Supplementary Information

Table S1. Meta-analysis statistics

ARG Class	Q-test for Heterogeneity	I-Squared Statistic
Beta-Lactam	80.89	96%
Macrolide	5.48	63%
Quinolone	9.22	67%
Sulfonamide	119.89	96%
Tetracycline	32.32	88%
Integrons	7.62	74%

Table S2. All studies included in the systematic review

Country	Surface water	Sampling points per subject	Sampling points as defined by the authors	Samples obtained per sampling points	Method	Data presentation	Reference
Australia	Brisbane River	12	forested hills and grazing land; peri-urban site	500 mL x four sampling events	qPCR	Mean Abundance (gene copies/uL)	Ahmed *et al.,* 2021
	Oxley Creek	1	highly populated, industrial, residential, and urban areas				
	Boggy Creek	1					
Nepal	Rivers near Kathmandu Valley	1	N/A	6 x 10 mL	ddPCR	Relative Abundance (gene copies/ 100 mL)	Amarasiri et. al. 2022
Brazil	Diluvio River	6	undefined	2 L x 8 sampling events	qPCR	absolute abundance (gene copies/mL)	Arsand *et al.,* 2020
France	Lez River	6	baseline, entrance of urban area,	2 L	qPCR	absolute abundance (gene copies/mL)	Aujoulat *et al.,* 2021
	Verdanson River	3	urban zones, peri-urban zones, residential-influenced area,				
	Font d'Aurelle River	2	hospital-influenced area				
	Mosson River	2					
	Lantissargues River	1					
	Rieu-Coulon River	1					
Japan	Yodo River	2	1 km downstream of effluent discharge point Main stream of Yodo River	300 mL x 4	qPCR	relative abundance (gene copies/mL)	Azuma *et al.,* 2022

Czech Republic	Svratka river	4	upstream and downstream of a WWTP	unknown	qPCR	relative abundance (gene copies/16srRNA)	Buriánková *et al.,* 2021
India	Ganga, Gomti, Yamuna, and Hindon Rivers	3	Start-point, mid-point, end-point	1-liter in triplicates	Conventional PCR	presence/absence	Chaturvedi *et al.,* 2021
China	"ponds and lakes adjacent livestock farms"	1	ponds and lakes adjacent or nearby livestock farms	1	qPCR	absolute abundance (gene copies/16srRNA)	Chen *et al.,* 2015
China	Unspecified River	2	Upstream Downstream	250 mL (triplicate)	qPCR	absolute abundance (copies/mL)	Chen et.al 2020a
China	Yangtze Estuary	19 sites (categorized into three sections)	inlet, turbidity maximum zone (TMZ), and outlet	1	qPCR	relative abundance (gene copies/16srRNA)	Chen *et al.,* 2020b
China	Linshan River	4	N/A	3 subsamples, pooled into one 2 L sample	HT-qPCR	Absolute Abundance (gene copies/L)	Cheng, et. al 2020
	Wujia Fishpond	1					
Georgia, USA	Upper Oconee watershed	115	various streams throughout the Upper Oconee Watershed Network	the number of samples collected varied	qPCR	unspecified abundance (copies/mL)	Damashek *et al.,* 2022
Puerto Rico	RLI	16	rural low-impact	2L	Metagenomic Sequencing and qPCR	Relative Abundance (gene copies/16srRNA)	Davis *et al.,* 2020
	PMI		PMI - per-urban medium impact				
	UHI		UHI - urban- high impact				
India	Mula-Mutha River	8	Upstream Downstream Confluence	400 mL, 3 samplings	Conventional PCR	Presence/Absence	Dhawde, et. al 2018
Uruguay	Montevideo Coastline	12	coastal areas	200 mL	Metagenomic Sequencing	Presence/Absence	Fresia et. al 2019
China	Liaohe River	10	Liaohe (L1 to L10), Daliaohe (D1 to D4), Hunhe (H1 to H7), Taizi (T1 to T8)	4L	HT-qPCR	Absolute Abundance (gene copies/L)	Gao *et al.,* 2022
	Daliaohe	4					

