The Preliminary Research on Shifts in Maize Rhizosphere Soil Microbial Communities and Symbiotic Networks under Different Fertilizer Sources

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CK (without any treatments), NPK (with only mineral NPK fertilizer (360 kg N ha^{-1}, 120 kg P$_2$O$_5$ ha^{-1}, and 45 kg K$_2$O ha^{-1})), OF (with only organic fertilizer 9000 kg ha^{-1}), and NPK+OF (mineral NPK fertilizer with organic fertilizer).

Table S1. The differences in the bacterial and fungal community structures among samples. The results were analyzed using ANOSIM analysis. p-value < 0.05 (*) and p-value < 0.01 (**) represent the significant difference between the two treatments. CK indicates without any treatments, NPK indicates NPK fertilizer treatment, OF indicates organic fertilizer treatment, NPK+OF indicates treatment of NPK fertilizer combined with organic fertilizer.

Group	Bacteria		Fungi	
	R statistic	p-value	R statistic	p-value
CK-NPK	1.0000	0.107	1.0000	0.103
CK-OF	1.0000	0.101	0.6667	0.110
CK-NPK+OF	0.7778	0.104	1.0000	0.099
NPK-OF	1.0000	0.108	1.0000	0.106
NPK-NPK+OF	0.2222	0.318	1.0000	0.099
OF-NPK+OF	0.5185	0.187	1.0000	0.101
all	0.6975	0.001**	0.8704	0.001**

Table S2. The relative abundance of phyla and genera (top 10) for bacteria. The asterisk (*) follows the taxonomic name represents significant differences ($p < 0.05$) among the four treatments, respectively.

Classification level	Top 10 bacteria	Relative abundance			
		CK	NPK	OF	NPK+OF
Phylum	Proteobacteria*	0.2715	0.2224	0.2253	0.2066
	Acidobacteriota*	0.0917	0.1490	0.1348	0.1504
	Gemmatimonadota*	0.0682	0.1174	0.1116	0.1084
	Actinobacteriota	0.1055	0.0873	0.0949	0.1012
	Chloroflexi	0.1014	0.0917	0.0933	0.0834
	Planctomycetota	0.0758	0.0803	0.0835	0.0700
	Bacteroidota*	0.0712	0.0514	0.0614	0.0855
	Myxococcota	0.0502	0.0453	0.0440	0.0438
	Crenarchaeota	0.0288	0.0337	0.0300	0.0311
	Desulfobacterota*	0.0426	0.0276	0.0284	0.0243
Genus	*MND1* *	0.0246	0.0200	0.0227	0.0241
	RB41 *	0.0111	0.0208	0.0224	0.0219
	Pseudomonas	0.0124	0.0267	0.0107	0.0179
	Haliangium	0.0118	0.0129	0.0122	0.0119
	Citrifermentans *	0.0143	0.0100	0.0094	0.0076
	Metagenome *	0.0096	0.0095	0.0104	0.0078
	Subgroup_10 *	0.0081	0.0086	0.0077	0.0119
	Lysobacter *	0.0112	0.0076	0.0074	0.0085
	Sphingomonas *	0.0097	0.0080	0.0100	0.0062
	Defluviicoccus	0.0115	0.0063	0.0093	0.0048

Table S3. The relative abundance of phyla and genera (top 10) for bacteria. The asterisk (*) follows the taxonomic name represents significant differences ($p < 0.05$) among the four treatments, respectively.

Classification level	Top 10 fungi	Relative abundance			
		CK	NPK	OF	NPK+OF
Phylum	Ascomycota*	0.6118	0.5464	0.4849	0.6549
	Basidiomycota*	0.0335	0.1076	0.0735	0.0592
	Mortierellomycota	0.0692	0.0534	0.0429	0.0555
	Glomeromycota	0.0227	0.0086	0.0184	0.0212
	Chytridiomycota	0.0227	0.0177	0.0101	0.0113
	Blastocladiomycota	0.0001	0.0002	0.0008	0.0000
	Rozellomycota	0.0001	0.0003	0.0001	0.0003
	Olpidiomycota	0.0000	0.0002	0.0000	0.0004
	Kickxellomycota	0.0002	0.0000	0.0003	0.0001
	Zoopagomycota	0.0002	0.0001	0.0000	0.0001
Genus	*Botryotrichum*	0.2692	0.1328	0.1895	0.1950
	Mortierella	0.0691	0.0531	0.0428	0.0554
	*Fusarium**	0.0186	0.0724	0.0193	0.0138
	*Acremonium**	0.0821	0.0098	0.0086	0.0058
	Chaetomium	0.0187	0.0136	0.0139	0.0364
	*Clitocybe**	0.0036	0.0005	0.0252	0.0080
	*Neopaxillus**	0.0073	0.0284	0.0001	0.0003
	*Stachybotrys**	0.0058	0.0137	0.0081	0.0070
	Lophotrichus	0.0210	0.0018	0.0046	0.0009
	*Plectosphaerella**	0.0190	0.0023	0.0038	0.0008

