

Table S1. Relative abundance of microbial phylum in soil samples

	Samples	W1/%	T1/%	X1/%	W2/%	T2/%	X2/%
Bacteria	Actinobacteria	40.36	22.99	31.35	44.19	34.99	40.89
	Proteobacteria	32.93	30.05	21.32	29.31	24.69	15.47
	Acidobacteria	10.12	10.62	8.43	6.87	9.55	10.19
	Firmicutes	4.37	9.96	5.04	7.85	14.05	12.25
	Chloroflexi	0.93	6.90	16.99	2.26	3.71	11.40
	Myxococcota	3.33	8.21	5.03	3.63	5.23	3.78
	Verrucomicrobia	1.72	8.31	7.73	1.97	4.77	2.92
	Gemmatimonadetes	0.84	0.92	1.91	1.70	1.24	1.36
	Bacteroidetes	2.09	0.66	0.67	0.58	0.31	0.47
	Planctomycetes	0.45	0.69	0.49	0.61	1.24	0.56
	Nitrospirae	1.88	0.28	0.34	0.57	0.01	0.12
	Samples	W1/%	T1/%	X1/%	W2/%	T2/%	X2/%
Fungi	Ascomycota	68.57	43.28	61.16	47.36	53.56	50.21
	Basidiomycota	23.42	52.09	35.27	47.08	37.83	45.75
	Mortierellomycota	5.73	2.49	0.92	2.77	6.27	1.41
	Glomeromycota	1.99	0.53	1.69	0.46	0.26	1.66
	Kickxellomycota	0.10	0.44	0.07	1.65	1.68	0.04

Note: W1, rhizosphere soil sample of bending type in May; W2, rhizosphere soil sample of bending type in August; T1, rhizosphere soil sample of straight type in May; T2, rhizosphere soil sample of straight type in August; X1, rhizosphere soil sample of introduced straight type in May; X2, rhizosphere soil sample of introduced straight type in August.

Table S2. Analysis of differences in main microbial genera among soil samples

		W1	T1	X1	W2	T2	X2
Bacteria	<i>Bacillus</i>	178.8±39.26 c	560.6±53.92 ab	204.4±48.81 c	322.2±86.28 bc	803.0±181.50 a	577.6±131.31 ab
	<i>Bradyrhizobium</i>	279.4±12.05 c	691.8±34.76 a	454.6±66.68 b	665.0±60.95 a	737.8±18.92 a	324.0±24.12 c
	<i>Mycobacterium</i>	104.0±17.99 c	122.0±18.06 bc	213.2±37.27 ab	228.4±51.97 a	193.2±19.23 abc	197.4±32.73 abc
	<i>Kitasatospora</i>	178.4±10.82 bc	132.2±30.21 c	120.0±10.07 c	327.0±17.50 a	277.8±79.15 ab	237.2±37.97 abc
	<i>Sphingomonas</i>	240.8±38.22 ab	146.4±21.56b	308.4±71.09 a	126.2±18.75b	130.0±36.60b	214.4±18.10 ab
	<i>RB41</i>	486.2±49.86 a	300.4±56.21 b	186.2±53.96 b	210.6±69.40 b	230.6±83.25 b	233.4±39.66 b
	<i>Gaiella</i>	453.6±15.32 a	198.6±90.19 bc	212.6±48.42 bc	357.8±75.52 ab	143.2±36.22 c	241.8±46.58 bc
	<i>Haliangium</i>	162.0±17.46 ab	195.4±26.66 a	114.8±17.84 b	133.0±9.71 b	162.6±10.45 ab	128.6±10.16 b
		W1	T1	X1	W2	T2	X2
Fungi	<i>Cladophialophora</i>	278.8±70.54 ab	117.0±24.76 ab	491.4±112.76 ab	149.4±52.66 b	232.8±44.55 a	334.6±111.77 ab
	<i>Trichoderma</i>	599.2±119.50 ab	666.2±239.99 ab	306.6±45.35 b	520.4±220.65 ab	877.6±115.64 a	344.2±138.47 b
	<i>Penicillium</i>	307.8±132.28 ab	497.6±70.26 ab	247.0±70.18 ab	198.2±55.15 b	651.4±272.98 a	295.0±58.60 ab
	<i>Apiotrichum</i>	776.6±331.59 a	12.4±6.87 b	1.3±1.18 b	155.0±106.93 b	42.6±23.40 b	1.7±1.35 b
	<i>Fusarium</i>	390.2±101.87 a	27.8±7.08 c	171.0±42.73 bc	53.2±16.73 c	94.4±39.97 bc	230.2±44.66 b
	<i>Exophiala</i>	234.6±76.41 a	62.0±12.21 b	47.0±11.14 b	140.2±71.47 ab	162.8±49.16 ab	16.0±12.50 b
	<i>Acremonium</i>	204.4±33.82 a	48.4±16.76 bc	35.4±6.85 c	106.0±15.11 b	76.6±22.51 bc	67.0±23.87 bc
	<i>Cordana</i>	177.2±76.60 a	5.82±2.28 b	8.22±4.15 b	252.8±77.48 a	24.2±12.96 b	3.04±1.66 b
	<i>Neocosmospora</i>	199.2±29.57 a	2.42±1.02 c	100.2±26.22 b	22.8±9.90 c	1.02±0.30 c	105.4±34.68 b
	<i>Tremellodendropsis</i>	0.1±0.00 b	575.4±421.57 a	0.1±0.00 b	0.28±0.18 b	105.42±67.38 ab	0.1±0.00 b
	<i>Archaeorhizomyces</i>	0.1±0.00 b	382.0±120.49 a	37.82±26.52 b	2.82±1.23 b	320.0±147.58 a	5.46±4.25 b
	<i>Camarophyllus</i>	0.1±0.00 b	617.46±394.69 a	1.06±0.61 b	0.1±0.00 b	0.1±0.00 b	0.1±0.00 b
	<i>Leohumicola</i>	0.1±0.00 b	393.4±149.62 a	39.62±11.04 b	100.2±56.84 b	60.8±18.77 b	0.46±0.22 b

