



1 **Soil microbial necromass shapes global carbon stocks in agricultural and natural**  
2 **ecosystems**

3 Jing-li Lu<sup>a</sup>, Thomas W. Crowther<sup>b</sup>, Manuel Delgado-Baquerizo<sup>c</sup>, Wenjie Liu<sup>a</sup>, Yamin

4 Jiang<sup>a</sup>, Hongyang Sun<sup>d</sup>, Zhiqiang Wang<sup>d</sup>, \*

5

6 <sup>a</sup> Center for Eco-Environment Restoration Engineering of Hainan Province, School of  
7 Ecology, Hainan University, Haikou, 570228, People's Republic of China;

8 <sup>b</sup> Institute of Integrative Biology, Department of Environmental Systems Science,  
9 ETH Zürich, 8092 Zürich, Switzerland;

10 <sup>c</sup> Laboratorio de Biodiversidad y Funcionamiento Ecosistémico, Instituto de Recursos  
11 Naturales y Agrobiología de Sevilla (IRNAS), CSIC, Seville, 41013, Spain;

12 <sup>d</sup> Sichuan Zoige Alpine Wetland Ecosystem National Observation and Research  
13 Station, College of Grassland Resources, Southwest Minzu University, Chengdu,  
14 610041, People's Republic of China

15

16

17 \* Corresponding author: Zhiqiang Wang

18 *E-mail address:* [wangzq@swun.edu.cn](mailto:wangzq@swun.edu.cn)

19



20 **Abstract**

21 Soil carbon (C) plays an essential role in regulating global C cycle and climate.  
22 Microbial necromass is an important component of soil C, and yet the relative  
23 contribution of microbial necromass in shaping the global C stocks in agricultural and  
24 natural ecosystems worldwide remains virtually unknown. In this study, we compiled  
25 data on fungal and bacterial necromass along with soil organic carbon (SOC) from the  
26 0–20 cm soil layer across 486 study sites (145 agricultural and 341 natural ecosystems)  
27 to evaluate the relative contribution of fungal necromass C (FNC) and bacterial  
28 necromass C (BNC) to SOC and the FNC/BNC ratio, after accounting for other biotic  
29 and abiotic factors. Our results indicated that, in both agricultural and natural  
30 ecosystems, the contribution of FNC to SOC significantly exceeded that of BNC, with  
31 FNC contributing approximately twice as much as BNC to SOC. However, the  
32 contributions of FNC and BNC to SOC were markedly higher in agricultural  
33 ecosystems than those in natural ecosystems, with a contrasting trend in the  
34 FNC/BNC ratio. Soil physicochemical properties (C/N and clay) were the most  
35 important predictors of the contributions of FNC and BNC to SOC in both ecosystems,  
36 while geographical factor (elevation) was the most important predictor of the  
37 FNC/BNC ratio. Our study enhances the current level of understanding regarding  
38 microbially mediated biogeochemical cycling and SOC dynamics, underscoring the  
39 critical role of microbial necromass in the global C cycle.

40

41 **Keywords:** agricultural ecosystems, bacterial necromass carbon, fungal necromass



42 carbon, microbial necromass carbon, natural ecosystems

43

## 44 **1 Introduction**

45 As the largest carbon (C) pool in the terrestrial biosphere, soil organic carbon (SOC)  
46 plays a pivotal role in shaping the global C cycle and climate system (Bellamy et al.,  
47 2005; Crowther et al., 2015). The traditional paradigm is that SOC storage is  
48 primarily formed directly based on plant material (Zhu and Miller, 2003; von Lützow  
49 et al., 2008). However, emerging evidence demonstrates that the stable SOC pool is  
50 predominantly composed of microbially derived organic compounds rather than  
51 plant-derived residues, indicating that microbial necromass may in fact be a primary  
52 source of stable SOC (Kallenbach et al., 2016; Liang et al., 2017). Microbes generate  
53 biomass by degrading plant-derived C, which is subsequently stabilized as microbial  
54 necromass through interactions with minerals and various processes within soil  
55 aggregates (Liang et al., 2017). Although the living soil microbial biomass constitutes  
56 only about 2% of SOC, microbial necromass carbon (MNC) can contribute up to  
57 50%–80% of SOC (Liang and Balser, 2011; Kallenbach et al., 2016; Liang et al.,  
58 2019). As such, there is growing scientific attention on the forces driving the  
59 accumulation of MNC and its contribution to SOC (Liang et al., 2017; Ni et al., 2020;  
60 Luo et al., 2022; Zhou et al., 2023). In order to gain a comprehensive and in-depth  
61 understanding of the role of MNC in the global C cycle, many studies have focused  
62 on the relative contributions of fungal (FNC) versus bacterial necromass (BNC;  
63 Zhang et al., 2021; Zhou et al., 2023; Xu et al., 2024).



64       The distinct roles of fungi and bacteria in stabilizing and decomposing SOC,  
65       enable their necromass C to elucidate the kinetics of SOC storage and decomposition  
66       (Malik et al., 2016). To be more specific, the chemical composition and functional  
67       characteristics of fungi and bacteria differ considerably, which may also contribute to  
68       different mechanisms of SOC formation. The cell walls of fungi primarily consist of  
69       chitin (a nitrogen-containing polysaccharide) and  $\beta$ -glucans, whereas bacterial cell  
70       walls are mainly composed of peptidoglycan—a complex of sugars and amino acids  
71       (Lenardon et al., 2007). The intricate structures of chitin and  $\beta$ -glucans in fungal  
72       necromass make them more resistant to decomposition compared to the typically  
73       more degradable bacterial necromass, leading to differences in their C decomposition  
74       rates in soil (Xu et al., 2022). Wang et al. (2021a) suggested that the higher  
75       contribution of FNC to SOC (exceeding 65%) than BNC (32–36%) may be not only  
76       due to the slower decomposition rates of fungal cellular compounds but also  
77       attributable to the higher living fungal biomass relative to bacterial biomass in  
78       terrestrial ecosystems. Previous studies have also indicated that the contributions of  
79       FNC and BNC to SOC depended on the type of ecosystems (Wang et al., 2021a; Cao  
80       et al., 2023; Xu et al., 2024), and they were mainly affected by climatic and soil  
81       physicochemical factors (e.g., soil pH and clay content; He et al., 2020; Zhang et al.,  
82       2023). However, these studies on the relative contributions of fungal necromass  
83       carbon (FNC) and BNC to SOC, and their ratio (FNC/BNC), have predominantly  
84       focused on ecosystems categorized based on biotic communities and vegetation types,  
85       such as forests (Chen et al., 2020), with limited attention given to ecosystems



86 classified by levels of human interference.

87 Terrestrial ecosystems can be broadly categorized into managed (agricultural) and  
88 natural ecosystems (Hobbs et al., 2011; Keith et al., 2022). The agricultural  
89 ecosystems, heavily reliant on human management, typically exhibit uniform plant  
90 litter influenced by agricultural activities (Bohan et al., 2013). In contrast, natural  
91 ecosystems, which are self-sustaining, display greater diversity in litter and root  
92 deposits, encompassing various plants and biological remains (Wu et al., 2019).  
93 Minimal human interference enhances fungal mycelial networks and stable soil  
94 aggregates, leading to higher FNC sequestration and contributions to SOC (Sanaullah  
95 et al., 2020; Sae-Tun et al., 2022). As key decomposers, fungi can break down  
96 cellulose and other complex organic compounds (Hättenschwiler et al., 2005). Choi et  
97 al. (2018) indicated that soil cellulose-degrading genes are associated with fungal  
98 activity and abundance. This suggests cellulose-rich soils may support higher fungal  
99 diversity and abundance. The low cellulose and chitin abundance in agricultural  
100 ecosystems might result from plant monoculture, while diverse plant inputs in natural  
101 ecosystems lead to rich soil cellulose content and higher fungal abundance and FNC  
102 (Song et al., 2022). These findings suggest that FNC and BNC accumulation respond  
103 differently to human interference and ecosystem characteristics, causing disparities in  
104 the FNC/BNC ratio across ecosystems. Therefore, understanding global patterns and  
105 drivers of FNC, BNC, and the FNC/BNC ratio in agricultural and natural ecosystems  
106 is crucial amid intensifying human activities and global changes.

107 In order to explore the global patterns and drivers of FNC, BNC and the



108 FNC/BNC ratio in agricultural and natural ecosystems, we compiled data from 486  
109 study sites worldwide. The aims of this study were: (1) to quantify the contributions  
110 of FNC and BNC to SOC and the FNC/BNC ratio in agricultural and natural  
111 ecosystems; and (2) to investigate the primary driving factors influencing the  
112 contributions of FNC and BNC to SOC and the FNC/BNC ratio, and determine  
113 whether the influencing factors were consistent across these two ecosystem types.

114

## 115 **2 Materials and methods**

### 116 2.1 Data collection

117 To clarify the contributions of FNC and BNC to SOC and the FNC/BNC ratio at  
118 global scale, we compiled a comprehensive dataset from a range of peer-reviewed  
119 papers published before 2022 through the Web of Science  
120 (<http://apps.webofknowledge.com>), Google Scholar (<http://scholar.google.com>), and  
121 the China National Knowledge Infrastructure (<http://cnki.net>), using the keywords  
122 ‘amino sugars’, ‘microbial necromass’, ‘microbial residue’, ‘fungal residue’, and  
123 ‘bacterial residue’. Data compilation was conducted following four stringent criteria  
124 to reduce bias from selected publications: (1) fungal and bacterial necromass (or  
125 glucosamine [GluN] and muramic acid [MurA]) had to be reported simultaneously for  
126 the same samples; (2) only data from agricultural and natural ecosystems (i.e.,  
127 grasslands and forests) were used; (3) for natural ecosystems, we excluded the data  
128 from fertilized, polluted, treated, or anthropogenically disturbed sites; and (4) we only  
129 included data from the top 0–20 cm of the soil profile reported in the publications,



130 with other depths or unspecified soil depths excluded from our dataset. In total, the  
131 final dataset consisted of 2094 observations from 486 sites worldwide (Figure 1)  
132 reported in 164 peer-reviewed papers. Among them, there were 1001 observations  
133 from agricultural ecosystems and 1093 observations from natural ecosystems.

