

Occurrence and drivers of Antibiotics in the rural-urban River Network: A case study of Hongze Lake basin, China

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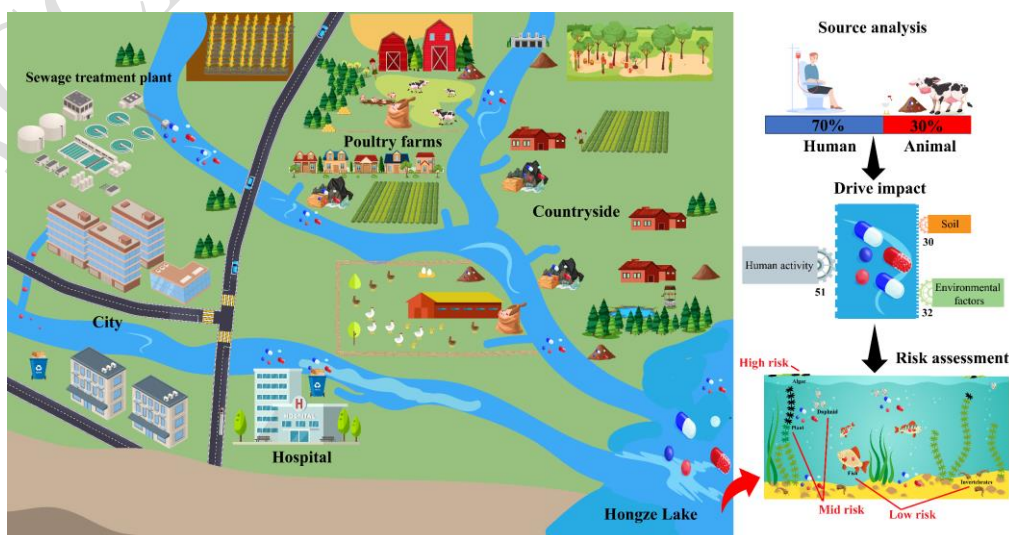
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Abstract:

The massive use of antibiotics and the consequent antibiotic pollution have become a major risk to river ecosystems, water quality, and human health. In this study, 28 antibiotics were analyzed in the rural-urban river water of Suzhou City, the inflow rivers of Hongze Lake. The total concentration of antibiotics in the rural-urban river was $nd-85.87 \text{ ng L}^{-1}$, mainly containing veterinary antibiotics, quinolones, and tetracyclines. The distribution of antibiotics was found to be closely related to the population density and the development of the breeding industry along the bank through structural equation model and correlation analysis. Meanwhile, the human activities (70%), livestock and poultry breeding (30%) were the main sources of antibiotics in the study area through the principal component analysis-multiple linear regression (PCA-MLR) source analysis. Finally, the risk assessment was carried out by the Risk Quotient (RQ) method, and indicated that antibiotics pose a low risk to plant and invertebrates, but Ofloxacin, Ciprofloxacin, Erythromycin, Norfloxacin, and Chlortetracycline posed a mid ecological risk to algae. This work provides a valuable data set across the rural-urban river network and revealed the antibiotic contamination profile. Prevention and management to reduce the antibiotic inputs are needed for the rural-urban zones.

Keywords: Antibiotics, rural-urban river network, drivers and sources, risk assessment



1. Introduction

Antibiotics are one class of emerging pollutants with a wide presence in the environment, and widely used to be the medicines of human and veterinary (Wang et al., 2021). The global consumption of antibiotics was 4.02 billion defined daily dose (DDD) in 2018, up 45% since 2000, of which 14.3 DDD of antibiotics were consumed per 1,000 people daily (Browne et al., 2021). China is the largest producer and user of antibiotics in the world and uses more than 25000 tons each year (Ci et al., 2021). Antibiotics could enter the aquatic environment through medical waste, animal excreta, and domestic sewage (Ci et al., 2021). Residual antibiotics in the water would lead to the reduction of microbial diversity and alteration of bacterial ecology through migration, adsorption, and bioaccumulation (Zhou et al., 2020). In addition, antibiotics in water might accumulate in the human body through drinking water and the food chain, causing the human body to develop drug-resistant genes and pose a serious threat to human health (Xiao et al., 2023). In summary, antibiotic pollution in water bodies should be widely concerned in the world.