Note: W1, rhizosphere soil sample of bending type in May; W2, rhizosphere soil sample of bending type in August; T1, rhizosphere soil sample of straight type in May; T2, rhizosphere soil sample of straight type in August; X1, rhizosphere soil sample of introduced straight type in May; X2, rhizosphere soil sample of introduced straight type in August. Different letters in the same line indicate significant differences ( $p < 0.05$ ).

Table S3. Analysis of differences in some bacterial functions among soil samples

	W1	T1	X1	W2	T2	X2
chemoheterotrophy	3319.8±105.53 b	2649.8±75.37 c	2905.4±247.40 bc	3922.2±128.44 a	3280.4±255.51 b	3025.4±159.04 bc
aerobic_chemoheterotrophy	3233.4±101.86 b	2618.4±76.90 c	2872.8±246.90 bc	3849.2±119.35 a	3249.4±257.56 b	2985.2±157.73 bc
nitrogen_fixation	283.2±12.00 c	695.2±33.92 a	457.8±67.04 b	668.8±59.63 a	740.2±18.82 a	325.4±23.82 c
cellulolysis	66.2±17.79 b	482.0±127.48 a	634.8±74.05 a	565.6±184.83 a	660.0±133.57 a	422.6±45.80 a
nitrate_reduction	394.2±28.72 a	128.0±25.82 c	131.4±12.14 c	255.0±39.59 b	178.8±17.30 bc	197.4±40.84 bc
ureolysis	73.4±4.69 b	59.2±7.98 b	65.0±5.62 b	65.8±19.38 b	67.6±7.03 b	144.8±44.62 a

Note: W1, rhizosphere soil sample of bending type in May; W2, rhizosphere soil sample of bending type in August; T1, rhizosphere soil sample of straight type in May; T2, rhizosphere soil sample of straight type in August; X1, rhizosphere soil sample of introduced straight type in May; X2, rhizosphere soil sample of introduced straight type in August. Different letters in the same line indicate significant differences ( $p < 0.05$ ).