134 We calculated the FNC and BNC based on the contents of fungal GluN and  
135 bacterial MurA using the following equations (Liang et al., 2019):

$$136 \quad FNC = \left( \frac{GluN}{179.17} - 2 \times \frac{MurA}{251.23} \right) \times 179.17 \times 9,$$
$$137 \quad BNC = MurA \times 45,$$

138 where 9 is the conversion factor from GluN to FNC, and, 179.17 and 251.23 are  
139 the molecular weights of GluN and MurA, respectively; 45 is the conversion factor  
140 from MurA to BNC.

141 Additional information including site geographic location (latitude and longitude),  
142 topographical condition (elevation), climatic factors (mean annual temperature [MAT])  
143 and mean annual precipitation [MAP]), soil physicochemical properties (pH, SOC,  
144 total nitrogen (TN), clay content, and soil temperature), and biotic (microbial and  
145 plant) factors were recorded. Specifically, biotic factors included microbial biomass  
146 carbon (MBC), microbial biomass nitrogen (MBN), MBC/MBN, net primary  
147 production (NPP), and belowground biomass C density (BGBC). The data of  
148 topographical condition (elevation) was classified as geographical factor in this study.  
149 When MAT and MAP were unavailable in the original articles, we extracted them  
150 from the global climate layers of WorldClim (<http://www.worldclim.org/>) with a grid  
151 precision of  $30 \times 30$  arc sec according to geographic location. Missing elevation data



152 were extracted using the *elevatr* package v.0.4.2 (Hollister, 2021) in the R  
153 environment. We acquired the data on annual mean soil temperature from the study of  
154 Lembrechts et al. (2022), while other absent soil physicochemical data were extracted  
155 from the Harmonized World Soil Database  
156 ([https://www.fao.org/soils-portal/data-hub/soil-maps-and-databases/harmonized-world](https://www.fao.org/soils-portal/data-hub/soil-maps-and-databases/harmonized-world-soil-database-v12/en/)  
157 [-soil-database-v12/en/](https://www.fao.org/soils-portal/data-hub/soil-maps-and-databases/harmonized-world-soil-database-v12/en/)) and SoilGrids 2.0 (Poggio et al., 2021;  
158 <https://www.soilgrids.org/>) using ArcGIS 10.3. In addition, the data on NPP and  
159 BGBC were acquired from the studies of Zhao and Running (2010) and Spawn et al.  
160 (2020), respectively. Missing MBC and MBN data were acquired using a global  
161 database with a high resolution of  $30 \times 30$  arc sec (Wang et al., 2022).

162

## 163 2.2 Statistical analysis

164 All the statistical analyses were performed using R v4.1.3 (R Core Team, 2021).  
165 Initially, the Shapiro–Wilk test was employed to assess the normality of our data,  
166 followed by the application of Levene's test to evaluate the homogeneity of variances  
167 across different groups. To detect the significant differences in the contributions of  
168 FNC and BNC to SOC and the FNC/BNC ratio between agricultural and natural  
169 ecosystems, as well as between forest and grassland ecosystems, the Wilcoxon rank  
170 sum test was conducted. We used Spearman's rank correlation coefficient to explore  
171 the connections between the 16 variables considered in this study, including  
172 geographical and climatic factors, soil physicochemical properties, and biotic factors.  
173 Since there was a strong positive correlation between MAT and soil temperature



174 (Figure S1), soil temperature was excluded from our subsequent analyses. Linear  
175 regressions between different factors and the contributions of FNC and BNC to SOC  
176 and the FNC/BNC ratio were performed. Dots and smoothing curves were drawn  
177 using the *geom\_point* and *geom\_smooth* functions, respectively, in the *ggplot2*  
178 package v.3.4.0 (Wickham, 2016).

179 Variation partitioning analysis was conducted using the *vegan* package v.2.5.7  
180 (Oksanen et al., 2020) to evaluate the effects of four types of factors on the  
181 contributions of FNC and BNC to SOC and the FNC/BNC ratio in agricultural and  
182 natural ecosystems at global scale. We used a variance inflation factor threshold of 3.3  
183 to eliminate those variables that were strongly correlated and avoid multicollinearity  
184 (Figure S2; Kock, 2015; Fanin et al., 2020). Following factor selection, boosted  
185 regression trees (BRTs) were used to partition independent influences of geographical  
186 (elevation) and climatic (MAT and MAP) factors, soil physicochemical properties (pH,  
187 clay, C/N, and SOC), and biotic factors (NPP, BGBC, MBC, and MBC/MBN) on the  
188 contributions of FNC and BNC to SOC and the FNC/BNC ratio with the *gbm* package  
189 v.2.1.8.1 (Greenwell et al., 2022).

190 Utilizing the selected factors, we performed structural equation models (SEMs)  
191 to quantify the effects (direct, indirect and both) of four types of factors on the  
192 contributions of FNC and BNC to SOC and the FNC/BNC ratio using *lavaan* package  
193 v.0.6.19 (Rosseel, 2012). According to the previously reported potential causal  
194 relationships between explanatory and response variables (Wang et al., 2021a, 2021b;  
195 Li et al., 2024), we established the *priori* structural equation models for agro- and



196 natural ecosystems, respectively (Figure S3). The SEMs were fitted via maximum  
197 likelihood estimation, with non-significant paths iteratively pruned through stepwise  
198 exclusion, followed by model evaluation using modification indices and  
199 goodness-of-fit criteria. The fit indices included degrees of freedom (df), chi-square  
200 ( $\chi^2$ ,  $0 \leq \chi^2/df \leq 2$ ), comparative fit index (CFI > 0.9), and root mean square error of  
201 approximation (RMSEA < 0.08), which were used to assess the adequacy of the SEM.

202 Map, box, bar, bubble, and lollipop charts were plotted with the *ggplot2* package  
203 v.3.4.0 (Wickham, 2016). To enhance map visualization, the *ggnewscale* package  
204 v.0.4.8 (Campitelli, 2022) was necessary alongside the *ggplot2* package v.3.4.0  
205 (Wickham, 2016). Similarly, the *ggpubr* package v.0.5.0 (Kassambara, 2022) was an  
206 additional necessity when creating lollipop charts.

207

### 208 **3 Results**

209 3.1 Contributions of FNC and BNC to SOC and their ratio in agricultural and natural  
210 ecosystems

211 There were no significant differences in the contributions of FNC and BNC to SOC  
212 and the FNC/BNC ratio between forest and grassland ecosystems ( $P > 0.05$ ; Figure  
213 S4). Specifically, FNC contributed, on average, 29.11% to SOC in forests and 26.75%  
214 in grasslands, while BNC contributed 13.48% in forests and 14.34% in grasslands  
215 (Table 1). The average FNC/BNC ratios for forests and grasslands were 2.80 and 3.58,  
216 respectively.

217 In contrast, our analysis revealed statistically significant disparities in the



218 contributions of FNC and BNC to SOC and the FNC/BNC ratio in agricultural and  
219 natural ecosystems at the global scale ( $P < 0.05$ ; Figure 2). Notably, the average  
220 contributions of FNC and BNC to SOC were substantially higher in agricultural  
221 ecosystems than in natural ecosystems ( $P < 0.001$ ; see Figures 2a, b). For FNC, the  
222 average contribution was 34.39% in agricultural ecosystems, versus 29.24% in natural  
223 ecosystems. BNC contributed an average of 15.65% to SOC in agricultural  
224 ecosystems, compared to 14.02% in natural ecosystems (Table 1). Additionally,  
225 natural ecosystems exhibited a higher average FNC/BNC ratio of 3.22, surpassing the  
226 average of 2.61 observed in agricultural ecosystems (Figure 2c, Table 1).

227

### 228 3.2 Effects of driving factors on the contributions of FNC and BNC to SOC and the 229 FNC/BNC ratio

230 To investigate the reasons behind the significant differences in the contributions of  
231 FNC and BNC to SOC and the FNC/BNC ratio between agricultural and natural  
232 ecosystems, we quantified the impact of four types of factors (geographical, climatic,  
233 soil physicochemical, and biotic) upon them. Soil physicochemical factors were the  
234 most important influence on the contributions of FNC and BNC to SOC in  
235 agricultural and natural ecosystems (Figures 3a–d, 4a–d). Specifically, in agricultural  
236 ecosystems, soil physicochemical factors accounted for 16% and 17% of variance in  
237 the contributions of FNC and BNC to SOC, respectively (Figures 3a, c). In  
238 comparison, soil physicochemical factors accounted for 20% and 24% of variance in  
239 the contributions of FNC and BNC to SOC in natural ecosystems, respectively



240 (Figures 3b, d). Conversely, geographical factors, rather than soil physicochemical  
241 factors, were the most important contributors to explain the FNC/BNC ratio in both  
242 agricultural and natural ecosystems, accounting for 21% and 10% of the explained  
243 variance in the FNC/BNC ratio, respectively (Figures 3e, f).

