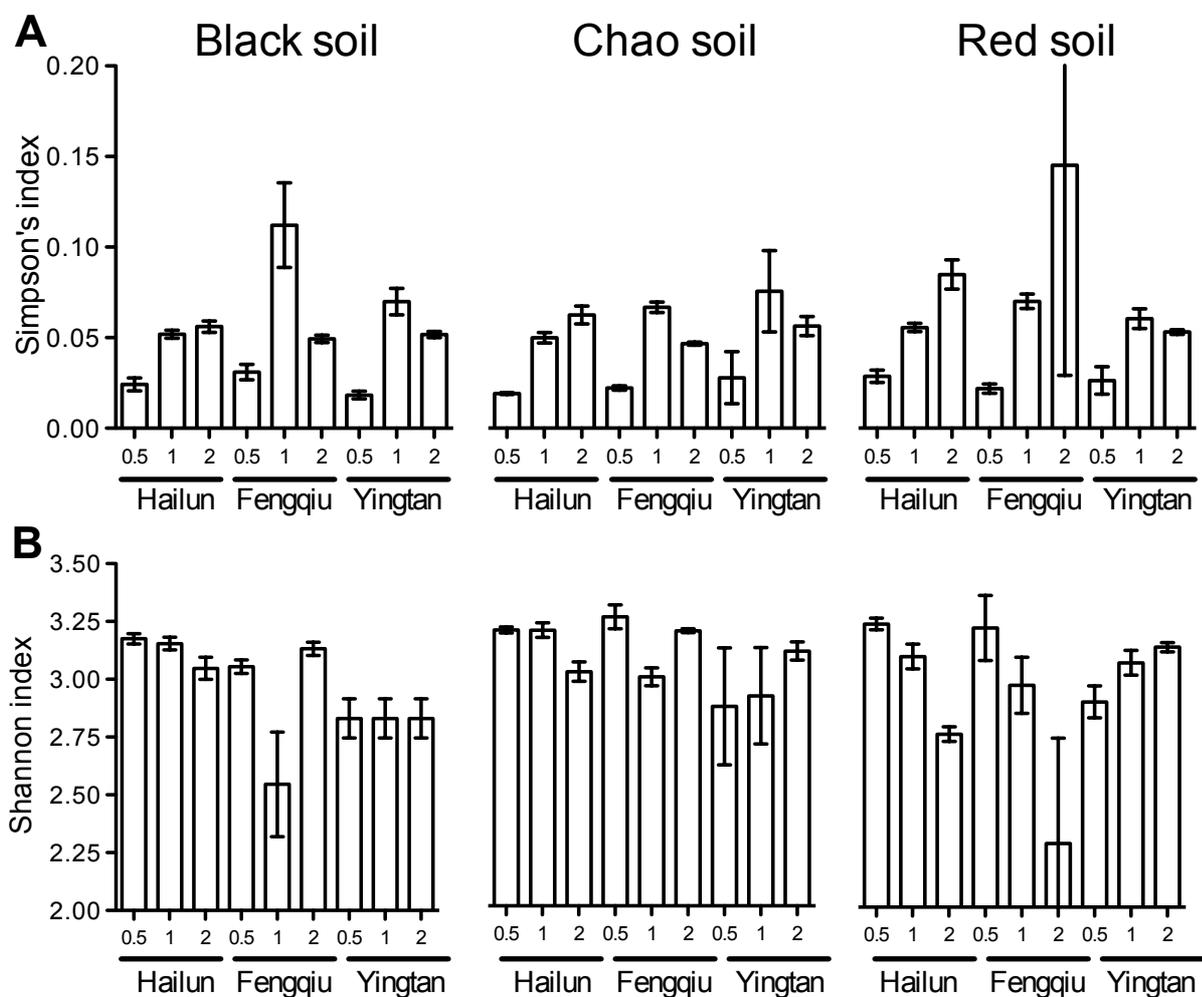
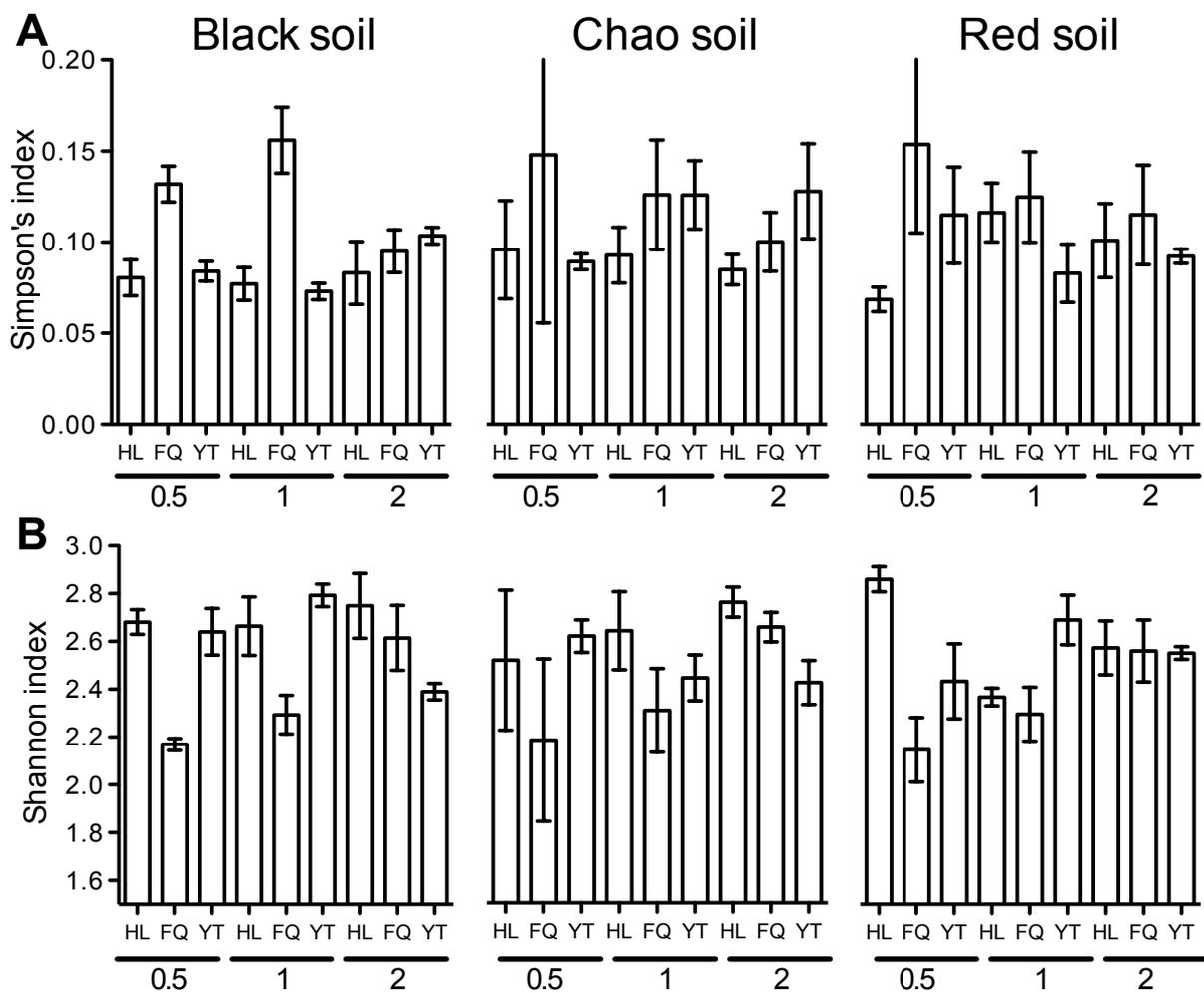