Table S4. Relative abundance of different functional fungal groups

	Guild	W1/%	T1/%	X1/%	W2/%	T2/%	X2/%
Saprotrophic	Dung Saprotroph	2.59	0.12	5.75	0.09	0.03	0.37
	Leaf Saprotroph	0.13	0.02	0.05	0.18	0.03	0.05
	Plant Saprotroph	0.79	0.08	1.36	0.11	0.18	1.47
	Saprotrophic	0.00	0.00	0.02	0.00	0.00	0.00
	Soil Saprotroph	14.48	6.21	0.74	3.51	6.72	0.36
	Undefined Saprotroph	58.45	84.48	71.80	67.80	71.09	76.71
	Wood Saprotroph	5.45	2.76	2.52	13.87	2.88	5.89
	Sum	81.90	93.67	82.24	85.57	80.93	84.84
	Guild	W1/%	T1/%	X1/%	W2/%	T2/%	X2/%
Pathogen	Animal Pathogen	6.36	1.99	3.16	8.38	1.73	7.30
	Plant Pathogen	3.17	2.97	5.83	1.44	1.47	3.40
	Fungal Parasite	2.93	0.14	0.56	2.16	1.19	0.74
	Lichen Parasite	0.00	0.01	0.00	0.00	0.00	0.01
	Sum	12.46	5.11	9.55	11.98	4.39	11.44
	Guild	W1/%	T1/%	X1/%	W2/%	T2/%	X2/%
Symbiotroph	Animal Endosymbiont	0.00	0.00	0.00	0.00	0.00	0.02
	Arbuscular Mycorrhizal	2.93	0.69	2.39	0.86	0.40	2.55
	Ectomycorrhizal	0.34	0.06	0.36	0.39	11.94	0.14
	Endophyte	0.29	0.10	4.06	1.04	0.36	0.88
	Lichenized	2.08	0.36	1.40	0.16	1.18	0.13
	Orchid Mycorrhizal	0.00	0.01	0.00	0.00	0.81	0.00
	Sum	5.64	1.22	8.21	2.44	14.69	3.72

Note: W1, rhizosphere soil sample of bending type in May; W2, rhizosphere soil sample of bending type in August; T1, rhizosphere soil sample of straight type in May; T2, rhizosphere soil sample of straight type in August; X1, rhizosphere soil sample of introduced straight type in May; X2, rhizosphere soil sample of introduced straight type in August. Different letters in the same line indicate significant differences ( $p < 0.05$ ).

Table S5. Soil microbial communities with significant differences

	Species name	group	Mean	LDA_value	Pvalue
Bacteria	<i>Pedomicrobium</i>	W1	4.767345	4.433512	0.000579
	<i>Solirubrobacter</i>	W1	4.687853	4.405673	0.000112
	<i>Gaiella</i>	W1	5.023153	4.621723	0.007118
	<i>Micromonospora</i>	W1	4.481648	4.164797	0.004619
	<i>Arthrobacter</i>	W1	4.527378	4.231651	0.002643
	<i>Nocardioides</i>	W1	4.780194	4.442551	0.000762
	<i>Reyranella</i>	W1	4.354520	4.155697	0.000342
	<i>RB41</i>	W1	5.050913	4.607000	0.022805
	<i>MND1</i>	W1	4.682856	4.424279	0.000602
	<i>Haliangium</i>	W1	4.574262	4.020340	0.030672
	<i>Kitasatospora</i>	W2	4.777100	4.286802	0.006644
	<i>Streptomyces</i>	W2	4.774355	4.383982	0.016476
	<i>Luedemannella</i>	W2	4.663654	4.295329	0.000374
	<i>Candidatus_Solibacter</i>	T1	4.689228	4.236479	0.013984
	<i>Anaeromyxobacter</i>	T1	4.749679	4.408057	0.000350
	<i>Bacillus</i>	T2	5.134566	4.689938	0.007352
	<i>Bradyrhizobium</i>	T2	5.097985	4.523772	0.000654
	<i>Candidatus_Udaeobacter</i>	X1	4.987426	4.565805	0.012744
	<i>Acidothermus</i>	X1	5.072493	4.749311	0.011610
	<i>Sphingomonas</i>	X1	4.759445	4.293756	0.005530
	<i>HSB_OF53-F07</i>	X1	4.761487	4.419299	0.020989
	<i>Bryobacter</i>	X2	4.515087	4.105184	0.001488
	<i>Actinoallomurus</i>	X2	4.420967	4.148947	0.026955
	<i>Pseudonocardia</i>	X2	4.376521	4.064796	0.000294
	<i>Conexibacter</i>	X2	4.766628	4.370470	0.003992
	<i>FCPS473</i>	X2	4.876113	4.561331	0.000403
Fungi	<i>Species name</i>	<i>group</i>	<i>Mean</i>	<i>LDA_value</i>	<i>Pvalue</i>
	<i>Gonytrichum</i>	W1	4.486678	4.303970	0.009794
	<i>Acremonium</i>	W1	4.650954	4.478092	0.009031
	<i>Neocosmospora</i>	W1	4.627346	4.478850	0.000169
	<i>Mortierella</i>	W1	4.994712	4.649244	0.030236
	<i>Apiotrichum</i>	W1	5.198802	4.886796	0.000625
	<i>Exophiala</i>	W1	4.713527	4.482962	0.005590
	<i>Fusarium</i>	W1	4.914217	4.566031	0.000530
	<i>Saitozyma</i>	W2	5.205070	4.836008	0.016033
	<i>Trechispora</i>	W2	5.037194	4.684383	0.016924
	<i>Cordana</i>	W2	4.666829	4.458914	0.001406
	<i>Hygrocybe</i>	W2	4.731303	4.435804	0.012853
	<i>Metarhizium</i>	W2	4.857473	4.494690	0.028028
	<i>Leohumicola</i>	T1	4.827901	4.510476	0.000859
	<i>Archaeorhizomyces</i>	T1	4.765919	4.576460	0.000825
	<i>Pseudallescheria</i>	T2	4.847206	4.694836	0.044360

