

Supplementary Information for

Unraveling the Sources and Influencing Mechanism of Soil Antibiotic Resistance Genes in Urban

Micro Green Spaces

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10 pages, 4 tables and 2 figures.

Table S1. List of characteristics for 21 micro green spaces

Number	Latitude and Longitude	Urban Type
1	117.19,39.10	intra-urban
2	117.28,39.16	intra-urban
3	117.27,39.11	intra-urban
4	117.17,39.12	intra-urban
5	117.15,39.13	intra-urban
6	117.15,39.09	intra-urban
7	117.25,39.10	intra-urban
8	117.22,39.08	intra-urban
9	117.19,39.17	intra-urban
10	117.16,39.16	intra-urban
11	117.14,39.17	intra-urban
12	117.20,39.13	intra-urban
13	117.33,39.10	intra-urban
14	117.29,39.14	intra-urban
15	117.23,39.21	intra-urban
16	117.19,39.19	intra-urban
17	117.51,38.73	extra-urban
18	117.14,38.88	extra-urban
19	116.95,38.91	extra-urban
20	117.02,39.15	extra-urban
21	117.03,39.62	extra-urban

Table S2. List of sample collection quantity

Site Number	Soil Samples	Trash Samples	Water Samples	Feces Samples
1	3	2	2	2
2	3	2	2	2
3	3	2	2	2
4	3	2	2	2
5	3	2	2	2
6	3	2	2	2
7	3	2	2	2
8	3	2	2	2
9	3	2	2	2
10	3	2	2	2
11	3	2	2	2
12	3	2	2	2
13	3	2	2	2
14	3	2	2	2
15	3	2	2	2
16	3	2	2	2
17	3	2	2	2
18	3	2	2	2
19	3	2	2	2
20	3	2	2	2
21	3	2	2	2

Table S3. Primer and classification list for 48 target ARGs.

Number	ARGs	ForwardPrimer	ReversePrimer	Class	Mechanism
1	16S	GGGTTGCGCTCGTTGC	ATGGYTGTCGTCAGCTCGTG	0	0
2	aad A1	AGCTAAGCGCGAACTGCAAT	TGGCTCGAAGATACCTGCAA	Aminoglycoside	antibiotic deactivate
3	aadA2-1	ACGGCTCCGCAGTGGAT	GGCCACAGTAACCAACAAATCA	Aminoglycoside	antibiotic deactivate
4	blaPSE	TTGTGACCTATTCCCCTGTAATAGAA	TGCGAAGCACGCATCATC	Beta_Lactamase	antibiotic deactivate
5	blaVIM	GCACTTCTCGCGGAGATTG	CGACGGTGATGCGTACGTT	Beta_Lactamase	antibiotic deactivate
6	cfr	GCAAAATTCAGAGCAAGTTACGAA	AAAATGACTCCCAACCTGCTTTAT	Others	antibiotic deactivate
7	intI-1	CGAACGAGTGGCGGAGGGTG	TACCCGAGAGCTTGGCACCCA	Integron	Integrase
8	dfrA1	GGAATGGCCCTGATATTCCA	AGTCTTGCGTCCAACCAACAG	Sulfonamide	antibiotic deactivate
9	erm(F)	CAGCTTTGGTTGAACATTTACGAA	AAATTCCTAAAATCACAACCGACAA	MLSB	cellular protection
10	ermT	GTTCACTAGCACTATTTTAAATGACAGAAGT	GAAGGGTGTCTTTTAAATACAATTAACGA	MLSB	cellular protection
11	cIntI-1	GGCATCCAAGCAGCAAG	AAGCAGACTTGACCTGA	Integron	Integrase

