Supplementary Information

Supplementary materials and methods

Qualitative PCR and quantitative real-time PCR

According to Liang et al. (2017), all qualitative PCR tests were performed in a 50 μ L reaction system with an ABI 2720 Thermocycler (ABI-2720, Applied Biosystems, USA). The specific components of the reaction system are shown in Table S3. The specific primers designed are presented in Table S4. The specificity tested was for each of them. The thermocycler was programmed to denature at 94°C for 4 min, followed by 35 cycles of 30 s at 94°C, 30 s at different annealing temperatures and 30 s at 72°C, with a final extension step for 7 min at 72°C. The annealing temperature varied depending on the target gene: 55°C for *tet*W, *tet*M, *tet*O, *tet*Q, *tet*H, *gyr*A, and *qnr*A and 60°C for *sul*1, *sul*2, *erm*F, and 16S rRNA. To ensure reproducibility, triplicate PCRs were performed for each sample. Sterile water was used as the negative control in every run.

PCR products were excised and purified using a TIANGEN Universal DNA Purification Kit (Tiangen, China) according to the manufacturer's instructions. The purified PCR products were ligated into a pEASY-T3 Cloning Kit (TransGen) and then transformed into Trans1-T1 Phage Resistant Chemically Competent Cells (TransGen), as described in the manufacturer's manual. Plasmids carrying the target genes were extracted using a TIAN Pure Midi Plasmid Kit (Tiangen) and used as standards for real-time fluorescent quantitative PCR. The CFX96 real-time PCR System (CFX96, Bio-Rad, USA) was used for quantitative real-time PCR analysis of target ARGs and 16S rRNA. The real-time PCR primers for ARGs and the 16S rRNA gene were the same as those used in the qualitative PCR (Table S4). Each reaction was performed in a 20 µL system, including 10 µL SYBR®Premix Ex TaqTM (TaKaRa, Japan).

GeoChip hybridization to detect ARGs

The DNA extracted from the samples was labeled fluorescently, purified, and resuspended in 50 μ L of hybridization solution containing 45% formamide, 5 × SSC, 0.1% SDS, 0.1 mg/mL salmon sperm DNA, and 2 μ L of common oligonucleotide reference standard (0.1 pmol/ μ L) (Liang et al., 2010). The labeled DNA was hybridized with GeoChip 5.0 on a MAUI® Hybridization System (BioMicro Systems, UT, USA). A ScanArray 5000 Microarray Analysis System (PerkinElmer, Wellesley, USA) was used to scan microarrays at 95% laser power and 68% photomultiplier tube gain. The scanned images were quantified using ImaGene® version 6.0 (BioDiscovery, Inc., Los Angeles, USA) to extract the digital signal at each spot and obtain the original data. The spots with signal-to-noise ratios lower than 2.0 were removed (Zhou et al., 2015). And those data were processed in the Microarray Data Manager system on the Institute for Environmental Genomics website.