<i>Cladophialophora</i>	X1	5.075464	4.736573	0.015213
<i>Entoloma</i>	X1	4.902233	4.647627	0.006644
<i>Agaricus</i>	X1	5.189211	4.852097	0.010651
<i>Clavaria</i>	X2	5.492799	5.165414	0.006982
<i>Chaetomium</i>	X2	4.996272	4.708027	0.002541

Note: W1, rhizosphere soil sample of bending type in May; W2, rhizosphere soil sample of bending type in August; T1, rhizosphere soil sample of straight type in May; T2, rhizosphere soil sample of straight type in August; X1, rhizosphere soil sample of introduced straight type in May; X2, rhizosphere soil sample of introduced straight type in August.

Table S6. RDA analysis results of microbial (bacterial, fungal) communities

		RDA1	RDA2	r <sup>2</sup>	<i>p</i> values
Bacteria	SWC	-0.4303	0.9027	0.5924	0.001
	pH	0.7565	0.654	0.7109	0.001
	SOC	-0.4547	0.8907	0.7487	0.001
	AP	-0.8914	-0.4532	0.4533	0.001
	AK	0.0756	0.9971	0.6416	0.001
	NH <sub>4</sub> <sup>+</sup> -N	-0.1984	0.9801	0.6989	0.001
	C: N	-0.1186	-0.9929	0.0452	0.524
	NH <sub>4</sub> <sup>+</sup> : NO <sub>3</sub> <sup>-</sup>	-0.9512	0.3085	0.3666	0.001
		CCA1	CCA2	r <sup>2</sup>	<i>p</i> values
Fungi	SWC	-0.9517	-0.3069	0.5736	0.001
	pH	-0.0908	-0.9959	0.7727	0.001
	SOC	-0.997	-0.0778	0.8020	0.001
	AP	-0.3842	0.9233	0.7794	0.001
	AK	-0.7637	-0.6455	0.8171	0.001
	NH <sub>4</sub> <sup>+</sup> -N	-0.8827	-0.4699	0.5437	0.001
	C: N	-0.4829	0.8757	0.0298	0.668
	NH <sub>4</sub> <sup>+</sup> : NO <sub>3</sub> <sup>-</sup>	-0.7987	0.6017	0.2737	0.010

Note: SWC, soil water content; SOC, soil organic carbon; AP, available phosphorus; AK, available potassium; NH<sub>4</sub><sup>+</sup>-N, ammonia nitrogen; C: N, the ratio between soil organic carbon and soil total nitrogen; NH<sub>4</sub><sup>+</sup>: NO<sub>3</sub><sup>-</sup>, the ratio between ammonia nitrogen and nitrate nitrogen.