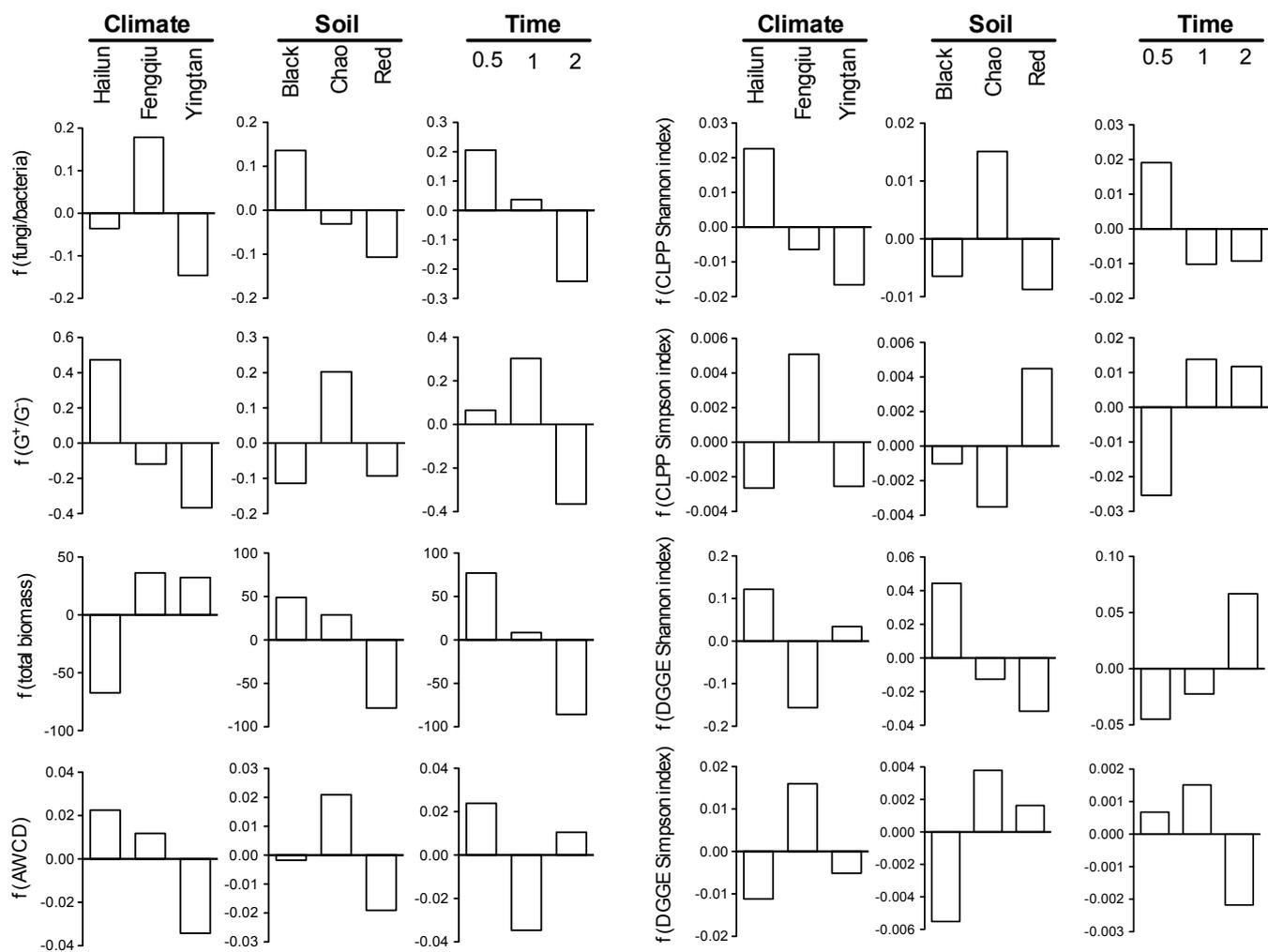
**Figure S1.** Geographic locations of the three reciprocal soil transplantation sites (A) and an overview of the experimental plot in Yingtan (B).



