Continuous organic mulching enhances the stability of soil organic carbon in *Phyllostachys praecox*: A 5-year in situ experiment

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Table S1 Results of one-way ANOVA on the effects of mulching on the relative abundance of dominant bacterial phylum in the bamboo soil.

	CK	T1	T3	T5
Acidobacteriota	42.16±0.73a	27.83±4.40b	23.17±1.71b	36.41±2.99a
Firmicutes	40.10±2.18b	55.17±5.36a	26.48±4.59c	3.30±0.76d
Proteobacteria	5.21±0.57b	6.51±1.56b	16.44±1.61a	16.65±1.59a
Chloroflexota	3.23±0.45b	2.25±0.86b	7.68±2.15a	11.19±3.19a
Eremiobacterota	2.68±0.30b	1.93±0.55b	10.00±0.63a	9.07±0.84a
Planctomycetota	1.11±0.10c	1.85±0.57bc	8.67±1.10a	2.62±0.37b
Verrucomicrobiota	1.71±0.13b	0.68±0.25c	0.44±0.26c	8.17±1.26a
Patescibacteria	0.17±0.03b	0.12±0.03b	2.35±0.28a	2.62±0.38a
Actinobacteriota	0.24±0.03b	0.11±0.02b	1.05±0.68b	2.98±1.27a
Cyanobacteria	1.69±0.46a	0.13±0.06b	0.35±0.09b	1.69±0.62a
other	1.70±0.15c	3.42±0.25b	3.38±0.43b	5.30±0.44

CK indicates the control group without any mulching, while T1, T3, and T5 denote the groups that have been mulched for one, three, and five years, respectively. Lowercase letters indicate significant differences between years of mulching application ($P < 0.05$).

Table S2 Results of one-way ANOVA on the effects of mulching on the relative abundance of dominant fungal phylum in the bamboo soil.

	CK	T1	T3	T5
Ascomycota	60.37±10.70b	80.19±0.67a	25.66±14.55c	49.66±5.10b
unclassified	30.03±8.64b	17.06±0.66c	43.39±11.00a	41.85±5.44a
Basidiomycota	7.78±2.39b	2.20±0.21b	28.69±6.70a	5.10±1.12b
Rozellomycota	0.03±0.03b	0.04±0.04b	0.04±0.05b	1.61±0.94a
Cercozoa	0.02±0.02c	0.29±0.10b	1.05±0.19a	0.05±0.02c
Chlorophyta	0.09±0.04b	0.01±0.00b	0.49±0.35a	0.63±0.32a
Glomeromycota	0.90±0.30a	0.00±0.00b	0.04±0.05b	0.02±0.01b
Aphelidiomycota	0.02±0.04b	0.02±0.03b	0.54±0.47a	0.16±0.09b
Chytridiomycota	0.04±0.07b	0.05±0.06b	0.00±0.00b	0.40±0.16a
Anthophyta	0.35±0.36a	0.01±0.02b	0.03±0.02b	0.02±0.02b
other	0.36±0.27ab	0.12±0.13bc	0.08±0.08c	0.51±0.13a

Table S3 The r value and *p* value in the Mantel test that describes the relationship between environmental variables and soil microorganisms.

	Bacterial community composition		Fungal community composition		Bacterial diversity		Fungal diversity	
	r	*p*	r	*p*	r	*p*	r	*p*
SOC	0.6247	0.001	0.5034	0.001	0.2110	0.037	0.2888	0.013
POC	0.4040	0.001	0.3867	0.001	0.5566	0.001	0.2929	0.014
MAOC	0.6916	0.001	0.4568	0.001	0.3478	0.006	0.4044	0.002
TN	-0.0723	0.771	0.0774	0.19	-0.1295	0.951	-0.0325	0.563
TP	0.3392	0.001	0.3105	0.004	0.0842	0.158	0.0958	0.14
AP	0.7193	0.001	0.6238	0.001	0.1128	0.098	0.3383	0.014
NO_3^--N	0.1805	0.055	0.4406	0.001	-0.1329	0.883	0.2872	0.013
NH_4^+-N	0.5255	0.001	0.5233	0.001	0.5592	0.001	0.2204	0.037
K^+	-0.1206	0.941	0.0475	0.245	-0.1665	0.902	-0.0689	0.744
Ca^{2+}	0.0405	0.261	0.0665	0.204	0.0441	0.332	-0.0328	0.601
Mg^{2+}	0.0360	0.346	0.0709	0.18	0.0392	0.388	0.0793	0.18
pH	0.8448	0.001	0.5673	0.001	0.3303	0.005	0.4301	0.003
Polyphenol oxidase	0.2021	0.037	0.0921	0.137	0.2620	0.035	0.1596	0.067
Urease	0.4993	0.001	0.3305	0.003	0.5449	0.002	0.0048	0.425
Phosphatase	0.2663	0.016	0.4737	0.001	0.0372	0.371	0.1627	0.06
β-xylosidase	0.3147	0.004	0.3434	0.003	0.0380	0.259	-0.0264	0.507
Peroxidase	0.0545	0.222	0.3083	0.002	-0.0774	0.636	-0.0993	0.878
Sucrase	0.1569	0.069	0.3297	0.004	0.0403	0.299	-0.0458	0.667
β-glucosidas	0.1294	0.076	0.4509	0.001	-0.1475	0.897	0.0183	0.349
Amylase	0.2784	0.02	0.3467	0.004	0.3559	0.003	0.2699	0.028