

## Supplementary Material

**Resistance profiles of microbial communities in maize rhizospheres  
to the introduction of exogenous antibiotics to agricultural systems  
with high arsenical geological backgrounds**

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**Table S1:** Primers and standard curves for the qPCR process. Standard curves of qPCR assays obtained from 10-fold serially diluted plasmids which carrying the target sequence.

Target	Primer or Probe	Sequence (5' → 3')	Annealing Temp (°C)	Amplicon Size (bp)	Standard Curves	R <sup>2</sup>
<i>sul2</i>	<i>sul2</i> -F	TCCGGTGGAGGCCGGTATCTGG	60.0	190	$y=-3.8834x+38.366$	0.9991
	<i>sul2</i> -R	CGGGAATGCCATCTGCCTTGAG				
<i>tetC</i>	<i>tetC</i> -F	GCGGGATATCGTCCATTCCG	60.0	207	$y=-3.7367x+35.817$	0.9998
	<i>tetC</i> -R	GCGTAGAGGATCCACAGGACG				
<i>tetG</i>	<i>tetG</i> -F	CGTTCTTCTGGCTTTTGC	60.0	132	$y=-3.8788x+37.426$	0.999
	<i>tetG</i> -R	GCCCCTTGCTTGTTACTG				
<i>tetM</i>	<i>tetM</i> -F	GAGCAAACCTCAACAAAG	60.0	154	$y=-3.562x+35.52$	0.9988
	<i>tetM</i> -R	CAGCAGAGCACAAAGTCAC				
<i>tetW</i>	<i>tetW</i> -F	CTTATGGGCGGTGTCTGT	60.0	176	$y=-4.0929x+39.437$	0.9977
	<i>tetW</i> -R	GCGTTTTCAAGGTGGAGT				
<i>tetX</i>	<i>tetX</i> -F	TGACTTAGCCTTACCAAT	60.0	256	$y=-4.024x+38.926$	0.9994
	<i>tetX</i> -R	AAGAATAACCAAATCTGC				
<i>aioA</i>	<i>aioA</i> -F	CCACTTCTGCATCGTGGG	60.0	1114	$y=-3.31x+39.24$	0.9956
	<i>aioA</i> -R	TGTCGTTGCCCCAGATGA				
<i>arsM</i>	<i>arsM</i> -F	TCYCTCGGCTGCGGCAAYCCVAC	60.0	347	$y=-3.33x+37.50$	0.9991
	<i>arsM</i> -R	CGWCCGCCWGGCTTWAGYACCCG				
16S rRNA	16s-F	GGGTTGCGCTCGTTGC	60.0	60	$y=-3.1251x+32.581$	0.9978
	16s-R	ATGGYTGTCTGTCAGCTCGTG				
<i>intI1</i>	<i>intI1</i> -F	GGCTTCGTGATGCCTGCTT	60.0	146	$y=-3.4363x+33.588$	0.9986
	<i>intI1</i> -R	CATTCTGGCCGTGGTTCT				

