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RESEARCH ARTICLE

Analysis of bacterial community distribution characteristics in the downstream section of a cross confluence in a polluted urban channel

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Abstract
Channel confluences are common in urban rivers and caused complex hydrodynamic conditions in the downstream section, significantly influencing the distribution of pollutants and the microbial community. So far, the principles of bacterial community assembly and their linkages with environmental factors are poorly understood. In the present study, the hydrodynamic and pollution conditions were investigated in a typical channel confluence of an urban river in the Yangtze River delta area, China, and their impacts on the bacterial community structure in the water and sediment were characterized using 16S rRNA gene high-throughput sequencing technology. Based on the results, the flow velocity was the crucial factor influencing the dispersal of nutrients, organic compounds, and bacterial communities in the river water. Moreover, the sediments exhibited higher α-diversity and bacterial richness for nitrogen and sulfur cycling than the water. In addition to flow velocity, the contents of total organic carbon, total phosphorus, and heavy metals determined the sediment bacterial communities at varying depths. The predictive analysis of functional gene category indicated differences between the water and sediment communities in metabolic potentials and pathogen risk and provided guidance for water pollution control and the eco-remediation of urban rivers.

Keywords Channel confluences · Bacterial community · Hydrodynamic conditions · Water pollution · Sediments · Correlation analysis

Introduction

In surface water, the dynamic interchange of material between water and sediment, driven by hydrodynamic diffusion, is a critical process influencing biogeochemical processes (Yang et al. 2019). In this context, sediments can provide a record of the upstream inputs of pollutants and a natural medium for microbe growth (Sun et al. 2012). Microbial communities not only function in the transformation of nutrients, the biodegradation of organics, and the conversion of energy but also are shaped by the hydrodynamic conditions, such as the velocity distribution of cross-section (Li et al. 2020b; Shao et al. 2011; Wu et al. 2017). For instance, Zhang et al. (2022c), by incorporating the bacteria-based index of biotic integrity (Ba-IBI), the path model, and the random forest regression model, found that the primary environmental factors affecting the sediment bacterial communities in river bends were flow velocity and ammonium concentration. Cai et al. (2019) observed that the microbial community assembly in black-odor rivers, which lose ecosystem functions, was mainly controlled by sulfur metabolism under oxygen-limited conditions. In another study, the transport of microorganisms and chemicals within and between water and sediments was identified as the rate-limiting step for the nitrogen dynamics in urban channel

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confluences using omics-based modeling (Hui et al. 2021). In addition, dam-induced environmental variations, especially hydrological and nutrient variables, potentially influence the microbial food web, intensifying the accumulation of organic carbon, ammonium, and inorganic phosphorus in river systems (Yang et al. 2021a, b). Given that the ecological selections of the microbial community assembly are governed by deterministic and stochastic processes (Li et al. 2020a, 2020c), it is necessary to identify the strong environmental factors that directionally shape the microbial community and specific functions. Such an approach can be used to support the self-purification capacity of water bodies.

The Yangtze-River-Delta is a well-developed mega-region; it contained around 11% of the permanent population in China, and economics of scale accounted for 20% of gross domestic product of the country by the end of 2016 (Wang et al. 2020a). Although the across-the-board Action Plan for the Prevention and Control of Water Pollution has been implemented since 2015, the improvement of the surface water quality remains a major challenge for urban sustainable development in this region, with the goal of ultimately eliminating black-odor water bodies in urban and rural areas by 2025 (GOJPG 2021).

As the junctions of different river systems, urban channel confluences exhibit sharp shifts in the pollutant distribution and flow dynamics on the cross section after the stream mixing (Li et al. 2020a; Hui et al. 2022). The confluence-induced heterogeneity in the microbial community would be mainly created by the diverse pollutant transport and transformation in overlying water and surface sediments, which is critical for the evaluation and improvement of aquatic ecosystem health (Burton and Johnston 2010). However, the principles of microbial community assembly and their linkages with hydrodynamic conditions and pollution levels in urban channel confluences are still poorly understood. In this sense, in situ investigations on the ecological function potentials of microbial communities are needed to provide solid evidence for guiding the eco-remediation of polluted urban rivers.

In this study, a typical cross confluence of an urban channel near the Yangtze River estuary was selected as the study site, with the following main objectives: (1) to characterize the differentiation of the hydrodynamic conditions, contaminant distributions, and bacterial communities in the same downstream section; (2) to analyze the correlation between bacterial community and environmental factors in water and sediment phases; (3) to investigate the metabolic potentials of bacterial communities in nutrient cycling and pollutant degradation.

Materials and methods

Site description and sample collection

The urban channel cross confluence is located in Suzhou City in the Yangtze-River-Delta, China (121°5′28″E, 31°25′53″N). Channel A is a local important shipping transport waterway, and the joining of Channel B and C changed the hydrodynamic conditions in the downstream section (Fig. 1a and b). There are numerous ports, agricultural land, and residential areas distributed along channels A, B, and C in the upstream, representing point and non-point effluent sources for inputs of nutrients and contaminants.

Two mixed water samples (W1 and W2, 5–20 cm in depth) were collected at the points near the right riverbank (P1) and the main channel (P2) in July 2020. The results of underwater sonar scanning (M9, SonTek, USA) indicated an average flow velocity (u) of 0.18 m/s in P2 and of 0.0 m/s in P1 (Fig. 1b), which created a sedimentation zone near the riverbank. Two groups of sediment samples (S1 and S2) were collected using a piston sampler (XDB0204, Pusen, China) at sediment depths of 0–10 cm (S1-1 and S2-1), 10–30 cm (S1-2 and S2-2), and 30–50 cm (S1-3 and S2-3) in P1 and P2, respectively. To avoid random sampling, the triple parallel sediments were sampled in the triangle (2 m side length) at the same depth. All samples were stored at − 80 °C for the extraction of bacterial DNA and freeze-dried for physicochemical analysis.

Physicochemical analysis

The dissolved oxygen (DO) concentration was determined in situ using a HACH HQ30d portable DO meter (Hach Co., Loveland, CO, USA). The concentrations of ammonia nitrogen (NH_4^+-N), total nitrogen (TN), total phosphorus (TP), and total organic carbon (TOC) in water samples were measured using the procedure described in Standard Methods (APHA 1998).