244 These findings were further substantiated by the results obtained from the BRTs.  
245 These results indicated that soil physicochemical factors accounted for a substantial  
246 portion of the variance in the contributions of FNC and BNC to SOC in agricultural  
247 and natural ecosystems (Figures 4a–d), and geographical factors played a similar role  
248 in explaining the FNC/BNC ratio (Figures 4e, f). More precisely, soil  
249 physicochemical factors were identified as the primary contributors for the  
250 contributions of FNC and BNC to SOC, with their contributions amounting to 51%  
251 and 44% in agricultural ecosystems (Figures 4a, c), and 44% in natural ecosystems  
252 (Figures 4b, d), respectively. This underscores soil physicochemical factors as the  
253 primary influencers on the contributions of FNC and BNC to SOC in both ecosystems.  
254 Similarly, in the BRT models, geographical factors emerged as the primary  
255 influencers of the FNC/BNC ratio in agricultural and natural ecosystems, accounting  
256 for 32% and 44% of the variance in each case, respectively (Figures 4e, f). In both  
257 ecosystems, the BRT models used to quantify the relative influence of the four types  
258 of factors on the contributions of FNC and BNC to SOC and the FNC/BNC ratio were  
259 all significant ( $P < 0.001$ ), with explained model variances ranging from 23% to 66%  
260 (Figure 4). Although soil physicochemical factors were the primary factors  
261 influencing the contributions of FNC and BNC to SOC in both ecosystems, the



262 response of the contributions to individual soil physicochemical factors was not  
263 entirely consistent between agricultural and natural ecosystems. Specifically, in the  
264 BRT models, the C/N ratio was the third most influential factor, following clay and  
265 SOC, influencing the contribution of FNC to SOC in agricultural ecosystems (Figure  
266 4a). However, the C/N ratio emerged as the most important factor influencing the  
267 contribution of FNC to SOC in natural ecosystems and the contribution of BNC to  
268 SOC in both ecosystems (Figures 4b–d). Linear regression models indicated that the  
269 contributions of FNC and BNC to SOC decreased with increasing C/N ratio in both  
270 ecosystems (Figures S5g, S6g). Elevation was the most significant geographical  
271 factors influencing the FNC/BNC ratio in both ecosystems (Figures 4e, f). Moreover,  
272 the FNC/BNC ratio in agricultural and natural ecosystems show significantly  
273 increased with an increase elevation (Figure S7a).

274 The SEMs revealed similar results, indicating that soil physicochemical factors  
275 were the most influential factors for the contributions of FNC and BNC to SOC in  
276 both agricultural and natural ecosystems, and the factor can affect the contributions of  
277 FNC and BNC to SOC in two ecosystems both directly and indirectly (Figures 5a–d,  
278 6a–d). Notably, the direct and standardized total effects of soil physicochemical  
279 factors on the contribution of FNC to SOC in natural ecosystem were both positive  
280 (Figures 6a, b). Geographical factors were the most influential factors for the  
281 FNC/BNC ratio in agricultural and natural ecosystems, exerting both direct and  
282 indirect effects on this ratio (Figures 5e, 6e), with the standardized total effect being  
283 positive (Figures 5f, 6f).



284

#### 285 **4 Discussion**

286 MNC is an important component of SOC (Ma et al., 2018), and its variations can  
287 influence the feedback effects on the C cycle and global climate change (Zhao et al.,  
288 2023). Our study indicated that the contributions of FNC to SOC were approximately  
289 twice those of BNC in agricultural and natural ecosystems. Although the contributions  
290 of FNC and BNC to SOC were significantly higher in agricultural ecosystems than in  
291 natural ecosystems, the FNC/BNC ratio was significantly higher in the latter. In  
292 addition, soil physicochemical properties and geographical factors were the most  
293 important predictors of the contributions of MNC (FNC and BNC) to SOC and the  
294 FNC/BNC ratio in the two ecosystems, respectively. These findings enhance our  
295 understanding of microbially mediated biogeochemical cycling processes under  
296 current and future climate scenarios.

297

#### 298 **4.1 Variation in the contributions of FNC and BNC to SOC and the FNC/BNC ratio in** 299 **agricultural and natural ecosystems**

300 With growing appreciation for the critical role of microbial necromass constituents in  
301 forming SOC, it is critical to understand the different drivers of this process across the  
302 globe. In this study, we found that the contribution of FNC to SOC significantly  
303 exceeded that of BNC, with the former contributing approximately twice as much as  
304 BNC to SOC in both agricultural and natural ecosystems (including forests and  
305 grasslands; Table 1). These findings were consistent with previous studies (Liang et



306 al., 2019; Wang et al., 2021a; Zhang et al., 2023; Ding et al., 2024). On the one hand,  
307 this might be attributable to the various nutrient utilization strategies of the different  
308 microbial groups. Labile compounds in bacterial cell walls are preferentially utilized  
309 by microbes, resulting in a lower content of bacterial residue in soil (Hu et al., 2020).  
310 In contrast, fungi, with their more recalcitrant compounds (e.g., chitin), decompose  
311 slowly, allowing them to persist longer in soil. Over time, fungal residue contributes  
312 more significantly to SOC pools (Wang et al., 2021a). On the other hand, the thicker  
313 cell walls of fungi result in a lower surface area-to-volume ratio of their residual  
314 fragments, facilitating the easy formation of complex macromolecular aggregates  
315 (Zhao et al., 2023). This contributes significantly to the stability of fungal necromass  
316 and plays a crucial role in the accumulation of SOC. Additionally, the comparatively  
317 larger biomass of fungi may be a contributing factor to the predominance of FNC over  
318 BNC in terms of contributing to SOC in agricultural and natural ecosystems (He et al.,  
319 2020).

320 In the present study, their contributions were found to be consistently higher in  
321 agricultural ecosystems as compared to natural ecosystems, with respective values of  
322 34.39% vs. 29.24% for FNC, and 15.65% vs. 14.02% for BNC (Figures 2a, b, Table  
323 1). The higher contributions of FNC and BNC to SOC in agricultural ecosystems  
324 compared to natural ecosystems may be attributable to two main factors. First, owing  
325 to the diverse range of plant communities and minimal human interference in natural  
326 ecosystems, the content of plant-derived organic C significantly exceeds that in  
327 agricultural ecosystems impacted by farming activities, potentially resulting in a



328 greater proportion of microbially derived C within SOC (Angst et al., 2021). Second,  
329 the concept of the microbial efficiency–substrate stability framework suggests that  
330 high-quality substrates (characterized by low C/N ratio) allow for greater  
331 accumulation of microbial residue because of a higher rate of microbial residue  
332 production (Castellano et al., 2015; Chen et al., 2020; Ni et al., 2020). In this study,  
333 the average C/N ratio in agricultural ecosystems was found to be significantly lower  
334 than in natural ecosystems—approximately one-third that of natural ecosystems  
335 (10.78 vs. 27.44). Therefore, the contribution of MNC (primarily from FNC and BNC)  
336 to SOC in agricultural ecosystems was significantly higher than that in natural  
337 ecosystems.

338 Significant differences in the FNC/BNC ratio were also observed between  
339 agricultural and natural ecosystems, with natural ecosystems exhibiting a higher  
340 FNC/BNC ratio (3.22 vs. 2.61; Figure 2c, Table 1). This finding is consistent with that  
341 of Wang et al. (2021a), providing additional confidence to the critical differences  
342 between these major microbial functional groups. The observed differences in the  
343 FNC/BNC ratio between agricultural and natural ecosystems may be attributable to  
344 the intrinsic characteristics of these two ecosystems. Zhou et al. (2023) suggested that  
345 soils with minimal human interference, such as those in natural ecosystems, tend to  
346 have higher FNC. Conversely, human interference (e.g., the application of organic  
347 fertilizers) is associated with an increase in BNC content in soil. Other studies have  
348 also demonstrated that minimizing soil disturbance can be advantageous for microbial  
349 growth, particularly fungi (Sanaullah et al., 2020; Sae-Tun et al., 2022). The mycelial



350 networks of fungi contribute to the formation of more stable soil aggregates, which in  
351 turn promotes the sequestration of FNC (Sae-Tun et al., 2022). Furthermore, bacteria  
352 tend to dominate in soil with high nutrient content, such as agricultural ecosystems,  
353 while in soil with relatively lower nutrient levels, like natural ecosystems, fungi  
354 assume a dominant position owing to their enhanced and more extensive substrate  
355 degradation capabilities (Strickland and Rousk, 2010; Yu et al., 2022). Hence,  
356 comparatively speaking, natural ecosystems, characterized by minimal human  
357 interference and relatively lower nutrient levels, are more conducive to fungal growth  
358 and the accumulation of their necromass C, consequently resulting in a higher  
359 FNC/BNC ratio compared to agricultural ecosystems.

360

#### 361 4.2 Important driving factors for the contributions of FNC and BNC to SOC and the 362 FNC/BNC ratio

363 Our results indicated that soil physicochemical factors were key in determining the  
364 contributions of FNC and BNC to SOC (Figures 3a–d, 4a–d, 5a–d). Deng and Liang  
365 (2022) suggested that the potential contribution of microbial residue to the SOC pool  
366 was governed by the C/N ratio. This finding was corroborated by our results, which  
367 further indicated that the contributions of FNC and BNC to SOC decreased as the soil  
368 C/N ratio increased (Figures 4b–d, S5g, S6g). Several factors may account for the  
369 results. On the one hand, the soil C/N ratio regulates microbial community  
370 composition, thereby influencing the accumulation of FNC and BNC (Han et al.,  
371 2023). Specifically, a high C/N ratio often indicates a relative surplus of C and a



372 limitation of N, which constrains microbial metabolism, reduces microbial turnover  
373 and biomass input, and consequently decreases the accumulation of FNC and BNC  
374 (Wu et al., 2025). On the other hand, under high C/N conditions, microbes tend to  
375 allocate more C to maintenance respiration or CO<sub>2</sub> release rather than biomass  
376 synthesis, leading to a lower efficiency of necromass production and diminished  
377 contribution to SOC (Liu et al., 2024). In addition, a high C/N ratio may also impair  
378 the binding capacity of microbial residues to soil minerals, thereby reducing their  
379 long-term stabilization and further weakening their contribution to SOC (Li et al.,  
380 2024). In contrast, soil clay content was the most predominant factor influencing the  
381 contribution of FNC to SOC in agricultural ecosystems (Figure 4a), and this  
382 contribution increased with increasing clay content (Figure S5g). Consistent findings  
383 have been reported by Six et al. (2006) and Liang et al. (2017), demonstrating that  
384 soils with higher clay and silt contents generally harbor greater quantities of microbial  
385 residues, particularly fungal-derived residues, due to the enhanced formation of stable  
386 organo-mineral complexes promoted by abundant fine soil particles. Moreover,  
387 agricultural management practices frequently disturb soil structure but simultaneously  
388 enhance clay enrichment and aggregate formation, thereby providing effective  
389 physical protection for the long-term stabilization of fungal-derived C (Chen et al.,  
390 2020; Mou et al., 2021; Zhou et al., 2023).

