

Table S1. Results of PERMANOVA (A), pairwise PERMANOVA (B), and tests for homogeneity of multivariate dispersion (betadisper) results (C) for bacterial and fungal communities under different fertilization treatments.

(A) Overall PERMANOVA results

Community	Source	Df	Sum of squares	R ²	F	P value	Significance
Bacteria	Group	3	0.25	0.11	0.79	0.98	ns
Bacteria	Residual	20	2.09	0.89	—	—	—
Bacteria	Total	23	2.34				
Fungi	Group	3	0.30	0.11	0.82	0.88	ns
Fungi	Residual	20	2.49	0.89	—	—	—
Fungi	Total	23	2.79				

(B) Pairwise PERMANOVA results

Groups	F	R ²	P value	Significance
Bacteria NF vs CF	0.66	0.06	0.98	ns
Bacteria NF vs SOCF	0.74	0.07	0.96	ns
Bacteria NF vs BSOCF	0.91	0.08	0.64	ns
Bacteria CF vs SOCF	0.71	0.07	0.96	ns
Bacteria CF vs BSOCF	0.90	0.08	0.61	ns
Bacteria SOCF vs BSOCF	0.81	0.08	0.88	ns
Fungi NF vs CF	0.70	0.06	0.92	ns
Fungi NF vs SOCF	0.64	0.06	0.98	ns
Fungi NF vs BSOCF	1.07	0.10	0.35	ns
Fungi CF vs SOCF	0.65	0.06	0.86	ns
Fungi CF vs BSOCF	1.02	0.09	0.41	ns
Fungi SOCF vs BSOCF	0.88	0.0	0.57	ns

(C) Tests for homogeneity of multivariate dispersion (betadisper) results

Community	Source	Df	Sum of squares	Mean square	F	P value	Significance
Bacteria	Groups	3	0.0010	0.0003	0.28	0.82	ns
Bacteria	Residuals	20	0.0229	0.0011	—	—	—
Fungi	Groups	3	0.0211	0.0070	1.26	0.32	ns
Fungi	Residuals	20	0.1122	0.0056	—	—	—

Beta diversity was calculated based on Bray–Curtis dissimilarity. NF, no fertilization; CF, compound fertilizer; SOCF, sheep manure organic fertilizer plus compound fertilizer; BSOCF, biochar-based sheep manure organic fertilizer plus compound fertilizer. “ns” indicates no significant difference at $P < 0.05$.

Table S2. Relative abundances (%) of the bacterial (A) and fungal phyla (B) shown in Figure 5 under different fertilization treatments.

(A) Relative abundances (%) of the bacterial phyla shown in Figure 5A.