The TOC contents in the sediments were analyzed by the thermodilution method, applying sulfuric acid and potassium dichromate; sediment total phosphorus (TP) was determined using the Murphy-Riley method after digestion with H_2SO_4–$HClO_4$, and the sulfide contents were determined using methylene blue spectrophotometry (Bao 2008). Sediment total nitrogen (TN) was analyzed with a continuous-flow automated analyzer after digestion with H_2SO_4–H_2O_2 (Soon and Kalra 1995). The typical heavy metals, including cadmium (Cd), arsenic (As), lead (Pb), chromium (Cr), and copper (Cu), were quantified via inductively coupled plasma (ICP) spectra, following the sample pretreatment described in the literature (Ning et al. 2014).

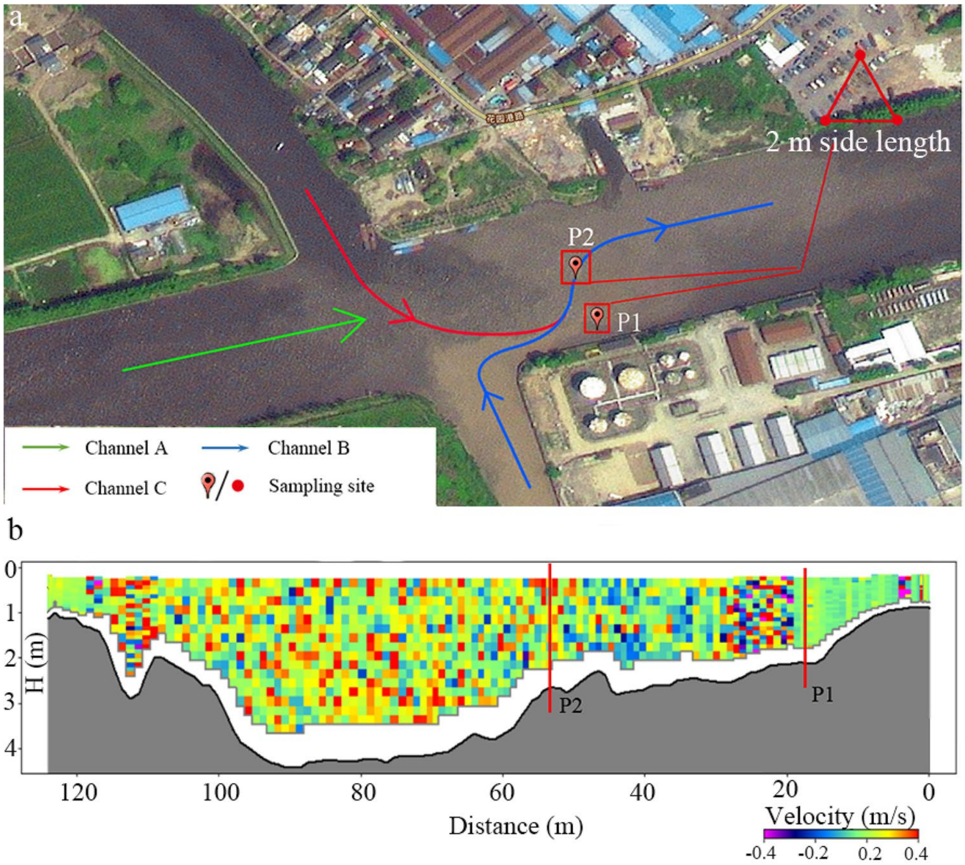


Fig. 1 **a** Location of sampling sites and **b** flow velocity distribution in the downstream section of channel A

3D-EEM fluorescence analysis

A three-dimensional excitation-emission matrix (3D-EEM) fluorescence spectrophotometer (FSS, Edinburgh Instrument Ltd., UK) was employed to analyze dissolved organic matter (DOM) in the water samples, using corresponding scanning emission (E_m) spectra from 260 to 550 nm by varying the excitation (E_x) wavelength from 200 to 400 nm at 10-nm increments; the scanning speed was set at 2,000 nm·min^{-1}. Two alternative fluorescence indices are proposed for characterizing DOM, with the following calculations (Ohno 2002; Huguet et al. 2009):

$$\textit{Humification index}\ (HIX) = (\Sigma I_{\mathrm{Em435-480}})/(\Sigma I_{\mathrm{Em300-345}}) \tag{1}$$

where $I_{\mathrm{Em435-480}}$ and $I_{\mathrm{Em300-345}}$ are the fluorescence intensities at the E_m of 435–480 and 300–345 nm using an E_x of 254 nm, respectively. A large *HIX* value indicates an increase in the humification degree of DOM (Ohno 2002).

$$\textit{Biological activity index}\ (BIX) = I_{\mathrm{Em380}}/I_{\mathrm{Em430}} \tag{2}$$

where I_{Em380} and I_{Em430} are the fluorescence intensities at the E_m of 380 and 430 nm using an E_x of 310 nm, respectively. The $BIX < 0.8$ indicates that terrestrial origin inputs (such as anthropogenic activity) dominate the DOM, while the $\mathrm{BIX} > 1.0$ suggests the dominant role of aquatic microbe sources (such as plankton, bacteria, and algae) (Huguet et al. 2009).

DNA extraction, PCR amplification, and sequencing

Microbial DNA was extracted from all samples using the E.Z.N.A.® soil DNA Kit (Omega Bio-tek, Norcross, GA, USA) according to the manufacturer's protocols. The V3–V4 hypervariable regions of the bacteria 16S rRNA gene were amplified with primers 338F (5′-ACTCCTACGGGAGGCAGCAG-3′) and 806R (5′-GGACTACHVGGGTWTCTAAT-3′) by the thermocycler PCR system (GeneAmp 9700, ABI, USA). The PCR reactions were conducted using the program in our previous report (Qian et al. 2018). Purified amplicons were pooled in equimolar concentrations and paired-end sequenced (2 × 300) on an Illumina MiSeq platform (Illumina, San Diego, USA) according to the standard protocols by Majorbio Bio-Pharm Technology Co. Ltd. (Shanghai, China).

Data analysis

The sequencing of 16S rRNA gene amplicons from 6 mixed water and 18 sediment samples produced 1,226,620 reads with an average length of 418 bp. The obtained sequences could be assigned to 7773 operational taxonomic units (OTUs) at a 97% similarity cutoff using UPARSE (version 7.1). The taxonomy of each 16S rRNA gene sequence was analyzed by the RDP Classifier algorithm (http://rdp.cme.msu.edu/) against the Silva (SSU123) 16S rRNA database using a confidence threshold of 70%.