	River						
	Hunhe River	7					
	Taizi River	8					
China	Ying Lake	3	Upstream region Fenced fish farming Box-type fish farming 10 cm below the surface for all	500 mL/corner, pooled (triplicate)	HT-qPCR	Relative Abundance (gene copies/16srRNA)	Gu et. al 2019
China	Ba River	7	W1 - upper reach of ecological wetland park of Ba River Bridge W2 - downstream of riverside park W3 - hundred meters upstream of W4 W4 - mouth of Chan River W5 - resident domestic sewage outlet W6 - WWTP discharge port W7 - close to Jing Wei Wetland	2 liters in triplicates	qPCR	relative abundance (gene copies/mL)	Guan *et al.,* 2018
UK India	Tyne River	3	high heavy metals vs. low heavy metal areas and high wastewater impact vs. low wastewater impact areas	500 mL in triplicates	qPCR	relative abundance (copies/16srRNA)	Gupta *et al.,* 2023
	Ouseburn River	2					
	Ganga River	3					
	Yamuna River	1					
Germany	Holtemme River	6	pristine (S1), urban (S2), WWTP discharge (S3), downstream of WWTP (S4-6)	1-L in triplicates	qPCR	absolute abundance (copy number/100mL)	Haenelt *et al.,* 2023
China	Taihu Lake	lake - 5 1 each for the river tributaries	Caoqiao river, Xitiao river, Shedu Bay, Xujiang River; and 5 sites within the lake	1L	qPCR	relative abundance (gene copies/16srRNA)	Han *et al.,* 2013
Poland	Pilica River catchment	7	Sampling Sites R1 to R7 are along the continuum of the river from upland to lowland	3000 mL in triplicates	qPCR	absolute abundance (gene copies/mL)	Harnisz *et al.,* 2020

California, USA	Agua Hedionfa Lagoon, Newport Bay, Los Angeles Harbor, San Pedro Ocean Time Series, Hawaii Ocean Time Series	1	1) Agua Hedionda Lagoon - aquaculture facility 2) Newport Bay - freshwater influence from San Diego Creek and Delhi Channel 3) Los Angeles Harbor - not mentioned 4) San Pedro Ocean Time Series - open ocean site that has coastal influence 5) Hawaiian Ocean Time Series - open-ocean site	8-16L in duplicates	functional metagenomics via sanger sequencing	Presence/Absence	Hatosy et al, 2015
China	Hainan Province	1	N/A	10 L x triplicates	qPCR	Relative abundance (gene copies/16S rRNA gene)	He et al, 2022
China	Wohushan Reservoir Yuqing Lake Reservoir Jinxiu Reservoir Mishan Reservoir Datun Reservoir Dongping Lake Jihongtan Reservoir Nanyang Lake	1	Wohushan Reservoir (WHS), Yuqing Lake Reservoir (YQ), Jinxiu Reservoir (JXC), Mishan Reservoir (MS), Datun Reservoir (JHT), Nanyang Lake (NYH), Datun Reservoir (DTH), Dongpin Lake (DP), and Xiashan Reservoir (XS)	1L water samples	Metagenomic Sequencing	Percent Relative Abundance	Hou et al., 2020

