

Supplementary materials

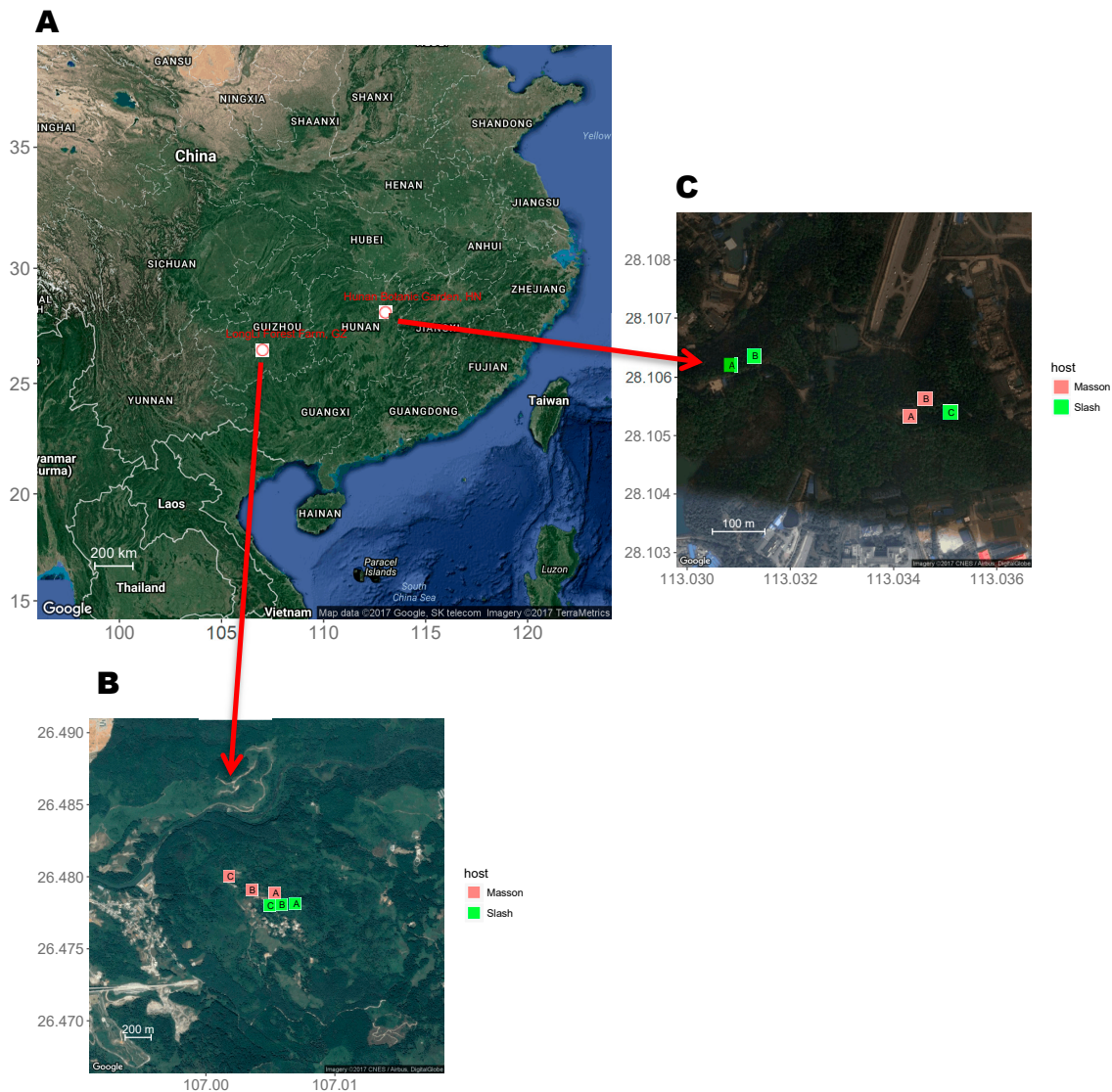


Figure S1. Map of sampling regime and sampling locations across the continental China. Circles represent individual sampling locations mapped on Google Map images. (A) Individual sampling plots are shown on a map of south China. (B) Individual plots 20-m $\times$ 20-m within a sampling site are shown in Longli Forest Farm, Guizhou. (C) Individual plots 20-m $\times$ 20-m within a sampling site are shown in Hunan Botanic Garden, Hunan. lat,

Table S1 Soil physico-chemical characteristics among different habitats.