391 On the contrary, geographical factor (elevation) was identified as the most  
392 influential predictors of the FNC/BNC ratio in both agricultural and natural  
393 ecosystems (Figures 4e, f, 5f, 6f), and the FNC/BNC ratio increased with increasing



394 elevation (Figure S7a). Increasing elevation typically leads to decreased temperature,  
395 and increased precipitation (Körner, 2007), conditions favoring fungi over bacteria  
396 due to higher enzymatic capabilities and resource-use efficiency of fungi under the  
397 environments (Chen et al., 2020; Yu et al., 2022; Zhang et al., 2025). High elevation  
398 also results in slower soil development, which can reduce the availability of soil  
399 nutrients (Guerrero-Ramírez et al., 2020). This in turn increases environmental stress  
400 and restricts bacterial activity, thereby favoring the accumulation and conversion of  
401 fungal residues into necromass (Li et al., 2024). Our study further demonstrated that  
402 although elevation had a direct effect on the FNC/BNC ratio, it also indirectly  
403 influenced the ratio by modulating climatic factors, soil physicochemical properties,  
404 and biological factors (Figures 5e, 6e). This may explain why elevation is always  
405 integrate other environmental factor effects in the studies of MNC (Cui et al., 2023;  
406 Zhang et al., 2025).

407

#### 408 4.3 Limitations and uncertainties

409 Although the present study provides important insights on global patterns and drivers  
410 of soil microbial necromass in agricultural and natural ecosystems, we must clarify  
411 two limitations. First, the limited data available on microbial characteristics, such as  
412 microbial community composition, enzymatic activities, and the content of soil  
413 aggregates and minerals hinder exploration of the drivers of soil microbial necromass.  
414 Second, it is undeniable that our dataset is unevenly distributed, primarily  
415 concentrating on the Northern Hemisphere, with sparse or nearly no data from other



416 regions such as Africa, South America, and Australia (see Figure 1). Moreover, the  
417 natural ecosystems in this study were limited to forests and grasslands, excluding  
418 other natural habitats such as wetlands and deserts. The uneven distribution of data  
419 may reduce the universality of MNC as a key driver of soil carbon pools in global  
420 terrestrial ecosystems. Therefore, more data from these important areas and biomes  
421 are clearly required, and further investigation is warranted to fill the data gaps  
422 regarding the contribution of MNC to SOC in terrestrial ecosystems.

423

#### 424 **5 Data availability**

425 The data and R code for this manuscript are available at  
426 <https://doi.org/10.6084/m9.figshare.28827386> (Lu, 2025).

427

#### 428 **6 Conclusions**

429 Our results suggest that the contribution of FNC to SOC is significantly greater than  
430 that of BNC in both agricultural and natural ecosystems. The relative contributions of  
431 FNC and BNC to SOC were found to be higher in agricultural ecosystems—an effect  
432 that is mediated by differences in soil physicochemical factors. The FNC/BNC ratio  
433 was significantly higher in natural ecosystems compared to agricultural ecosystems,  
434 primarily driven by geographical factors (elevation). Our results reveal consistent  
435 trends in the contributions of FNC and BNC to SOC, and the FNC/BNC ratio, which  
436 are indicative of ecosystem-level differences in C turnover and stabilization  
437 mechanisms across the globe. These insights are conducive to a better mechanistic



438 understanding of the role of microbes in the C cycle in terrestrial ecosystems, and  
439 could inform strategies for C sequestration and sustainable land management  
440 strategies in the context of global change.

441

#### 442 **Author contributions**

443 JL performed the data analysis and prepared the original draft. TC and MDB  
444 contributed to manuscript review and editing. WL and HS contributed to data  
445 collection. YJ contributed to data analysis. ZW supervised the project and contributed  
446 to the original draft.

447

#### 448 **Competing interests**

449 The contact author has declared that none of the authors has any competing interests.

450

#### 451 **Disclaimer**

452 Publisher's note: Copernicus Publications remains neutral with regard to jurisdictional  
453 claims in published figures and institutional affiliations.

454

#### 455 **Acknowledgements**

456 We are grateful for the data contributors and the scientific community which made the  
457 data accessible and useful for our study.

458

#### 459 **Financial support**



460 This work was supported financially by the National Natural Science Foundation of  
461 China (No. 32160291), the National Key Research and Development Program of  
462 China (No. 2021YFD2200403-04), the Natural Science Foundation of Hainan  
463 province (No. 423QN212), and the Hainan University Research start-up Fund (No.  
464 KYQD(ZR)22187).

465

#### 466 **References**

- 467 Angst, G., Mueller, K.E., Nierop, K.G., Simpson, M.J., 2021. Plant-or  
468 microbial-derived? A review on the molecular composition of stabilized soil  
469 organic matter. *Soil Biol. Biochem.* 156, 108189.  
470 <https://doi.org/10.1016/j.soilbio.2021.108189>
- 471 Bellamy, P.H., Loveland, P.J., Bradley, R.I., Lark, R.M., Kirk, G.J., 2005. Carbon  
472 losses from all soils across England and Wales 1978–2003. *Nature* 437, 245–248.  
473 <https://doi.org/10.1038/nature04038>
- 474 Bohan, D.A., Raybould, A., Mulder, C., Woodward, G., Tamaddoni-Nezhad, A.,  
475 Bluthgen, N., Pocock, M.J.O., Muggleton, S., Evans, D.M., Astegiano, J., Massol,  
476 F., Loeuille, N., Petit, S., Macfadyen, S., 2013. Networking agroecology:  
477 integrating the diversity of agroecosystem interactions. *Adv. Ecol. Res.* 49, 1–67.  
478 <https://doi.org/10.1016/B978-0-12-420002-9.00001-9>
- 479 Campitelli, E., 2022. *ggnewscale*: Multiple Fill and Colour Scales in 'ggplot2'. R  
480 package version 0.4.8. <https://CRAN.R-project.org/package=ggnewscale>



- 481 Cao, Y., Ding, J., Li, J., Xin, Z., Ren, S., Wang, T., 2023. Necromass-derived soil  
482 organic carbon and its drivers at the global scale. *Soil Biol. Biochem.* 181,  
483 109025. <https://doi.org/10.1016/j.soilbio.2023.109025>
- 484 Castellano, M.J., Mueller, K.E., Olk, D.C., Sawyer, J.E., Six, J., 2015. Integrating  
485 plant litter quality, soil organic matter stabilization, and the carbon saturation  
486 concept. *Global Change Biol.* 21, 3200–3209. <https://doi.org/10.1111/gcb.12982>
- 487 Chen, G., Ma, S., Tian, D., Xiao, W., Jiang, L., Xing, A., Zou, A., Zhou, L., Shen, H.,  
488 Zheng, C., Ji, C., He, H., Zhu, B., Liu, L., Fang, J., 2020. Patterns and  
489 determinants of soil microbial residues from tropical to boreal forests. *Soil Biol.*  
490 *Biochem.* 151, 108059. <https://doi.org/10.1016/j.soilbio.2020.108059>
- 491 Choi, J., Bach, E., Lee, J., Flater, J., Dooley, S., Howe, A., Hofmockel, K. S., 2018.  
492 Spatial structuring of cellulase gene abundance and activity in soil. *Front.*  
493 *Environ. Sci.* 6, 107. <https://doi.org/10.3389/fenvs.2018.00107>
- 494 Crowther, T.W., Sokol, N.W., Oldfield, E.E., Maynard, D.S., Thomas, S.M., Bradford,  
495 M.A., 2015. Environmental stress response limits microbial necromass  
496 contributions to soil organic carbon. *Soil Biol. Biochem.* 85, 153–161.  
497 <https://doi.org/10.1016/j.soilbio.2015.03.002>
- 498 Cui, W., Li, R., Fan, Z., Wu, L., Zhao, X., Wei, G., Shu, D., 2023. Weak  
499 environmental adaptation of rare phylotypes sustaining soil multi-element cycles  
500 in response to decades-long fertilization. *STOTEN.* 871, 162063.  
501 <https://doi.org/10.1016/j.scitotenv.2023.162063>



- 502 Deng, F., Liang, C., 2022. Revisiting the quantitative contribution of microbial  
503 necromass to soil carbon pool: stoichiometric control by microbes and soil. *Soil*  
504 *Biol. Biochem.* 165, 108486. <https://doi.org/10.1016/j.soilbio.2021.108486>
- 505 Ding, Z., Mou, Z., Li, Y., Liang, C., Xie, Z., Wang, J., Hui, D., Lambers, H., Sardans,  
506 J., Peñuelas, J., Xu, H., Liu, Z., 2024. Spatial variation and controls of soil  
507 microbial necromass carbon in a tropical montane rainforest. *STOTEN.* 921,  
508 170986. <https://doi.org/10.1016/j.scitotenv.2024.170986>
- 509 Fanin, N., Bezaud, S., Sarneel, J.M., Cecchini, S., Nicolas, M., Augusto, L., 2020.  
510 Relative importance of climate, soil and plant functional traits during the early  
511 decomposition stage of standardized litter. *Ecosystems* 23, 1004–1018.  
512 <https://doi.org/10.1007/s10021-019-00452-z>
- 513 Greenwell, B., Boehmke, B., Cunningham, J., Developers, G.B.M., 2022. *gbm*:  
514 Generalized Boosted Regression Models. R package version 2.1.8.1.  
515 <https://CRAN.R-project.org/package=gbm>
- 516 Han, B., Yao, Y., Wang, Y., Su, X., Ma, L., Chen, X., Li, Z., 2024. Microbial traits  
517 dictate soil necromass accumulation coefficient: A global synthesis. *Global Ecol.*  
518 *Biogeogr.* 33(1), 151–161. <https://doi.org/10.1111/geb.13776>
- 519 Hao, Z., Zhao, Y., Wang, X., Wu, J., Jiang, S., Xiao, J., Wang, K., Zhou, X., Liu, H., Li,  
520 J., Sun, Y., 2021. Thresholds in aridity and soil carbon-to-nitrogen ratio govern  
521 the accumulation of soil microbial residues. *Commun. Earth Environ.* 2, 236.  
522 <https://doi.org/10.1038/s43247-021-00306-4>



