

Microbial community composition in urban riverbank sediments: response to municipal effluents over spatial gradient

Yidong Guan^{a,b}, Zhang Li^c, Lidong Huang^d, Yin Luo^{e,*} and Jie Fu^c

^a Collaborative Innovation Center of Atmospheric Environment and Equipment Technology, Jiangsu Key Laboratory of Atmospheric Environment Monitoring and Pollution Control, School of Environmental Science and Engineering, Nanjing University of Information Science & Technology, Nanjing 210044, China

^b Key Laboratory of Environment Remediation and Ecological Health, Ministry of Education, College of Environmental Resource Sciences, Zhejiang University, Hangzhou 310058, China

^c School of Environmental Science and Engineering, Huazhong University of Science and Technology, Wuhan 430074, China

^d College of Applied Meteorology, Nanjing University of Information Science & Technology, Nanjing 210044, China

^e Department of Environmental Engineering, Wenhua College, Wuhan 430074, China

*Corresponding author. E-mail: luoyin147@163.com

 YL, 0000-0002-6948-5945

ABSTRACT

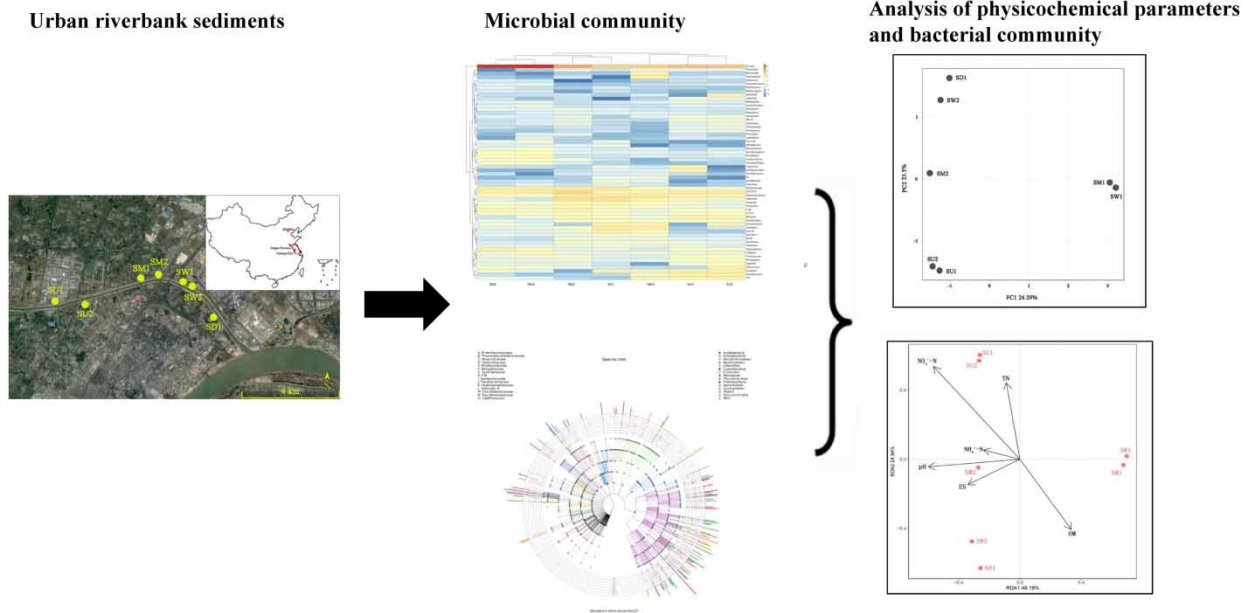
Municipal effluents have adverse impacts on the aquatic ecosystem and especially the microbial community. This study described the compositions of sediment bacterial communities in the urban riverbank over the spatial gradient. Sediments were collected from seven sampling sites of the Macha River. The physicochemical parameters of sediment samples were determined. The bacterial communities in sediments were analyzed by 16S rRNA gene sequencing. The results showed that these sites were affected by different types of effluents, leading to regional variations in the bacterial community. The higher microbial richness and biodiversity at SM2 and SD1 sites were correlated with the levels of $\text{NH}_4^+\text{-N}$, organic matter, effective sulphur, electrical conductivity, and total dissolved solids ($p < 0.01$). Organic matter, total nitrogen, $\text{NH}_4^+\text{-N}$, $\text{NO}_3\text{-N}$, pH, and effective sulphur were identified to be important drivers for bacterial community distribution. At the phylum level, Proteobacteria (32.8–71.7%) was predominant in sediments, and at the genus level, *Serratia* appeared at all sampling sites and accounted for the dominant genus. Sulphate-reducing bacteria, nitrifiers, and denitrifiers were detected and closely related to contaminants. This study expanded our understanding of municipal effluents on microbial communities in riverbank sediments, and also provided valuable information for further exploration of microbial community functions.