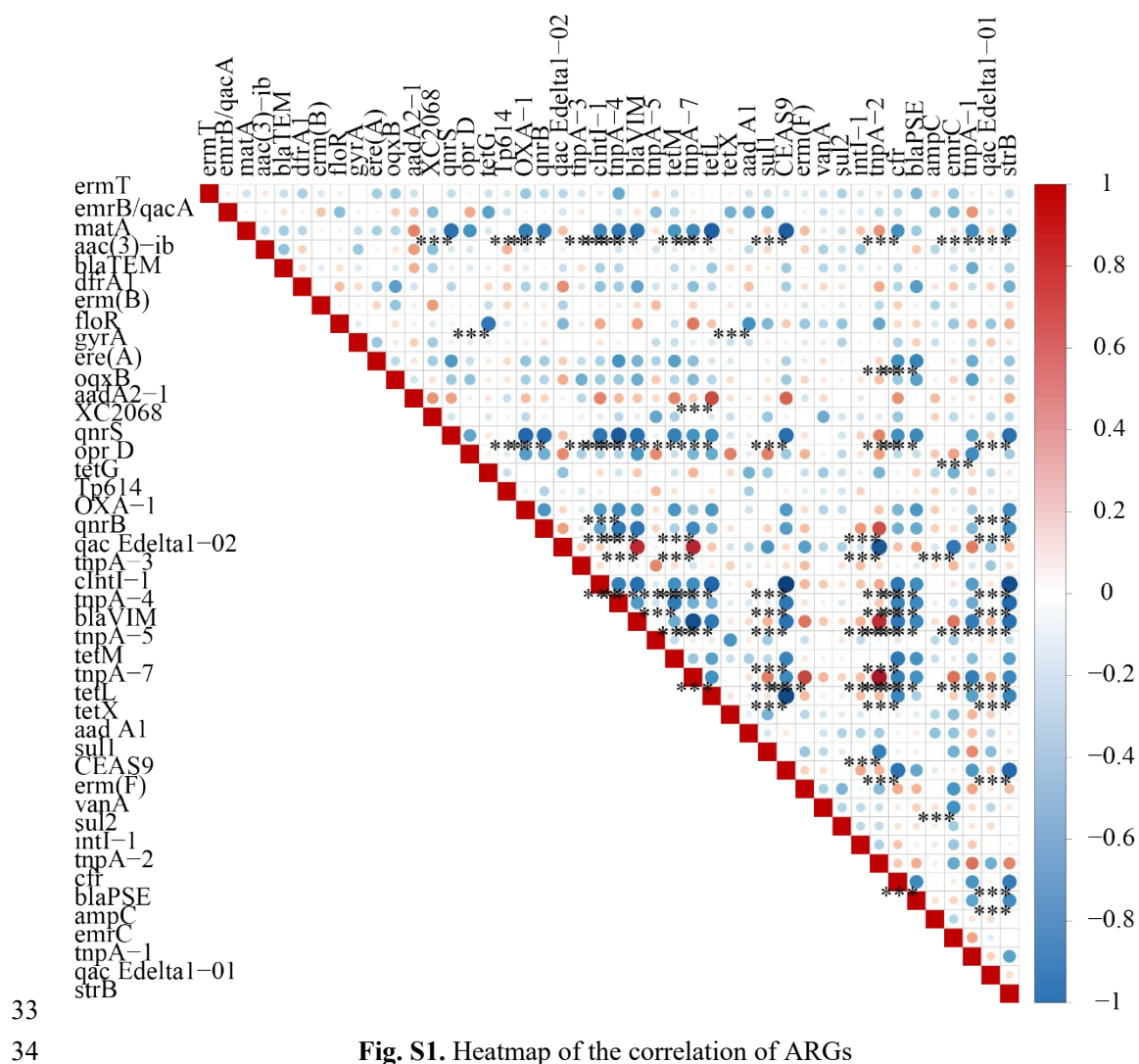
12	matA	TAGTAGGCAAGCTCGGTGTTGA	CCTGTGCTATTTTAAGCCTTGTTTCT	MLSB	efflux pump
13	opr D	ATGAAGTGGAGCGCCATTG	GGCCACGGCGAACTGA	Multidrug	efflux pump
14	qac Edelta1-01	TCGCAACATCCGCATTAAAA	ATGGATTTCAGAACCAGAGAAAGAAA	Multidrug	efflux pump
15	qac Edelta1-02	CCCCTTCCGCCGTTGT	CGACCAGACTGCATAAGCAACA	Multidrug	efflux pump
16	qnrA	AGGATTTCTCACGCCAGGATT	CCGCTTTCAATGAAACTGCAA	Others	cellular protection
17	strB	GCTCGGTCGTGAGAACAATCT	CAATTTCCGGTCGCCTGGTAGT	Aminoglycoside	antibiotic deactivate
18	sul2	TCATCTGCCAAACTCGTCGTTA	GTCAAAGAACGCCGCAATGT	Sulfonamide	cellular protection
19	tetB	AGTGCGCTTTGGATGCTGTA	AGCCCCAGTAGCTCCTGTGA	Tetracycline	efflux pump
20	tetL	ATGGTTGTAGTTGCGCGCTATAT	ATCGCTGGACCGACTCCTT	Tetracycline	efflux pump
21	tetX	AAATTTGTTACCGACACGGAAGTT	CATAGCTGAAAAAATCCAGGACAGTT	Tetracycline	other/unknown
22	tnpA-4	CATCATCGGACGGACAGAATT	GTCGGAGATGTGGGTGTAGAAAGT	Transposase	transposase
23	tnpA-3	GGGCGGGTCGATTGAAA	GTGGGCGGGATCTGCTT	Transposase	transposase
24	tnpA-7	AATTGATGCGGACGGCTTAA	TCACCAAAGTGTATGGAGTCGTT	Transposase	transposase
25	tnpA-2	CCGATCACGGAAGCTCAAG	GGCTCGCATGACTTCGAATC	Transposase	transposase

