Supplemental Data

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Table S1 The effect of elevated O_3 and cultivars on the soil and plant properties analyzed by ANOVA.

Soil or plant variable	O_3		Cultivar		O_3 x Cultivar	
	F value	P value	F value	P value	F value	P value
pH	6.814	**0.0311**	0.033	0.8612	0.061	0.8117
Microbial biomass carbon	0.047	0.8340	1.687	0.2300	3.355	0.1040
Dissolved organic carbon	15.215	**0.0045**	7.189	**0.0279**	1.439	0.2646
Total carbon (TC)	1.054	0.3350	1.419	0.2680	1.419	0.2680
Total nitrogen (TN)	0.299	0.5990	1.166	0.3120	0.454	0.5190
C/N ratio (CNR)	0.142	0.7160	0.273	0.6150	0.486	0.5060
TC-grain	15.949	**0.0040**	0.108	0.75068	2.121	0.1834
TN-grain	0.267	0.6190	1.902	0.2050	2.484	0.1540
CNR-grain	0.498	0.5000	3.159	0.1130	1.933	0.2020
TC-straw	6.211	**0.0374**	3.169	0.1129	0.014	0.9085
TN-straw	3.691	0.091	0.923	0.3650	2.700	0.1390
CNR-straw	3.032	0.1200	0.430	0.5300	2.810	0.1320
Panicle length	0.617	0.4550	0.137	0.7210	3.238	0.1100
Grain weight	12.110	**0.0083**	7.672	**0.0243**	0.000	0.9958
Plant weight	1.645	0.2360	0.888	0.3740	0.023	0.8840
Straw-root weight	2.740	0.1360	0.383	0.5530	1.567	0.2460

Table S2 The number of detected genes and their α-diversity, and evenness of rhizosphere microbial communities from Yannong 19 and Yangmai 16 wheat cultivars at aO_3 and eO_3 conditions.

	C-Y19	C-Y16	O-Y19	O-Y16
No. of detected genes	1901±224.5	2120±369.2	1998±203.3	2061±170.8
Archaea	70.1±10.1	76.3±17.1	76.7±11.4	76.3±6.7
Bacteria	1498±298.2	1674±324.1	1573±280.7	1612±219.7
Fungi	101.7±35.1	111±25.9	88.7±13.6	100.7±21.0
Shannon index (H’)	7.26±0.235	7.35±0.197	7.24±0.149	7.32±0.132
Simpson's reciprocal index (1 / D)	1074±313.5	1177±199.5	985±155.9	1087±148.4
Simpson evenness	$0.718±0.148^a$	$0.686±0.241^a$	$0.614±0.147^c$	$0.652±0.173^b$

C-Y19: O_3-sensitive wheat cultivar at aO_3; C-Y16: O_3-relatively sensitive wheat cultivar at aO_3; O-Y19: O_3-sensitive wheat cultivar at eO_3; O-Y16: O_3-relatively sensitive at eO_3. The significance was tested by the Student t-test at $p < 0.05$.

Table S3 Significantly changed genes with O_3 and wheat cultivar analyzed by ANOVA.

Gene or enzyme	Functional process	O_3		Cultivar		O_3:Cultivar	
		F value	P value	F value	P value	F value	P value
SMR	Antibiotic resistance	0.3109	0.5773	7.1749	**0.0075**	2.1681	0.1412
fhs/FTHFS	Acetogenesis	7.8243	**0.0054**	0.0052	0.9426	0.0508	0.8218
Exoglucanase	C degradation	0.1699	0.6806	5.2054	**0.0236**	0.0972	0.7555
limEH		3.3607	0.0774	4.7885	**0.0372**	0.5504	0.4643
lip		0.0275	0.8685	0.0317	0.8591	3.9740	**0.0486**
aclB	C fixation	0.7601	0.3962	4.5182	**0.0495**	0.1080	0.7467
CODH		0.2341	0.6287	7.2823	**0.0073**	3.5637	0.0598
chrA	Metal resistance	0.0548	0.8150	5.5815	**0.0183**	1.3816	0.2401
corC		7.6562	**0.0071**	0.0619	0.8042	0.1088	0.7425
copA		0.2675	0.6051	6.3048	**0.0121**	1.6811	0.1949
nifH	Nitrogen fixation	0.4097	0.5222	4.0418	**0.0445**	2.5435	0.1109
pimF	Organic remediation	0.2207	0.6386	4.4700	**0.0347**	3.7838	0.0520
pobA		1.5717	0.2108	9.3416	**0.0024**	1.7187	0.1907
alkH		0.0026	0.9960	0.7324	0.3936	5.0641	**0.0260**
chnB		0.0377	0.8463	1.6780	0.1976	4.4957	**0.0360**
ALN		2.6850	0.1399	5.8526	**0.0419**	0.5333	0.4860
dsrA	Sulfite reduction	0.6436	0.4226	3.9130	**0.0482**	2.8688	0.0906