Key words: bacterial community, denitrification, diversity, environmental heterogeneity, municipal effluents, urban riverbank sediments

HIGHLIGHTS

- This study described the compositions of sediment bacterial communities in the municipal effluent-affected urban riverbank over the spatial gradient.
- This study showed that different types of effluents led to regional variations in the bacterial community. Downstream effluents were more affected by effluents, accompanied by higher abundance and biodiversity of bacteria.

GRAPHICAL ABSTRACT



1. INTRODUCTION

Nowadays, the further development of urbanization and industrialization have caused an extreme shortage of water resources and led to the contamination of the major base flow of rivers in many regions by municipal and industrial wastewater effluent (Rice *et al.* 2013). Currently, China owns the world's largest municipal wastewater sector in terms of municipal wastewater treatment plants (WWTPs) (about 4,000) number and treatment capacity ($7.4 \times 10^{10} \text{ m}^3/\text{year}$) (Lu *et al.* 2019). Although with the implementation of stringent discharge limits and remarkable achievements in wastewater treatment, the treated effluent still contains large nutrients and toxic pollutants. These pollutants release into natural water, which has non-negligible adverse impacts on the aquatic ecosystem. Numerous studies have indicated that the parameters of treated effluent are still above the limit, which can cause eutrophication (Berehanu *et al.* 2015) and ecotoxicity problems. The problems can change the diversity and richness of microbial communities (Chonova *et al.* 2016; Qiu *et al.* 2021), and further have negative consequences for global biogeochemical cycling (Grob *et al.* 2013).

Microorganisms are vital to biogeochemical cycles. Once environmental conditions change, microorganisms are extremely sensitive and respond quickly to changes (Wu *et al.* 2019; Wang *et al.* 2020a), thus can be a reliable indicator for monitoring the quality of rivers and sediment. Riverbanks, part of riverine systems, are scoured by river water, periodically submerged, and provide habitat for wildlife and microorganisms (Meier *et al.* 2005; Buckley *et al.* 2012). The nutrients, metals, and other harmful contaminants in rivers can be deposited and sorbed on riverbank sediments, thereby affecting the quality and microbial community in sediments (Johnston & Leff 2015; Lynch *et al.* 2018). Zhang *et al.* (2014a) found pollutant-resistant genera in the sea sediment of an industrial area. Johnston & Leff (2015) revealed that bacterial community compositions were strongly influenced by polycyclic aromatic hydrocarbon (PAH) concentrations in highly PAH-contaminated sites. A study reported that river water characterized by high sulphate concentrations can facilitate the existence of bacteria involved in sulphur cycles in river sediments (Martínez-Santos *et al.* 2018). Under long-term pollution, some microbial populations will prevail over others to change the structure and function of the community (Lors *et al.* 2010; Machado *et al.* 2012).

Up to now, many studies about the responses and variations of microbial communities in various environmental conditions were performed, like constructed wetlands (Zhang *et al.* 2021), WWTP effluents (Yu *et al.* 2020), activated sludge (Thomsen *et al.* 2010), and reservoir (Shi *et al.* 2020). While the study on microbial community in urban riverbank sediments influenced by municipal effluents has attracted the attention of researchers in recent years. In this study, we examined the sediments along the riverbank of the Macha River. Until now, these studies carried out on the Macha River mainly focused on the

occurrence of organic matter (OM) (Zhang *et al.* 2014b). This study first focuses on the compositions of sediment bacterial communities along the riverbank of the Macha River.

The overall goal of this study is to describe the compositions of sediment bacterial communities in the municipal effluent-affected urban riverbank over the spatial gradient. The specific objectives include the following aspects: (1) measure the physicochemical parameters of sediments; (2) evaluate the bacterial community diversity and variation among sampling sites; and (3) assess the impact of environmental heterogeneity caused by anthropogenic activities on the biogeographic distribution of bacterial communities. The purpose of this study is to provide a further understanding of microbial ecology in contaminated riverbank sediments.

2. MATERIALS AND METHODS

2.1. Study site description and sampling

The Macha River (13.6 km long), an important flood diversion channel in the lower reaches of the Chu River, is located to the north of the Yangtze River, as well as is the main water source and sewage receiving water body of Luhe District, Nanjing, China. The effluents that come from industrial and domestic wastewater have been treated before discharging into the Macha River. According to the discharge standard of pollutants for municipal wastewater treatment plants in China (GB18918-2002), the residual effluent can still have adverse consequences for riverbank sediment quality.