Antibiotics have been widely detected in aquatic environments, including river water, seawater, groundwater and even drinking water (Fu et al., 2022; Wang et al., 2021). The rural-urban rivers serve as the main source of water supply for rural-urban users (Ci et al., 2021), but well known as a hotspot for antibiotics due to the receiving of massive wastes from rural-urban areas (Morina and Franklin, 2023). Therefore, to protect human health and ecosystem safety, it is important to investigate the environmental behavior process of antibiotics in the rural-urban rivers. However, there have been only a few studies on antibiotics in the rural-urban river network (Yang et al., 2020). Specifically, perhaps due to various factors that affect antibiotic enrichment and migration, researchers have until now known little about antibiotic drivers in urban and rural river networks (Zainab et al., 2021).

Mathematical statistics are the useful tools to identify the drivers of antibiotics in the river water (Wang et al., 2024). Recent studies have attempted to utilize the simple linear equation of correlations to study the influence factors of antibiotics in surface water (Wu et al., 2023). However, a simple linear equation can only present the relationship between one dependent variable and one independent variable at a time. Structural equation models was developed to identify the potential driving factors and interpret their direct and indirect effects on antibiotic concentrations, and can analyze the relationship between multiple independent and dependent variables at the same time (Tian et al., 2021). In short, structural equation models can comprehensive analysis the drivers of antibiotics and more accurate indicate the combined effects of variables, thus the structural equation method will be used to analyze the driving factors of antibiotics in the present study.

Suzhou City in Anhui Province of China, which is located in the upstream of Hongze Lake basin, is the core city of the Huaihai economic cooperation region, an important node of the Yangtze River Delta urban agglomeration, and the Central Plains Economic Zone in China. Lots of industrial and domestic sewage, agriculture and livestock wastewater would inflow into the rural-urban rivers of Suzhou city. In addition, the rural-urban river network in Suzhou has the various river channels, which could also lead to the complex antibiotic pollution situation. Therefore, the objectives of this study are as follows: (1) to investigate the occurrence of commonly used antibiotics (e.g. Quinolones (QNs), Macrolides (MLs), Sulfonamides (SAs), Tetracyclines (TCs)), (2) to study the sources and drives of the antibiotics (3) to estimate the risk assessment of antibiotics in the rural-urban river water of Suzhou City, China.

2. Materials and methods

2.1 Study area and sample collection

The rural-urban rivers in Suzhou were located in the upstream of Hongze Lake basin (Fig 1). At the study area, two rivers (W and X rivers) flow through five counties of Suzhou City (e.g. Dangshan County, Xiao County, Yongqiao District, Lingbi County, Si County). In July 2023, the surface water samples at 41 sampling sites were collected. In detail, the sampling sites of W1-W6 were located in Dangshan County, W7 and X1-X9 were located in Xiao County, W8-W10 and X10-X12 were located in Yongqiao District, W11 and X17-19 were located in Lingbi County, and W12-W15 and X20-X26 were located in Si County.

Approximately 1L of water (0.5m below the river surface) was drawn into a precleaned brown polypropylene bottle at each sampling site and stored at 4-10°C before analysis. The pH and water temperature (WT) for the surface water were tested at each sampling site using a combo quality meter (HACHDS5X, USA).

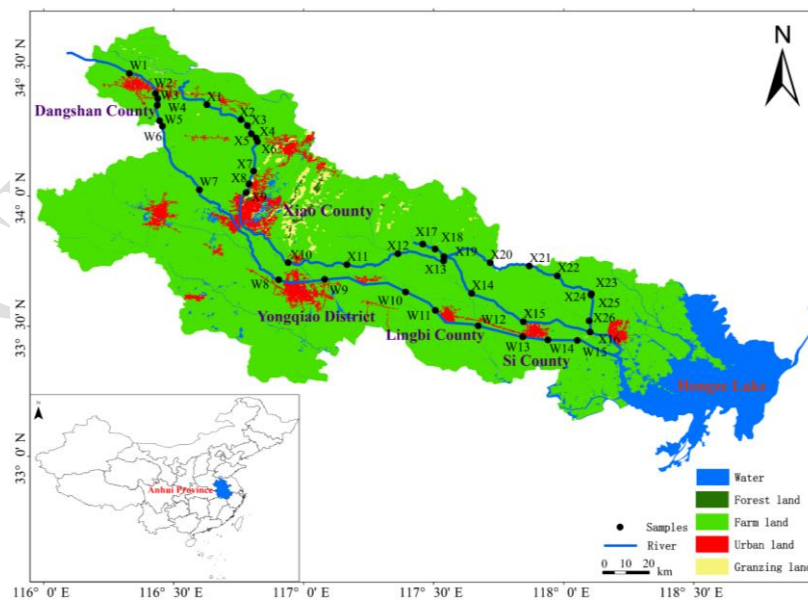


Figure 1. The location of study area and sampling sites in the rural-urban river of Suzhou City, China.