The α-diversity indices (OTUs richness, Ace, Chao, Shannon, and Simpson) of the 24 samples were calculated by Mothur. Composition analysis was conducted at the phylum and family levels. Principal component analysis (PCA) of environmental parameters was performed with the CANOCO 5 software. The *Z*-score method was used for normalization calculations, and the logarithmic value was displayed according to the logarithmic value Log, so that the change of the color bar was used to visually represent the changes in variables among different samples. Comparison of the relative abundances of the most abundant family among samples was performed using the heatmap package of R 3.2.4 (https://www.r-project.org/). Correlations between the environmental parameters and bacterial communities were measured using the Spearman correlation analysis (significance $P<0.05$) in SPSS 20.0. The software Gephi was applied to visualize and render all networks. According to the annotation of the 16S rDNA sequence classification by the KEGG database, the functional prediction of the output microbial community was conducted using Functional Annotation of Prokaryotic Taxa (FAPROTAX) (Qu et al. 2020).

Results and discussion

Physicochemical characteristics of samples

The main water quality parameters and 3D-EEM images of samples W1 and W2 are shown in Fig. 2. With the combined pollution of organics and nutrients (TOC and TN), the DO concentration of channel A was below the Standard V (DO ≥ 3 mg/L) in the Environmental Quality Standard for Surface Water of China (GB3838-2002), which was similar to the typical polluted urban channel located in the Yangtze-River-Delta region (Yang et al. 2021a). There were four characteristic peaks, located at E_x/E_m of 255–280/320–335 nm (peak T_1), 230–235/330–335 nm (peak T_2), 230–240/425–440 nm (peak A), and 305–340/420–430 nm (peak C) in 3D-EEM. According to previous studies (Huguet et al. 2009; Qian et al. 2022), the protein-like substances related to microbial activity (peak T_2) dominated in W1 and W2, followed by fulvic acid compounds (peak A). With the different *u* values in P1 and P2, W1 exhibited a relatively higher BIX and a lower HIX than W2. This indicates that aquatic microbe sources contributed more to the pollution of P1 near the riverbank than terrestrial origin inputs. The higher humification degree of DOM in the main channel (P2) was in agreement with terrestrial origin inputs from upstream runoff.

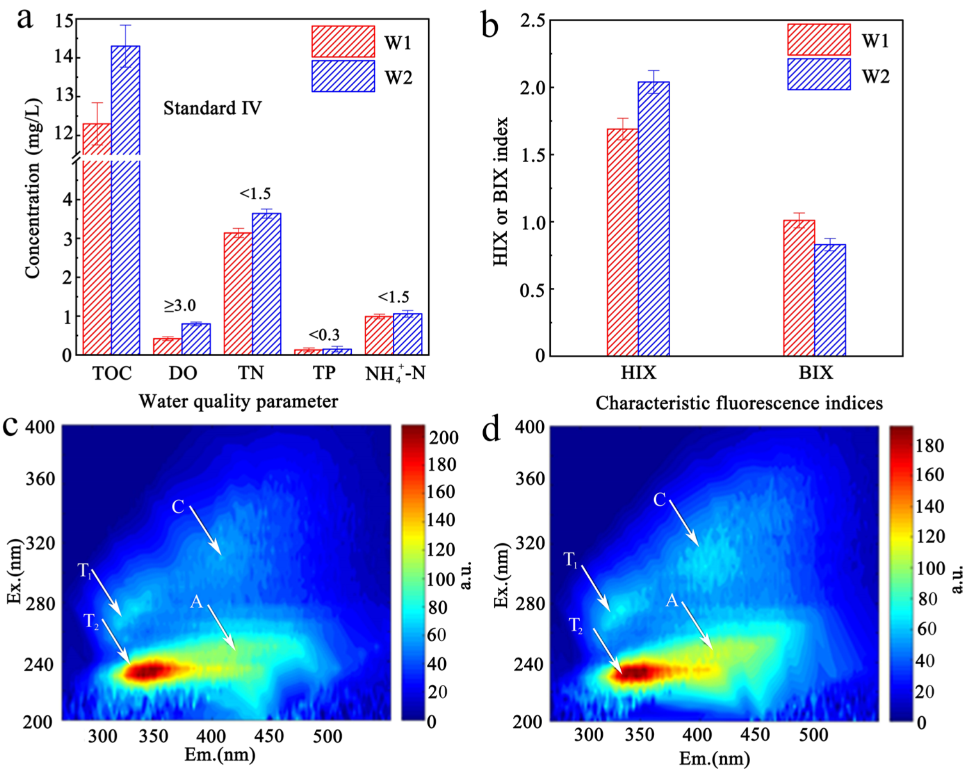


Fig. 2 **a** Water quality and **b** characteristic fluorescence indices of water samples and 3D EEM fluorescence spectroscopy of **c** W1 and **d** W2

Figure 3 displays the pollutant contents of sediments in P1 and P2 at various depths. The TOC contents in group S1 increased as increasing sampling depth, and the opposite pattern was found for group S2. Due to the terrestrial origin inputs and low flow velocity, the TOC level (3.5–5.7 g/kg) in the sediments was significantly higher 0.4–3.4 g/kg in the previous reports of this region (Wu et al. 2019; Zhang et al. 2022b). According to the Standard for Contaminated Sediments in Freshwater Ecosystems of USEPA (Cieniawski et al. 2002), the TN, TP, and sulfide contents of S1 and S2 were heavily polluted, with pollution levels above the median values in local urban rivers, namely, as 1.0–4.9 g/kg for TN, 0.4–2.0 g/kg for TP, and 0.02–0.2 g/kg for sulfide (Wu et al. 2019; Lei et al. 2020). In addition, the As, Cd, and Pb levels of S2 were higher than those of S1, and lower levels of total Cr and Cu were found in P2 close to the main channel. Notably, the average contents of total Cr, As, Cd, Pb, and Cu in the sediments were 1.03, 2.40, 3.10, 1.89, and 1.98 times those of the local background values (65.7 g/kg for total Cr, 8.8 g/kg for As, 0.12 g/kg for Cd, 22.8 g/kg for Pb, 20.4 g/kg for Cu) (Wang et al. 2020b), respectively (Vareda et al. 2019). Because of the considerable ecological risk of heavy metals, the channel cleanout or in situ stabilization of the polluted sediments should be conducted in the channel confluences (Ning et al. 2014; Li et al. 2020b).