Table S4 Effects of elevated O_3 and wheat cultivars on the abundances of key functional genes involved in N cycling analyzed by ANOVA. Only genes with > 3 probes detected were shown.

Gene or enzyme	Functional process	O_3 (%)[a]		Cult. (%)[b]		p-value[c]		
		Y19	Y16	aO_3	eO_3	O_3	Cult.	O_3:cult.
nifH	Nitrogen fixation	18.58	-6.11	29.97	2.91	0.5222	**0.0445**	0.1109
amoA	Nitrification	-20.32	-26.84	36.34	25.20	0.3613	0.3654	0.7940
narG	Denitrification	20.73	-8.53	43.99	9.09	0.8238	0.1480	0.3845
nirK		5.86	-5.38	7.17	-4.21	0.9972	0.9164	0.6531
nirS		18.14	-14.20	46.49	6.39	0.9453	0.1635	0.3151
norB		25.64	-1.39	36.24	6.93	0.7196	0.4973	0.6773
nosZ		24.47	-22.88	40.47	-12.96	0.9093	0.7176	0.4008
nirA	Assimilatory N reduction	35.04	-22.75	44.51	-17.33	0.9709	0.7225	0.2538
nirB		8.87	-4.07	20.30	6.01	0.9405	0.6138	0.7957
nasA		56.40	3.30	54.19	1.83	0.3710	0.4064	0.4551
napA	Dissimilatory N reduction	-61.67	-33.00	-33.16	16.82	0.0989	0.5972	0.4336
nrfA		3.52	-18.71	36.10	6.87	0.6576	0.3831	0.5583
gdh	Ammonification	177.15	-42.73	-25.52	-84.61	0.8592	0.1662	0.6703
ureC		-7.94	-22.71	19.24	0.11	0.1637	0.4413	0.4462
hzo	Anammox	15.76	-8.44	38.80	9.78	0.9301	0.2789	0.5516

a: Percent change by elevated O_3 was calculated using the following formula: $(eO_3 - aO_3)*100/aO_3$, where aO_3 and eO_3 were the average signal intensities of genes detected by GeoChip 3.0 at ambient O_3 or elevated O_3, respectively. b: Percentage change by cultivar is calculated using the following formula: $(cult_{Y16} - cult_{Y19})*100/cult_{Y19}$ under aO_3 or eO_3 conditions; c: p values based on ANOVA analysis using the model: $Y \sim O_3 + cultivar + O_3$: cultivar.

Table S5 Effects of elevated O_3 and wheat cultivars on the abundances of key functional genes involved in S and P cycling analyzed by ANOVA. Only genes with > 3 probes detected were shown.

Gene or enzyme	Functional process	O_3 (%)[a]		Cult. (%)[b]		p-value[c]		
		Y19	Y16	aO_3	eO_3	O_3	Cult.	O_3:cult.
Phytase	Phosphorus utilization	-1.87	-27.46	74.29	28.85	0.9326	0.6415	0.5178
ppk		29.38	-11.05	56.08	7.31	0.8320	0.2531	0.4158
ppx		24.66	-15.65	43.90	-2.63	0.9417	0.1634	0.1056
aprA	Sulfur metabolism	15.86	0.43	24.22	7.68	0.7463	0.5136	0.7624
dsrA	Sulfite reduction	25.85	-6.69	38.03	2.34	0.4226	**0.0482**	0.0906
dsrB		9.86	-0.26	19.32	8.32	0.8365	0.5388	0.8259
sox	Sulfur oxidation	9.96	-3.01	0.69	-11.19	0.9118	0.8528	0.8354