2.2 Sample extraction and analysis

For the total nitrogen (TN), nitrate (NO₃-N), and Suspended Solids (SS), all surface water samples were analyzed and determined by the national standards (TN: HJ 636—2012), (NO₃-N: HJ/T 346—2007), (SS: GB/11901—89).

For the antibiotics analysis, 1.0L of water of each sample was filtered through a glass microfiber filter with a pore size of 0.45 μm in the laboratory. The concentrated sulfuric acid was added into each water sample to adjust the pH at 3.0 for the biological activity inhibition, and then 0.5g Na₂EDTA was added to complex the metal ions (Li et al., 2019). Afterward, all water samples were extracted by solid phase extraction with Oasis HLB column (KANGZHIDA, 500mg, 6ml), Each water sample flowed through the column at a flow rate of 5 ml min⁻¹. then the column was with 5 ml of deionized water to eliminate impurities and dried for 20 minutes (Deng et al., 2016). Subsequently, each HLB column was eluted with 10 ml of methanol. All extracts were concentrated and dissolved into 1 ml methanol.

Concentrations of antibiotics were measured by liquid chromatography - electrospray tandem mass spectrometry (LC-MS / MS) (EXPEC 5210) with a Waters ACQUITY BEH C18 column (2.1×100 mm, 1.7 μm) (Hu et al., 2023). The injection volume was 10 μL with a flow rate of 0.3 mL min⁻¹. The mobile phase solvent was 0.1% (v v⁻¹) formic acid (phase A) and methanol (phase B). All extracts were analyzed in positive ion mode and positive ions were collected in multiple reaction monitoring (MRM) mode. The peak area of each compound was obtained from the chromatogram, and the peak area versus concentration was calculated using the standard curve (Zhou et al., 2022a).

The solved blanks, program blanks, and standards were analyzed every ten samples to check the analytical precision and accuracy. All experiments were carried out in triplicate, and the limit of

detection was from 0.001 to 0.106 depending on the target antibiotics. The surrogates (Sulfamethoxazole-d4, Tetracycline-d6, Ciprofloxacin-d8) were spiked into water samples, and their recoveries ranged from 68% to 83%.

2.3 Composite structural equation model

To determine the drivers of antibiotics in the rural-urban river water, the R4.3.0 analysis software was used to execute the composite structural equation model (SEM) (Tian et al., 2021). In the SEM, the data of land type (e.g. River, Water, Forest land, Farm land, Urban land, Grazing land), environment factors (e.g. pH, T, SS, TN, NH₃-N), and human activities (e.g. population density, discharge of livestock breeding wastewater, and manure) were chosen as the influence factors of antibiotics. The data of the land type and human activities were collected from satellite data and local statistical yearbooks (Kim et al., 2019), and the environment factors were analyzed in the present study. For livestock and poultry factories were collected as the livestock and poultry factors. Based on the various influence factors, all measured variables in the model were first classified as “complex variables”, and then incorporated into the SEM. For the stability of the model relationships, the piecewise SEM was used to rationalize the random effects of the sampling sites and to provide “marginal” and “conditional” contributions of environmental predictors in driving ecosystem stability (Tian et al., 2021).

2.4 Source apportionment of Antibiotics

The principal component analysis coupled with multiple linear regression (PCA-MLR) was used to determine the source apportionment of antibiotics in IBM SPSS Statistics 26.0 (Wang et al., 2013). PCA aimed to extract principal components (PCs) and suggest potential pollution sources, whereas

MLR could select the significant PCs ($p < 0.05$). The determine principal components (PCs) was revealed by using its characteristic antibiotics (loadings on $PC_i > 0.5$) together with the antibiotic usage in human or animals or their occurrence in wastewater. PCA-MLR analysis was performed for water samples and only the antibiotics with detection frequencies higher than 80% were included.

2.5 Risk assessment of antibiotics

The ecological risk of antibiotics can be assessed by the Risk Quotient (RQ) method (Du et al., 2017), which is widely used to assess the risk of various environmental pollutants. The RQ of antibiotics in the aquatic environment was calculated by the following equation:

$$RQ = \frac{MEC}{PNEC} \quad (1)$$

The MEC is the measured environmental concentration and PNEC is the predicted no-effect concentration in water (Zhou et al., 2022b). The PNEC in aqueous media was calculated according to the following formula:

$$PNEC = \frac{LC_{50}/EC_{50}}{AF} \quad (2)$$

LC_{50} or EC_{50} is the lowest median effective concentration value (Du et al., 2017). In previous studies, AF was represented as an appropriate standardized assessment factor (1000). Risks were categorized as high ($RQ > 1$), medium ($0.1 < RQ < 1$), and low ($0.01 < RQ < 0.1$) (Zhou et al., 2022b).