China	Xiashan Reservoir N/A	1	2 duck-fish ponds, 3 duck ponds, 3 fishponds, and control pond (no aquaculture activity)	4.5 liters	qPCR	relative abundance (gene copies/uL)	Huang *et al.,* 2017
China	Minjiang River	12	upstream of the dam (s1-7), downstream of the dam (s8-12)	2L x "three duplicate samples"	HT-qPCR	Relative abundance (ARG copies/16S rRNA gene)	Huang et al, 2022
Poland	NA	2	upstream and downstream of a WWTP	500 ml in triplicates	qPCR	absolute abundance (gene copies/mL)	Hubeny et al, 2021
Spain	La Llosa Reservoir Sau Reservoir Foix Reservoir	3	Tail, mid, and near the dam	5L	qPCR	relative abundance (gene copies/16srRNA)	Huerta et al, 2013
Benin	channel hydrographic complex of Cotonou-Lake Nokoue	10	Hinde, caniyeau hinde, dantokpa, gbogbanou, ladji, homel, lazaret, hotel du lac, restaurant le berlin	150 ml	Conventional PCR	Presence/Absence	Ichola *et al.,* 2021
South Korea	Pacific Ocean Southern Ocean	13 15	stations near some countries	150 -4000 mL	qPCR	absolute abundance (gene copies/mL)	Jang et. al, 2022
China	Hongqi River Yongan River Taihu Lake Taige River	uneven - total of 7 sampling points for all the rivers	Outlet of the sedimentation tank - S1 and S2 Without fecal wastewater discharge - S0 Receiver water along the river flow - S3-S6	10L	Metagenomic Sequencing	relative abundance in ppm	Jia *et al.,* 2017
Brazil	Uberabinha River	6	S1-S4 (Upstream to downstream perimeter), S5 (Artificially protected area), S6 (Small natural pond)	1L	qPCR	relative abundance (gene copies)/16s rRNA)	Jia *et al.,* 2021

China	Beijiang River	38	upstream vs downstream sites	1.5L	Conventional PCR and qPCR	presence/absence; copies/uL	Jiang *et al.,* 2018b
China	Danjiangkou Reservoir	8	Han River, Dan River and Danjiangkou Dam	1L (3 depths from each site)	qPCR	Relative Abundance (ARGs/16S rRNA gene)	Jiang et al, 2021
China	Huangpu River	7	S1, S2, S3, S6, and S7 suburban areas (agricultural activities) S4 and S5 urban area (industrial and residential activities)	8L water each site	qPCR	absolute abundance (copy/mL)	Jiang et al., 2013
China	Pearl River Delta Region	4	WA1 - intersection of a branch and main stream of beijiang river WA2 - downstream of Xijiang River WA3 - intersection of three tributaries of Pearl rive with complex dry environment WA4 - pearl river estuary where was intensively influenced by integrated aquaculture farms	1.5 L	Metagenomic Sequencing	Absolute Abundance (gene copies/cell)	Jiang et al., 2018a
Georgia, USA	Oakdale creek	3	upstream headwater region, mid-stream salmarsh, mouth of the creek	1L (triplicates 1L each)	qPCR	Quantitative (gene copies/ml of water)	Jones *et al.,* 2018
Japan	Urban Rivers in Japan	undefined/uneven as n = 30	Group A - no WWTP located upstream Group B - effluent are estimated to be <10% Group C - effluent could be >10% For Tamagawa, Iruma, and Arakawa Rivers, samples were collected from upstream and downstream sites to evaluate the impact of treated effluents between two sites 2 (upstream and downstream) and 2 (Influent and treated influent)	100 ml (n = 30)	HT-qPCR	Presence/Absence	Kasuga et al, 2022

Germany; Austria; Hungary; Croatia; Serbia; Romania; Bulgaria	Danube River	1	4 - downstream of megacities 2 - beginning of the river 2 - delta of the river 4 - rural sampling sites 2 - confluence of two biggest tributaries	1 L in triplicates	Conventional PCR	Presence/Absence	Kittinger *et al.,* 2018
Poland	Warta River	3	upstream, city, and downstream	unknown	qPCR	relative abundance (gene copies/mL)	Koczura *et al.,* 2016
Sri Lanka and India	Brahmaputra River	4	N/A	2 Liters	Conventional PCR	Presence/Absence	Kumar et al, 2020
	Kelani River	4					
Romania	Romanian aquatic fishery lowland salted lakes	NA	Balta Alba, Jirlau, Caineni, Amara	NA	Conventional PCR	Presence/Absence	Lazăr et al, 2021
France	unspecified river in northwest of France	1	upstream of river before discharge of wastewater	1 L	Conventional PCR	Presence/Absence	Leclercq *et al.,* 2013
Spain	Ter River	2	upstream and downstream of WWTP	1 L x 6 replicates	qPCR	absolute concentration - log(gene copies/mL)	Lekunberri *et al.,* 2017
Poland	Bilka River Zakopianka River	5 4	B1 - Outflow from the Tatra National Park (TNP) (protected area) B2 - Before STP B3 - STP B4 - Intake of water for artificial snowing of Kotelnica ski resort B5 - By the largest ski station in the region B6 - After passing through Białka Tatrzan´ska locality Z1 - Before the discharge of sewage from the hospital in Zakopane	1L	Conventional PCR	Presence/Absence	Lenart-Boroń 2017