1 Supplementary Tables

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Sites	Latitude	Longitudo	Climate zone	MAT	MAP	Soil type ^{a)}		
		Longitude	Climate zone		(mm)	Soil subgroup	Soil parent suborder	
TZ	32.40°N	119.58°E	Subtropical monsoon climate	14.7	1037.7	Typic Fe-accumuli-Stagnic Anthrosols	Udic Cambosols	
MG	32.32°N	118.11°E	Subtropical to warm temperate climate	15.0	934.1	Albic Fe-laechi-Stagnic Anthrosols	Udic Cambosols	
DY	32.00°N	119.27°E	Subtropical monsoon climate	15.8	1050.0	Albic Fe-laechi-Stagnic Anthrosols	Udic Cambosols	
CZ	31.60°N	119.48°E	Subtropical monsoon climate	15.4	1066.0	Typic Fe-accumuli-Stagnic Anthrosols	Udic Cambosols	
LA	32.01°N	116.41°E	Subtropical humid monsoon climate	15.1	1250.0	Typic Hapli-Stagnic Anthrosols	Udic Argosols	
SH	31.37°N	121.27°E	Subtropical monsoon climate	17.6	1173.4	Typic Fe-accumuli-Stagnic Anthrosols	Alluvic Primosols	
JX	30.79°N	120.73°E	Subtropical monsoon climate	15.9	1168.6	Typic Fe-accumuli-Stagnic Anthrosols	Alluvic Primosols	
YW	29.20°N	119.55°E	Subtropical monsoon climate	17.0	1350.0	Typic Hapli-Stagnic Anthrosols	Udic Ferralosols	
SG	28.14°N	115.00°E	Subtropical monsoon climate	17.6	1718.4	Typic Hapli-Stagnic Anthrosols	Udic Ferralosols	
ZS	28.01°N	115.54°E	Subtropical monsoon climate	17.7	1710.7	Typic Hapli-Stagnic Anthrosols	Udic Ferralosols	
FZ	26.00°N	119.27°E	Subtropical maritime monsoon climate	22.5	1500.0	Typic Hapli-Stagnic Anthrosols	Alluvic Primosols	

3 Table S1 Locations, climate zone, mean annual temperature, mean annual precipitation, and soil type of the sampling regions

4 Notes: TZ: Taizhou; MG: Mingguang; DY: Danyang; CZ: Changzhou; LA: Lu'an; SH: Shanghai; JX: Jiaxing; YW: Yiwu; SG: Shanggao; ZS: Zhangshu; FZ: Fuzhou. MAT: mean annual

5 temperature; MAP: mean annual precipitation. a) Soil type was classified according to Chinese Soil Taxonomy

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10 Table S2 The instrument detection limit (LOD) of four antibiotics in soils, quantitative limit (LOQ), method detection limit (MQL),

11 and the standard recoveries

Antibiotics	LOD (mg/L)	LOD LOQ (mg/L) (mg/L)		MQL in manure (mg/kg)	Recovery (%)	
Tetracyclines	0.029–0.086	0.090-0.260	0.750-1.700	0.030-0.180	63.200-89.300	
Sulfonamides	0.008-0.069	0.023-0.208	0.200-0.800	0.030-0.090	58.700-78.800	
Quinolones	0.002-0.046	0.007-0.138	0.450-1.900	0.060-0.150	68.100-83.900	
Macrolides	0.017-0.031	0.052-0.095	1.300-2.700	0.010-0.050	81.200–97.600	

17	Table S3	Reaction system for quantitative real time polymerase chain reaction (qPCR)

Component	Dosage (µ L)	
2×PCR Buffer	5	
Mg^{2+} (25 mM)	3	
dNTP (each 10 mM)	1	
forwarding primers (10-20 pmol)	2	
reverse primers (10–20 pmol)	2	
Taq DNA Polymerase (5 U/µL)	1	
template	1	
ddH ₂ O	35	
total system	50	

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Table S4	Primers used in this study for quantitative real time polymerase chain reaction (qPCR)								
Genes	Sequences (5'→3')	Amplicon size (bp)	Annealing temperature (°C)	Reference					
tetW	FW_GAGAGCCTGCTATATGCCAGC RV_GGGCGTATCCACAATGTTAAC	168	55	Aminov et al., 2001					
tetM	FW_ACAGAAAGCTTATTATATAAC RV_TGGCGTGTCTATGATGTTCAC	171	55	Aminov et al., 2001					
tetO	FW_ACGGARAGTTTATTGTATACC RV_TGGCGTATCTATAATGTTGAC	171	55	Aminov et al., 2001					
tetQ	FW_AGAATCTGCTGTTTGCCAGTG RV_CGGAGTGTCAATGATATTGCA	169	55	Aminov et al., 2001					
<i>tet</i> H	FW_CAACCCATTACGGTGTGCTA RV AAGTGTGGTTGAGAATGCCA	164	55	Tamminen et al., 2011					
sul1	FW_CGCACCGGAAACATCGCTGCAC RV TGAAGTTCCGCCGCAAGGCTCG	163	60	Pei et al., 2007					
sul2	FW_TCCGGTGGAGGCCGGTATCTGG RV_CGGGAATGCCATCTGCCTTGAG	191	60	Pei et al., 2007					
gyrA	FW_ACGTACTAGGCAATGACTGG RV_AGAAGTCGCCGTCGATAGAAC	192	55	Everett et al., 1996					
qnrA	FW_AGGATTTCTCACGCCAGGATT RV_CGCTTTCAATGAAACTGCA	124	55	Cummings et al., 2011					
<i>erm</i> F	FW_CGACACAGCTTTGGTTGAAC	309	60	Chen et al., 2007					
16S rDNA	515FW_GTGCCAGCMGCCGCGG 806RV_GGACTACHVGGGTWTCTA-AT	292	60	Caporaso et al., 2011					