Table S4. The results of Monte Carlo permutation test in the RDA in the vegan package of R. r^2 represents the coefficients of determination of soil properties that were related to OTUs. *$p<0.05$, **$p<0.01$, ***$p<0.001$. Soil organic matter (OM), total N (TN), total P (TP), total K (TK), dissolved organic C (AN), available P (AP), available K (AK).

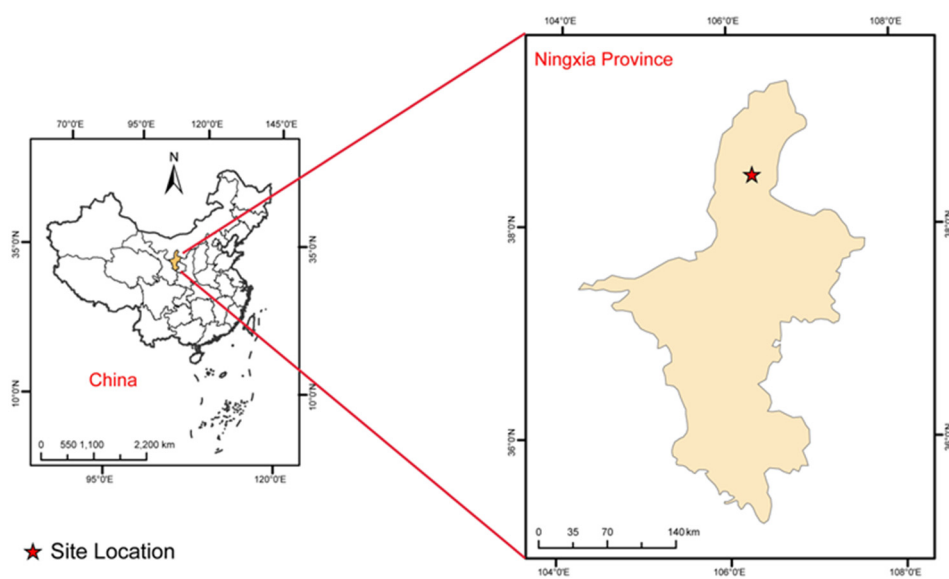| Soil properties	RDA1	RDA2	r^2	p-value
Bacteria				
Test: F= 1.4835, 0.004 **				
OM	0.76694	-0.64172	0.9196	0.001 ***
TN	0.49292	-0.87007	0.6166	0.011 *
TP	0.37449	-0.92723	0.2551	0.266
TK	-0.94021	0.34059	0.1833	0.411
AN	0.59796	-0.80153	0.9478	0.001 ***
AP	0.47998	-0.87728	0.8926	0.003 **
AK	-0.27171	-0.96238	0.7909	0.004 **
Fungi				
Test: F= 2.7082, 0.002 **				
OM	0.90045	-0.43495	0.5958	0.018 *
TN	0.65143	-0.75871	0.3091	0.184
TP	0.56482	-0.82521	0.4734	0.062
TK	-0.96626	-0.25758	0.0611	0.774
AN	0.73856	-0.67418	0.6279	0.020 *
AP	0.60415	-0.79687	0.6951	0.007 **
AK	-0.37200	-0.92823	0.5504	0.031 *