			Z2 - Downstream of the discharge of sewage from the Zakopane hospital Z3 - Downstream of the discharge from the Zakopane STP, intake of water for snowing of Harenda Z4 - After passing through Zakopane town Z5 - Center of Nowy Targ town				
China	Weihe River	4	upstream, urban area, town area, and village area	unknown	qPCR	absolute abundance (gene copies/L)	Li and Zhang 2020
China	Dapeng Cove of Daya Bay	9	site A1-3 - cage aquaculture area; site T - yacht tourism area; site S - domestic drainage channel	3 samples in site A1-3 - ; 1 sample in site T ; 3 samples in site S	qPCR	absolute abundance (gene copies/mL)	Li *et al.,* 2020
China	Beijiang River	20	Wujiang river, lishi, xibe bridge, shaoguan train station, xinshao town, baiwang bridge, baitu bridge, wushu, shakou, wangfu, lianjiangkou, lixi, feixia, qingyuan urban, shijiao town, lubao, beishui, sanshui, nanzhuang, jiujang town	1 liter in replicates	qPCR	relative abundance (gene copies/16s rDNA)	Ling *et al.,* 2013
China	Xidong reservoir	6	freshwater reservoir	300-500mL	metagenomic sequencing and qPCR	Relative abundance (gene copies/16srRNA)	Liu *et al.,* 2019
China	Yarlung Tsangpo River	7	2 pristine, 2 urbanized, 3 dam-regulated areas	2-liter in triplicates	Metagenomic Sequencing	Absolute Abundance (gene copies/cell)	Liu *et al.,* 2021
Sri Lanka	Canal: Kittampahuwa canal Sebastian canal Hemilton canal	11 Canal - 1 samples each 6 Rivers - 1 samples each Kelani River - 8	meandering zone of the Kelani River which covers three disticts	2 L in triplicates	qPCR	absolute abundance (gene copy/mL)	Liyanage *et al.,* 2021

	Old Dutch canal Raggahawatta canal Pugoda canal Thummodara Seethawaka Zone canal Arangala Rivers: Diyawanna Oya New Keleni river bridge Pusselli Oya Kelani River	sampling sites - 1 sample each					
China	Yellow river	6	river water and source water were taken from influent and effluent of SSRs	triplicates (500 ml each)	Metagenomic Sequencing and qPCR	Absolute Abundances (gene copies/ mL)	Lu *et al.,* 2018
Poland	Zimny Potol River	2	upstream and downstream effluent discharge	5 L x 4	qPCR	relative abundance (gene copies/mL)	Makowska *et al.,* 2016
Thailand	Canals and Ponds	12 for 2 ponds 41 for 7 canals	N/A	450 mL	Conventional PCR	Presence/Absence	Mala et. al, 2017
China	Haihe River	7	main stream and tributaries	0.2 L	qPCR	Presence/ Absence	Mao et al, 2014
Spain	Ter River	3	WWTP discharge point, 100 m upstream and downstream of the WWTP	duplicates	qPCR	relative abundance (gene copy/gram)	Marti *et al.,* 2013
China	Yellow Sea	16	sites: near WWTP aquaculture sea near tourism area medical wastewater area	1 (1L per sample)	qPCR	relative abundance (gene copies/mL)	Na *et al.,* 2014
Japan	Yae River	3	ST1: upper basin of the river, densely populated area ST2: midstream, flows through urban area surrounded by marshy area ST3: downstream in an estuarine	1L	Conventional PCR	Presence/Absence	Nishiyama *et al.,* 2017