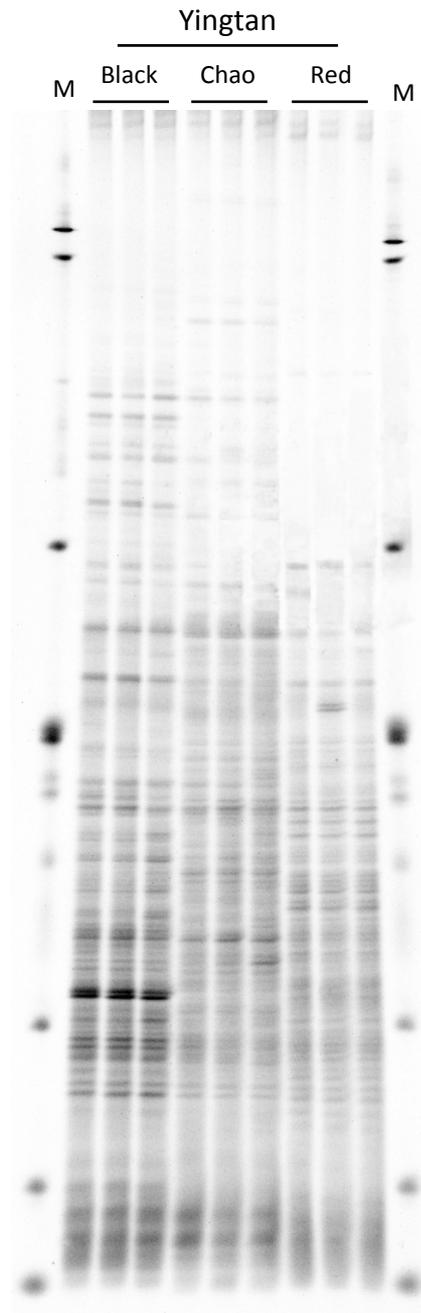
**Fig. S2.** Functional diversity of the bacterial community as expressed by the Simpson's and Shannon's indices calculated from the CLPP data. Results are means and standard errors of three replicates.