3. Results and discussion

3.1 Occurrence and distribution of Antibiotics

The concentration and composition of detected antibiotics in water samples were summarized. Among the 28 target antibiotics, 26 antibiotics were detected at least once in the water samples with concentrations up to 85.87 ng L^{-1} , indicating that antibiotics were widespread along the rural-urban

river network. The detection rate of 21 antibiotics in the study area reached more than 80%. The maximum number of detected antibiotics per site was 26 for the surface water, with 61% of target antibiotics. The antibiotics concentration in the surface waters ranged from not detected (ND) to 85.87 ng L⁻¹, with a mean value of 145.78 ng L⁻¹ (Fig. 2a, b). Overall NOR and OTC exhibited the highest mean concentrations of 17.39 ng L⁻¹, and 13.21 ng L⁻¹, with detection frequencies of 98%, and 100%, respectively.

Among the four classes of antibiotics, the antibiotics concentration in the surface water: FQs (46.12 ng L⁻¹) > TCs (44.79 ng L⁻¹) > MLs (38.00 ng L⁻¹) > SAs (16.85 ng L⁻¹) (Fig. 2d). FQs were considered as the bacteriostatic antimicrobial agents which widely used in human and animal, and the study area was densely populated with towns and cities (Population of Suzhou City: 1.94 million), resulting in relatively high usage (Miranda et al., 2022). Meanwhile, TCs were widely used in livestock and poultry breeding (Wang et al., 2017). According to the statistical yearbook, there were 2280 livestock and poultry farmers in Suzhou City in 2022, with a total of 690,000 tons of wastewater discharges per year, and these discharges contributed to high TCs pollution in the study area. MLs were widely used in the treatment of human bacterial infections, and as feed additives in livestock (Bandell et al., 2019). SAs were mainly used in animal treatment in the livestock industry (De Liguoro et al., 2018), but they were easily decomposed in sunlight (Hu et al., 2022). The abundant light in summer accelerated the decomposition of SAs, which resulted in low concentrations of SAs in water. Thus, it was found that the contents of antibiotics was significantly influenced mainly by human activities around the study area.

The distribution of antibiotic levels in water of the study area was found that Yongqiao District (mean value: 157.49 ng L⁻¹) > Xiao County (mean value: 151.11 ng L⁻¹) > Lingbi County (mean value:

141.96 ng L⁻¹) > Dangshan County (mean value: 141.30 ng L⁻¹) > Si County (mean value: 139.96 ng L⁻¹) (Fig. 2d). According to the statistical yearbook, Yongqiao District and Xiao County are the two most populous counties in Suzhou, accounting for 58.6% and 12.3% of the population respectively. In addition, there are significant regional differences in the distribution of agricultural and sideline products in Suzhou City. The fruit industry is dominated by Dangshan pear in the northern part of the study area (Dangshan County), while livestock, and poultry breeding are represented by Fuli roasted chicken in the southern part (Yongqiao District and Lingbi County). Based on the distribution of the antibiotics in the five zones, we found that the antibiotics levels in the densely inhabited area and livestock and poultry breeding area were higher than that in the planting region (Wei et al., 2024). The distribution of various antibiotics in each counties were shown that the antibiotics of the human medicinal using were dominant in Xiao County (OFI: 11.7 %, NOR: 11.8 %), Si County (NOR: 12.5 %) while the animal-derived antibiotics were dominant in the Yongqiao District (CTC: 9.0 %), Lingbi County (OTC: 9.4 %, CTC: 9.9 %). OFI and NOR is a common bacterial therapeutic drug which used by humans (Wain et al., 2021), CTC and OTC were most used in livestock Sun et al., 2017). It is worth noting that in animal excreta, TCs was difficult to remove due to their structural peculiarities and higher concentrations (Yang et al., 2022). These antibiotic residues in feces promote the production of ARGs, which might lead to increased drug resistance, making bacterial infections gradually difficult to treat with antibiotics and posing a significant threat to human health (He et al., 2020). In summary, the antibiotics contents in water were higher in the densely populated and

livestock breeding areas.