Bacterial community diversity in water and sediments

The *α*-diversity indices of water and sediment samples are listed in Table S1. The Ace, Chao, Shannon, and Simpson indices revealed significantly lower levels of bacterial community richness and *α*-diversity in water samples (average Ace 1837.5, Chao 1613.0, Shannon index 4.85, and Simpson index 0.03) compared to sediments (average Ace 4510.2, Chao 4433.8, Shannon index 6.53, and Simpson index 0.01). Because of the substrate gradients, good biocompatibility, and high enrichment capacity, the sediments could provide diverse niches for microbial growth under anthropogenic interference, facilitating the formation of integrated microecosystems (Crump et al. 2012; Meziti et al. 2016). For the same channel section, considerable differences between W1 and W2 or between S1 and S2 groups in terms of biodiversity were not found.

Figure 4a shows the results of PCA in the water and sediment samples. The dispersion degrees of W1 and W2 spots were significantly larger than those in the sediments (group S1 and S2) in both PCA1 (resolution 67.45%) and PCA2 (14.31%) levels. As shown in Fig. 4b, the shared OTUs between W1 and W2 accounted for 78.0% in W1

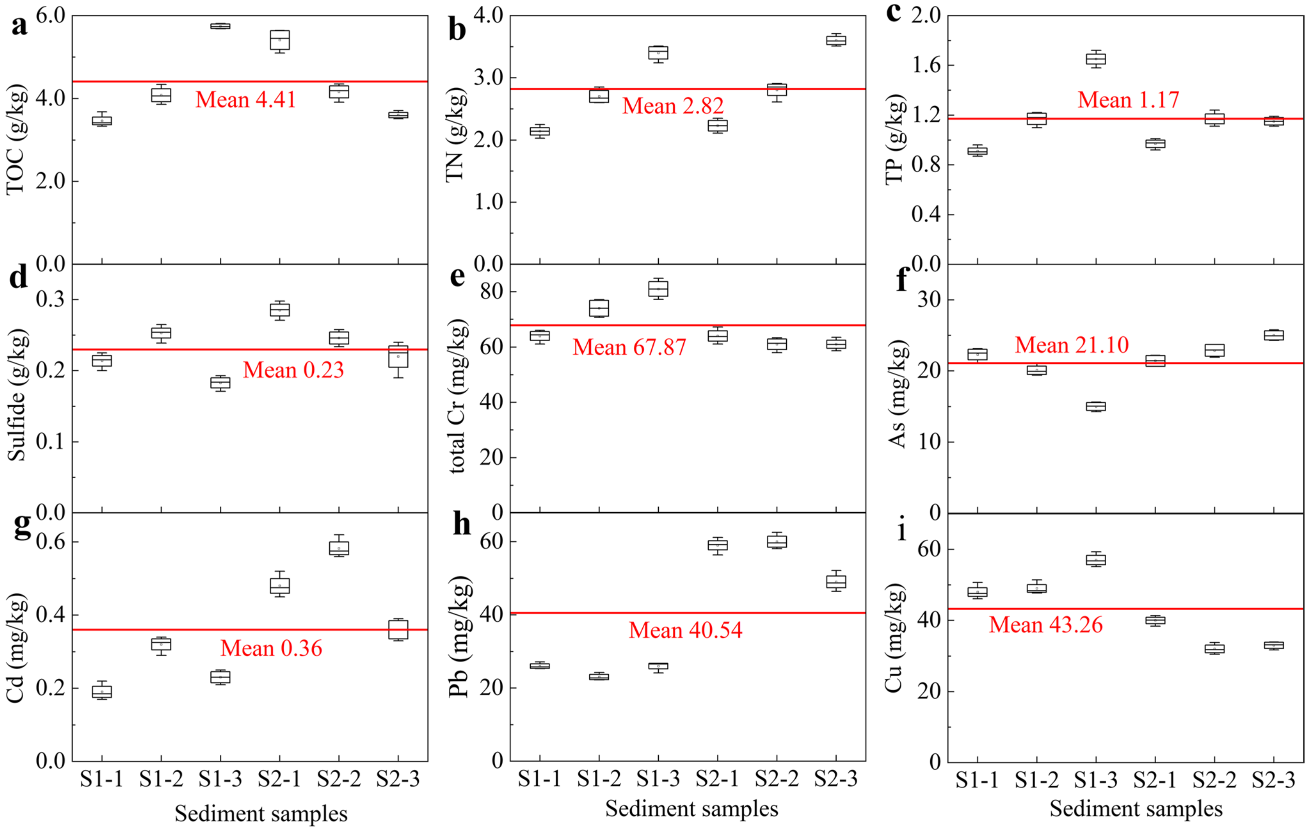


Fig. 3 (**a**) TOC, (**b**) TN, (**c**) TP, (**d**) sulfide, (**e**) total Cr, (**f**) As, (**g**) Cd, (**h**) Pb, and (**i**) Cu contents in sediment samples

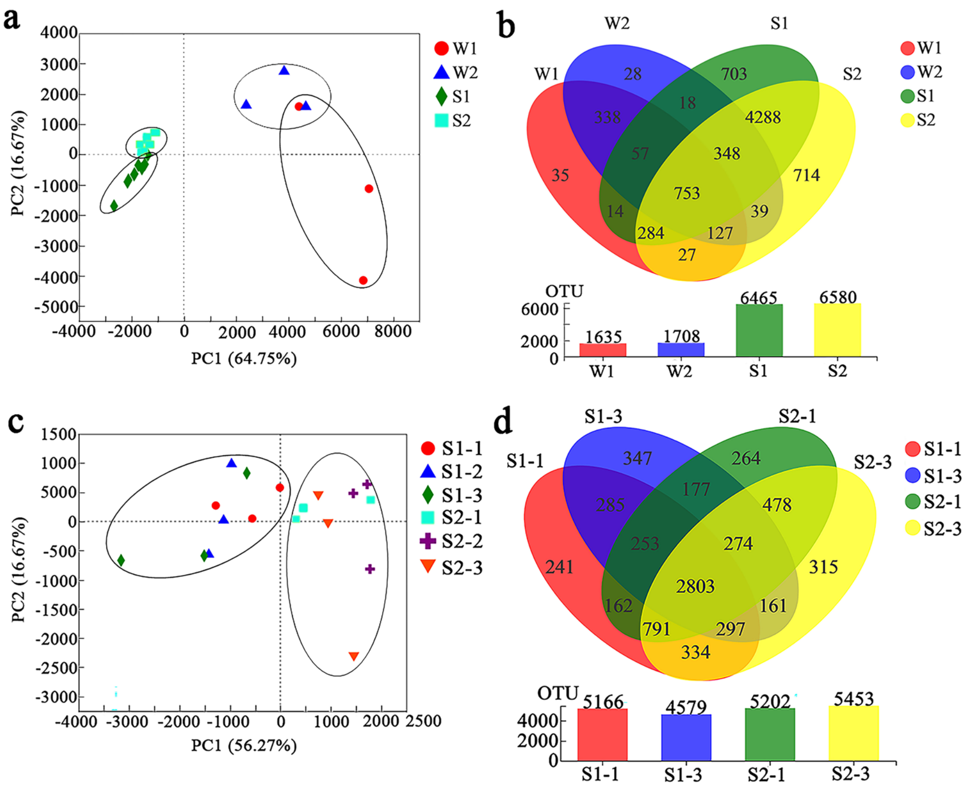


Fig. 4 **a** PCA analysis and **b** Venn diagram of water samples and sediment groups on the OTU level, and **c** PCA analysis and **d** Venn diagram of sediment samples in different depth