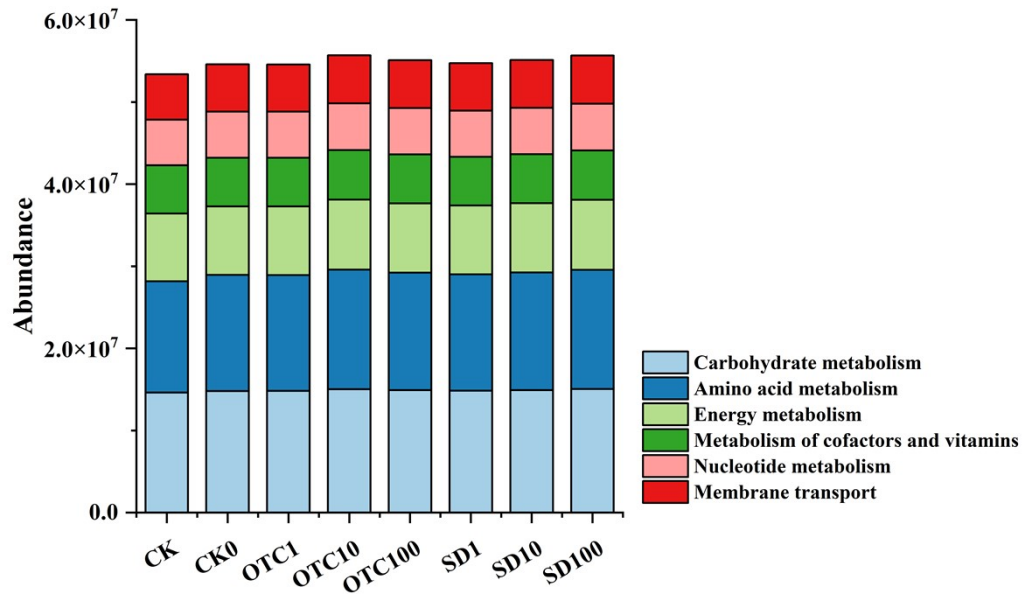


Figure S1. the functional composition at level 2 of Kyoto Encyclopedia of Genes and Genomes (KEGG) from all microcosms in soils of antibiotics exposure. CK0, without the application of manure and antibiotics; CK, manure with no antibiotics; OTC1, manure with OTC (1mg/kg); OTC10, manure with OTC (10mg/kg); OTC100, manure with OTC (100mg/kg); SD1, manure with SD (1mg/kg); SD10, manure with SD (10mg/kg); SD100, manure with SD (100mg/kg).