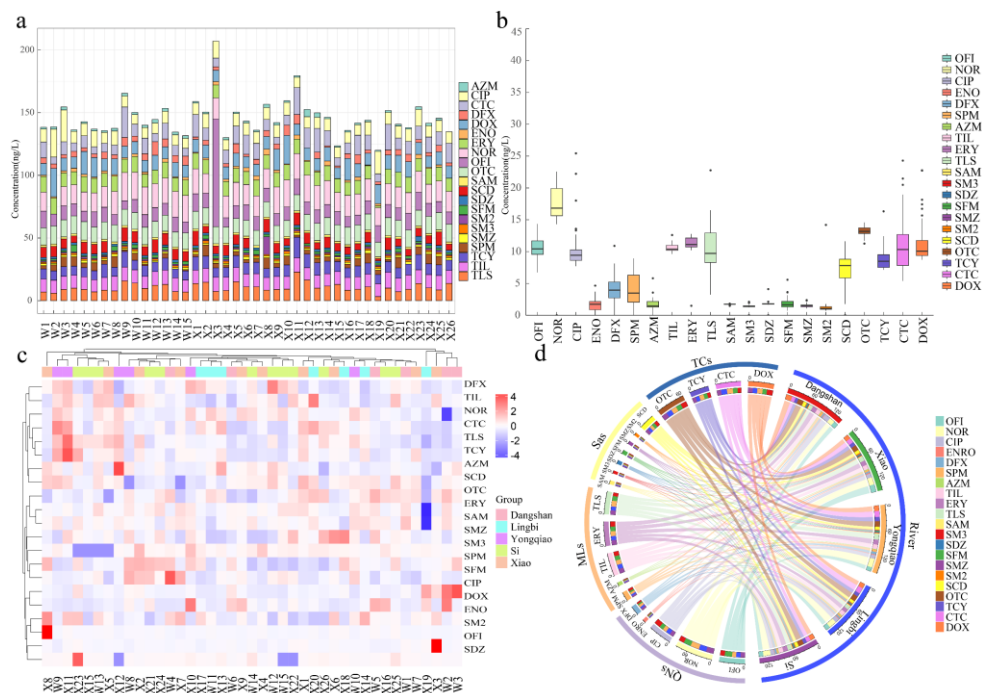


Figure 2. spatial changes of antibiotic in the rural-urban rivers of Suzhou City, China. (a) Antibiotic distribution in study area. (b) Concentration of each antibiotic in present study. (c) Clustered heat map of antibiotic concentrations in all samples, with each cell color representing z-score normalized concentration values. (d) The chordal graph demonstrates the levels of various types of antibiotics in different rivers.

3.2 Factors influencing the distribution of antibiotic levels

The driving factors of antibiotic migration and transformation in water bodies were complex (Anthony A et al., 2018). The Composite structural equation model, Mantel test, and correlation network model were utilized to analyze the correlation between antibiotics and their drivers in the present study. The structural equation model can be used to determine the degree of influence of individual and global composite variables on antibiotic distribution through multiple regression analysis (Tian et al., 2021). The results of the structural equation model indicated that human activities, environmental factors, and land uses were accounted for 69% of the drivers of antibiotics, while the land use had the least driving influence (path coefficient of 0.30) (Fig 3a). Among the complex

variables of the land use (e.g. farmland, building, water, forest and grassland), all the land uses have non correlation with antibiotics contents.

For the environment factors, the individual environmental factor (pH, T, SS, TN, NH₃-N) did not show a strong correlation with the total amount of antibiotics, but the environmental factors as a whole demonstrated a generally significant driving force of antibiotic distribution ($p=0.01$) (Fig. 3a).

In the Mantel test (Fig. 3b), NOR and CIP were affected by the whole environmental factors ($p<0.01$).

In detail, a negative correlation between NOR and pH was identified from the correlation analysis ($r=-0.4$, Table S1) (Fig. 3c). The result was attributed to the impact of pH on the ionic form of NOR, and the previous study suggested that the degradation of NOR at pH=11 was twice as efficient as at pH=3 (Wang et al., 2020). Furthermore, a significant correlation was shown between CIP and SS ($r=0.82$), due to the high adsorption of CIP to suspended matters and sediments (Dinh et al., 2017).