- 523 Hättenschwiler, S., Tiunov, A.V., Scheu, S., 2005. Biodiversity and litter  
524 decomposition in terrestrial ecosystems. *Rev. Ecol. Evol. S.* 36, 191–218.  
525 <https://doi.org/10.1146/annurev.ecolsys.36.112904.151932>
- 526 He, L., Rodrigues, J.L.M., Soudzilovskaia, N.A., Barceló, M., Olsson, P.A., Song, C.,  
527 Tedersoo, L., Yuan, F., Yuan, F., Lipson, D.A., Xu, X., 2020. Global  
528 biogeography of fungal and bacterial biomass carbon in topsoil. *Soil Biol.*  
529 *Biochem.* 151, 108024. <https://doi.org/10.1016/j.soilbio.2020.108024>
- 530 Hobbs, R.J., Hallett, L.M., Ehrlich, P.R., Mooney, H.A., 2011. Intervention ecology:  
531 applying ecological science in the twenty-first century. *BioScience* 61, 442–450.  
532 <https://doi.org/10.1525/bio.2011.61.6.6>
- 533 Hollister, J. W., 2021. *elevatr*: Access Elevation Data from Various APIs. R package  
534 version 0.4.2. <https://CRAN.R-project.org/package=elevatr/>
- 535 Hu, Y., Zheng, Q., Noll, L., Zhang, S., Wanek, W., 2020. Direct measurement of the *in*  
536 *situ* decomposition of microbial-derived soil organic matter. *Soil Biol. Biochem.*  
537 141, 107660. <https://doi.org/10.1016/j.soilbio.2019.107660>
- 538 Kallenbach, C.M., Frey, S.D., Grandy, A.S., 2016. Direct evidence for  
539 microbial-derived soil organic matter formation and its ecophysiological controls.  
540 *Nat. Commun.* 7, 13630. <https://doi.org/10.1038/ncomms13630>
- 541 Kassambara, A., 2022. *ggpubr*: 'ggplot2' Based Publication Ready Plots. R package  
542 version 0.5.0. <https://CRAN.R-project.org/package=ggpubr>
- 543 Keith, D.A., Ferrer-Paris, J.R., Nicholson, E., Bishop, M.J., Polidoro, B.A.,  
544 Ramirez-Llodra, E., Tozer, M.G., Nel, J.L., Nally, R.M., Gregr, E.J., Watermeyer,



- 545 K.E., Essl, F., Faber-Langendoen, D., Franklin, J., Lehmann, C.E.R., Etter, A.,  
546 Roux, D.J., Stark, J.S., Rowland, J.A., Brummitt, N.A., Fernandez-Arcaya, U.C.,  
547 Suthers, I.M., Wiser, S.K., Donohue, I., Jackson, L.J., Pennington, R.T., Iliffe,  
548 T.M., Gerovasileiou, V., Giller, P., Robson, B.J., Pettoirelli, N., Andrade, A.,  
549 Lindgaard, A., Tahvanainen, T., Terauds, A., Chadwick, M.A., Murray, N.J.,  
550 Moat, J., Plissock, P., Zager, I., Kingsford, R.T., 2022. A function-based typology  
551 for Earth's ecosystems. *Nature* 610, 513–518.  
552 <https://doi.org/10.1038/s41586-022-05318-4>
- 553 Kock, N., 2015. Common method bias in PLS-SEM: A full collinearity assessment  
554 approach. *International Journal of e-Collaboration (IJeC)* 11, 1–10.  
555 <https://doi.org/10.4018/ijec.2015100101>
- 556 Körner, C., 2007. The use of 'altitude' in ecological research. *Trends Ecol. Evol.*  
557 22(11), 569–574. <https://doi.org/10.1016/j.tree.2007.09.006>
- 558 Lembrechts, J.J., van den Hoogen, J., Aalto, J., Ashcroft, M.B., De Frenne, P.,  
559 Kempainen, J., Kopecký, M., Luoto, Maclean, M.I.M.D, Crowther, T.W., Bailey,  
560 J.J., Haesen, S., Klinges, D.H., Niittynen, P., Scheffers, B.R., Van Meerbeek, K.,  
561 Aartsma, P., Abdalaze, O., Abedi, M., Aerts, R., Ahmadian, N., Ahrends, A.,  
562 Alatalo, J.M., Alexander, J.M., Allonsius, C.N., Altman, J., Ammann, C.,  
563 Andres, C., Andrews, C., Ardö, J., Arriga, N., Arzac, A., Aschero, V., Assis, R.L.,  
564 Assmann, J.J., Bader, M.Y., Bahalkeh, K., Barančok, P., Barrio, I.C., Barros, A.,  
565 Barthe, M., Basham, E.W., Bauters, M., Bazzichetto, M., Marchesini, L.B., Bell,  
566 M.C., Benavides, J.C., Alonso, J.L.B., Berauer, B.J., Bjerke, J.W., Björk, R.G.,



- 567 Björkman, M.P., Björnsdóttir, K., Blonder, B., Boeckx, P., Boike, J., Bokhorst, S.,  
568 Brum, B.N.S., Brúna, J., Buchmann, N., Buysse, P., Camargo, J.L., Campoe,  
569 O.C., Candan, O., Canessa, R., Cannone, N., ... Hik, D. S., 2022. Global maps of  
570 soil temperature. *Global Change Biol.* 28, 3110–3144.  
571 <https://doi.org/10.1111/gcb.16060>
- 572 Lenardon, M.D., Whitton, R.K., Munro, C.A., Marshall, D., Gow, N.A.R., 2007.  
573 Individual chitin synthase enzymes synthesize microfibrils of differing structure  
574 at specific locations in the *Candida albicans* cell wall. *Mol. Microbiol.* 66, 1164–  
575 1173. <https://doi.org/10.1111/j.1365-2958.2007.05990.x>
- 576 Liang, C., Amelung, W., Lehmann, J., Kästner, M., 2019. Quantitative assessment of  
577 microbial necromass contribution to soil organic matter. *Global Change Biol.* 25,  
578 3578–3590. <https://doi.org/10.1111/gcb.14781>
- 579 Liang, C., Balser, T.C., 2011. Microbial production of recalcitrant organic matter in  
580 global soils: implications for productivity and climate policy. *Nat. Rev.*  
581 *Microbiol.* 9, 75–75. <https://doi.org/10.1038/nrmicro2386-c1>
- 582 Liang, C., Schimel, J.P., Jastrow, J.D., 2017. The importance of anabolism in  
583 microbial control over soil carbon storage. *Nat. Microbiol.* 2, 17105.  
584 <https://doi.org/10.1038/nmicrobiol.2017.105>
- 585 Liu, X., Tian, Y., Heinzle, J., Salas, E., Kwatcho-Kengdo, S., Borken, W.,  
586 Schindlbacher, A., Wanek, W., 2024. Long-term soil warming decreases soil  
587 microbial necromass carbon by adversely affecting its production and



- 588 decomposition. *Global Change Biol.* 30(6), e17379.  
589 <https://doi.org/10.1111/gcb.17379>
- 590 Li, Y., Wang, S., Yang, Y., Ren, L., Wang, Z., Liao, Y., Yong, T., 2024. Global  
591 synthesis on the response of soil microbial necromass carbon to climate-smart  
592 agriculture. *Global Change Biol.* 30(5), e17302.  
593 <https://doi.org/10.1111/gcb.17302>
- 594 Luo, R., Kuzyakov, Y., Zhu, B., Qiang, W., Zhang, Y., Pang, X., 2022. Phosphorus  
595 addition decreases plant lignin but increases microbial necromass contribution to  
596 soil organic carbon in a subalpine forest. *Global Change Biol.* 28, 4194–4210.  
597 <https://doi.org/10.1111/gcb.16205>
- 598 Malik, A.A., Chowdhury, S., Schlager, V., Oliver, A., Puissant, J., Vazquez, P.G.,  
599 Jehmlich, N., von Bergen, M., Griffiths, R., Gleixner, G., 2016. Soil fungal:  
600 bacterial ratios are linked to altered carbon cycling. *Front. Microbiol.* 7, 1247.  
601 <https://doi.org/10.3389/fmicb.2016.01247>
- 602 Ma, T., Zhu, S., Wang, Z., Chen, D., Dai, G., Feng, B., Su, X., Hu, H., Li, K., Han, W.,  
603 Liang, C., Bai, Y., Feng, X., 2018. Divergent accumulation of microbial  
604 necromass and plant lignin components in grassland soils. *Nat. Commun.* 9,  
605 3480. <https://doi.org/10.1038/s41467-018-05891-1>
- 606 Mou, Z., Kuang, L., He, L., Zhang, J., Zhang, X., Hui, D., Li, Y., Wu, W., Mei, Q., He,  
607 X., Kuang, Y., Wang, J., Wang, Y., Lambers, H., Sardans, J., Peñuelas, J., Liu, Z.,  
608 2021. Climatic and edaphic controls over the elevational pattern of microbial