			environment flowing into the sea				
China	Bohai Bay	7	polluted estuary, aquaculture area, tourism area, area not influenced by human activities	1 L	qPCR	relative abundance (gene copies/16srRNA)	Niu *et al.,* 2016
Japan	Kaeda River	1	natural water vs. urban water	1 L	Whole Genome Sequencing	presence/absence	Ogura *et al.,* 2020
China	Kiyotake River Jiulongjiang River	3	major tributaries situated at the center of the city; remote suburban mountain (pristine control)	4-12L each sampling site in triplicates	HT-qPCR	Absolute Abundance (gene copies/L)	Ouyang *et al.,* 2015
Bolivia	Lake Alalay	3	n/a	100 mL	Metagenomic Sequencing	Presence/Absence	Quillaguamán *et al.,* 2021
India	Ghaghara River	14	Upper stream, middle stream, lower stream	100 ml	Conventional PCR	Presence/Absence	Ravi et al, 2022
Germany	Kraichbach River	10	5 upstream, 5 downstream	250 to 400 ml	qPCR	absolute abundance (gene copies/mL)	Reichert *et al.,* 2021
Ireland	River Liffey River Tolka Elm Park Stream Trimleston Stream	1	pristine, near agriculture and industrual land, main river, completely urban areas	100 ml	Conventional PCR	Presence/Absence	Sala-Comorera *et al.,* 2021
Iran	unspecified surface waters within 60km radius from City of Isfahan, Iran	1	N/A	200 - 250 mL	Conventional PCR	Presence/Absence	Shahin et. al, 2019
China	Lake Tai	6	Northern region of Lake Tai	100 - 600 mL	qPCR	absolute abundance (gene copies/ mL)	Stange et. al 2018
	N/A	3	3 different steps of DWTP	1000 mL			
Nepal	Bagmati River	3	Sundarijal (upstream), Thapathali (midstream) and Chovar (downstream)	100 ml	qPCR	absolute abundance (log copies/mL)	Thakali *et al.,* 2020
Nigeria	Rivers of Southwestern Nigeria	1	undefined/random	1.5L	Conventional PCR	Presence/Absence	Titilawo *et al.,* 2015

China	Honghu Lake	12	N/A	1 L for lake waters	qPCR	fold change in gene expression	Tong *et al.,* 2020
	4 ponds nearby the Honghu Lake	1 per pond		500 mL for pond waters			
Vietnam	Saigon River	10	less impacted areas, agricultural areas, industrial areas, residential areas	5 L in triplicates	qPCR	relative abundance (gene copies/mL)	Truong *et al.,* 2021
	Dong Nai River	2					
China	Funan River	10	river intersections, streams near parks; sewage outlets near residential areas, hospital, and municipal wastewater treatment plant.	3	qPCR	absolute abundance (- log10 gene copies/mL)	Tuo *et al.,* 2018
China	Pinghu Creek	6	N/A	2 L	qPCR	relative abundance (gene copies/16srRNA)	Wang *et al.,* 2020
	Huanggu Creek	8					
China	"coastal area in Dalian, China"	1	N/A	5 L	qPCR	relative abundance (gene copies/16srRNA)	Wang *et al.,* 2017
China	Weihe River	13	7 urban areas, 6 rural areas	1-liter in triplicates	ddPCR	Absolute Abundance (gene copies/mL)	Wang *et al.,* 2018
China	Yangtze River	8	no specific definitions but the sampling sites are the river estuaries	1.5 L	qPCR	absolute abundance (gene copies/L)	Wang *et al.,* 2019
China	Weihe River	4	W1-4 (high population density area with aquaculture and sewage discharge)	triplicates	Metagenomic Sequencing	Absolute Abundance (gene copies/16srRNA)	Wang *et al.,* 2023
	Fenhe River	5	Y3 (Confluence of river)				
	Yellow River	3	F1-3 (urban area with large population density F4 (large population density) F5 (confluence of river)				
China	Liuxi River	12	(Site A, Upstream), (Site B, downstream), (Site C, Downstream), (Site D, Downstream)	3 L	qPCR	relative abundance (gene copies/mL)	Xiong *et al.,* 2014