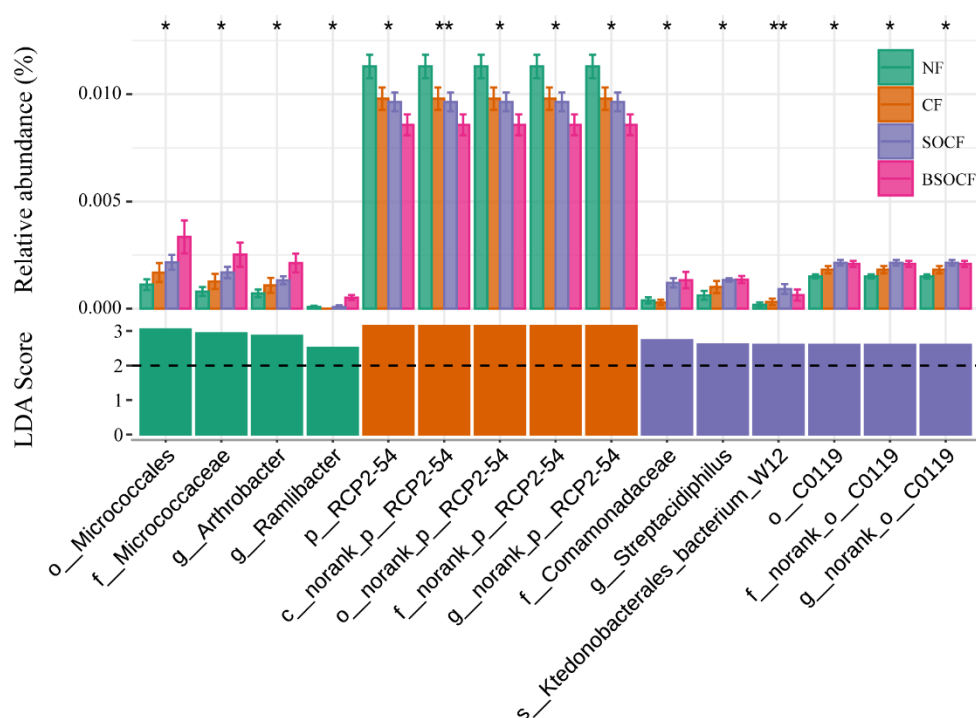
Phylum	NF	CF	SOCF	BSOCF	Significance
<i>Acidobacteriota</i>	30.09 ± 0.60	30.16 ± 0.81	29.67 ± 0.97	28.71 ± 1.19	n.s.
<i>Pseudomonadota</i>	23.06 ± 1.03	22.83 ± 0.62	22.86 ± 0.64	23.89 ± 0.66	n.s.
<i>Chloroflexota</i>	21.30 ± 1.26	21.04 ± 0.66	22.09 ± 0.60	20.44 ± 1.76	n.s.
<i>Actinomycetota</i>	8.90 ± 0.38	8.98 ± 0.31	9.22 ± 0.36	9.91 ± 0.60	n.s.
<i>Planctomycetota</i>	6.34 ± 0.28	5.77 ± 0.25	5.51 ± 0.29	5.83 ± 0.24	
	a	ab	b	ab	
<i>Bacillota</i>	1.80 ± 0.14	1.86 ± 0.31	2.13 ± 0.26	2.17 ± 0.14	n.s.
<i>Gemmatimonadota</i>	0.97 ± 0.09	1.02 ± 0.05	1.05 ± 0.08	1.21 ± 0.11	n.s.
<i>Candidatus</i>	0.98 ± 0.12	1.08 ± 0.10	1.11 ± 0.11	1.05 ± 0.09	n.s.
<i>Eremiobacterota</i>					
<i>Verrucomicrobiota</i>	1.02 ± 0.36	1.32 ± 0.37	0.82 ± 0.25	0.93 ± 0.08	n.s.
<i>RCP2-54</i>	1.13 ± 0.05	0.98 ± 0.05	0.96 ± 0.04 a	0.86 ± 0.05 b	
	a	ab			
Others	4.41	4.97	4.58	5	

(B) Relative abundances (%) of the fungal phyla shown in Figure 5B.

Phylum	NF	CF	SOCF	BSOCF	Significance
<i>Ascomycota</i>	62.60 ± 5.13	61.11 ± 3.48	62.16 ± 2.26	63.21 ± 3.64	n.s.
<i>Basidiomycota</i>	27.53 ± 4.78	26.82 ± 2.04	26.63 ± 2.58	28.25 ± 2.75	n.s.
<i>Mortierellomycota</i>	7.13 ± 0.97	9.42 ± 1.50	8.92 ± 1.60	6.91 ± 1.10	n.s.
<i>Rozellomycota</i>	1.18 ± 0.36	0.91 ± 0.24	1.06 ± 0.44	0.66 ± 0.20	n.s.
<i>Kickxellomycota</i>	0.99 ± 0.16	0.98 ± 0.38	0.57 ± 0.06	0.35 ± 0.06	n.s.
<i>Mucoromycota</i>	0.23 ± 0.07	0.29 ± 0.08	0.28 ± 0.07	0.31 ± 0.07	n.s.
<i>Chytridiomycota</i>	0.12 ± 0.05	0.27 ± 0.09	0.27 ± 0.04	0.18 ± 0.03	n.s.
<i>Calcarisporiellomycota</i>	0.06 ± 0.02	0.10 ± 0.07	0.08 ± 0.04	0.09 ± 0.04	n.s.
<i>Glomeromycota</i>	0.13 ± 0.09	0.06 ± 0.04	0.02 ± 0.01	0.04 ± 0.01	n.s.
<i>Zoopagomycota</i>	0.03 ± 0.03	0.04 ± 0.02	0.00 b	0.00 b	
	ab	a			
Others	0.01	0.01	0.02	0	

Note: NF, no fertilization; CF, compound fertilizer; SOCF, sheep manure organic fertilizer plus compound fertilizer; BSOCF, biochar-based sheep manure organic fertilizer plus compound fertilizer. Values are presented as mean ± SE (%) for the phyla individually shown in Figure 5 (n = 6). “Others” was calculated as the sum of all remaining bacterial phyla. Groups sharing the same lowercase letter do not differ significantly at $P < 0.05$.