In November 2016, sediments were collected from the seven sampling sites along the riverbank of the Macha River in triplicate (Figure 1). The sampling sites were selected according to the different types of effluents they received. Briefly, SU1 (32°15'9.36"N, 118°42'53.76"E) near a fishing farm, SU2 (32°15'15.3"N, 118°43'33.48"E) was located downstream of SU1. SM2 (32°15'45"N, 118°45'29.52"E) was sampled at the intersection of a tributary into the Macha River, and the contamination source was from municipal wastewater. SM1 (32°15'38.58"N, 118°45'11.52"E) was close to SM2 and located at upstream of SM2. SW2 (32°15'29.82"N, 118°46'28.32"E) represented the sampling site located at the downstream of a WWTP. SW1 (32°15'34.26"N, 118°46'18.06"E) and SD1 (32°14'57.84"N, 118°47'3.96"E) were, respectively, sampled above and below SW2. In order to maintain the anaerobic environment, the sediments were quickly wrapped and sealed in a plastic bag after sampling, and then transported to the laboratory in an ice box for subsequent physicochemical and microbial analyses. In addition, salinity, total

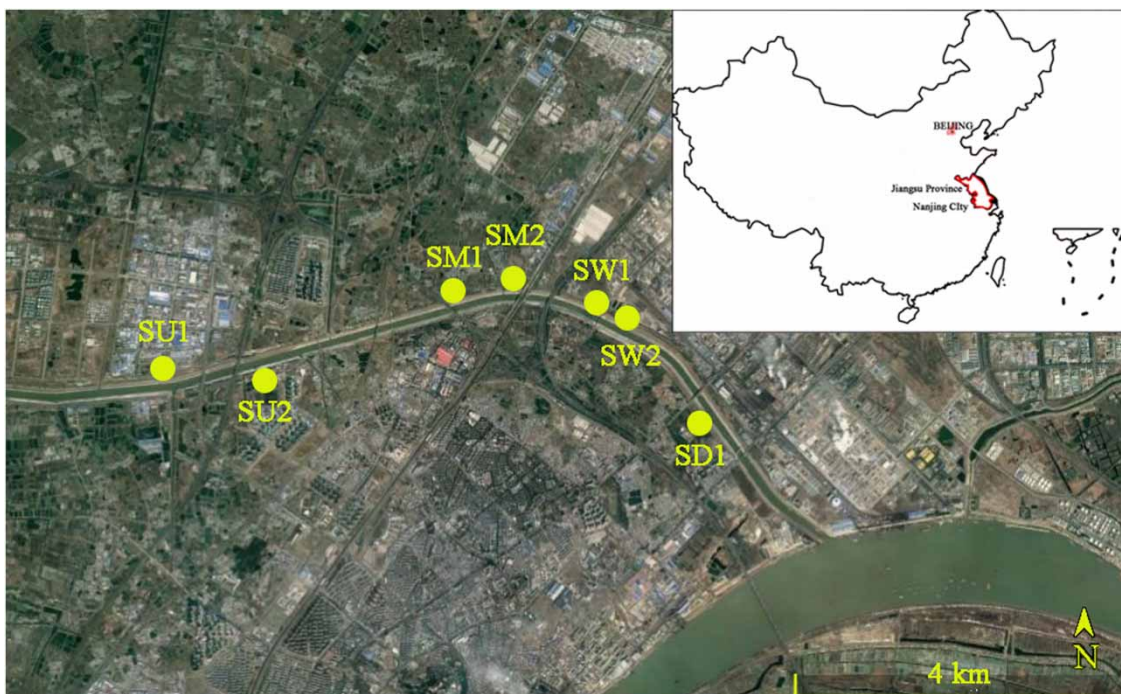


Figure 1 | Location of sampling sites along the Macha River in Nanjing City, China.

dissolved solids (TDS), and temperature (T) of interstitial water were measured on-site using a multi-parameter water quality analyzer (HQ30d, HACH).