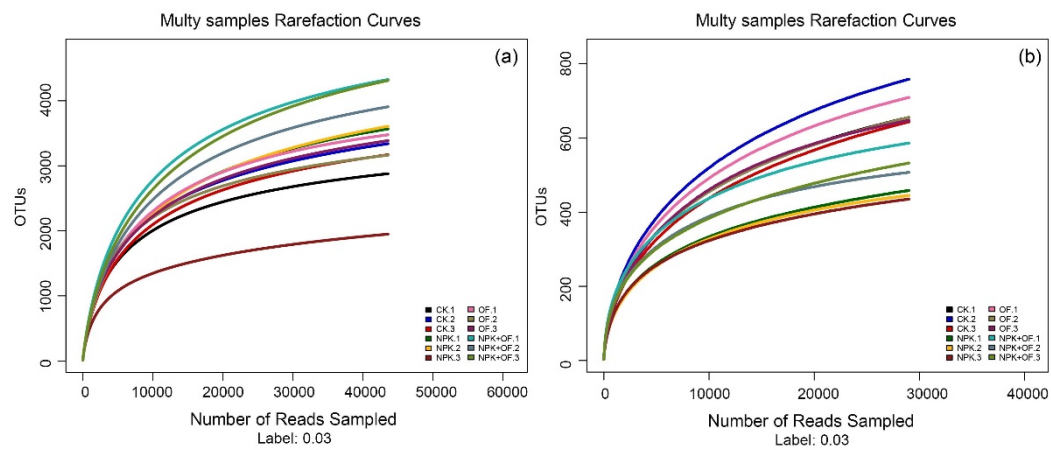**Figure S1.** The geographical location of the experimental field.

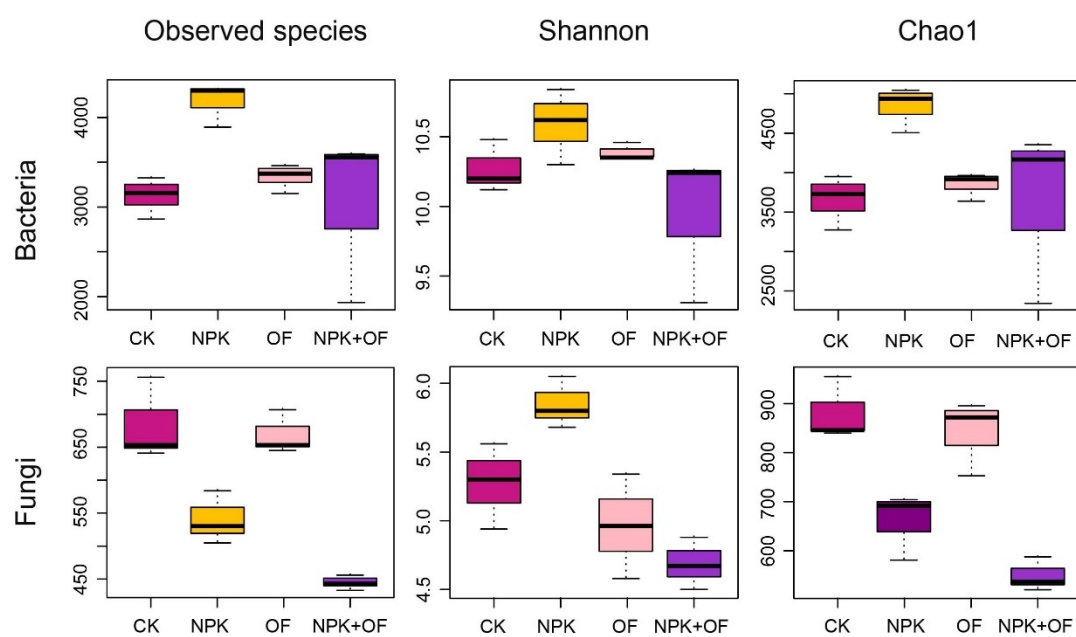**Figure S2.** Rarefaction curves of bacteria (a) and fungi (b).

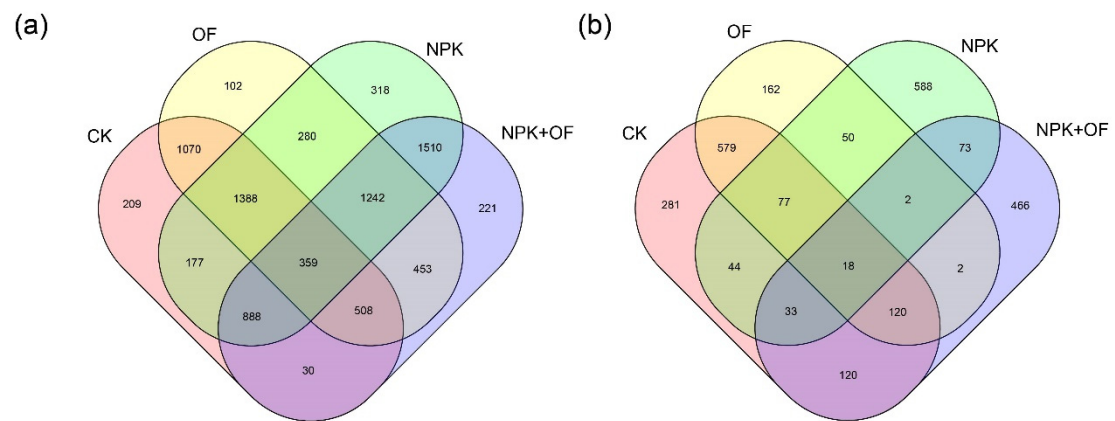**Figure S3.** Comparison of microbial diversity indices among all four treatments.