and 74.6% in W2, respectively, and group S1 shared more than 90% of OTUs with S2. Liu et al. (2018) investigated the integrated biogeography of sedimentary bacterial communities in the Yangtze River and found that the estimated immigration rate (*m*) of sediment communities (0.1463–0.1640) was considerably lower than that for water communities (0.1814–0.1997). The relatively stable sediment communities were mainly attributed to the serious dispersal limits (Liu et al. 2018). The flow of river water would not only drive the transports of nutrients, organic matter, and suspend solids in different environmental but also enhance microbial community coalescence and further control habitat biodiversity and metabolic processes (Li et al. 2015; Meziti et al. 2016; Zhang et al. 2022a). The slow *u* in P1 resulted in a higher bacterial community difference in group S1 than that in group S2, in terms of the longer PAC1 (56.27%) distance in Fig. 4c. The 3638 shared OTUs between S1-1 and S1-3 were less than the 4346 OTUs between S2-1 and S2-3 (Fig. 4d), whereas the surface sediments (4009 OTUs shared by S1-1 and S2-1) exhibited a higher similarity than the deep ones (3535 OTUs shared by S1-3 and S2-3).

As seen in Fig. 5, the dominant bacterial phyla in the water samples were Proteobacteria (relative abundance 23.9% in W1, 38.1% in W2), Actinobacteriota (46.0% in W1, 33.3% in W2), Bacteroidota (12.5% in W1, 10.9% in W2), Cyanobacteria (10.8% in W1, 10.5% in W2), and Chloroflexi (1.5% in W1, 2.3% in W2), which were different from those in the sediment groups, where Proteobacteria (28.0% in S1, 19.8% in S2), Chloroflexi (23.4% in S1, 27.9% in S2), Acidobacteriota (9.6% in S1, 11.1% in S2), Desulfobacterota (7.5% in S1, 5.9% in S2), and Firmicutes (6.1% in S1, 3.9% in S2) were dominant. Notably, slow-growth nitrite-oxidizing bacteria, such as Nitrospirota, were only detected in the sediments (2.1–2.6%). According to Lei et al. (2020), considering phylogenetic turnover deviation, dispersal and variable selection are the most crucial factors dominating microbial community assemblies in water and sediments of urban rivers, respectively. The differences in the spatial distribution of substrates (such as oxygen, nutrients, and organics) and mass transfer resistance result in the heterogeneity of microbial niche in various environmental media (Hollister et al. 2010; Gao et al. 2021). The excess inputs of pollutants with low-flow velocity would promote the enrichment of functional bacteria in the sediments, which are responsible for labile organic matter degradation (Chloroflexi, Acidobacteriota, and Firmicutes) (Ji et al. 2022; Wang et al. 2022), nitrogen cycling (Proteobacteria, Nitrospirota, and Bacteroidota) (Yang et al. 2021b; Deveautour et al. 2022), and ferric or sulfate reduction (Desulfobacterota) (Cai et al. 2019) under anoxic conditions; similar findings have been widely reported for polluted lake bays (Haller et al. 2011; Wu et al. 2017) and urban rivers (Wu et al. 2019; Zhang et al. 2022b). In addition, the different hydrodynamic