2.2. Physicochemical analysis of sediment samples

Sediments were air-dried and ground to 100 mesh. Total nitrogen (TN) was determined by the semi-micro Kjeldahl method (Ran *et al.* 2016). Ammonia nitrogen ($\text{NH}_4^+\text{-N}$) and nitrate nitrogen ($\text{NO}_3^-\text{-N}$) were determined after 50 mL of KCl extraction using a spectrophotometer (UV-1800PC) (Mulvaney 1996). OM was measured by a colorimetric method developed by Bartlett and Ross (Bartlett & Ross 1988). Effective sulphur (ES) was quantified using ion chromatography (Dionex Ion Chromatograph Model ICS-1100, Dionex Corp., Sunnyvale, California) (Li *et al.* 2009). Electrical conductivity (EC) and sediment pH were measured in the dissolved solution with a ratio of sediment to ultrapure water (18.2 M Ω cm) of 1:5 (w/v) using an electric conductometer (CM-230) and a pH meter (PHS-3C), respectively. The above-mentioned measurements were performed in triplicate to count the mean value and standard deviation.

2.3. DNA extraction and bacterial community analysis

On arrival at the laboratory, the DNA samples of fresh sediment samples were extracted using Power soil™ DNA Isolation kit (Mobio Laboratories, Carlsbad, CA, USA) and carried out as described in Kowalchuk *et al.* (2003). The integrity of extracted DNA was checked on 1% agarose gel electrophoresis and placed at -80°C until use. The primer pairs 338F (ACTCCTACGG-GAGGCAGCAG) and 806R (GGACTACHVGGGTWTCTAAT) were used to amplify the V4 regions of bacterial 16S rRNA genes (Zhang *et al.* 2018), and the polymerase chain reaction (PCR) conditions were as follows: 3 min at 95°C ; 30 cycles for 30 s at 95°C ; 30 s at 55°C , and a final extension of 72°C for 45 s. Subsequently, the PCR products were sequenced by Guheinfo (Hangzhou, China). All 16S rRNA sequences were analyzed by QIIME for quality filtration, then the filtered sequences were clustered into bacterial operational taxonomic units (OTUs) with a 97% similarity cutoff by Mothur software. Sequences obtained in this study are deposited in National Omics Data Encyclopedia (NODE) database with the accession number OEP002636.

2.4. Statistical analyses

Rarefaction and Shannon–Winner curves were calculated by Mothur according to the clustered OTUs, which also could be utilized to determine the alpha diversity, like Chao 1, Shannon, Simpson, PD-Whole-Tree, and Good's coverage. Significant differences in the variance of parameters were evaluated with analysis of variance (ANOVA) or Kruskal–Wallis tests. The similarity between the sediment samples was measured by principle coordinate analysis (PcoA) based on Bray–Curtis distances. The heatmap was conducted by R software to reveal the composition of the community structure. Pearson correlation analysis for the relationships between physiochemical parameters and dominant genera was performed using SPSS software. Redundancy analysis (RDA) was used to reflect the relationship between environmental parameters and bacterial communities by means of the R software package.

3. RESULTS

3.1. Physicochemical properties of sediment samples

The physicochemical properties of sediments over spatial gradient are summarized in Table 1. The TN ranged from 0.03 to 0.11%, and high contents were observed in the SU1, SM2, and SD1 sites. Meanwhile, the concentrations of $\text{NH}_4^+\text{-N}$ and $\text{NO}_3^-\text{-N}$ in the above three sites were relatively high; sites SU1 and SD1 had the highest $\text{NO}_3^-\text{-N}$ (0.69 ± 0.04 mg/kg) and $\text{NH}_4^+\text{-N}$ (85.9 ± 2.23 mg/kg) concentrations, respectively. The nitrogen level in sediments of Macha River is much lower than that of the Jialu River (Zhengzhou, China) with a TN of $0.21 \pm 0.12\%$, $\text{NH}_4^+\text{-N}$ of 173.5 ± 105.4 mg/kg, and $\text{NO}_3^-\text{-N}$ of 0.96 ± 0.26 mg/kg, which has been severely polluted by a variety of contaminant sources such as industrial and domestic wastewater, trade wastes, and untreated or lightly treated sewage wastes (Fu *et al.* 2014). As for the OM and ES, sites SM2 (OM = 2.16%, ES = 119.9 mg/kg) and SD1 (OM = 2.22%, ES = 62.7 mg/kg) had higher values than SU1 (OM = 1.37%, ES = 59.8 mg/kg), which may be attributed to the different sources of contamination at these sites. SU1 was mainly subjected to the effluent from a fish farm that discharged uneaten feed and fish excreta into the nearby river, and then led to the high concentrations of TN, $\text{NH}_4^+\text{-N}$, and $\text{NO}_3^-\text{-N}$ in the sediments, which is consistent with previous studies (Zivic *et al.* 2010; Huang *et al.* 2012). The EC in sediment of SM2 was 180.5 $\mu\text{S}/\text{cm}$ and much higher than the average value of 116 $\mu\text{S}/\text{cm}$ of all samples, and similarly, the interstitial water at SM2 had the highest TDS of 126.5 mg/L. This means the site had

