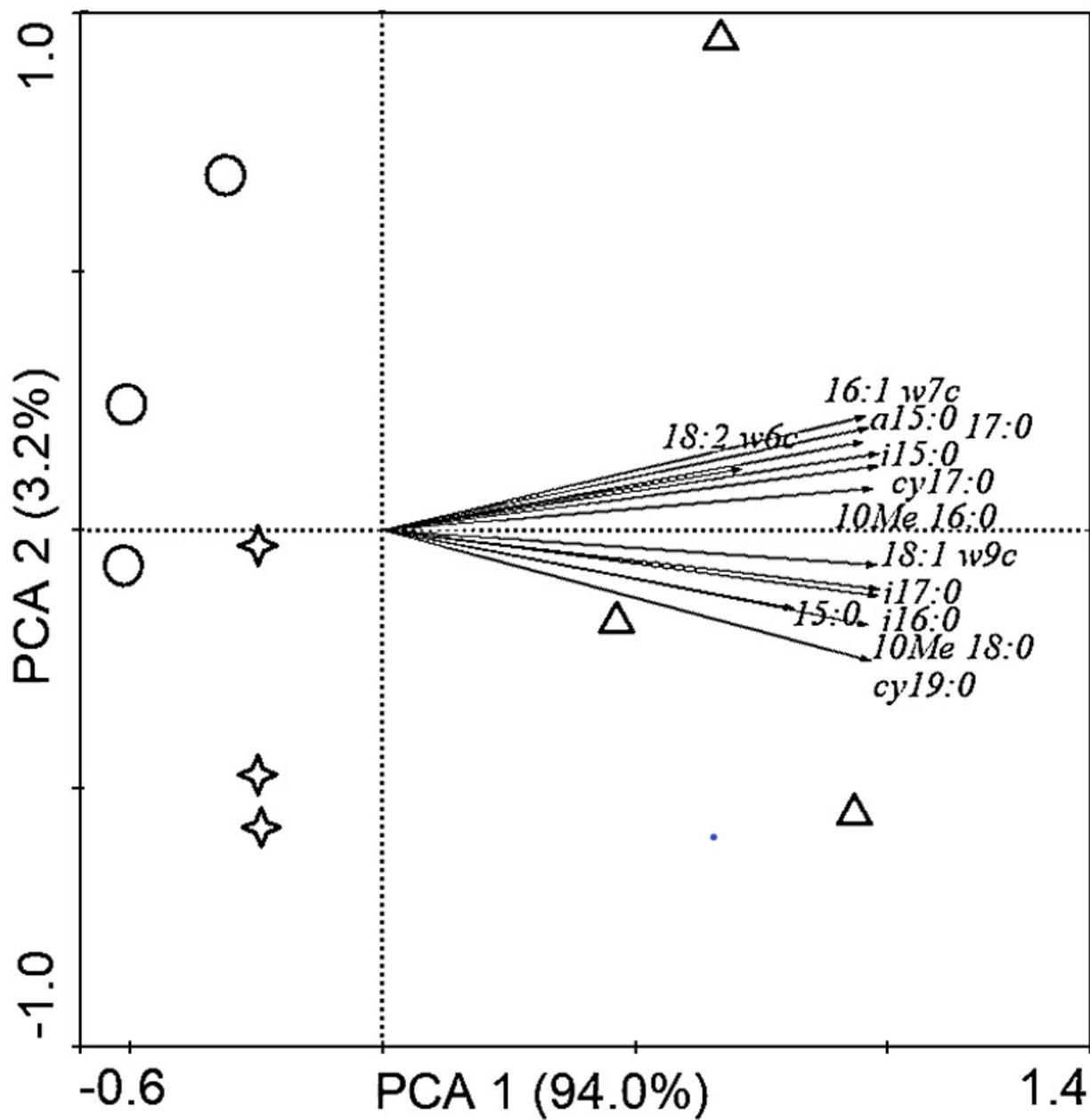


Figure 5

Results of variation partitioning analyses illustrating the relative contribution of soil microbial community and soil physicochemical properties to soil organic carbon