25 Table S4 Primers used in this study for quantitative real time polymerase chain reaction (qPCR)

26 Notes: FW: forward; RV: reverse

28 Table S5 Paddy soil physicochemical properties in 11 rice planting regions with inorganic-fertilization and manure-fertilization

	NH4 ⁺ -N (mg/kg)			TP (g/kg)			AP (mg/kg)			TK (g/kg)		
Site	Inorganic-	Manure-		Inorganic-	Manure-		Inorganic-	Manure-		Inorganic-	Manure-	
	amended	amended	р	amended	amended	р	amended	amended	р	amended	amended	р
	soils	soils		soils	soils		soils	soils		soils	soils	
TZ	28.1	20.9	< 0.001	0.9	0.7	< 0.001	0.6	0.4	0.062	14.6	14.6	0.974
MG	56.3	30.3	0.157	1.2	0.4	< 0.001	1.5	2.2	0.187	15.3	18.7	0.004
DY	70.0	48.9	0.007	0.9	0.4	< 0.001	1.5	0.5	< 0.001	14.8	14.7	0.603
CZ	47.8	31.2	0.004	0.4	0.7	< 0.001	0.5	0.8	< 0.001	12.3	17.1	< 0.001
LA	48.5	26.6	0.003	0.4	0.8	< 0.001	0.6	3.7	< 0.001	14.8	11.8	< 0.001
SH	36.3	36.6	< 0.001	0.8	2.5	< 0.001	0.3	8.0	< 0.001	17.6	17.4	0.405
JX	51.5	41.7	0.130	0.7	2.2	< 0.001	0.8	11.7	< 0.001	17.3	18.0	0.005
YW	60.5	83.3	0.386	0.4	1.9	< 0.001	0.4	6.2	< 0.001	16.5	20.9	< 0.001
SG	20.9	35.4	0.002	0.9	0.6	< 0.001	3.0	1.8	0.018	18.9	16.1	< 0.001
ZS	71.4	36.6	< 0.001	1.0	1.5	0.074	1.4	8.2	0.008	8.0	13.2	< 0.001
FZ	15.9	22.8	0.014	1.5	1.6	0.425	3.3	7.9	< 0.001	44.5	52.9	< 0.001

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Notes: TZ: Taizhou; MG: Mingguang; DY: Danyang; CZ: Changzhou; LA: Lu'an; SH: Shanghai; JX: Jiaxing; YW: Yiwu; SG: Shanggao; ZS: Zhangshu; FZ: Fuzhou. TOC: total organic carbon; TN: total 31 nitrogen; TP: total phosphorus; AP: available phosphorus; TK: total potassium. The significant differences (p < 0.05) between inorganic-amended (n = 143) and manure-amended soils (n = 143) are colored in red

33 Supplementary Figures

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Fig. S1 'L-shaped' sampling layout. A 50 m \times 50 m rectangular plot was established at each sampling site. Thirteen subplots were placed apart along the transect, resembling an "L", with distances between the adjacent subplots of 0, 1, 1, 3, 6, 14, and 25 m