A. Lefse identified bacteria biomarkers



B. Lefse identified bacteria biomarkers Correlated with environment factors

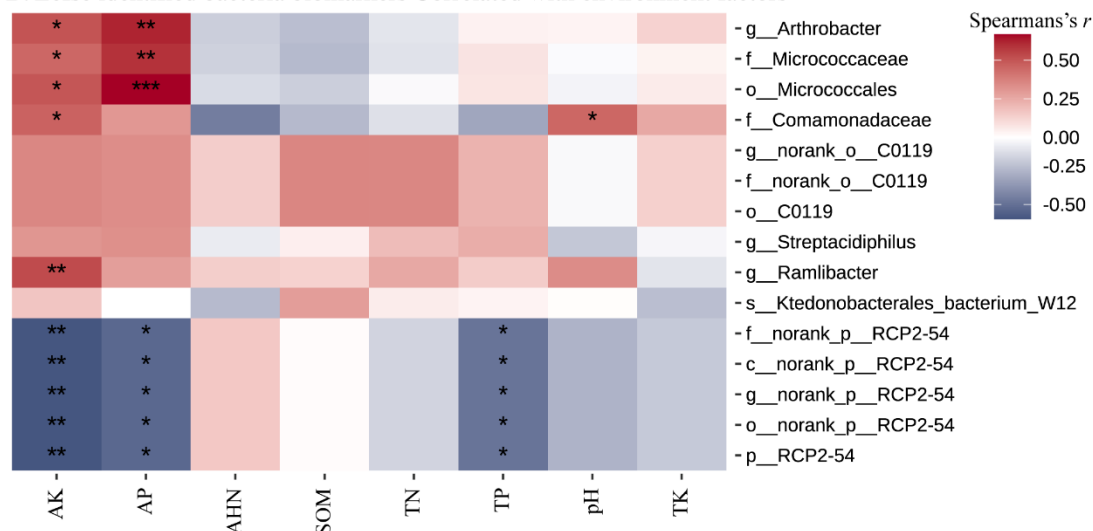
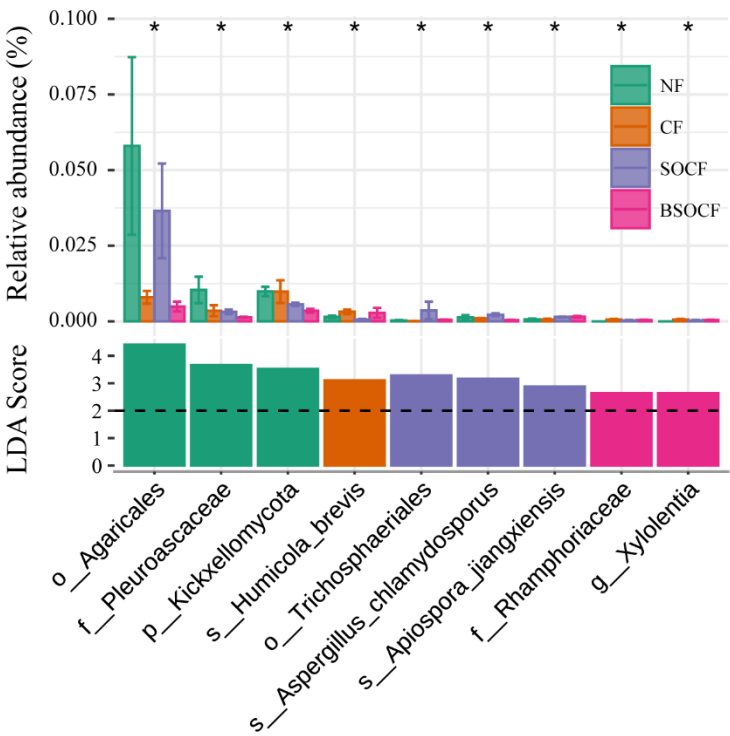


Figure S1. LEfSe-identified bacterial biomarkers and their correlations with soil physicochemical properties under different fertilization treatments in a moso bamboo forest. (A) Relative abundances and LDA scores of bacterial biomarkers identified by LEfSe. Colors of the LDA bars indicate the treatment in which each taxon was enriched, and the dashed line indicates the LDA threshold of 2.0. Asterisks above the bar plots indicate significant differences among treatments. (B) Spearman correlation heatmap between LEfSe-identified bacterial biomarkers and soil physicochemical properties. The color gradient represents Spearman's correlation coefficients. pH, soil pH; SOM, soil organic matter; TN, total nitrogen; TP, total phosphorus; TK, total potassium; AHN, alkali-hydrolyzable nitrogen; AP, available phosphorus; AK, available potassium.