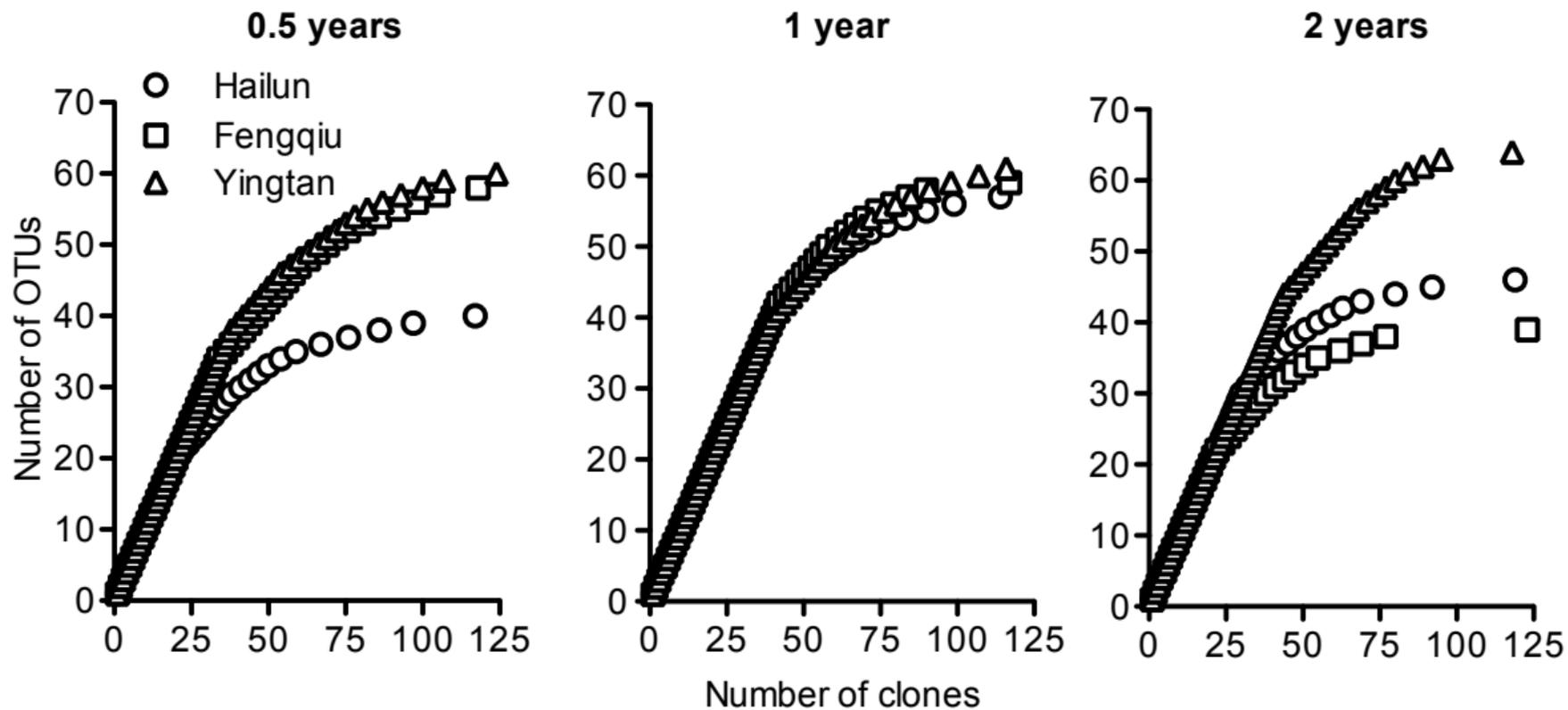
**Fig. S3.** Phylogenetic diversity of the bacterial community as expressed by the Simpson's and Shannon's indices calculated from the 16S rDNA DGGE data. Results are means and standard errors of three replicates. HL, Hailun; FQ, Fengqiu; YT, Yingtan.