a: Percent change by elevated O_3 was calculated using the following formula: $(eO_3 - aO_3)*100/aO_3$, where aO_3 and eO_3 were the average signal intensities of genes detected by GeoChip 3.0 at ambient O_3 or elevated O_3, respectively. b: Percentage change by cultivar is calculated using the following formula: $(cult_{Y16} - cult_{Y19})*100/cult_{Y19}$ under aO_3 or eO_3 conditions; c: p values based on ANOVA analysis using the model: $Y \sim O_3 + cultivar + O_3: cultivar$.

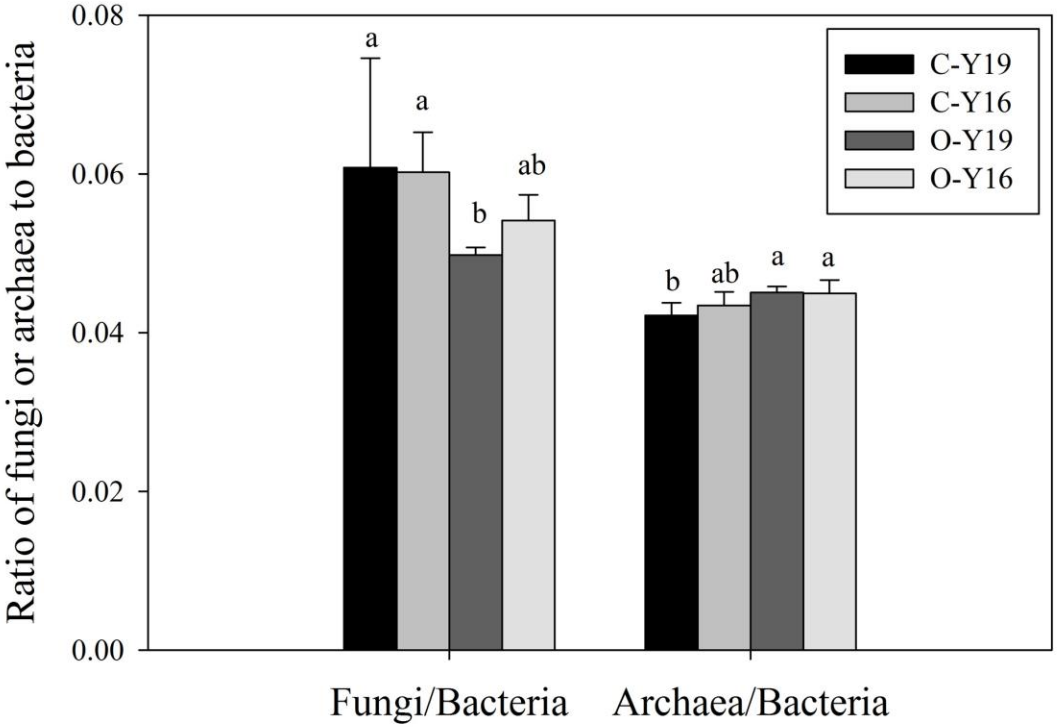

Fig. S1 The ratios of fungi to bacteria and archaea to bacteria based on the sum of the signal intensities detected by GeoChip 3.0. The significance was tested by the Student t-test at $p < 0.05$. from O_3-sensitive and O_3-tolerant wheat cultivars at aO_3 and eO_3 conditions. C-Y19: O_3-sensitive wheat cultivar at aO_3; C-Y16: O_3-relatively sensitive wheat cultivar at aO_3; O-Y19: O_3-sensitive wheat cultivar at eO_3; O-Y16: O_3-relatively sensitive at eO_3.