China	Receiving river of an STP	2	upstream, downstream	4 L	qPCR	relative abundance (genes copies/16s rRNA)	Xu *et al.,* 2015
China	Sha River	2	N/A	1000 mL	qPCR	absolute abundance (gene copies/mL)	Xu *et al.,* 2016
	Wenyu River	10					
	Qinghe River	9					
	Beixiao River	3					
	Ba River						
	Tonghui River	5					
	Xhiaozhong River	7					
		1					
China	Coastal area in Guandgong China	13	N/A	2 L x 3, combined	qPCR	absolute abundance (gene copies/mL)	Xu *et al.,* 2019
China	Artificial city park lakes - Lingjiao, Yuehu, and Ziyang	2 sampling sites for each artificial lakes	N/A	2L	Conventional PCR and qPCR	quantitative - ARG copies/16srRNA	Yang *et al.,* 2017
	Semi-natural urban lakes - East Lake, Nanhu, and Shahu	Semi-natural urban lakes - East Lake (9), Nanhu (3), and Shahu (3)					
China	Funan River	12	upper reach, middle reach, downstream region	3 x 2 L	Conventional PCR and qPCR	Presence/Absence; absolute abundance in copies/mL	Yang *et al.,* 2018
China	unnamed river receiving	2	upstream and downstream	5 x 4 L	qPCR	absolute abundance (log copies/mL)	Yang *et al.,* 2019

	wastewater from a large-scale pig farm						
Ethiopia	Big Akaki River Little Akaki River	1 3	Little Akaki: Gefersa (GE) - reservoir for drinking water, restricted for anthropogenic activities Mekanissa (MK) - irrigation and residential area directly discharging its wastes to the river Batu (BA) - industry dominated area directly discharging wastes to the river Big Akaki: Zewditu (ZE) - residential area with healthcare facilities Aba-Samuel (AB) - convergence of both rivers	1 L	qPCR	relative Abundance	Yitayew *et al.,* 2022
China	Ili River	5	upstream tributary Kashi River (BGC), Yining City (YN), Cokdara (KKDL), Huiyuan City (HY), and the National Highway 219 (B219)	10L x triplicates	Metagenomic Sequencing	relative abundance in ppm	Yang *et al.,* 2022
Nebraska, USA	swine wastewater treatment lagoon; cattle storage pond	1	N/A	1 L	qPCR	absolute abundance (gene copies/mL)	Zhang *et al.,* 2013
China	Taihu Lake Tributary Rivers of Taihu Lake	8 17 Tributaries	undefined	undefined sample amount. Taihu Lake - 2 samples per sampling site (n=16)	Conventional PCR	Presence/Absence	Zhang *et al.,* 2015

				one sample per tributaries (n=17)			
China	Yangtze River (Jiangsu Section)	12	upstream and downstream	1 L x 3	qPCR	absolute abundance (gene copies/mL)	Zhang *et al.,* 2020a
China	Sishili Bay	32	Different Functional zones: aquaculture farm ecological aquaculture Bathing beach Yantai Port WWTPs River	10 L x triplicates	qPCR	absolute abundance (gene copies/mL)	Zhang *et al.,* 2020b
China	Ci River Hao River Hutuo River Wangyanggon River Xiao River	3	Urban River and Rural River	5 L x 3	Metagenomic Sequencing	Frequency: detection frequency % or log read numbers	Zhang *et al.,* 2022
China	Inflowing rivers in the Fuxian Lake	unevenly distributed number of sampling points per river. Total of 23 water samples.	living quarter sites, mining area, agricultural district, tourist area	1 L	qPCR	absolute abundance (gene copies/mL)	Zhao *et al.,* 2021
China	East Tiaoxi River	13	confluence locations downstream of each catchment area; country and urban areas	1	HT-PCR	quantitative - absolute abundance (copies/L) and relative abundance (copies/cell)	Zheng *et al.,* 2017
China	Bosten Lake	17	"various sites"	2 L	qPCR	relative abundance (gene copies/16srRNA)	Zhou *et al.,* 2014