**Fig. S4.** Partial dependency plots for the aggregated boosted tree (ABT) analysis of fungi/bacteria,  $G^+/G^-$  bacteria, total biomass and the community-level physiological profiles (AWCD) and DGGE in terms of the Shannon's and Simpson's indices. The associated importance scores are shown in Table 1.



**Figure S5.** A representative photograph of DGGE gel of microbial communities from the three bulk soils located in Yingtán. Soil samples were taken at the beginning of the straw decomposition and the analysis was performed with 3 replicates for each soil. M: DNA ladder N3233 from New England BioLabs (UK) Ltd.



**Fig. S6.** Rarefaction curve of the total number of unique restriction profiles (OTUs) against the total number of clones for each of the nine residue samples.

**Table S1.** Chemical properties of the soils at the beginning of the reciprocal soil transplantation (Time 0).

Soil <sup>a</sup>	pH	OM (g/kg)	TN (g/kg)	TP (g/kg)	TK (g/kg)	AP (mg/kg)	AK (mg/kg)
Black	6.06 ± 0.03	52.99 ± 0.35	2.47 ± 0.05	0.27 ± 0.00	13.62 ± 0.11	31.13 ± 1.15	150.1 ± 7.0
Chao	8.23 ± 0.02	8.35 ± 0.16	0.66 ± 0.01	0.18 ± 0.03	12.99 ± 0.22	11.80 ± 3.04	68.9 ± 0.1
Red	4.98 ± 0.01	8.28 ± 0.16	0.79 ± 0.13	0.07 ± 0.00	7.93 ± 0.10	27.46 ± 2.88	180.5 ± 2.7

<sup>a</sup>Data are means and standard errors of three replicates: OM, organic matter; TN, total nitrogen; TP, total phosphate; TK, total potassium; AP, available phosphate; AK, available potassium.

**Table S2.** Chemical properties of soils at the end of the maize straw decomposition experiment (2 years after the straw burial and 4.5 years after soil transplantation).