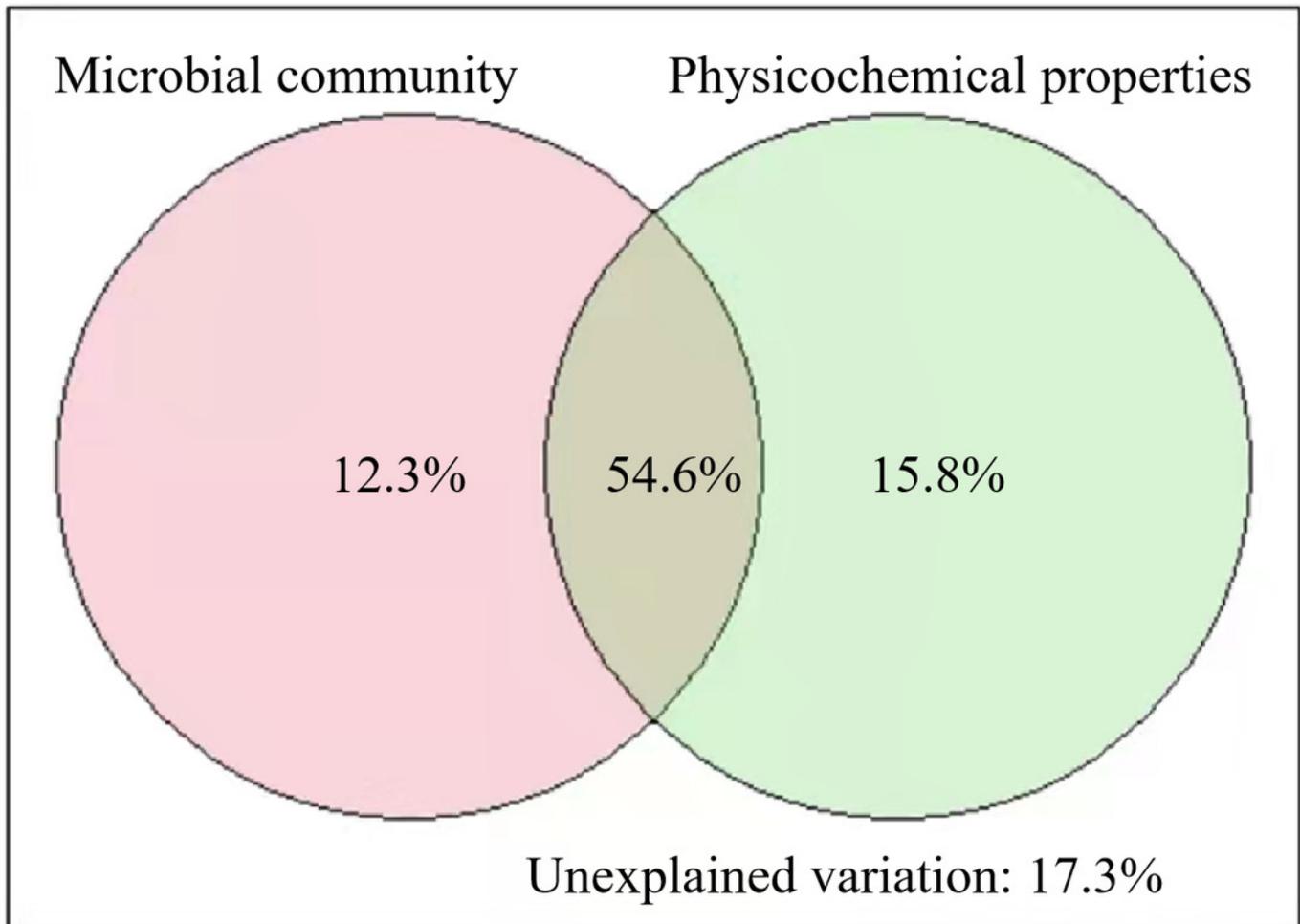


Table 1 (on next page)

Soil physicochemical properties in *Cunninghamia lanceolata* plantations of three different stand ages

The data shown in the table is the mean \pm standard error (n=3). Different lower case letters indicated a significant difference among plantations of different stand ages at 0.05

level. SWC, Soil water content; BD, Bulk density; TN, Total nitrogen; C/N, the ratio of organic carbon to total nitrogen; NH_4^+ -N, Ammonium nitrogen; NO_3^- -N, Nitrate nitrogen; DOC, Dissolved organic carbon.