- 609 necromass in subtropical forests. *Catena* 207, 105707.  
610 <https://doi.org/10.1016/j.catena.2021.105707>
- 611 Ni, X., Liao, S., Tan, S., Peng, Y., Wang, D., Yue, K., Wu, F., Yang, Y., 2020. The  
612 vertical distribution and control of microbial necromass carbon in forest soils.  
613 *Global Ecol. Biogeogr.* 29, 1829–1839. <https://doi.org/10.1111/geb.13159>
- 614 Oksanen, J., Blanchet, F.G., Friendly, M., Kindt, R., Legendre, P., McGlinn, D.,  
615 Wagner, H., 2020. *vegan*: Community Ecology Package. R package version 2.5.7.  
616 <https://CRAN.R-project.org/package=vegan>
- 617 Poggio, L., De Sousa, L.M., Batjes, N.H., Heuvelink, G., Kempen, B., Ribeiro, E.,  
618 Rossiter, D., 2021. SoilGrids 2.0: producing soil information for the globe with  
619 quantified spatial uncertainty. *Soil* 7, 217–240.  
620 <https://doi.org/10.5194/soil-7-217-2021>
- 621 R Core Team, 2021. R: A language and environment for statistical computing. R  
622 Foundation for Statistical Computing, Vienna, Austria. <https://www.R-project.org>
- 623 Rosseel, Y. 2012. *lavaan*: An R package for structural equation modeling. *J. Stat.*  
624 *Softw.* 48, 1–36. <https://doi.org/10.18637/jss.v048.i02>
- 625 Sae-Tun, O., Bodner, G., Rosinger, C., Zechmeister-Boltenstern, S., Mentler, A.,  
626 Keiblinger, K., 2022. Fungal biomass and microbial necromass facilitate soil  
627 carbon sequestration and aggregate stability under different soil tillage intensities.  
628 *Appl. Soil Ecol.* 179, 104599. <https://doi.org/10.1016/j.apsoil.2022.104599>
- 629 Sanaullah, M., Usman, M., Wakeel, A., Cheema, S.A., Ashraf, I., Farooq, M., 2020.  
630 Terrestrial ecosystem functioning affected by agricultural management systems:



631 A review. *Soil Tillage Res.* 196, 104464.  
632 <https://doi.org/10.1016/j.still.2019.104464>

633 Six, J., Frey, S.D., Thiet, R.K., Batten, K.M., 2006. Bacterial and fungal contributions  
634 to carbon sequestration in agroecosystems. *Soil Sci. Soc. Am. J.* 70, 555–569.  
635 <https://doi.org/10.2136/sssaj2004.0347>

636 Song, A., Zhang, J., Xu, D., Wang, E., Bi, J., Asante-Badu, B., Njyenawe, M.C., Sun,  
637 M., Xue, P., Wang, S., Fan, F., 2022. Keystone microbial taxa drive the  
638 accelerated decompositions of cellulose and lignin by long-term resource  
639 enrichments. *STOTEN* 842, 156814.  
640 <https://doi.org/10.1016/j.scitotenv.2022.156814>

641 Spawn, S.A., Sullivan, C.C., Lark, T.J., Gibbs, H.K., 2020. Harmonized global maps  
642 of above and belowground biomass carbon density in the year 2010. *Sci. Data* 7,  
643 112. <https://doi.org/10.1038/s41597-020-0444-4>

644 Strickland, M.S., Rousk, J., 2010. Considering fungal: bacterial dominance in soils–  
645 methods, controls, and ecosystem implications. *Soil Biol. Biochem.* 42, 1385–  
646 1395. <https://doi.org/10.1016/j.soilbio.2010.05.007>

647 von Lützow, M., Kögel-Knabner, I., Ludwig, B., Matzner, E., Flessa, H., Ekschmitt,  
648 K., Guggenberger, G., Marschner, B., Kalbitz, K., 2008. Stabilization  
649 mechanisms of organic matter in four temperate soils: Development and  
650 application of a conceptual model. *J. Plant Nutr. Soil Sci.* 171, 111–124.  
651 <https://doi.org/10.1002/jpln.200700047>



- 652 Wang, B., An, S., Liang, C., Liu, Y., Kuzyakov, Y., 2021a. Microbial necromass as the  
653 source of soil organic carbon in global ecosystems. *Soil Biol. Biochem.* 162,  
654 108422. <https://doi.org/10.1016/j.soilbio.2021.108422>
- 655 Wang, B., Liang, C., Yao, H., Yang, E., An, S., 2021b. The accumulation of microbial  
656 necromass carbon from litter to mineral soil and its contribution to soil organic  
657 carbon sequestration. *Catena* 207, 105622.  
658 <https://doi.org/10.1016/j.catena.2021.105622>
- 659 Wang, Z., Zhao, M., Yan, Z., Yang, Y., Niklas, K.J., Huang, H., Mipam, T.D., He, X.,  
660 Hu, H., Wright, S.J., 2022. Global patterns and predictors of soil microbial  
661 biomass carbon, nitrogen, and phosphorus in terrestrial ecosystems. *Catena* 211,  
662 106037. <https://doi.org/10.1016/j.catena.2022.106037>
- 663 Wickham, H., 2016. *ggplot2: elegant graphics for data analysis*. Springer-Verlag New  
664 York. <https://ggplot2.tidyverse.org>
- 665 Wu, H., Xiang, W., Ouyang, S., Forrester, D. I., Zhou, B., Chen, L., Ge, T., Lei, P.,  
666 Chen, L., Zeng, Y., Song, X., Peñuelas, J., Peng, C., 2019. Linkage between tree  
667 species richness and soil microbial diversity improves phosphorus bioavailability.  
668 *Funct. Ecol.* 33, 1549–1560. <https://doi.org/10.1111/1365-2435.13355>
- 669 Wu, W., Feng, J., Wang, X., Xiao, J., Qin, W., Zhu, B., 2025. The response of soil  
670 microbial necromass carbon to global change: A global meta-analysis. *Catena*  
671 249, 108693. <https://doi.org/10.1016/j.catena.2024.108693>



- 672 Xu, S., Song, X., Zeng, H., Wang, J., 2024. Soil microbial necromass carbon in forests:  
673 A global synthesis of patterns and controlling factors. *Soil Ecol. Lett.* 6(4),  
674 240237. <https://doi.org/10.1007/s42832-024-0237-3>
- 675 Xu, Y., Sun, L., Gao, X., Wang, J., 2022. Contrasting response of fungal versus  
676 bacterial residue accumulation within soil aggregates to long-term fertilization.  
677 *Sci. Rep.* 12, 17834. <https://doi.org/10.1038/s41598-022-22064-9>
- 678 Yu, K., van den Hoogen, J., Wang, Z., Averill, C., Routh, D., Smith, G.R., Drenovsky,  
679 R.E., Scow, K.M., Mo, F., Waldrop, M.P., Yang, Y., Tang, W., Vries, F.T.D.,  
680 Bardgett, R.D., Manning, P., Bastida, F., Baer, S.G., Bach, E.M., García, C.,  
681 Wang, Q., Ma, L., Chen, B., He, X., Teurlincx, S., Heijboer, A., Bradley, J.A.,  
682 Crowther, T. W., 2022. The biogeography of relative abundance of soil fungi  
683 versus bacteria in surface topsoil. *Earth Syst. Sci. Data* 14, 4339–4350.  
684 <https://doi.org/10.5194/essd-14-4339-2022>
- 685 Zhang, B., Zhu, S., Guo, L., Chen, G., Zhang, G., Li, J., 2025. Elevation-dependent  
686 distribution of soil microbial necromass carbon in *Pinus densata* Mast. forests.  
687 *Appl. Soil Ecol.* 209, 106049. <https://doi.org/10.1016/j.apsoil.2025.106049>
- 688 Zhang, Q., Li, X., Liu, J., Liu, J., Han, L., Wang, X., Liu, H., Xu, M., Yang, G., Ren,  
689 C., Han, X., 2023. The contribution of microbial necromass carbon to soil  
690 organic carbon in soil aggregates. *Appl. Soil Ecol.* 190, 104985.  
691 <https://doi.org/10.1016/j.apsoil.2023.104985>



- 692 Zhao, M., Running, S.W., 2010. Drought-induced reduction in global terrestrial net  
693 primary production from 2000 through 2009. *Science* 329, 940–943.  
694 <https://doi.org/10.1126/science.1192666>
- 695 Zhang, X., Jia, J., Chen, L., Chu, H., He, J.S., Zhang, Y., Feng, X., 2021. Aridity and  
696 NPP constrain contribution of microbial necromass to soil organic carbon in the  
697 Qinghai-Tibet alpine grasslands. *Soil Biol. Biochem.* 156, 108213.  
698 <https://doi.org/10.1016/j.soilbio.2021.108213>
- 699 Zhao, X., Tian, P., Liu, S., Yin, P., Sun, Z., Wang, Q., 2023. Mean annual temperature  
700 and carbon availability respectively controlled the contributions of bacterial and  
701 fungal necromass to organic carbon accumulation in topsoil across China's  
702 forests. *Global Ecol. Biogeogr.* 32, 120–131. <https://doi.org/10.1111/geb.13605>
- 703 Zhou, R., Liu, Y., Dungait, J.A., Kumar, A., Wang, J., Tiemann, L.K., Zhang, F.,  
704 Kuzyakov, Y., Tian, J., 2023. Microbial necromass in cropland soils: A global  
705 meta-analysis of management effects. *Global Change Biol.* 29, 1998–2014.  
706 <https://doi.org/10.1111/gcb.16613>
- 707 Zhu, Y.G., Miller, R.M., 2003. Carbon cycling by arbuscular mycorrhizal fungi in  
708 soil–plant systems. *Trends Plant Sci.* 8, 407–409.  
709 [https://doi.org/10.1016/S1360-1385\(03\)00184-5](https://doi.org/10.1016/S1360-1385(03)00184-5)



710 **Table 1. Summary of the contributions of fungal necromass carbon (FNC) and**  
 711 **bacterial necromass carbon (BNC) to SOC and the FNC/BNC ratio in**  
 712 **agricultural and natural ecosystems at the global scale investigated in this study.**

Ecosystem	FNC/SOC (%)		BNC/SOC (%)		FNC/BNC	
	Range	Mean± SE	Range	Mean± SE	Range	Mean± SE
<b>Natural ecosystem<sup>&amp;</sup></b> ( <i>N</i> = 341)	0.92– 96.29	29.24 ± 0.51 b*	0.25– 89.45	14.02 ± 0.36 b	0.12– 44.24	3.22 ± 0.11 a
<i>Forest</i> ( <i>N</i> = 195)	0.92– 96.29	29.11 ± 0.63 A <sup>#</sup>	0.94– 96.47	13.48 ± 0.43 A	0.22– 11.56	2.80 ± 0.07 A
<i>Grassland</i> ( <i>N</i> = 146)	0.96– 93.89	26.75 ± 0.74 A	0.25– 89.45	14.34 ± 0.60 A	0.05– 44.24	3.58 ± 0.22 A
<b>Agricultural ecosystem</b> ( <i>N</i> = 145)	0.09– 97.53	34.39 ± 0.67 a	0.81– 65.00	15.65 ± 0.33 a	0.02– 12.74	2.61 ± 0.06 b

713 Note: *N* refers to the number of study sites;

714 <sup>&</sup>Natural ecosystem includes forest and grassland;

715 <sup>\*</sup>Within the same column, values with different lowercase letters indicate a significant  
 716 difference in the same variable between agricultural and natural ecosystems ( $P < 0.05$ ,  
 717 Wilcoxon rank-sum test);

718 <sup>#</sup>Within the same column, values with different capital letters indicate a significant  
 719 difference in the same variable between forests and grasslands ( $P < 0.05$ , Wilcoxon  
 720 rank-sum test).