The structural equation model revealed that human activities (e.g., population density, discharge of livestock breeding wastewater, and manure) had the highest path coefficient (0.51), as the most direct driving factor (Fig. 3a). Among the complex variables of human activities, population factor was strongly associated with antibiotics ($p<0.001$) indicating that population was the main driving factor for antibiotics in the model (Fig. 3a). In the study area, as the human-derived antibiotics (Norrby and Jonsson, 1983), OFI and NOR were the high antibiotics in the rural-urban rivers. In the Mantel test, human activities showed a significant correlation with TLS, TCY, and CTC ($p<0.01$) (Fig. 3b), and the correlation analysis revealed that this correlation was primarily influenced by discharges from livestock and poultry breeding (Fig. 3c). Livestock breeding was booming in the study area, and TCY was widely used for antimicrobial therapy in animals (Amangelsin et al., 2023). Besides, CTC and TLS were often added to feeds to promote growth and assist in antimicrobial therapy (Kobashi et al.,

2008; Thomas et al., 2017). These residual antibiotics in urine and feces were flown into the river water. In short, antibiotics were widely used and the main drivers were human activities in the rural-urban rivers.

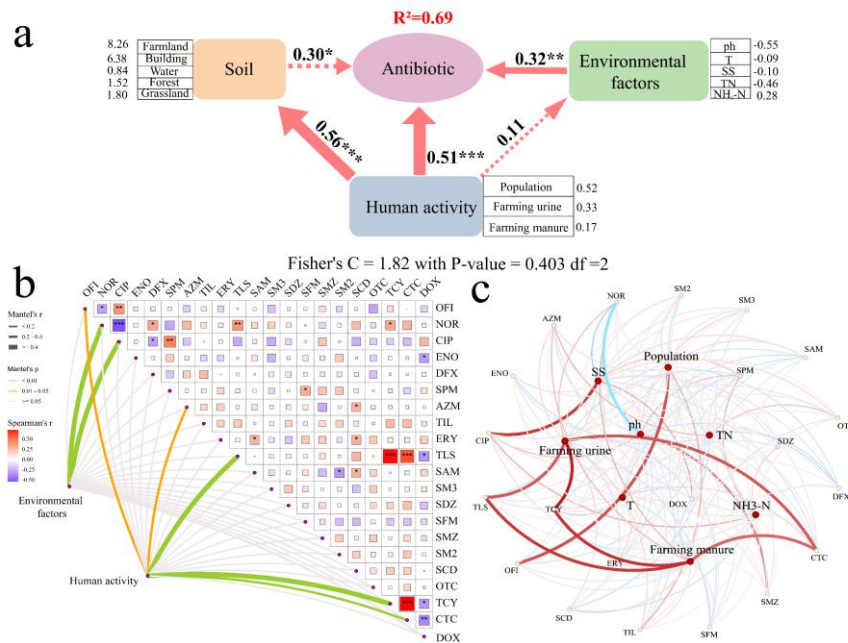


Figure 3. The driving factors of the distribution of antibiotics. (a) The composite structural equation model of antibiotic distribution in the study area. Numbers adjacent to measured variables are their coefficients with composite variables. The numbers next to the arrows are path coefficients showing the direct standardized effect of the relationship. The thickness of the arrows indicates the strength of the relationship. The total standardized effect of the complex variables is shown in marginal, and condition R^2 represents the variance proportion explained by all predictors of the random effect. (b) The correlation between antibiotics and different influencing factor groups by Mantel Test. (c) The correlation between antibiotics and each influencing factors. Red lines representing positive feedback effects, blue representing negative feedback effects

3.3 Source analysis of antibiotics

To enhance the reliability of the antibiotic source apportionment, the PCA-MLR method was used in the present study (Wang et al., 2013). The majority of the variance (84.7%) in the water antibiotics was accounted by four principal components (PCs). PC 1 explained 57.6 % of the total variance, PC 2 accounted for 17.0 %, PC 3 accounted for 6.3 %, and PC 4 accounted for 3.7 %. Along the PC 1

axis, PC 1 had a strong correlation with CTC (0.58), which was commonly used in the livestock and poultry breeding (Kobashi et al., 2008; Thomas et al., 2017). PC 2 presented significant correlation loading for NOR (0.48), which was closely related to the treatment of urinary tract infections in humans (Norrby and Jonsson, 1983). PC 3 had a strong correlations with DOX (0.72), which is often used in the treatment of human skin (Korbi et al., 2021). PC 4 presented strong positive loading for OFI (0.996), which was a medication used for treating Typhoid fever in humans (Wain et al., 2021). The contributions of the major inputs of antibiotics in the rural-urban river water were estimated with MLR from the PCA scores. Based on the calculation, the sources of antibiotics were predominated by medicinal use for humans (70%), followed by medicinal use for livestock (30%) in the rural-urban rivers of Suzhou City.