- 1 Table 1. Soil physicochemical properties in *Cunninghamia lanceolata* plantations of three
 2 different stand ages

Soil physicochemical properties	Young plantation	Middle-aged plantation	Mature plantation
pH	4.88±0.03b	5.10±0.08a	4.67±0.06b
SWC (%)	20.83±0.46ab	22.50±0.77a	19.74±0.41b
BD (g cm ⁻³)	1.07±0.14a	1.30±0.03a	1.33±0.04a
TN (g kg ⁻¹)	0.60±0.06b	1.07±0.03a	0.67±0.07b
C/N	9.35±1.50a	9.96±0.48a	11.34±0.35a
NH ₄ ⁺ -N (mg kg ⁻¹)	12.37±0.98b	15.27±2.10b	22.13±1.25a
NO ₃ ⁻ -N (mg kg ⁻¹)	0.68±0.13a	1.55±0.34a	1.40±0.28a
DOC (mg kg ⁻¹)	17.67±6.13a	14.74±2.92a	6.44±1.15a

- 3 The data shown in the table is the mean ± standard error (n=3). Different lower case letters indicated a significant
 4 difference among plantations of different stand ages at 0.05 level. SWC, Soil water content; BD, Bulk density; TN, Total
 5 nitrogen; C/N, the ratio of organic carbon to total nitrogen; NH₄⁺-N, Ammonium nitrogen; NO₃⁻-N, Nitrate nitrogen; DOC,
 6 Dissolved organic carbon.
 7

Table 2 (on next page)

Pearson correlations between SOC and soil microbial/physicochemical properties.

TPLFA, Total phospholipid fatty acids; B, Bacteria; F, Fungi; ACT, Actinobacteria; G⁺, Gram-positive bacteria; G⁻, Gram-negative bacteria; F/B, Ratio of fungi to bacteria; G⁺ /G⁻, Ratio of gram-positive bacteria to gram-negative bacteria; SWC, Soil water content; BD, Bulk density; TN, Total nitrogen; C/N, the ration of organic carbon to total nitrogen; NH₄⁺-N, Ammonium nitrogen; NO₃⁻-N, Nitrate nitrogen; DOC, Dissolved organic carbon; SC, Mineral-associated organic carbon; SA, Organic carbon protected within microaggregates; POM, Particulate organic matter.

1 Table 2. Pearson correlations between SOC and soil microbial/physicochemical properties.

2

	Microbial community		Physicochemical properties					
	<i>r</i> -value	<i>P</i> -value		<i>r</i> -value	<i>P</i> -value		<i>r</i> -value	<i>P</i> -value
3 TPLFA	0.87	<0.001	pH	0.48	0.11	SC	-0.22	0.50
4 B	0.87	<0.001	SWC	0.49	0.10	SA	0.62	0.03
5 F	0.72	0.008	BD	0.44	0.15	POM	-0.22	0.50
6 ACT	0.89	<0.001	TN	0.90	<0.001			
7 G ⁺	0.89	<0.001	C/N	0.32	0.31			
8 G ⁻	0.85	<0.001	NH ₄ ⁺ -N	0.34	0.29			
	-0.68	0.02	NO ₃ ⁻ -N	0.63	0.03			
	-0.34	0.28	DOC	0.12	0.72			

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10 TPLFA, Total phospholipid fatty acids; B, Bacteria; F, Fungi; ACT, Actinobacteria; G⁺, Gram-positive bacteria; G⁻, Gram-
 11 negative bacteria; F/B, Ratio of fungi to bacteria; G⁺/G⁻, Ratio of gram-positive bacteria to gram-negative bacteria;
 12 SWC, Soil water content; BD, Bulk density; TN, Total nitrogen; C/N, the ration of organic carbon to total nitrogen; NH₄⁺-N,
 13 Ammonium nitrogen; NO₃⁻-N, Nitrate nitrogen; DOC, Dissolved organic carbon; SC, Mineral-associated organic carbon; SA,
 14 Organic carbon protected within microaggregates; POM, Particulate organic matter.

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