Soil <sup>a</sup>	Location	pH	OM (g/kg)	TN (g/kg)	TP (g/kg)	TK (g/kg)	AP (mg/kg)	AK (mg/kg)
<b>Black</b>	<b>Hailun</b>	6.25 ± 0.09	46.39 ± 0.45	1.79 ± 0.16	0.79 ± 0.01	18.69 ± 0.04	39.57 ± 2.19	201.7 ± 23.2
Black	Fengqiu	6.33 ± 0.03	43.85 ± 1.34	2.02 ± 0.10	0.85 ± 0.01	19.40 ± 0.39	45.93 ± 7.06	168.3 ± 8.0
Black	Yingtian	6.20 ± 0.01	41.34 ± 0.24	1.66 ± 0.02	0.80 ± 0.01	18.98 ± 0.17	33.85 ± 0.40	164.2 ± 0.8
Chao	Hailun	7.87 ± 0.05	9.49 ± 0.54	0.59 ± 0.06	0.58 ± 0.01	16.97 ± 0.22	8.74 ± 2.02	129.2 ± 9.3
<b>Chao</b>	<b>Fengqiu</b>	7.90 ± 0.08	8.72 ± 0.25	0.56 ± 0.01	0.73 ± 0.07	20.60 ± 2.20	7.31 ± 0.15	99.2 ± 4.4
Chao	Yingtian	8.05 ± 0.03	7.93 ± 0.41	0.50 ± 0.09	0.58 ± 0.03	18.32 ± 0.65	8.69 ± 0.49	71.7 ± 4.6
Red	Hailun	5.11 ± 0.01	9.59 ± 0.46	0.56 ± 0.01	0.32 ± 0.01	9.78 ± 0.17	12.93 ± 0.82	202.5 ± 5.2
Red	Fengqiu	5.75 ± 0.08	10.27 ± 0.08	0.66 ± 0.14	0.45 ± 0.01	10.38 ± 0.18	21.82 ± 1.28	208.3 ± 13.1
<b>Red</b>	<b>Yingtian</b>	5.28 ± 0.05	9.83 ± 0.08	0.58 ± 0.03	0.44 ± 0.00	9.73 ± 0.28	17.27 ± 0.40	109.2 ± 0.8

<sup>a</sup>Data are means and standard errors of three replicates: OM, organic matter; TN, total nitrogen; TP, total phosphate; TK, total potassium; AP, available phosphate; AK, available potassium.  
Data of soils in their original location are highlighted in bold format.

**Table S3.** Comparison of pH values between bulk soil and residual maize straw buried at the same site.

Soil <sup>a</sup>	Location	Soil	Maize residue
Black	Hailun	6.26 ± 0.10	7.24 ± 0.11
Black	Fengqiu	5.97 ± 0.05	7.29 ± 0.01
Black	Yingtian	6.50 ± 0.08	7.47 ± 0.03
Chao	Hailun	7.68 ± 0.14	7.44 ± 0.02
Chao	Fengqiu	7.70 ± 0.12	7.48 ± 0.07
Chao	Yingtian	7.24 ± 0.47	7.62 ± 0.01
Red	Hailun	5.80 ± 0.15	7.21 ± 0.06
Red	Fengqiu	6.54 ± 0.54	7.76 ± 0.07
Red	Yingtian	5.97 ± 0.22	7.26 ± 0.04

<sup>a</sup>Data are means and standard errors of three replicates and samples were taken at 1 year after the straw burial (i.e., ~3.5 years after soil transplantation).

**Table S4.** Climate conditions at the experimental sites during the period of straw decomposition experiment.

Location <sup>a</sup>	Time (year)	Temperature (°C)	Relative humidity (%)	Precipitation (mm)
Hailun	0.5	12.5	54.0	65.0
	1	3.5	53.7	36.9
	2	2.0	64.3	40.1
Fengqiu	0.5	20.6	74.3	50.1
	1	14.8	69.8	36.1
	2	14.1	70.3	32.6
Yingtian	0.5	24.2	67.0	120.3
	1	19.0	72.7	133.6
	2	16.3	71.6	83.3

<sup>a</sup>Data shown are monthly average during the whole period of straw decomposition.

**Table S5.** Multivariate analysis of the decomposition rate and microbial biomass (PLFA) of residual maize straws.

Results are three-way crossed ANOVA with climate conditions (Hailun, Fengqiu, Yingtian), soil types (Black soil, Chao soil, Red soil), decomposition time (0.5 year, 1 year, 2 year) as the fixed factors.

Source	Rate of straw decomposition						Microbial biomass (PLFA)		
	relative decrease of C/N per year			Residual loss of mass per year					
	DF	F ratio	Significance	DF	F ratio	Significance	DF	F ratio	Significance
location	2	50.731	0.000	2	92.943	0.000	2	16.317	0.000
soil	2	5.191	0.009	2	17.638	0.000	2	10.262	0.000
time	2	16.328	0.000	2	883.585	0.000	3	8.051	0.000
location*soil	4	1.510	0.212	4	2.166	0.085	4	3.313	0.016
location*time	4	13.051	0.000	4	13.908	0.000	6	5.186	0.000
soil*time	4	1.598	0.188	4	1.765	0.149	5	5.122	0.001
location*soil*time	8	1.041	0.417	8	2.499	0.022	9	2.697	0.010
Error	54			54			64		
Total	81			81			96		
Corrected total	80			80			95		

**Table S6.** Multivariate analysis of microbial biomass (PLFA).

Results are two-way crossed ANOVA with climate conditions (Hailun, Fengqiu, Yingtan), soil types (black soil, chao soil, red soil) as the fixed factors.