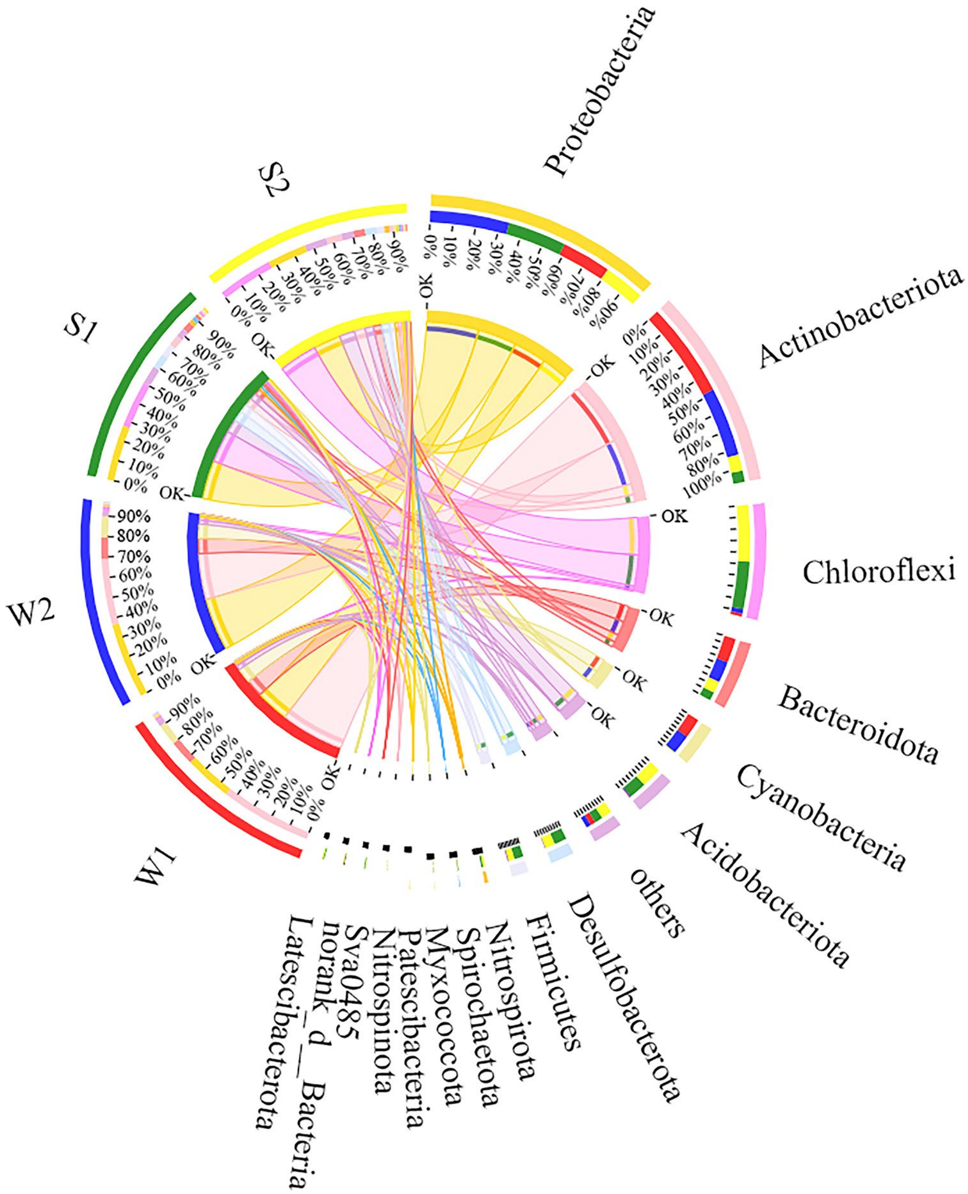
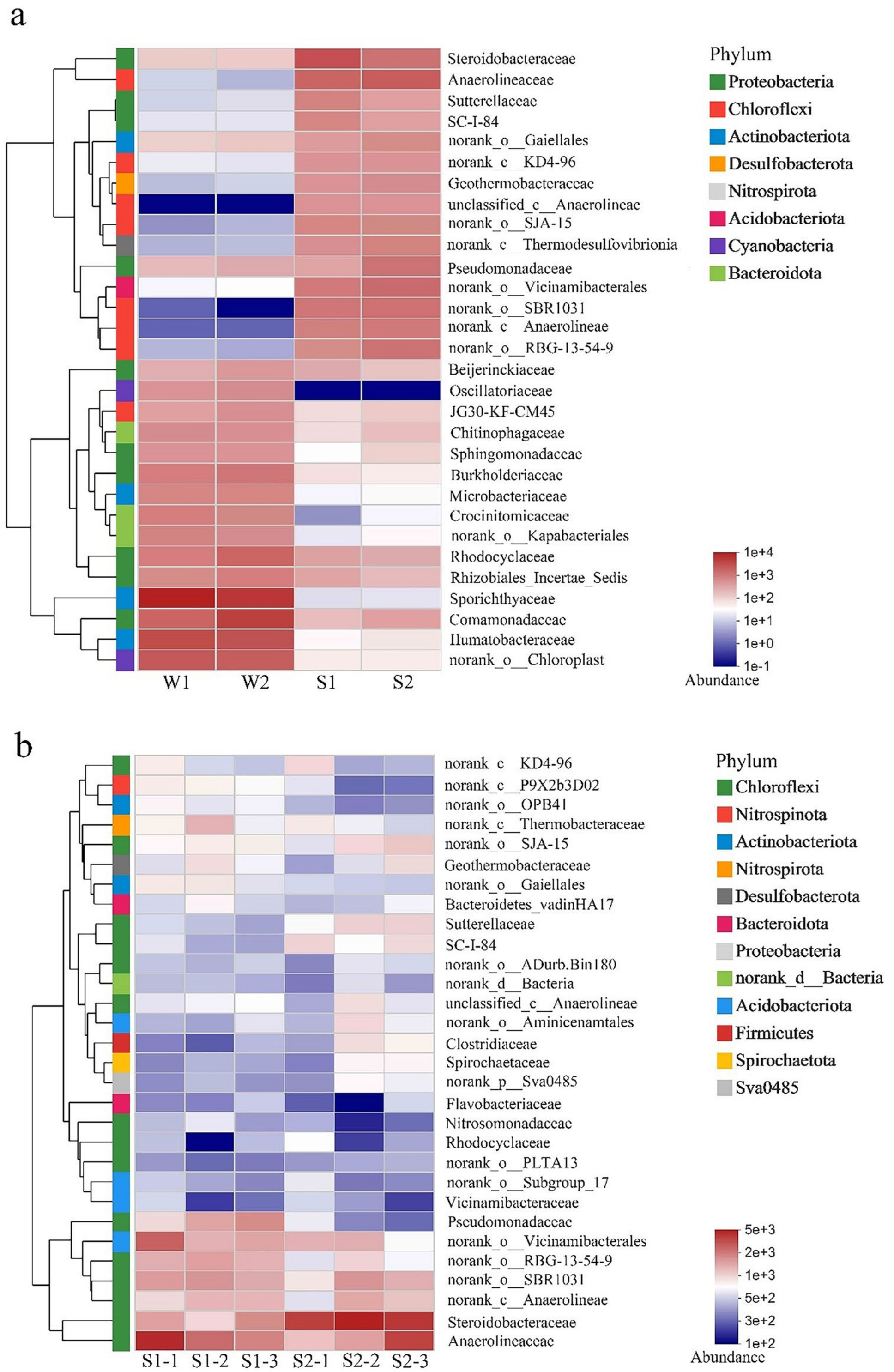


Fig. 5 Bacterial community structures in the water and sediments on the phylum level

conditions also influenced the abundances of dominant bacterial phyla in the sediments (Fig. S1). For example, the relative abundance of Chloroflexi in S2-1 (26.7%) was significantly higher than the 18.6% in S1-1, due to abundant substrate in the center of the urban channel. Moreover, the fraction of Desulfobacterota in S1-3 (7.1%) was 1.5 times higher than that in S2-3 (4.8%), which indicated that sulfur biotransformation (such as dissimilated sulfate reduction) preferably occurs in the deeper layer of the static flow field (P1), with a high oxidation–reduction potential (Cai et al. 2019).

Comparison of the bacterial community assembly in the water and sediments at the family level provided detailed information of ecological niche and biogeochemical processes. As shown in Fig. 6, the predominant bacterial family in the water samples was Sporichthyaceae (30.9% in W1, 17.9% in W2), followed by Ilumatobacteraceae (9.6% in W1, 8.9% in W2), norank_o__Chloroplast (7.3% in W1, 6.6% in W2), and Comamonadaceae (5.3% in W1, 13.7% in W2); the other families accounted for less than 5%. In contrast, the total relative abundances of the abovementioned families were only 0.8% in S1 and 1.5% in S2. The most abundant taxa were Steroidobacteraceae (9.5%, Proteobacteria-affiliated denitrifiers) (Liu et al. 2019) in S1 and Anaerolineaceae (6.9%, Chloroflexi-affiliated anaerobe) (Qian et al. 2017) in S2. In particular, the fractions of Nitrosomonadaceae as ammonia-oxidizing bacteria were stable at 1.0–1.5% in group S2 at various depths, whereas those in group S1 experienced a decrease from 1.1 to 0.4% with increasing depth (Fig. 6b).