Figure S4. Shared and unique OTUs in all treatments for bacteria (a) and fungi (b).
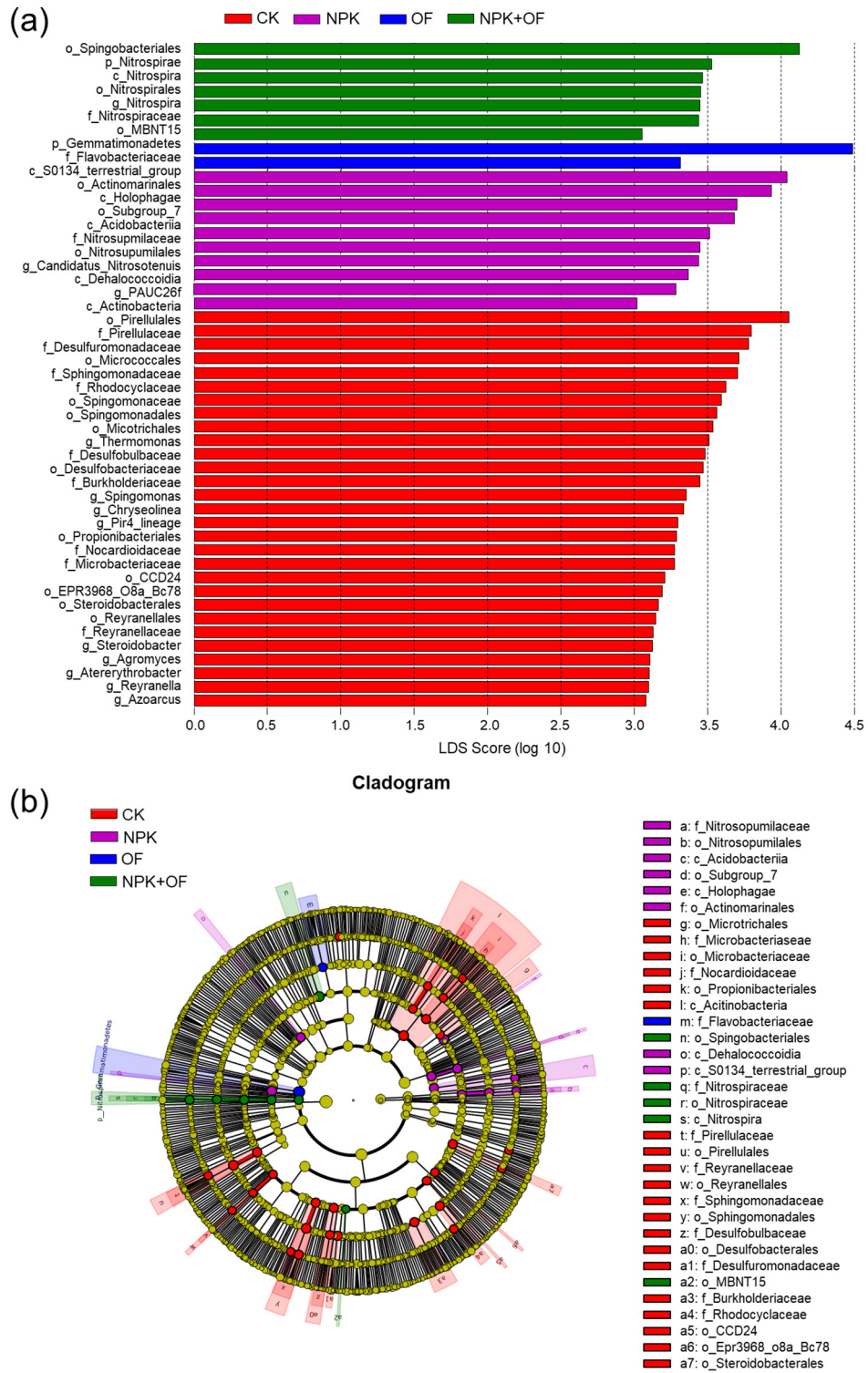
Figure S5. Results of LEfSe analysis showing bacterial taxa that significantly differed in the four treatments (a). Cladogram plotted from LEfSe analysis showing the significant differences (*p* <0.05) in relative abundance of bacterial taxon among four treatments (b).