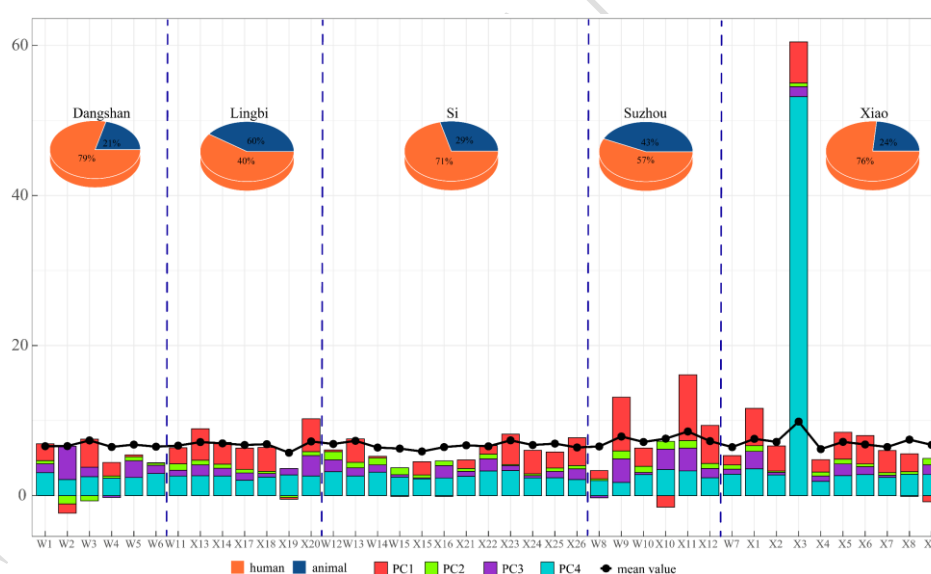


Figure 4. Source contributions of antibiotics by PCA-MLR in study area

3.4 Environmental risk assessment

The risk Quotient (RQ) method has been widely used to evaluate the risk assessment of antibiotics (Li et al., 2023). However, due to the different hazards of antibiotics to different species (Tian et al., 2023), the representative algae, invertebrates, fish, daphnia, and plants were collected for risk

assessment in present study. The ecological risk posed by antibiotics was similar in the different counties as shown in Fig. 5.

For algae, most antibiotics have the medium risk in the rural-urban rivers. In detail, 15.4% of the antibiotics have the low risk, and 38.5% of the antibiotics have the medium ecological risk. It is noteworthy that the mean RQ values of OFI, CIP, ERY, NOR, and CTC of algae were 0.76, 0.60, 0.57, and 0.44, respectively, indicating OFI, CIP, ERY, NOR, and CTC posed a medium ecological risk to algae. In addition, OFI posed a high risk in the sampling site of X3 at the Xiao county (RQ = 5.37), and CIP posed a high risk in the sampling site of W2, W3 at the Xiao county (RQ = 1.31, 1.35), which induced ARG profiles in algae and allowed more bacteria carrying ARGs to spread from algae to the ecology, cultivating superbugs and posing a threat to the ecology and human health (Xue et al., 2023).

For plants, most antibiotics (80 %) have the low risk in the rural-urban rivers. Interestingly, SM2 which belongs to SAs has the lower value in present study (the mean value of 1.44 ng L⁻¹), but has the highest RQ value for plants (RQ = 0.07). Similarly with previous studies, SM2 were potentially significant in causing the ecotoxicological effects (Deng et al., 2016; Li et al., 2018). The antibiotics have the low risk for animals in the rural-urban rivers, as the least exposing to antibiotics in the study area. In detail, OTC, ERY, and CTC posed low risk to invertebrates and daphnia, but no significant risk to fish in rural-urban rivers (Li et al., 2022). In a word, algae was most sensitive to antibiotics in rural-urban rivers of Suzhou City, and the management of antibiotic contamination in the present study is urgent. In recent years, because of the antibiotic pollution in economically developed areas, the ecological risk of antibiotic in rural-urban river network is likely to be more serious (Wu et al., 2024). In summary, there is a great need for research on the contamination of the rural-urban river

network to prevent the ecological hazards of antibiotic pollution.