Table 1 | Physicochemical parameters of sediments measured at each sampling site

Sample	TN ^a (%)	NH ₄ ⁺ -N (mg/kg)	NO ₃ ⁻ N (mg/kg)	OM ^b (%)	ES ^c (mg/kg)	pH	EC ^d (μS/cm)	TDS ^e of IW ^f (mg/L)	T ^g of IW (°C)	Salinity of IW (ppt)
SU1	0.10 (0.004) ^h	28.5 (0.71)	0.69 (0.04)	1.37 (0.02)	59.8 (4.39)	7.46 (0.07)	115.5 (5)	80.4 (2.55)	21.2 (0.07)	0.1
SU2	0.08 (0.002)	15.1 (0.48)	0.45 (0.04)	0.17 (0.02)	41.7 (1.86)	7.49 (0.02)	41.7 (1.86)	77.7 (0)	21.4(0.28)	0.1
SM1	0.07 (0.004)	15.6 (0.72)	0.24 (0.01)	1.69 (0.01)	59.9 (1.08)	7.18 (0.04)	115.5 (2.12)	80.7 (0.99)	21.1	0.1
SM2	0.11 (0.001)**	43.7 (0.48)**	0.38 (0.06)	2.16 (0.01)**	119.9 (2.92)**	7.38 (0.01)	180.5 (2.12)**	126.5 (0.7)**	20.8	0.1
SW1	0.03 (0.001)	8.82 (0.30)	0.09 (0.03)	0.69 (0)	33.3 (0.66)	7.58 (0.04)	91 (2.83)	64.1 (2.05)	21 (0.07)	0.1
SW2	0.07 (0.001)	23.6 (4.82)	0.06 (0.02)	2.09 (0.02)	30.9 (1.76)	7.46 (0.05)	135.5 (0.7)	108.7 (19.02)	20.8	0.1
SD1	0.11 (0.004)**	85.9 (2.23)**	0.36 (0.02)	2.22 (0.13)**	62.7 (3.19) ^v	7.67 (0.17)	132.5 (2.12)**	92.8 (3.75)**	21 (0.07)	0.1
<i>p</i> value ⁱ	<i>p</i> < 0.001	<i>p</i> < 0.001	<i>p</i> < 0.001	<i>p</i> < 0.001	<i>p</i> < 0.001	<i>p</i> < 0.05	<i>p</i> < 0.001	<i>p</i> < 0.05	<i>p</i> < 0.01	/

^aTotal nitrogen.^bOrganic matter.^cEffective sulphur.^dElectrical conductivity.^eTotal dissolved solids.^fInterstitial water.^gTemperature.^hAverage value (standard deviation).ⁱAnalyzed by one-way AVONA.**p* < 0.05, ***p* < 0.01, '/' represents Cannot be calculated.

higher ionic concentrations, which may be due to strong anthropogenic activity (Das 2005). In addition, low concentrations of contaminants were observed in the rest sites SU2, SM1, and SW1, indicating the low pollution degree in these sites. That is because these three sites are relatively farther away from the origin points of effluent discharge and subjected to lower influence by effluents (Martínez-Santos *et al.* 2018). Macha River is the main flood diversion channel in the middle and lower reaches of the Chu River, the hydrodynamic process of seasonal flood could influence the physiochemical parameters of riverbank sediments by flushing the riverbank and transporting part of sediments to downstream (Tang *et al.* 2019). In addition, the pH of sediments was basically alkalescence (7.18–7.67), the temperature of interstitial water was in the range of 20.8–21.4 °C, and the salinity of interstitial water was 0.1 ppt. These basic parameters showed no obvious difference among sites.

In general, the physicochemical properties of sediments are impacted by complex interactions including periodic inundation, river hydrology, and anthropogenic pollution (Johnston & Leff 2015; Martínez-Santos *et al.* 2018).