721 **Figure legends**

722 **Figure 1. Global distribution of the sites used in this study.** Ecosystem types are  
723 distinguished by distinct shapes and colors, with the numbers in parentheses  
724 indicating the number of study sites for each ecosystem type.

725 **Figure 2. Comparison of the contributions of MNC to SOC and their ratio in**  
726 **agricultural and natural ecosystems.** Colors indicate different ecosystems types.  
727 Significance levels: \*\*\* $P < 0.001$  and \* $P < 0.05$ .

728 **Figure 3. Variations in the contributions of MNC to SOC and their ratio**  
729 **explained by four types of factors in agricultural and natural ecosystems.** Colors  
730 indicate different types of factors.

731 **Figure 4. Relative influence of different factors on the contributions of MNC to**  
732 **SOC and their ratio in agricultural and natural ecosystems.** MAT, mean annual  
733 temperature; MAP, mean annual precipitation; MBC, microbial biomass carbon; SOC,  
734 soil organic carbon; C/N, the ratio of SOC to total nitrogen (TN); MBC/MBN, the  
735 ratio of MBC to microbial biomass nitrogen (MBN); NPP, net primary production;  
736 BGBC, belowground biomass carbon density. Colors indicate different types of  
737 factors.

738 **Figure 5. The influence pathways of four types of factors on the contributions of**  
739 **MNC to SOC and their ratio in agricultural ecosystems.** Direct and indirect effects  
740 (a, c, e) and the standardized total effects (b, d, f) of different factors on the  
741 contributions of MNC to SOC and their ratio of agricultural ecosystems are shown.  
742 Standardized path coefficients representing the effect sizes of potential causal factors

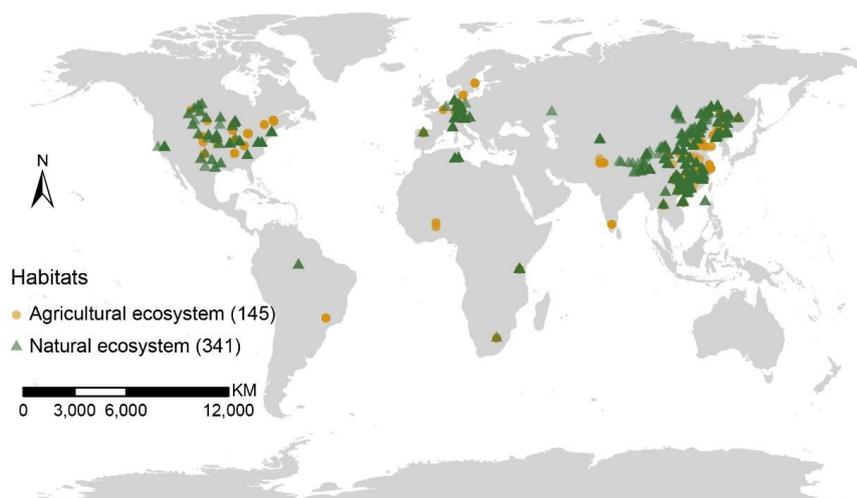


743 are indicated by numbers adjacent to arrows. The width of arrows is proportional to  
744 the potential causal effect between variables. The red arrows indicate positive effects,  
745 and the blue arrows indicate negative effects. The numbers adjacent to boxes of  
746 response variables denote the explained variance ( $R^2$ ). Right-angled rectangles denote  
747 single variables, whereas rounded rectangles represent composite variables. Colors  
748 indicate different types of factors. Significance levels:  $***P < 0.001$ ,  $**P < 0.01$  and  
749  $*P < 0.05$ . The *priori* models are shown in Figure S7.

750 **Figure 6. The influence pathways of four types of factors on the contributions of**  
751 **MNC to SOC and their ratio in natural ecosystems.** Direct and indirect effects (**a, c,**  
752 **e**) and the standardized total effects (**b, d, f**) of different factors on the contributions of  
753 MNC to SOC and their ratio of natural ecosystems are shown. Standardized path  
754 coefficients representing the effect sizes of potential causal factors are indicated by  
755 numbers adjacent to arrows. The width of arrows is proportional to the potential  
756 causal effect between variables. The red arrows indicate positive effects, and the blue  
757 arrows indicate negative effects. The numbers adjacent to boxes of response variables  
758 denote the explained variance ( $R^2$ ). Right-angled rectangles denote single variables,  
759 whereas rounded rectangles represent composite variables. Colors indicate different  
760 types of factors. Significance levels:  $***P < 0.001$ ,  $**P < 0.01$  and  $*P < 0.05$ . The  
761 *priori* models are shown in Figure S7.