39 Fig. S2 The absolute abundance of β-lactam resistance genes in inorganic-amended and manure-amended paddy soils in 3

40 rice planting regions in eastern China. CZ: Changzhou; SG: Shanggao; FZ: Fuzhou. Different letters above the bars indicate the

41 difference in the sum abundance of antibiotic resistance genes between inorganic-amended and manure-amended paddy soils at p < 0.05



Fig. S3 Pearson correlations between the antibiotic resistance genes and the metals and others environmental variables in inorganic-amended paddy soils. The color points indicate the significant correlation coefficient (p < 0.05; bluer indicates stronger negative correlation and redder indicates stronger positive correlation). MC: moisture content; MAT: mean annual temperature; SO₄²⁻: sulfate; TOC: total organic carbon; TN: total nitrogen; NO₃⁻: nitrate nitrogen; NH₄⁺: ammonium nitrogen; TON: total organic nitrogen; TP: total phosphorus; AP: available phosphorus; TK: total potassium

References

Aminov R I, Garrigues-Jeanjean N, Mackie R I (2001). Molecular ecology of tetracycline resistance: development and validation of primers for detection of tetracycline resistance genes encoding ribosomal protection proteins. Applied and Environmental Microbiology, 67(1): 22–32

Caporaso J G, Kuczynski J, Stombaugh J, Bittinger K, Bushman F D, Costello E K, Fierer N, Peña A G, Goodrich J K, Gordon J I, Huttley G A, Kelley S T, Knights D, Koenig J E, Ley R E, Lozupone C A, McDonald D, Muegge B D, Pirrung M, Reeder J, Sevinsky J R, Turnbaugh P J, Walters W A, Widmann J, Yatsunenko T, Zaneveld J, Knight R (2010). QIIME allows analysis of high-throughput community sequencing data. Nature Methods, 7(5): 335–336

Chen J, Yu Z, Michel F C Jr, Wittum T, Morrison M (2007). Development and application of real-time PCR assays for quantification of erm genes conferring resistance to macrolides-lincosamides-streptogramin B in livestock manure and manure management systems. Applied and Environmental Microbiology, 73(14): 4407–4416

Cummings D E, Archer K F, Arriola D J, Baker P A, Faucett K G, Laroya J B, Pfeil K L, Ryan C R, Ryan K R U, Zuill D E (2011). Broad dissemination of plasmid-mediated quinolone resistance genes in sediments of two urban coastal wetlands. Environmental Science & Technology, 45(2): 447–454

Everett M J, Jin Y F, Ricci V, Piddock L J (1996). Contributions of individual mechanisms to fluoroquinolone resistance in 36 Escherichia coli strains isolated from humans and animals. Antimicrobial Agents and Chemotherapy, 40(10): 2380–2386

Liang Y, He Z, Wu L, Deng Y, Li G, Zhou J (2010). Development of a common oligonucleotide reference standard for microarray data normalization and comparison across different microbial communities. Applied and Environmental Microbiology, 76(4): 1088–1094

Liang Y, Pei M, Wang D, Cao S, Xiao X, Sun B (2017). Improvement of soil ecosystem multifunctionality by dissipating Manure-Induced antibiotics and resistance genes. Environmental Science & Technology, 51(9): 4988–4998

Pei R, Cha J, Carlson K H, Pruden A (2007). Response of antibiotic resistance genes (ARG) to biological treatment in dairy lagoon water. Environmental Science & Technology, 41(14): 5108–5113

Tamminen M, Karkman A, Lõhmus A, Muziasari W I, Takasu H, Wada S, Suzuki S, Virta M (2011). Tetracycline resistance genes persist at aquaculture farms in the absence of selection pressure. Environmental Science & Technology, 45(2): 386–391

Zhou J, He Z, Yang Y, Deng Y, Tringe S G, Alvarez-Cohen L (2015). High-throughput metagenomic technologies for complex microbial community analysis: open and closed formats. mBio, 6(1): e2214–e2288