3.2. Bacterial community diversity

A total of 508,723 quality sequences in 16S rRNA sequencing were obtained, with a range of 52,985–115,191 for each site, and the identified OTUs in each site ranged from 2,418 to 3,678. The number of sequence and OTUs, alpha richness, and diversity estimator/index are shown in Table 2. Good's coverage ranged from 0.97 to 0.99, indicating the libraries could well reflect the bacterial community in the sediments. There was no significant difference in bacterial community diversity among all sites (Kruskal–Wallis test, $p > 0.05$) (Table 2). The higher estimators/indices of sites SM2 (Chao1: 3,813.73, Shannon: 9.76, Simpson: 0.995, and PD-Whole-Tree:172.79) and SD1 (Chao1: 3,577.32, Shannon: 9.55, Simpson: 0.995, and PD-Whole-Tree:173.72) suggested the higher microbial richness and biodiversity at these sites. The lowest alpha richness and diversity estimator/index were found at site SW1 (Chao1: 3,188.50, Shannon:5.33, Simpson: 0.677, and PD-Whole-Tree: 149.37). Likewise, rarefaction (Figure 2) and Shannon–Winner (Figure 3) curves demonstrated the same results with Table 2. Combing the above-mentioned results of physicochemical parameters, it may be concluded that contaminants contained in wastewater effluent would stimulate the increase in the bacterial diversity and richness of the effluent receiving area.

PcoA based on Bray–Curtis distance was carried out to study the similarity of community structures among sampling sites. As shown in Figure 4, the first two PcoA components explained 49.59% variance for bacteria in sediments. The adjacent sampling sites (SW2 and SD1; SU2 and SU1; SM1 and SW1) showed a similarity in bacterial communities, and it is worth noting that the bacterial communities were distinct among sites suffering from different effluents. Chemical characteristics of the river ecosystem (e.g., nutrients and NO_3^-) can affect the composition, spatial-distribution, and abundance of bacterial communities in the sediments (Weisener *et al.* 2017; Yu *et al.* 2017). Therefore, due to the analogous physiochemical parameters of sediments at sites SM1 and SW1, a similarity in the bacterial community was observed at the two sites. Although site SM2 is closer to SM1 relative to SW1, the sediment bacterial community at site SM2 showed a relatively larger disparity with SM1 owing to the difference in sediment properties. Furthermore, the hierarchical cluster analysis (Figure 5) at the genus level also showed that the bacteria assemblage of SM1 was similar to that of SW1 due to the analogous

Table 2 | Number of sequence and OTUs, alpha richness, and diversity estimator/index of microbial communities in sediment samples

Sample	Sequence	OTUs ^a	Chao1	Shannon	Simpson	PD-Whole-Tree	Coverage
SU1	66,198 (5,654) ^b	2,867(292)	3,130(42)	9.53(0.42)	0.994(0.006)	146.62 (14.14)	0.98(0.01)
SU2	52,895 (2,828)	2,655(431)	2,884(113)	9.58(0.14)	0.994(0.004)	143.13 (4.24)	0.98(0.01)
SM1	73,881 (4,243)	2,919(424)	3,253(70)	5.59(0.13)	0.709(0.007)	149.11 (12.73)	0.97(0.01)
SM2	74,662 (5,374)	3,483(268)	3,813(141)	9.76(0.28)	0.995(0.006)	172.79 (11.31)	0.97(0.01)
SW1	77,188 (2,828)	2,926(127)	3,188(282)	5.33(0.04)	0.677(0.007)	149.37 (11.45)	0.97(0.01)
SW2	48,708 (2,546)	2,418(42)	2,931(113)	8.93(0.18)	0.993(0.006)	134.89 (8.49)	0.97(0.01)
SD1	115,191 (14,142)	3,678(396)	3,577(424)	9.55(0.31)	0.995(0.003)	173.72 (15.56)	0.99(0.01)
<i>p</i> value ^c	<i>p</i> > 0.05	<i>p</i> > 0.05	<i>p</i> > 0.05	<i>p</i> > 0.05	<i>p</i> > 0.05	<i>p</i> > 0.05	<i>p</i> > 0.05

^aOperational taxonomic units.

^bAverage value (standard deviation).

^cAnalyzed by one-way Kruskal–Wallis test.