China	Wen Rui Tang River	17	main stem sites, first-branch tributaries, second-branch tributaries, sub-urban site	1	HT-qPCR	quantitative - absolute abundance (copies/bacterial cell)	Zhou *et al.,* 2017
China	unnamed aquaculture ponds in Baiyun, Guangdong China	1	N/A	15L	HT qPCR	relative abundance - log2 (gene copy number of ARGs)	Zhou *et al.,* 2023
China	Hengshi river	6	sampling sites along the river from Dabaoshan Mine to Shangba Village	2 liters in triplicates	qPCR	relative abundance (gene copies/mL)	Zou *et al.,* 2021

Table S3. Antibiotic resistance genes (ARGs) in various surface waters detected through sequencing methods

Surface Water	Number of ARG subtypes	Data Type	ARG Abundance	ARGs Detected	Reference
Puerto Rican Watersheds	816	relative abundance	N/A	aminocoumarin, aminoglycoside, beta-lactam, elfamycin, fluoroquinolone, fosfomycin, glycopeptide, MLS, multidrug, phenicol, quinolone, rifamycin, streptogramin, sulfonamide, tetracycline, trimethoprim	Davis *et al.,* 2020
Pearl River Delta Region	115	absolute abundance	0.55 - 1.34 copies/cell	aminoglycoside, bacitracin, beta-lactam, macrolide, phenicol, fosfomycin (phosphonic antibiotics), MLS, multidrug resistance, polymyxin, aminonucleoside, quinolone, sulfonamide, tetracycline, diaminopyrimidines, vancomycin	Jiang *et al.,* 2018a
Yarlung Tsangpo River	119	absolute abundance	0.55 - 1.34 copies/cell	aminoglycoside, bacitracin, cephalosporin, phenicol, beta-lactam, macrolide, aminocyclitol, streptogramin, sulfonamide, tetracycline, glycylcycline	Liu *et al.,* 2021
Yellow river	17	absolute abundance	$1.51 \times 104 \pm 1.49 \times 10^4$ copies/mL	aminoglycoside, macrolide, tetracycline, sulfonamide, integrase	Lu *et al.,* 2018
Weihe River Fenhe River Yellow River	102	absolute abundance	1.86×10^{-2} - 7.26×10^{-2} copies/16S rRNA copies	polymyxin, phenicol, multidrug, beta-lactam, tetracycline, aminoglycoside, rifamycin, sulfonamide, vancomycin, macrolide-lincosamide-streptogramin, phosphonic, bacitracin	Wang *et al.,* 2023
Ci River, Hao River, Hutuo, Wangyanggon River, Xiao River	165	Frequency: detection frequency % or log read numbers	N/A	quinolone, fluoroquinolone, quinolone, pyridopyrimidine	Zhang *et al.,* 2022
Kaeda River Kiyotake River	30	presence/absence	N/A	beta-lactams, aminoglycoside, diaminopyrimidine, fluoroquinolone, phenicol, tetracycline, sulfonamide, macrolide, rifamycin	Ogura *et al.,* 2020
Montevideo Coastline	108	presence/absence	N/A	aminoglycosides, beta lactams, tetracyclines, elfamycins, fluoroquinolones, sulfonamides, macrolides, lincosamides, streptogramins, phenicols	Fresia *et al.,* 2019
Agua Hedionfa Lagoon, Newport Bay, Los Angeles Harbor, San Pedro Ocean Time Series, Hawaii Ocean Time Series	33	presence/absence	N/A	beta-lactam, aminoglycoside, tetracycline, vancomycin, sulfonamide	Hatosy *et al.,* 2015