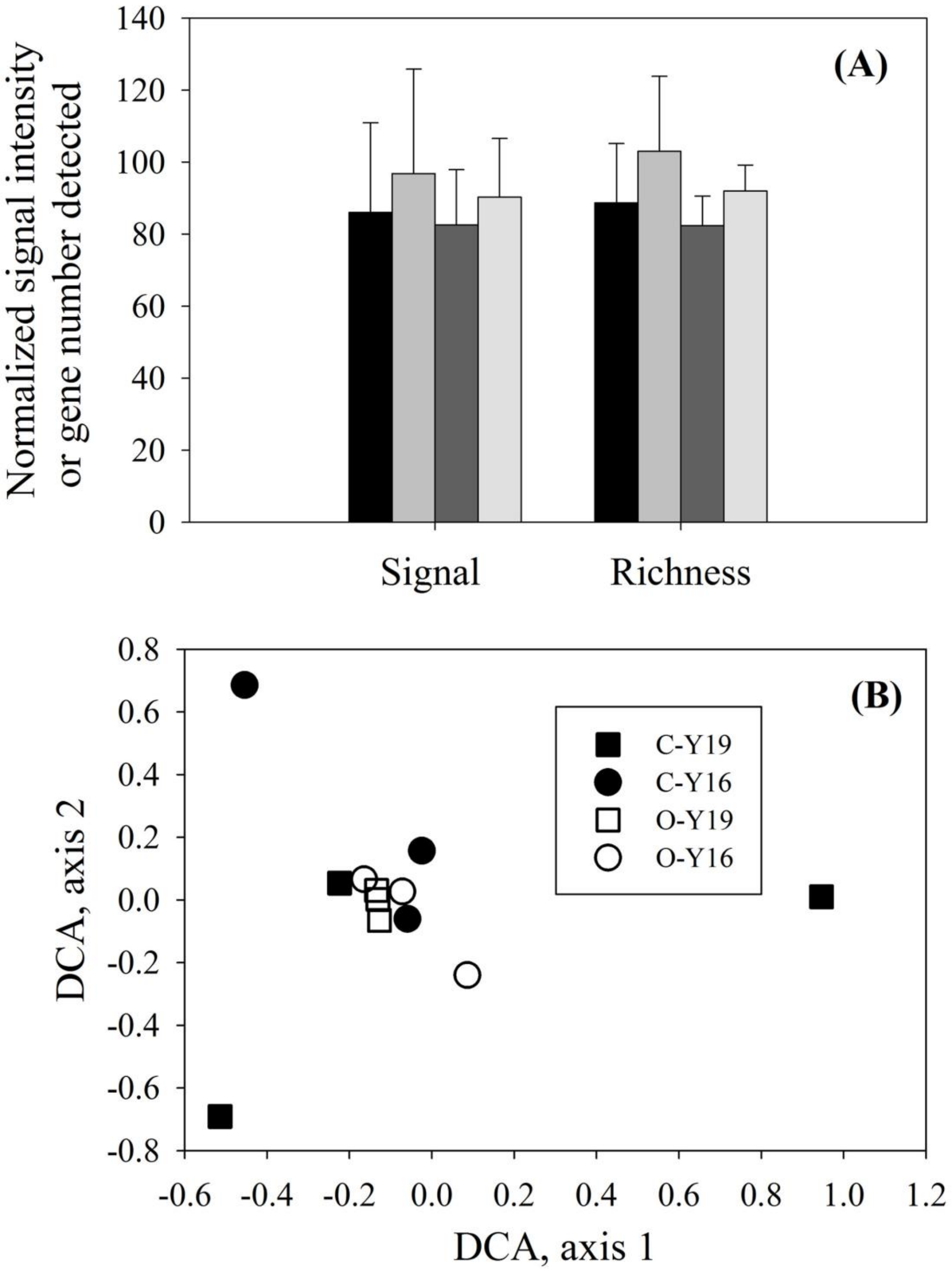

Fig. S2 The number and abundance of detected *gyrB* genes (A) and DCA analysis of phylogenetic structure (B) of microbial communities of Yannong Y19 and Yangmai 16 wheat cultivars under aO_3 and eO_3. C-Y19: O_3-sensitive wheat cultivar at aO_3; C-Y16: O_3-relatively sensitive wheat cultivar at aO_3; O-Y19: O_3-sensitive wheat cultivar at eO_3; O-Y16: O_3-relatively sensitive at eO_3.