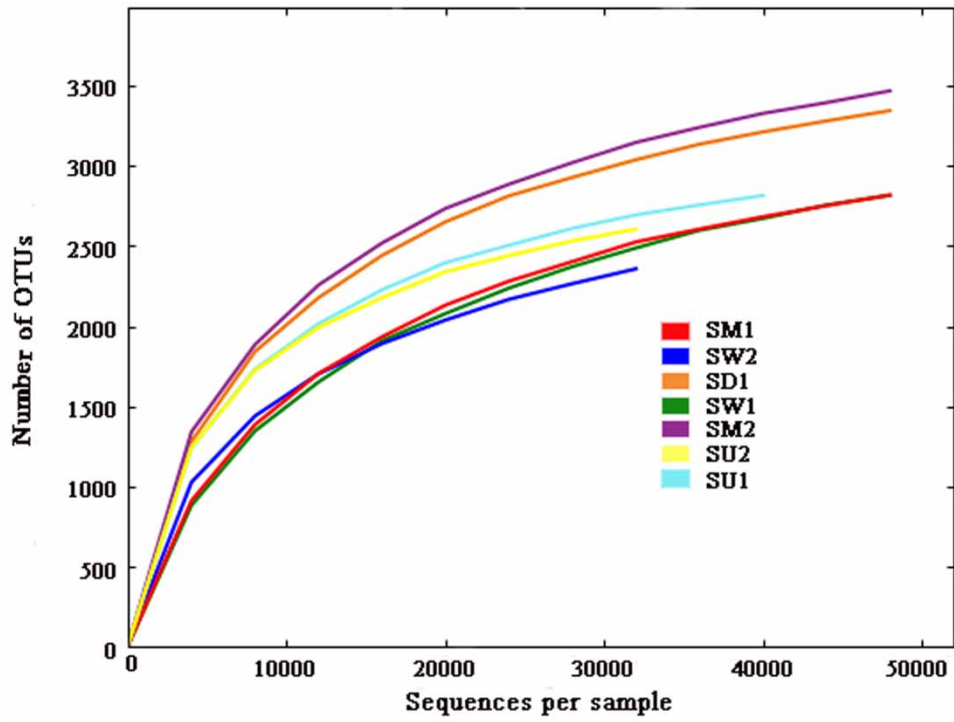


Figure 2 | Rarefaction curve based on sequencing of microbial communities in sediment samples.

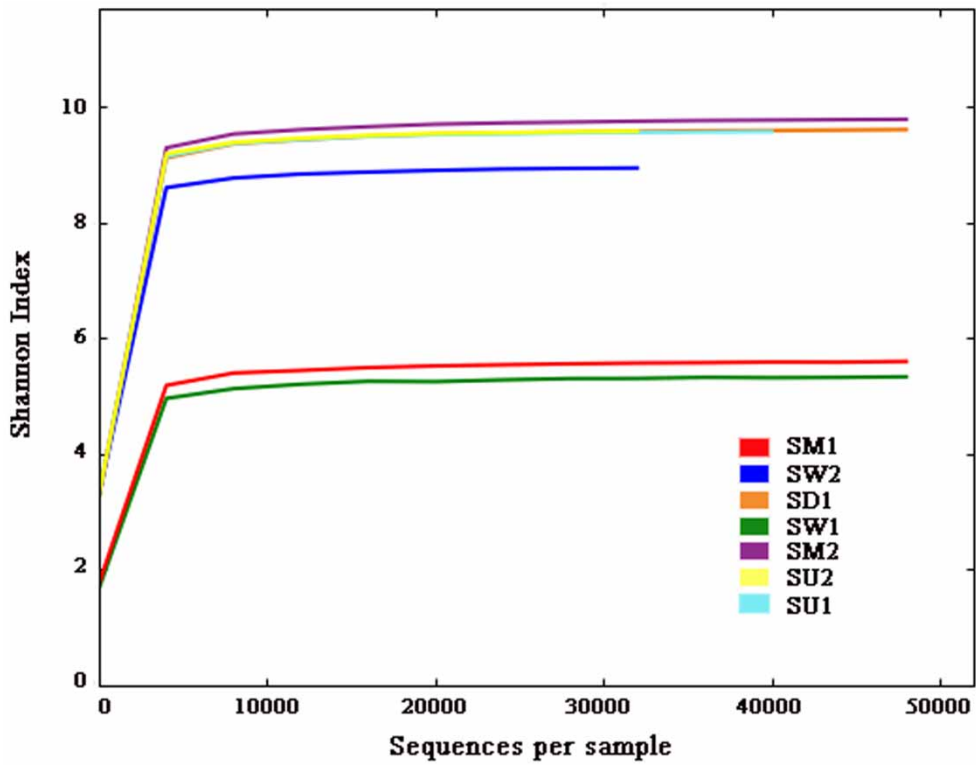


Figure 3 | Shannon-Winner curve of microbial communities in sediment samples.