Fig. 6 Bacterial community structures of **a** water samples and sediment groups and **b** of sediment samples at different depths depth at the family level



Correlation analysis of bacterial communities and environmental variables

As shown in Fig. 7a, 14 of the top 16 bacterial families (including Rhodocyclaceae, Halieaceae and Comamonadaceae) in the water samples (W1 and W2) exhibited positive correlations (red lines) with the *u* value, as the same as TOC, DO, TN, NH_4^+-N, and TP concentrations in water. The correlations between sediment bacterial communities and water environmental factors were more complex (Fig. 7b), and 7 (such as Pseudomonadaceae, Anaerolineae, and Geothermobacteraceae) and 11 (such as Desulfosarcinaceae, Gemmatimonadaceae. and Vicinamibacteraceae) of the top 18 bacterial families in the surface sediments (S1-1

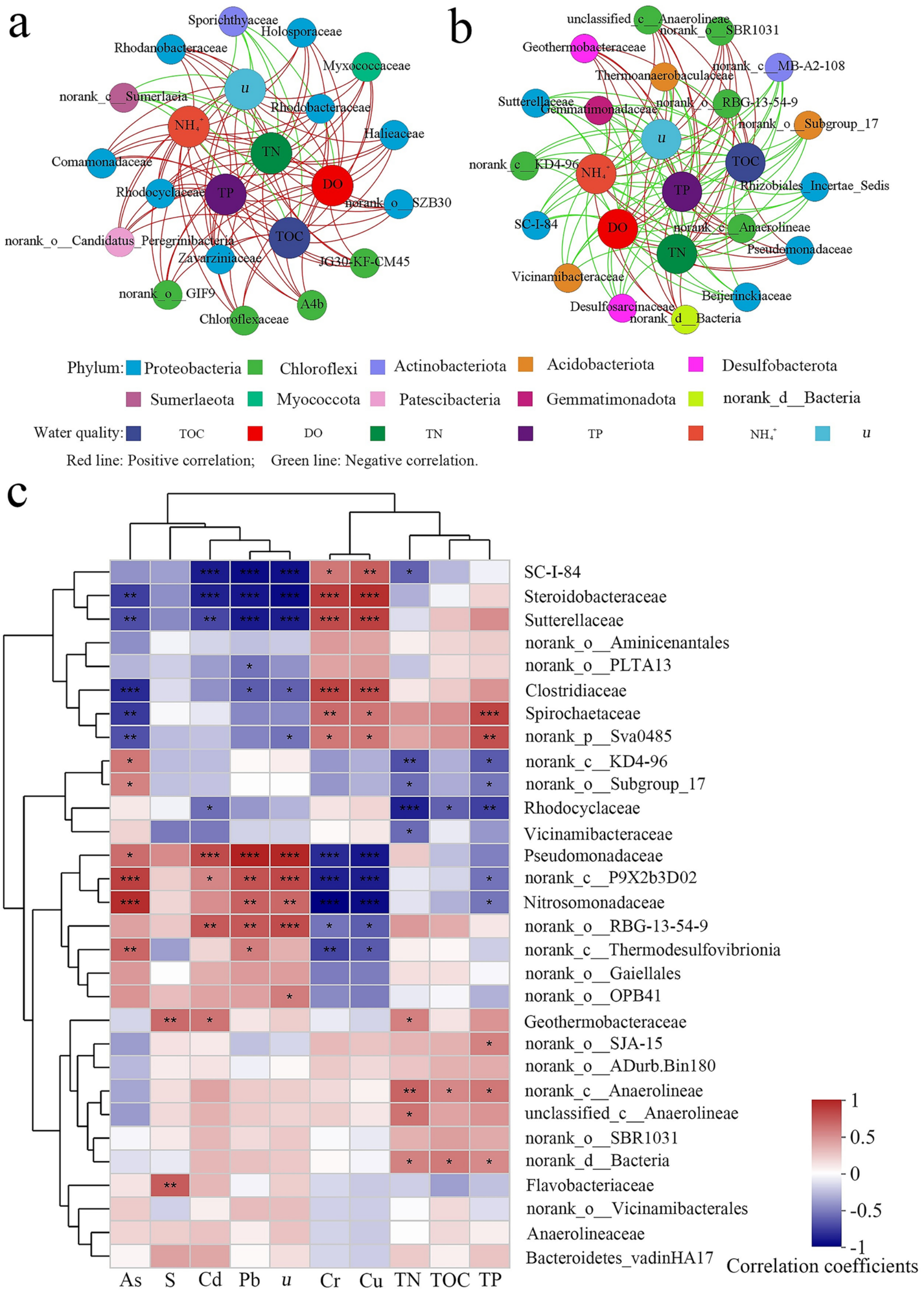


Fig. 7 Correlation analysis of **a** water and **b** surface sediment bacterial communities with water environmental characteristics and **c** correlation heatmap for the top 30 bacterial families and main pollutants in the sediments ($*P<0.05$; $**P<0.01$; $***P<0.005$; ns, $P>0.05$, according to two-tailed *t*-tests)

and S2-1) showed positive and negative correlations with the *u* value, respectively. As described in previous reports (Li et al. 2015, 2020a; Lei et al. 2020), the hydrodynamic conditions determined the water microbial communities by significantly influencing the DO level and the oxidation–reduction potential. Thus, the combination of aeration and push flow can improve the hydrodynamic conditions and self-purification capacity of rivers in eco-remediation engineering (Sun et al. 2022).