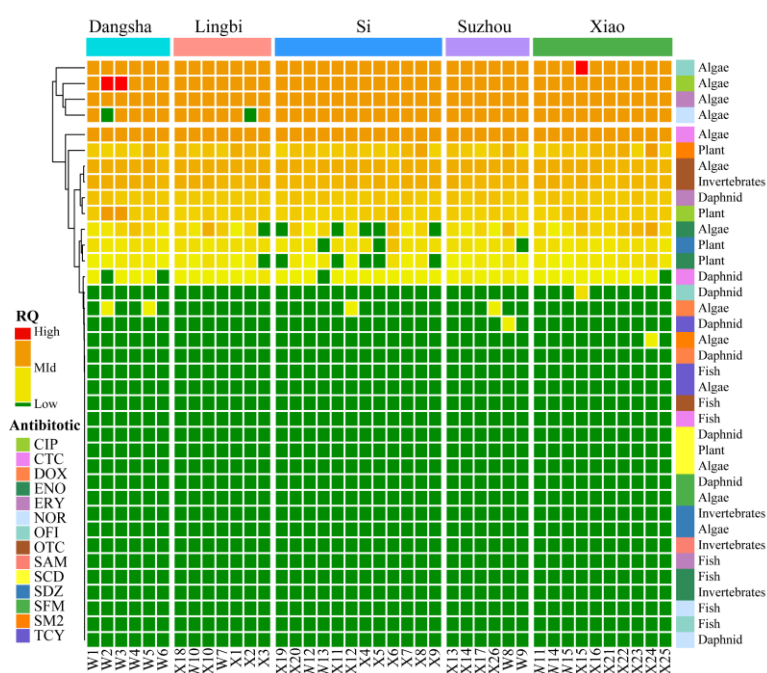


Figure 5. Ecological risk of antibiotics in the study area

4. Discussion

This study presented insights into four antibiotic classes variations throughout the rural-urban river network. Twenty-one antibiotics were detected in the river water with total concentrations in the range of nd-85.87 ng L⁻¹. Antibiotic concentrations in water were following: FQs > TCs > MLs > SAs, and the antibiotic values were higher in the densely populated and breeding areas. The regional variations of antibiotic profiles in water along the rivers can be explained by the main influence of population, and followed by livestock according on the composite structural equation model, Mantel test, and correlation network model . The PCA-MLR analysis suggests that the antibiotics in river water are mainly from human (70 %) and livestock (30 %) medical using. Finally, antibiotics pose a medium risk to algae, while the risk to plants and Invertebrates is low. The results of the present study will fill the knowledge gap of the antibiotic in the typical rural-urban river network, and also help to provide guidance and suggestions for the management of antibiotic pollution in this study area.

Acknowledgment

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Supporting Information

Table S1. Pearson values of correlation networks.

Antibiotic	ph	T	SS	TN	NH3-N	population	Cultured urine	Farming manure
OFI	0.08	0.02	-0.04	-0.19	-0.06	0.7	-0.05	-0.1
NOR	-0.4	0.03	-0.71	0.07	-0.04	-0.06	0.25	0.32
CIP	0.27	-0.03	0.8	0.13	0.33	0.14	-0.09	-0.15
ENO	-0.09	-0.07	-0.07	-0.26	-0.1	0.12	0.09	0.07
DFX	-0.33	0.1	-0.14	-0.33	-0.03	-0.19	0.05	-0.05
SPM	0.26	-0.05	0.23	0.15	0.3	0.1	-0.18	-0.1
AZM	-0.19	0.07	0.04	0.3	0.13	-0.14	0.17	0.27
TIL	-0.16	-0.02	-0.07	-0.03	0.04	0.3	0.16	0.12
ERY	-0.19	-0.17	0.13	-0.03	0.04	0.11	-0.17	-0.07
TLS	-0.09	0.07	-0.21	-0.09	-0.05	-0.07	0.67	0.8
SAM	-0.29	-0.3	0.16	-0.07	0	0.14	-0.18	-0.05
SM3	0.17	0.07	-0.09	0	-0.12	-0.05	-0.04	-0.07
SDZ	0.03	-0.1	0.12	0.05	0.2	0.04	0.04	0.03
SFM	-0.05	-0.2	-0.14	0.09	0.03	-0.05	-0.23	-0.1
SMZ	0.48	0.12	-0.05	0.07	0.06	-0.01	0.06	0.04
SM2	0.01	0.05	-0.06	-0.2	-0.11	0.15	-0.03	-0.04

SCD	-0.1	0.08	0.06	-0.31	-0.23	-0.01	0.15	0.16
OTC	-0.02	0	0.15	0.24	0.1	0.08	-0.1	-0.11
TCY	-0.02	0.25	-0.14	-0.08	-0.05	-0.03	0.9	0.82
CTC	-0.06	0.19	-0.17	-0.06	-0.01	-0.05	0.67	0.61
DOX	0.01	-0.29	0.36	0.06	0.04	-0.13	-0.25	-0.23

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