A. Lefse identified fungi biomarkers



B. Lefse identified fungal biomarkers Correlated with environment factors

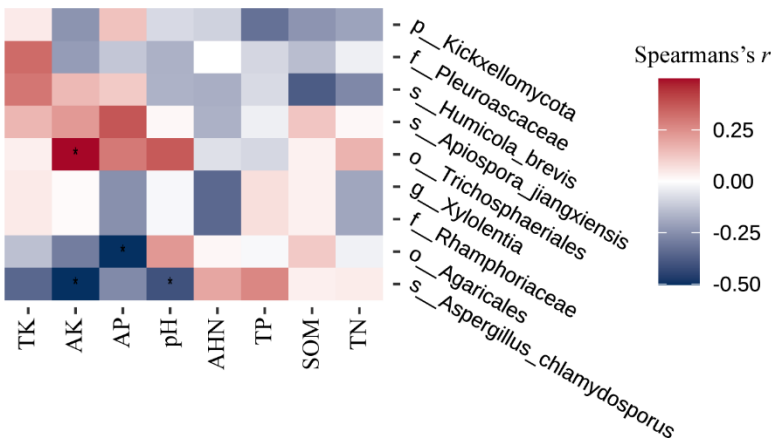


Figure S2. LEfSe-identified fungal biomarkers and their correlations with soil physicochemical properties under different fertilization treatments in a moso bamboo forest. (A) Relative abundances and LDA scores of fungal biomarkers identified by LEfSe. Colors of the LDA bars indicate the treatment in which each taxon was enriched, and the dashed line indicates the LDA threshold of 2.0. Asterisks above the bar plots indicate significant differences among treatments. (B) Spearman correlation heatmap between LEfSe-identified fungal biomarkers and soil physicochemical properties. The color gradient represents Spearman's correlation coefficients. pH, soil pH; SOM, soil organic matter; TN, total nitrogen; TP, total phosphorus; TK, total potassium; AHN, alkali-hydrolyzable nitrogen; AP, available phosphorus; AK, available potassium.

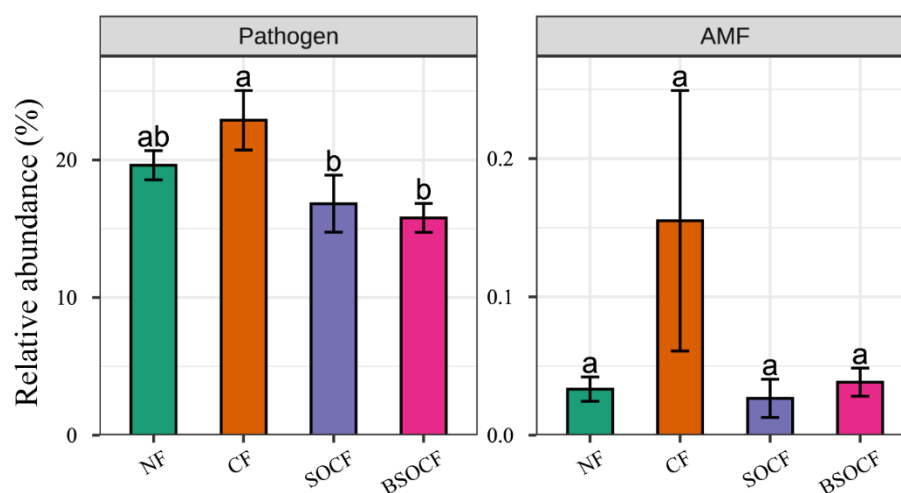


Figure S3. Relative abundances of FUNGuild-predicted plant pathogens and arbuscular mycorrhizal fungi (AMF) under different fertilization treatments in a moso bamboo forest. Values are presented as mean $\pm$ SE ($n = 6$). Different lowercase letters indicate significant differences among treatments according to Tukey's honestly significant difference (HSD) test at $P < 0.05$. NF, no fertilization; CF, compound fertilizer; SOCF, sheep manure organic fertilizer plus compound fertilizer; BSOCF, biochar-based sheep manure organic fertilizer plus compound fertilizer.