Properties	Forest types			
	LFF-Masson (n=15)	LFF-Slash (n=15)	HBG-Masson (n=10)	HBG-Slash (n=15)
pH (H ₂ O)	4.11 ± 0.03ab	4.1 ± 0.03b	4.18 ± 0.03ab	4.24 ± 0.04a
Sand (%)	57.9 ± 4.3a	49.6 ± 3.1ab	43.0 ± 0.2b	45.9 ± 0.9b
Silt (%)	33.0 ± 4.1a	40.0 ± 3.8a	12.3 ± 1.0b	20.5 ± 1.4b
Clay (%)	9.1 ± 1.0a	10.4 ± 1.6a	44.7 ± 0.9b	33.6 ± 1.9c
C (g kg ⁻¹ soil)	11.5 ± 1.4a	14.6 ± 1.5a	21.5 ± 3.9ab	29.0 ± 2.9b
N (g kg ⁻¹ soil)	0.8 ± 0.1a	1.2 ± 0.1a	1.7 ± 0.2b	2.3 ± 0.2c
C/N	14.5 ± 1.6	12.6 ± 1.1	11.6 ± 0.9	12.6 ± 0.9
NH ₄ -N (mg kg ⁻¹ soil)	162.7 ± 9.2	167.3 ± 16.2	192.1 ± 16.2	171.5 ± 6.5
NO ₃ -N (mg kg ⁻¹ soil)	1.9 ± 0.3a	1.7 ± 0.2a	8.3 ± 1.6b	5.4 ± 0.6c
PO ₄ -P (mg kg ⁻¹ soil)	3.2 ± 0.2	3.7 ± 0.2	3.5 ± 0.2	3.1 ± 0.3
Available K (mg kg ⁻¹ soil)	15.9 ± 1.0a	26.3 ± 1.7a	46.5 ± 4.9b	55.1 ± 7.3b
P (mg kg ⁻¹ soil)	48.2 ± 2.1a	45.0 ± 2.6a	93.1 ± 8.2b	100.3 ± 3.4b
K (mg kg ⁻¹ soil)	794.2 ± 6.1a	810.2 ± 19.4a	4061.5 ± 219.3b	3959.5 ± 156.5b
Ca (mg kg ⁻¹ soil)	496.1 ± 17.0a	413.5 ± 11.4ab	326.3 ± 52.3bc	266.8 ± 27.0c
Mg (mg kg ⁻¹ soil)	1531.9 ± 52.2a	1430.4 ± 109.0a	614.6 ± 18.7b	754.2 ± 33.3b
Fe (mg kg ⁻¹ soil)	564.9 ± 4.7a	560.0 ± 28.5a	3698.2 ± 28.2b	3700.5 ± 17.2b
Cu (mg kg ⁻¹ soil)	1.7 ± 0.2a	3.0 ± 0.4a	14.0 ± 0.7b	12.7 ± 0.7b
Pb (mg kg ⁻¹ soil)	35.5 ± 0.5a	33.9 ± 0.8a	18.6 ± 2.8b	23.9 ± 1.7b
Zn (mg kg ⁻¹ soil)	20.0 ± 2.1a	30.7 ± 4.0b	46.2 ± 1.0c	38.8 ± 1.0bc
Mn (mg kg ⁻¹ soil)	47.2 ± 5.7a	47.8 ± 5.8a	19.6 ± 2.8b	16.3 ± 2.9b

Notes: Values represent means ± standard errors. Different letters indicate significant ($P < 0.05$) differences between individual means were assessed by two-way factorial analysis of variance (ANOVA) followed by Tukey's HSD post-hoc testing.

Table S2 Comparison of sequence abundances and operational taxonomic unit (OTU) counts in a mock community of 18 Basidiomycota species collected in local area.

Mock community taxa	NCBI	Initial DNA concentration in pooled DNA (ng/ul)	Relative abundance in pooled DNA (%)	Read abundance	Relative abundance in total read (%)
<i>Lactarius sp.1</i>	GU258227 (99)	1.47	18.95	2698	14.15
<i>Russula sp.1</i>	AB597666 (100)	0.19	2.41	1026	5.38
<i>Xerocomus. Sp.</i>	UDB013362 (96)	0.05	0.6	0	0
<i>Suillus bovinus</i>	FJ481028 (100)	0.39	5.07	1054	5.53
<i>Russula cascadiensis</i>	KP406549 (98)	0.21	2.72	182	0.95
<i>Russula sp.2</i>	AB636419 (99)	0.99	12.82	3513	18.42
<i>Strobilomyces confusus</i>	KT121567 (99)	1.48	19.18	0	0
<i>Lactarius horakii</i>	EF685070 (99)	0.42	5.47	1302	6.83
<i>Clavulina cristata</i>	KF359593 (97)	0.42	5.44	674	3.53
<i>Lactarius sp.1</i>	KR025614 (99)	0.43	5.63	3610	18.92
<i>Laccaria amethystina</i>	JN942783 (99)	0.10	1.23	88	0.46
<i>Rhizopogon sp.1</i>	LC096919 (100)	0.22	2.89	5	<0.1
<i>Phliota multicingulata</i>	HQ533029 (99)	0.18	2.28	1420	7.45
<i>Tomentella stuposa</i>	UDB018520 (98)	0.24	3.09	994	5.21
<i>Atheliaceae sp.</i>	AB839405 (89)	0.48	6.16	2143	11.24
<i>Amanita spiacea</i>	KU139516 (100)	0.32	4.09	298	1.56
<i>Russula sp.3</i>	JN129410 (86)	0.11	1.41	55	0.29
<i>Tomentella sp.</i>	JX556209 (99)	0.04	0.54	15	0.08

Notes: The mock community was built by mixing equimolar amounts of DNA from each species and then processed in the same way as all other samples. The datasets were treated identically in the bioinformatics quality filtering and OTU clustering using the multi-step full-linkage OTU clustering approach implemented in QIIME.