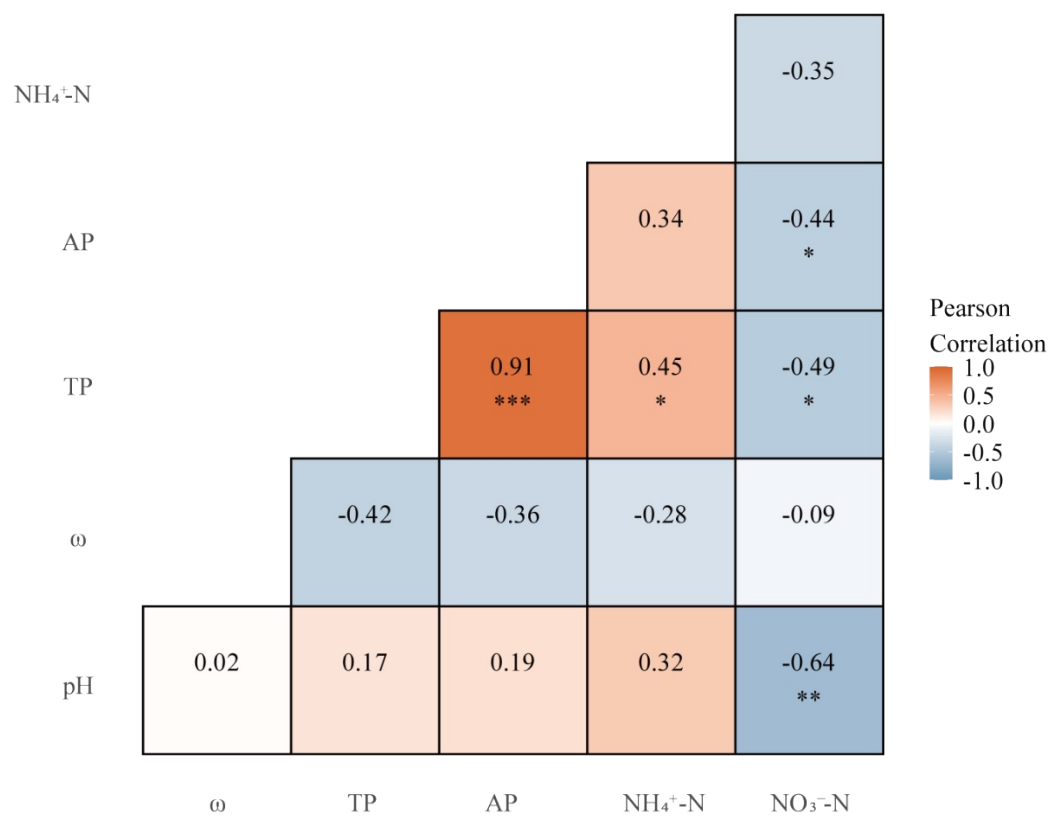
26	tnpA-1	GCCGCACTGTCGATTTTTATC	GCGGGATCTGCCACTTCTT	Transposase	transposase
27	tnpA-5	GAAACCGATGCTACAATATCCAATTT	CAGCACCGTTTGCAGTGTAAG	Transposase	transposase
28	Tp614	GGAAATCAACGGCATCCAGTT	CATCCATGCGCTTTTGTCTCT	Transposase	transposase
29	vanA	AAAAGGCTCTGAAAACGCAGTTAT	CGGCCGTTATCTTGTA AAAACAT	Vancomycin	cellular protection
30	aac(3)-ib	CAGCGAGACGTTTCATCGC	CACGCTTCAGGTGGCTAATC	Aminoglycoside	deactivate
31	ampC	CTGGCGCATACCTGGATTAC	GCCAGTTCAGCATCTCCCA	Beta_Lactamase	deactivate
32	blaTEM	CGCCGCATACACTATTCTCAG	GCTTCATTGAGCTCCGGTTC	Beta_Lactamase	deactivate
33	ere(A)	GATAATTCTGCTGGCGCACA	GCAGGCGTGGTCACAAC	Beta_Lactamase	deactivate
34	erm(B)	GAACACTAGGGTTGTTCTTGCA	CTGGAACATCTGTGGTATGGC	Beta_Lactamase	regulator
35	floR	AACCCGCCCTCTGGATCA	GCCGTCGAGAAGAAGACGAA	Beta_Lactamase	efflux
36	sulI	GCCGATGAGATCAGACGTATTG	CGCATAGCGCTGGGTTTC	Beta_Lactamase	regulator
37	tetG	TTATCGCCGCCGCCCTTCT	TCATCCAGCCGTAACAGAAC	Beta_Lactamase	efflux
38	tetM	GGAGCGATTACAGAATTAGGAAGC	TCCATATGTCCTGGCGTGTC	Beta_Lactamase	protection
39	emrB/qacA	CTTTTCTCTAACCGTACATTATCTACGATAAA	AGAACGTAGCGACTGATAAAATGCT	Beta_Lactamase	efflux