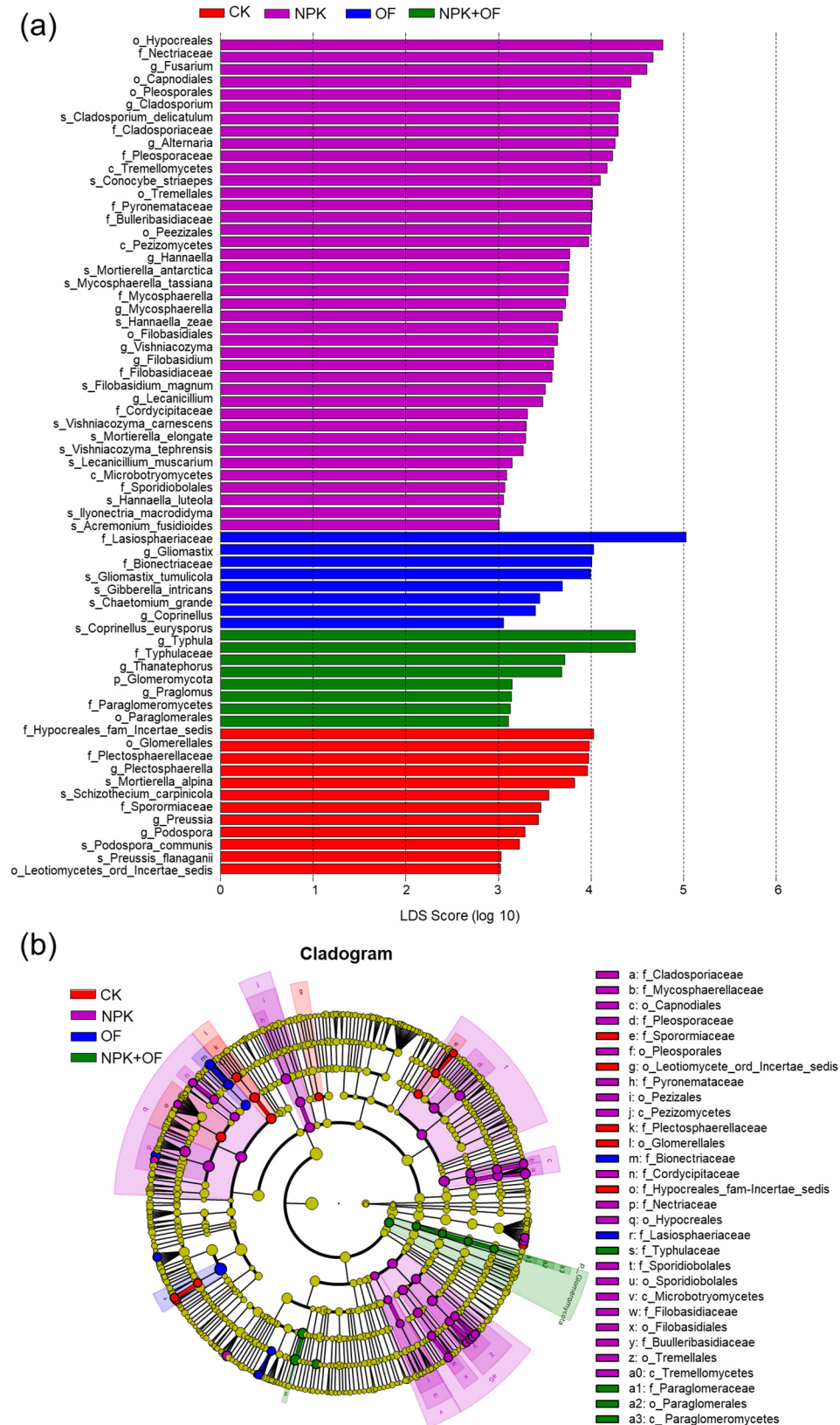
Figure S6. Results of LEfSe analysis showing fungal taxa that significantly differed in the four treatments (a). Cladogram plotted from LEfSe analysis showing the significant differences ($p < 0.05$) in relative abundance of fungal taxon among four treatments (b).