Source	0.5 year			1 year			2 year		
	DF	F ratio	Significance	DF	F ratio	Significance	DF	F ratio	Significance
location	2	4.017	0.036	2	1.938	0.173	2	3.528	0.051
soil	2	5.339	0.015	2	2.596	0.102	2	0.078	0.925
location*soil	4	1.440	0.261	4	3.534	0.027	4	2.000	0.138
Error	18			18			18		
Total	27			27			27		
Corrected total	26			26			26		

**Table S7.** Multivariate analysis of microbial functional diversity (CLPP).

Results are three-way crossed ANOVA with climate conditions (Hailun, Fengqiu, Yingtan), soil types (Black soil, Chao soil, Red soil), decomposition time (0.5 year, 1 year, 2 year) as the fixed factors.

Source	AWCD			Simpson's index			Shannon's index		
	DF	F ratio	Significance	DF	F ratio	Significance	DF	F ratio	Significance
location	2	20.224	0.000	2	7.133	0.002	2	6.605	0.003
soil	2	7.807	0.001	2	4.748	0.013	2	4.259	0.019
time	2	20.526	0.000	2	65.166	0.000	2	4.673	0.013
location*soil	4	5.647	0.001	4	3.752	0.009	4	4.098	0.006
location*time	4	9.513	0.000	4	3.577	0.012	4	6.794	0.000
soil*time	4	9.579	0.000	4	8.515	0.000	4	5.900	0.001
location*soil*time	8	5.506	0.000	8	4.727	0.000	8	4.106	0.001
Error	54			54			54		
Total	81			81			81		
Corrected total	80			80			80		

**Table S8.** Multivariate analysis of phylogenetic diversity (DGGE).

Results are three-way crossed ANOVA with climate conditions (Hailun, Fengqiu, Yingtan), soil types (Black soil, Chao soil, Red soil), decomposition time (0.5 year, 1 year, 2 year) as the fixed factors.

Source	Shannon's index			Simpson's index		
	DF	F ratio	Significance	DF	F ratio	Significance
location	2	34.192	0.000	2	16.204	0.000
soil	2	2.826	0.068	2	1.552	0.221
time	2	5.642	0.006	2	0.757	0.474
location*soil	4	0.901	0.470	4	0.979	0.427
location*time	4	14.804	0.000	4	3.420	0.015
soil*time	4	1.039	0.396	4	0.075	0.990
location*soil*time	8	4.047	0.001	8	1.977	0.067
Error	54			54		
Total	81			81		
Corrected total	80			80		

**Table S9.** Similarity of the straw-decomposing bacterial populations in Black soil located in three geographic regions as estimated by Sørensen similarity index of the RFLP data.

	HL-0.5	FQ-0.5	YT-0.5	HL-1	FQ-1	YT-1	HL-2	FQ-2	YT-2
HL-0.5	1								
FQ-0.5	0.408	1							
YT-0.5	0.320	0.339	1						
HL-1	<b>0.454</b>	0.383	0.410	1					
FQ-1	0.343	<b>0.444</b>	0.403	0.397	1				
YT-1	0.416	0.403	<b>0.446</b>	0.492	0.417	1			
HL-2	<b>0.269</b>	0.279	0.306	0.248	0.325	0.288	1		
FQ-2	0.329	<b>0.351</b>	0.303	0.313	0.265	0.380	0.252	1	
YT-2	0.327	0.377	<b>0.371</b>	0.347	0.341	0.448	0.219	0.330	1

Note: bacterial populations are designated by the location (HL, Hailun; FQ, Fengqiu; YT, Yingtian) and the time of sampling (0.5, 1 or 2 years) which are separated by a hyphen.