Lake Alalay	277	presence/absence	N/A	fluoroquinolones, tetracyclines, phenicols, macrolides, beta-lactams, rifamycin, diaminopyrimidine, aminoglycosides, acridine dye, aminocoumarin, peptides, lincosamides, mupirocin (monocycliccarbolic acid), nitroimidazoles, oxazolidinones, sulfonamides, nitrofurans, streptogramins, triclosan	Quillaguaman *et al.,* 2021
Various lakes and reservoirs in Northern China	213 to 242	relative abundance	1.3% to 2.0%	vancomycin, penicillin, cephalosporin, multidrug, phenicol, fluroquinolone, tetracycline, macrolide	Hou *et al.,* 2020
Xidong reservoir	104 (HT-qPRC); 160 (meta)	relative abundance	N/A	aminoglycoside, bacitracin, beta-lactam, phenicol, phosphonic, MLS (macrolide, lincosamide and streptogramin), nitroimidazole, lantibiotic, pyrazinamide, polymyxin, aminonucleoside, quinolone, rifamycin, sulfonamide, tetracenomycin, tetracycline, diaminopyrimidine, vancomycin	Liu *et al.,* 2019
Hongqi river, Yongan River, Taihu Lake, Taige River	194	relative abundance	relative abundance in percentage only	tetracycline, aminoglycoside, macrolide, bacitracin, beta-lactam, phenicol, quinolone, dihydropyrimidine, phosphonic, polymyxin, vancomycin, sulfonamide, diamonopyrimidine	Jia *et al.,* 2017
Ili River	-	relative abundance	figures only	phosphonic, beta-lactam, polymyxin, fluoroquinolone, vancomycin, macrolide, phenicol, tetracycline, aminoglycoside	Yang *et al.,* 2022

Table S4. Summary of the correlation analyses of antibiotic resistance genes (ARGs) and bacteria done in the literature

Surface Water	Impacting Factors	Main Bacteria Associated with ARGs	Reference
Yarlung Tsangpo River	Urban areas and dam-regulated activities	*Acinetobacter, Aeromonas, Bordetella, Burkholderia, Dickeya, Escherichia, Francisella, Legionella, Mycobacterium, Mycoplasma, Neisseria, Pseudomonas, Staphylococcus, Yersinia*	Liu *et al.,* 2021
Yellow River	Sand Settling Reservoirs (SSRs) and Drinking Water Treatment plant (DWTP)	*Brevundimonas and Methylobacterium*	Lu *et al.,* 2018
Hongqi River Yongan River Taihu Lake Taige River	Wastewater and agriculture	*Clostridium, Bacteroides, Oscillibacter, Treponema, Prevotella*	Jia *et al.,* 2017
Weihe River Fenhe River Yellow River	Urban areas	*Proteobacteria, Lactococcus, Bacillus, Cloacibacterium, Hydrogenophaga, Polynucleobacter, Acidovorax, Sulfurospirillum, and Tolumonus*	Wang *et al.,* 2018
Ili River	Free-grazing farming, sewage discharge from community, animal husbandry, and medical waste	*Proteobacteria, Bacteroidetes*	Yang *et al.,* 2022
Various urban rivers in Japan	Sewage, wastewater treatment plant (WWTP), livestock industry, and decentralized treatment facilities	*Comamonadaceae, Flectobacillus, and Flavobacterium*	Kasuga *et al.,* 2022
Minjiang River	Anthopogenic disturbances, aquaculture, dam construction, and urban activities	*Phycisphaeraceae, Actinobacteriota, Sporichthyaceae*	Huang *et al.,* 2022
Ying Lake	Fish farming methods	*Proteobacteria, Actinobacteria*	Gu *et al.,* 2019
East Tiaoxi River	Uurban areas	*Proteobacteria*	Zheng *et al.,* 2017
Wen Rui Tang River	Wastewater	*Burkholderia, Zooglea, Bacteroides, Prevotella*	Zhou *et al.,* 2017
Unspecified aquaculture ponds in Baiyun, Guangdong China	Aquaculture	*Proteobacteria, Aerococcus, Selenomonas, Pseudoramibacter, Citrobacter, Mycobacterium, Pseudoalteromonas, Moraxella, Eikenella, Providencia, Proteus*	Zhou *et al.,* 2023

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