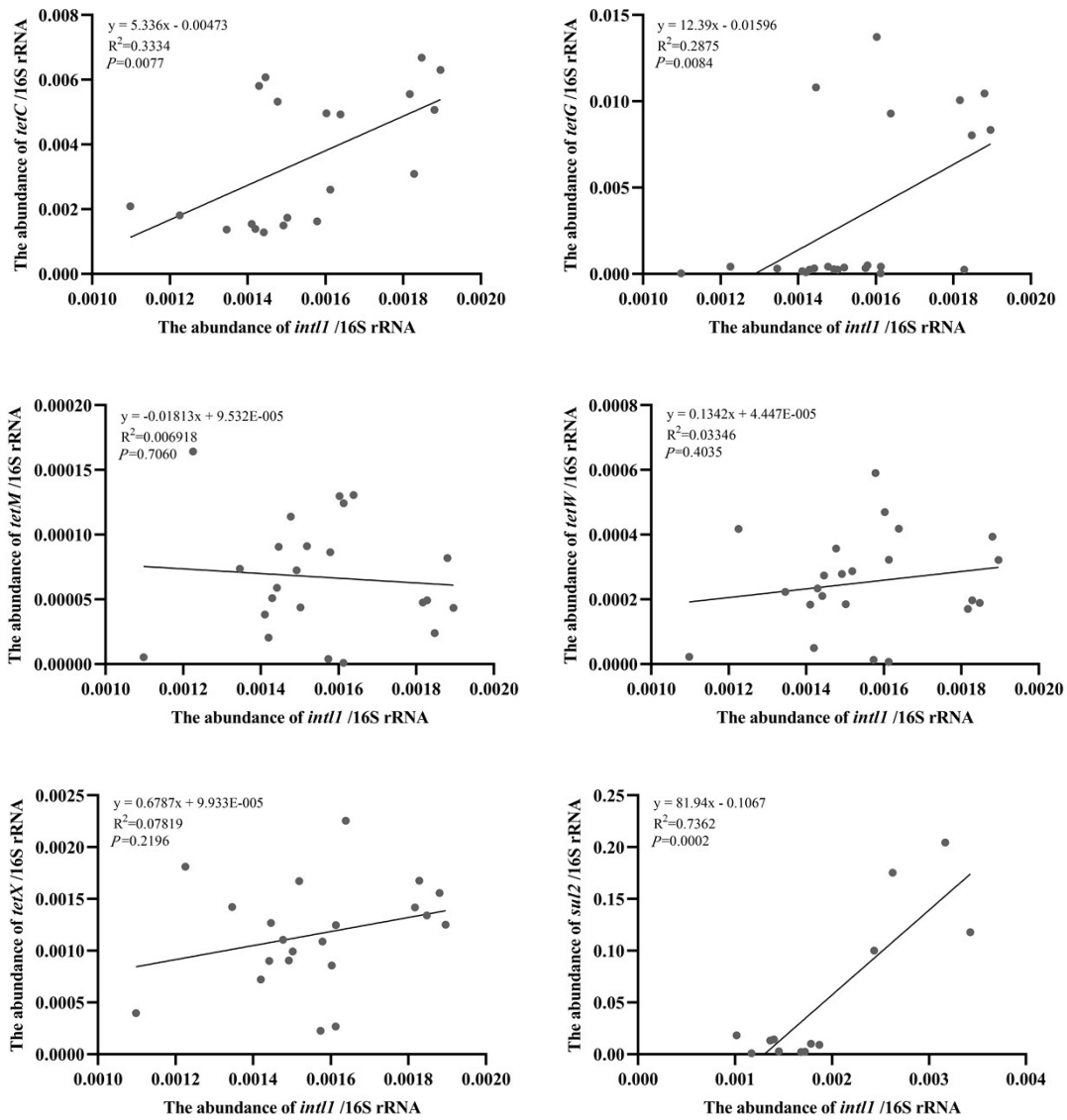


Figure S2 relationship between ARGs and *int1*. CK0, without the application of manure and antibiotics; CK, manure with no antibiotics; OTC1, manure with OTC (1mg/kg); OTC10, manure with OTC (10mg/kg); OTC100, manure with OTC (100mg/kg); SD1, manure with SD (1mg/kg); SD10, manure with SD (10mg/kg); SD100, manure with SD (100mg/kg).

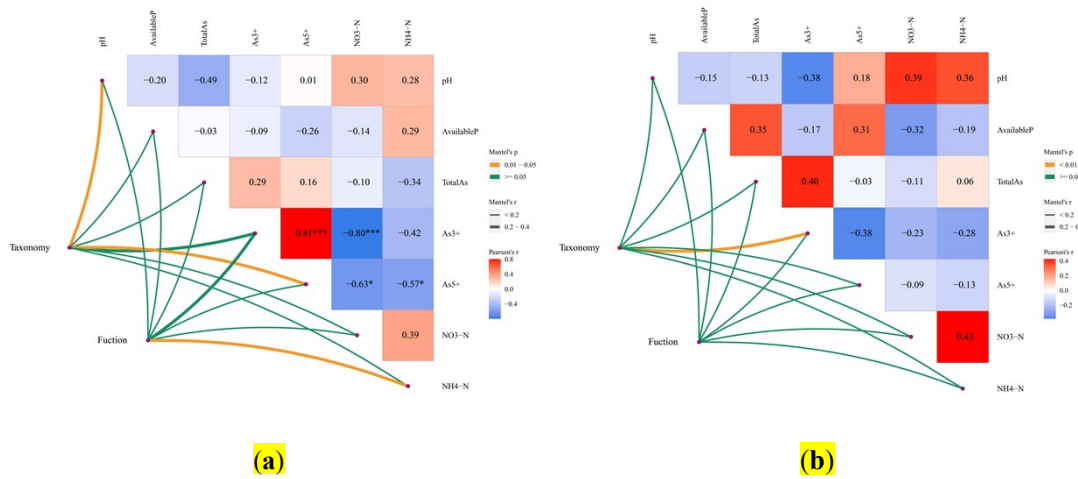


Figure S3. Environmental drivers of microbial community composition in antibiotic treatment groups: (a for OTC groups, b for SD groups) pairwise comparisons of environmental factors were shown, with color gradients representing Spearman's correlation coefficients. Taxonomic (based on genus-level bacteria) and functional (based on ARGs, AMGs, *intl1*) community composition was related to each environmental factor by Mantel tests. Edge width denotes the Mantel's  $r$  statistic for the corresponding distance correlations, and edge color represents the statistical significance.