According to the results of the correlation analysis (Fig. 7c), the assembly of sediment bacterial communities was mainly dependent on the *u* value and the toxic substance (heavy metals) rather than the contents of organics (TOC) and nutrients (TN and TP). Several previous reports have demonstrated that heavy metals transported along rivers are associated with colloids (Ning et al. 2014), and the complex flow field in the channel confluences benefits the settling of heavy metals into the sediments. In the present study, the higher *u* value combined with shipping disturbance promoted the growth of Pseudomonadaceae, Nitrosomonadaceae, norank_c__P9X2b3D02, and norank_o__RBG-13–54-9, but suppressed that of Steroidobacteraceae, Sutterellaceae, and SC-I-84 in the sediments. The families Steroidobacteraceae, Sutterellaceae, SC-I-84, and Clostridiaceae exhibited a high resistance capacity to Cr and Cu and were sensitive to the presence of Cd, Pb, and As. Pseudomonadaceae, Nitrosomonadaceae, and norank_c__P9X2b3D02 showed the opposite responses to these heavy metals, indicating that changes in the specific bacterial community can be used as indicators of excess exposure to heavy metals, such as Pseudomonadaceae for Cd (Wang et al. 2021) and Steroidobacteraceae for Cd, Cu, Pb, and Ni (Nyoyoko 2022). Phosphorous is often considered a critical growth-limiting substrate of sediment microbes in freshwater bodies (Shao et al. 2011), and TP and TOC showed more significant influences on the bacterial families than the TN contents (Fig. 7c). In polluted urban rivers, Spirochaetaceae (hydrolytic microorganisms) (Avila et al. 2019) and Rhodocyclaceae (denitrifying phosphate accumulating organisms, DPAOs)(Zhang et al. 2021) exhibited different growth trends, which could be explained by the phosphate production via organic solid hydrolysis and the phosphate release of DPAOs under anoxic conditions. In this context, the effects of different P forms on microbial growth in sediments deserve further elaboration.

Predictive analysis of functional gene category

According to high-throughput sequencing of the samples, predictive analyses of the top 30 functional gene categories involved in carbon (15 categories), sulfur (3 categories), nitrogen (6 categories), and chlorine (1 category) cycles; human diseases (2 categories); and cellular processes (3 categories) were conducted using the FAPROTAX tool. As shown in Fig. 8 and Table S2, the water had a greater metabolic potential for carbon cycling (organics metabolism and degradation) than the sediment in terms of dark_hydrogen_oxidation, methanol_oxidation, oxygenic_photoautotrophy, cyanobacteria, photoautotrophy, phototrophy, and chloroplasts. Both water and sediments exhibited comparable gene abundance in aerobic_chemoheterotrophy, chemoheterotrophy, methylotrophy, methanotrophy, and hydrocarbon_degradation. Similar to fermentation under anoxic conditions (Perez-Esteban et al. 2022), sulfur-related metabolism preferably occurred in the sediments, including dark_sulfide_oxidation, dark_oxidation_of_sulfur_compounds, and respiration_of_sulfur_compounds, whereas the transformations between organic sulfur and inorganic sulfide were considered as the critical reason for the black-odor phenomena in polluted water bodies (Cai et al. 2019; Qin et al. 2019; Jiang et al. 2021). Similar to the findings of Cai et al. (2021), in this study, there were no significant differences in the distribution of functional genes at the varying depths. Although the gene abundance of nitrite_ammonification and nitrite_respiration in the water was significantly lower than that in the sediments, W2 exhibited gene levels of nitrate_respiration, nitrate_reduction, nitrogen_respiration, and nitrogen_fixation similar to those of the surface sediments (S1-1 and S2-1). Because of the weak homogenization of static water, environmental selection resulted in lower metabolic potentials of W1 than W2 for nitrification processes (Massara et al. 2017; Li et al. 2020c). Compared to the sediments, the water samples (especially W2) had higher abundances of genes for human disease vector and cellular process (animal_parasites_or_symbionts). The inputs of upstream runoff were regarded as the main origin of pathogens in urban rivers (Sun et al. 2022). Considering the widespread residential areas, agricultural land, and ports in the upstream and busy shipping

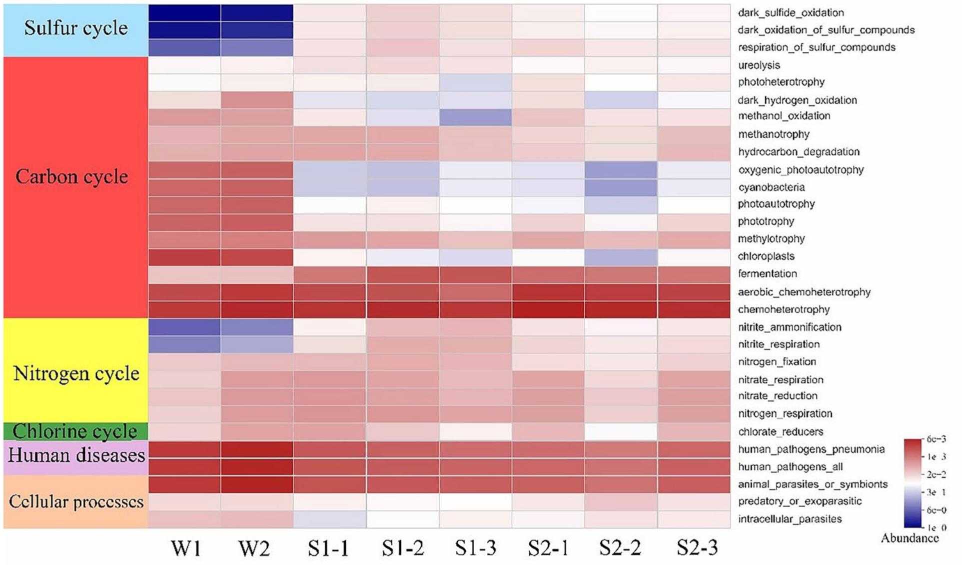


Fig. 8 Predictive analysis of the top 30 functional gene categories in the water and sediments using the FAPROTAX tool

transport in the channel, it was necessary to strictly control the unorganized discharging of livestock and poultry farming, distributed domestic wastewater, and ship sewage.

Conclusion

The results of this study provide evidence for the bacterial community distribution in the downstream section of urban channel confluences, closely associated with the pollution levels and hydrodynamic conditions. In comparison to the water, the sediments exhibited a higher bacterial diversity and richness. The larger u value in the main channel (P2) resulted in a stronger homogenizing dispersal compared to P1, which was close to the riverbank; the latter showed a higher dispersion degree in the bacterial communities. The slow water flow not only promoted the settling of sediments in the static water zone with the lower DO level but also diversified the sediment bacterial community at different depths, thereby influencing nitrogen metabolism and sulfur reduction processes. In addition to the u value, the TP and heavy metal contents also impacted the bacterial community in the same section. According to the predictive analysis of functional gene categories, the water had a greater metabolic potential for carbon cycling, and urban rivers potentially contain human pathogens. Regarding engineering, the combination of upstream runoff control and eco-remediation technologies (such as channel cleanout, plug flow aeration, and ship sewage treatment) is an effective approach for improving water quality.

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Declarations

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