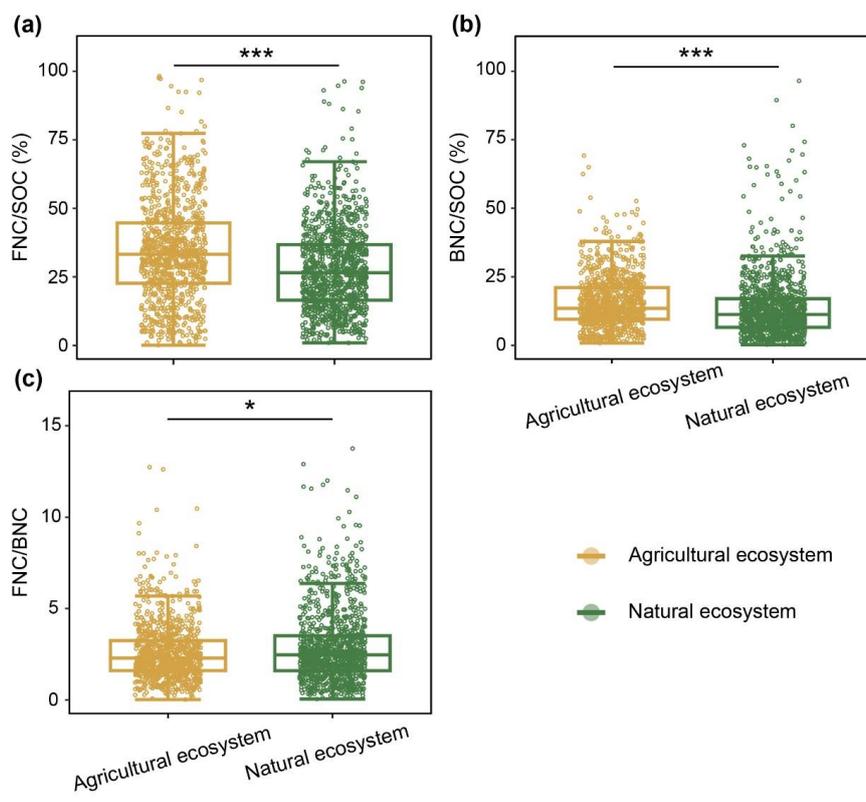
762 **Figure 1.**



763



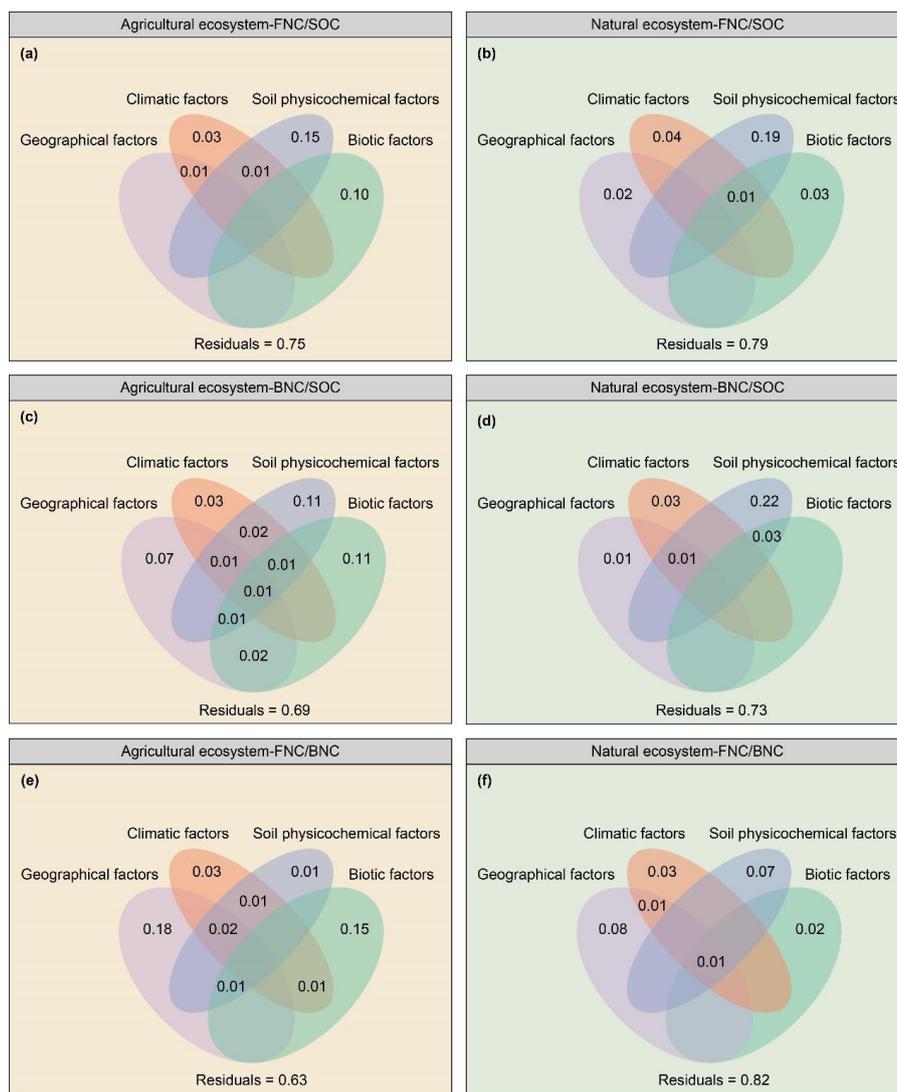
764 **Figure 2.**



765



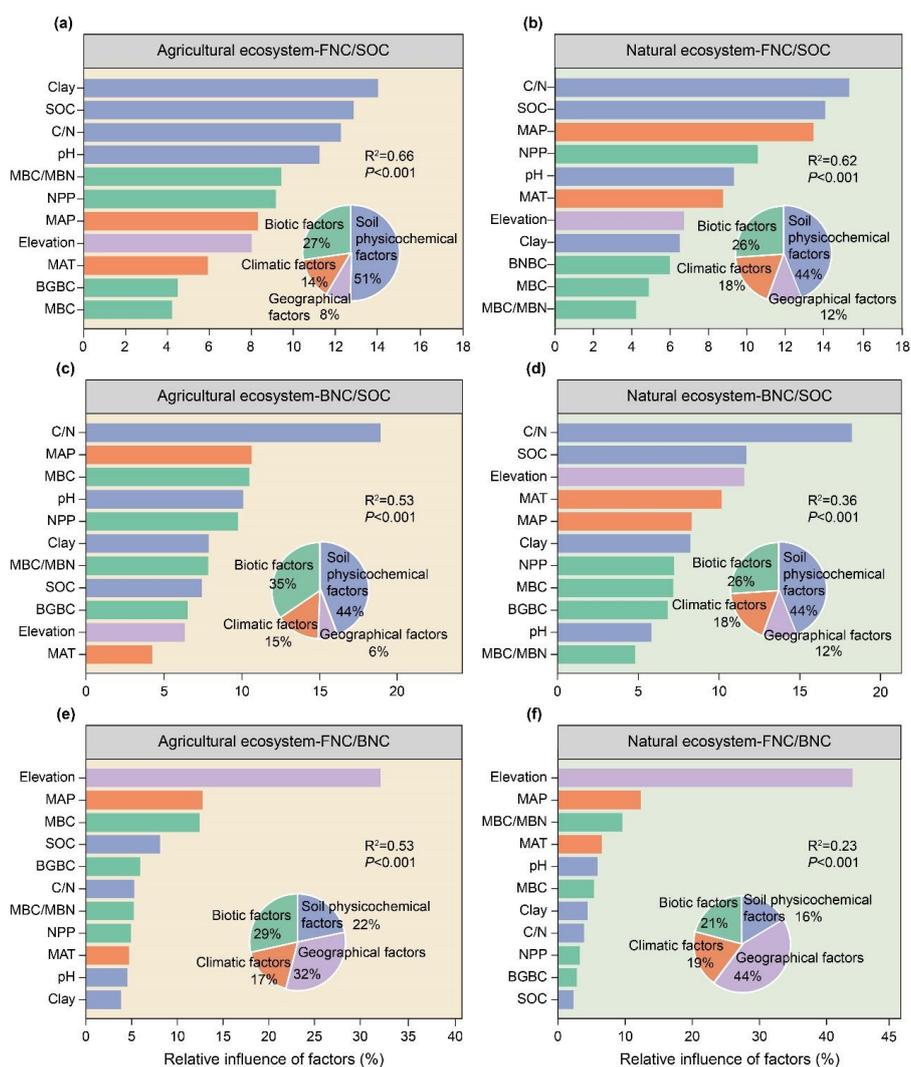
766 **Figure 3.**



767



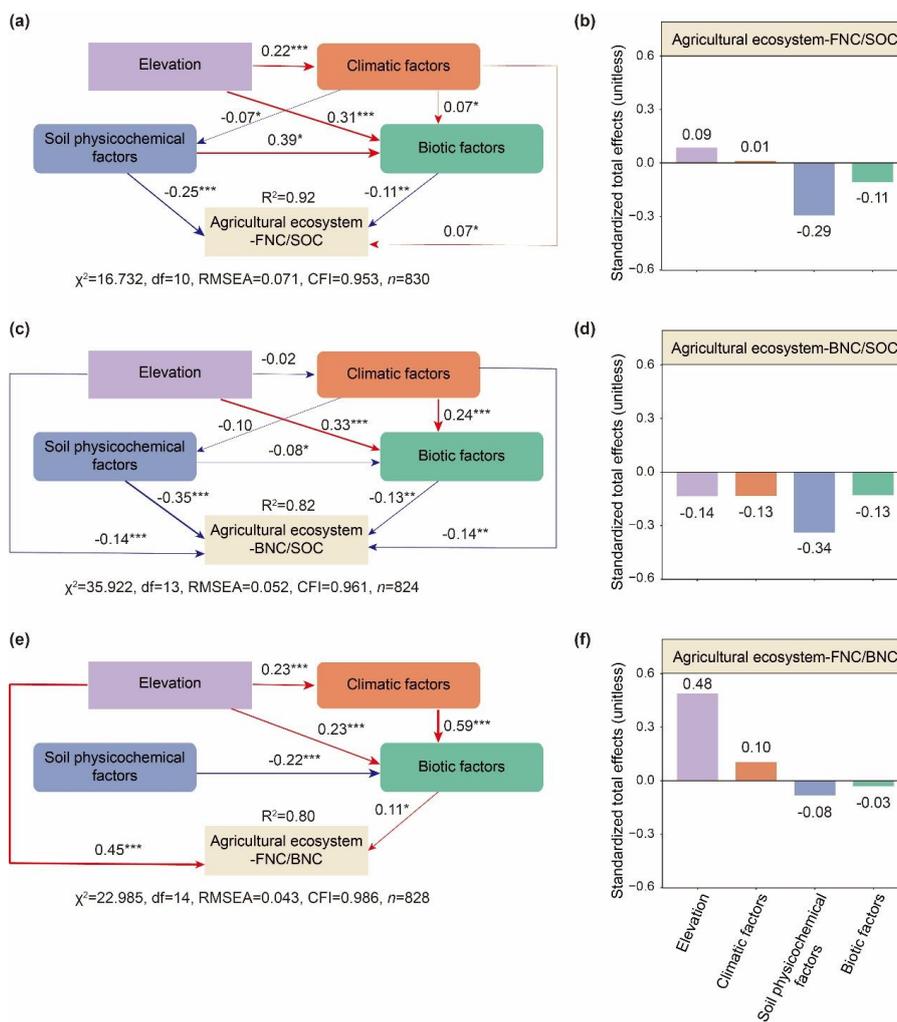
768 **Figure 4.**



769



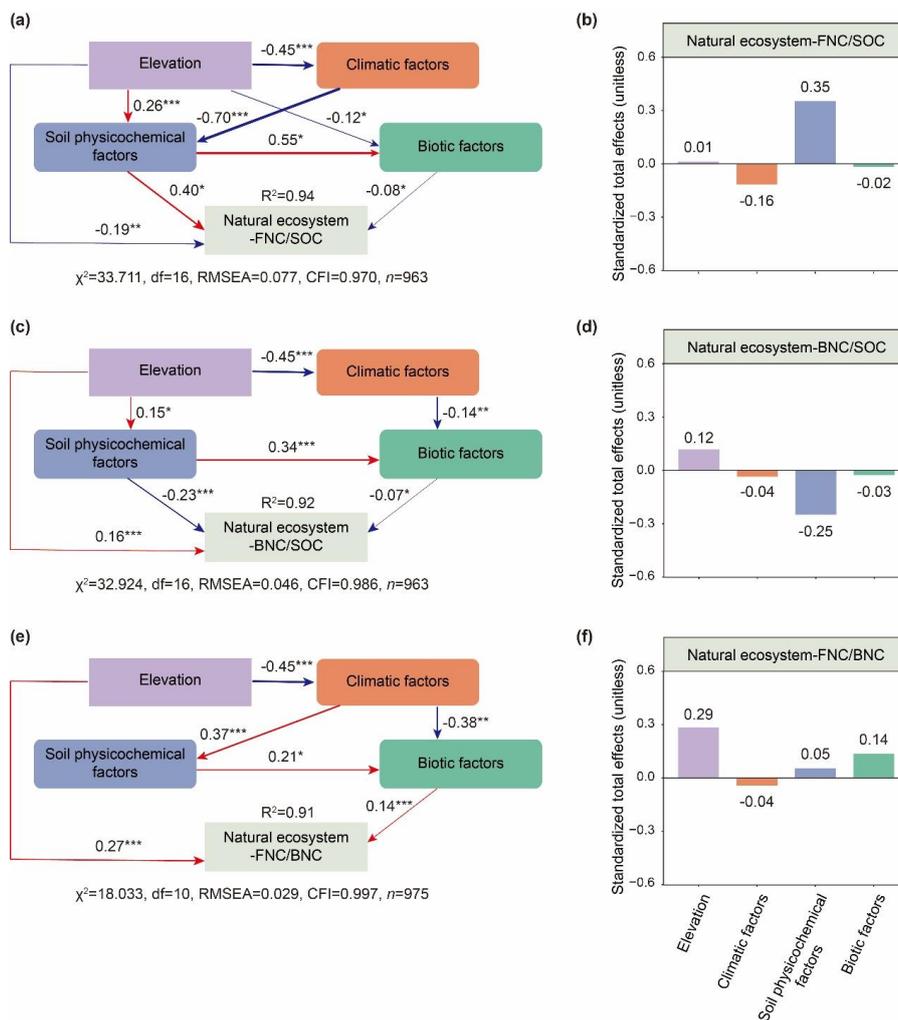
770 **Figure 5.**



771



772 **Figure 6.**



773