40	OXA-1	TATCTACAGCAGCGCCAGTG	TATCTACAGCAGCGCCAGTG	Beta_Lactamase	deactivate
41	gyrA	CAAGAATCGTGGGTGATG	GTGGAATATTTGTCGCCA	Fluoroquinolone	protection
42	qnrB	GCGACG TTCAGTGGTTCAG	TGTCCA ACTTAACGCCTTGTA	Fluoroquinolone	protection
43	qnrS	TAAATCACACGCACGGA ACT	AACAGGGTGATATCGAAGGC	Fluoroquinolone	protection
44	oqxB	TCCTGATCTCCATTAACGCCCA	ACCGGAACCCATCTCGATGC	Multidrug	efflux pump
45	emrC	GAAATCGGCTCAGGAAAAGG	TAGCAAACCCGTATTCCACG	Multidrug	efflux pump
46	XC2068	TCCTCGGCAACCTCTATGTG	ACAGCAGCGGGTCTTCCTC	Others	other/unknown
47	CEAS9	CAGCACGAACTTCACAGTCACA	AACAATCTCCCAAAAAGCGGTC	Others	other/unknown
48	clmA	TTGCAACAGTACGTGACAT	ACACAACGTGTACAACCAG	Others	other/unknown

Table S4. Table of soil physicochemical properties in 21 micro green spaces.

Number	pH	ω	TP(g/kg)	AP(mg/kg)	NH ₄ ⁺ -N(mg/kg)	NO ₃ ⁻ -N(mg/kg)
1	8.91	5.92%	0.70	26.14	10.02	22.19
2	8.57	4.53%	0.96	35.33	9.52	10.77
3	8.70	7.84%	0.88	30.99	9.52	5.70
4	8.41	7.06%	0.83	19.00	8.96	17.10
5	8.59	7.03%	1.24	59.66	9.84	2.85
6	8.81	11.33%	0.75	12.28	9.97	1.58
7	8.77	7.68%	0.89	27.59	11.69	7.18
8	8.40	6.80%	1.04	42.90	14.78	19.38
9	8.89	6.32%	0.81	58.68	10.11	7.43
10	8.40	5.59%	1.50	98.42	10.20	10.00
11	8.66	6.76%	0.90	44.21	11.86	3.17
12	8.37	6.24%	1.05	41.85	12.72	6.00
13	8.62	9.56%	0.97	44.19	11.80	2.81
14	8.66	6.04%	0.99	48.81	11.91	5.01
15	8.95	10.11%	1.02	49.22	19.39	3.18
16	8.70	4.41%	0.85	21.66	28.63	9.79
17	8.00	8.19%	0.43	2.86	3.10	38.64
18	8.34	12.03%	0.37	7.03	12.53	19.43
19	8.33	5.50%	0.55	8.26	3.37	43.24
20	8.58	16.93%	0.41	3.64	0.13	12.63
21	8.66	5.96%	0.41	1.23	0.68	6.61





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 36 **Fig. S2.** Correlation analysis of soil physicochemical properties. Significance levels are indicated
 37 by asterisks (*p < 0.05, ** p < 0.01, *** p < 0.001).