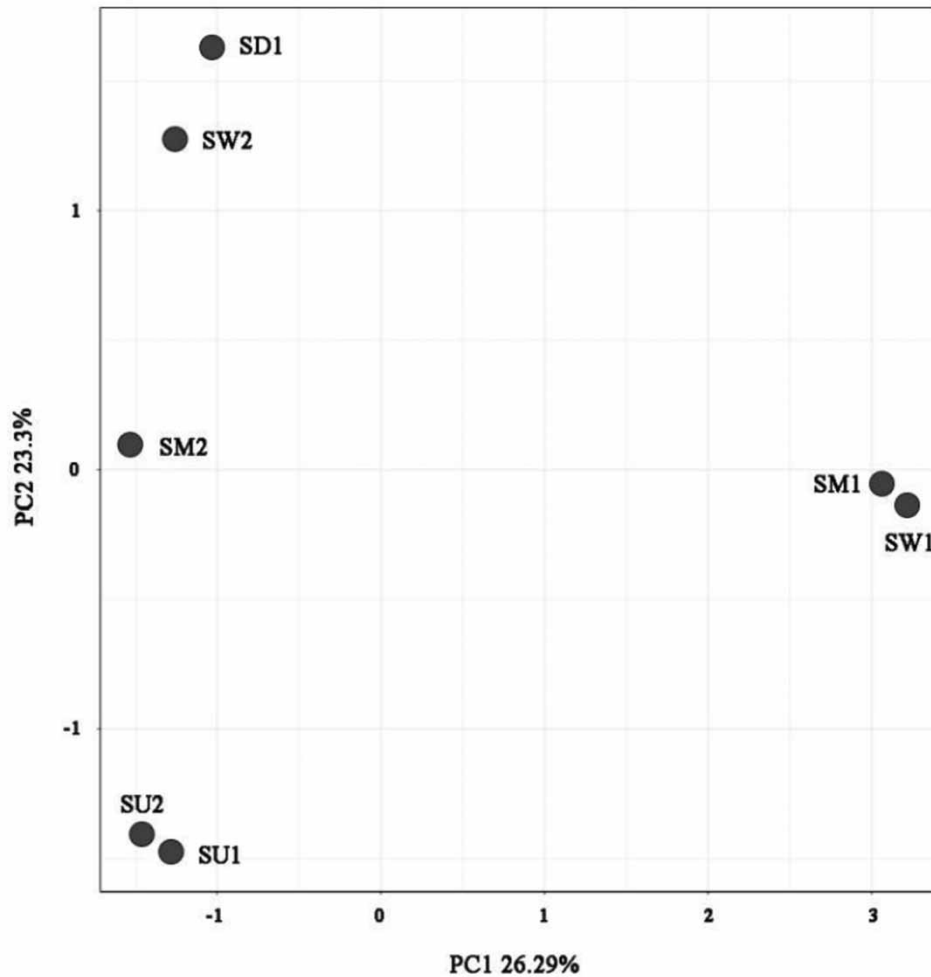


Figure 4 | PCoA of bacterial communities based on Bray–Curtis distances. The distance between two points indicates the similarity of microbial communities.

physiochemical parameters of sediments at these sites. Meanwhile, the bacterial assemblage at site SM2 showed a relatively less similarity with SM1.

3.3. Bacterial community composition

Microbial community compositions of sediments were determined by high-throughput sequencing analyses at different taxonomic levels. As shown in Figure 6, *Proteobacteria* (32.8–71.7%) was the dominant phylum, followed by *Acidobacteria* (5.75–22.59%), *Chloroflexi* (6.77–13.83%), *Bacteroidetes* (2.45–4.04%), and *Actinobacteria* (3.45–4.57%). At the family level, the abundant taxa were *Rhodocyclaceae* (from class *Betaproteobacteria*) (0.46–2.42%), *Syntrophaceae* (from class *Deltaproteobacteria*) (0.25–2.98%), and *Thermodesulfobivibrionaceae* (0.99–2.33%). *Rhodocyclaceae* contains many denitrifiers that can reduce NO_3^- -N to nitrogen (N_2), and has been commonly detected in districts suffered by wastewater (Niu *et al.* 2018). Correspondingly, a high proportion of some genera in *Rhodocyclaceae* family were detected at sites SW2, SM2, and SD1 in our study. *Syntrophaceae* family includes many sulphate-reducers and most of them act strictly under anaerobic conditions, thereby leading to the formation of insoluble metal sulphides through the reaction between reduced product hydrogen sulphide and divalent transition metals (Gray *et al.* 2011). And the fact is proved by an increased abundance of genera affiliated *Syntrophaceae*. Moreover, the *Syntrophaceae* plays an essential role in the biodegradation of hydrocarbons to methane (Kelemen *et al.* 2016), the high OM concentrations at sites SW2 ($2.09 \pm 0.02\%$) ($p < 0.0001$) and SD1

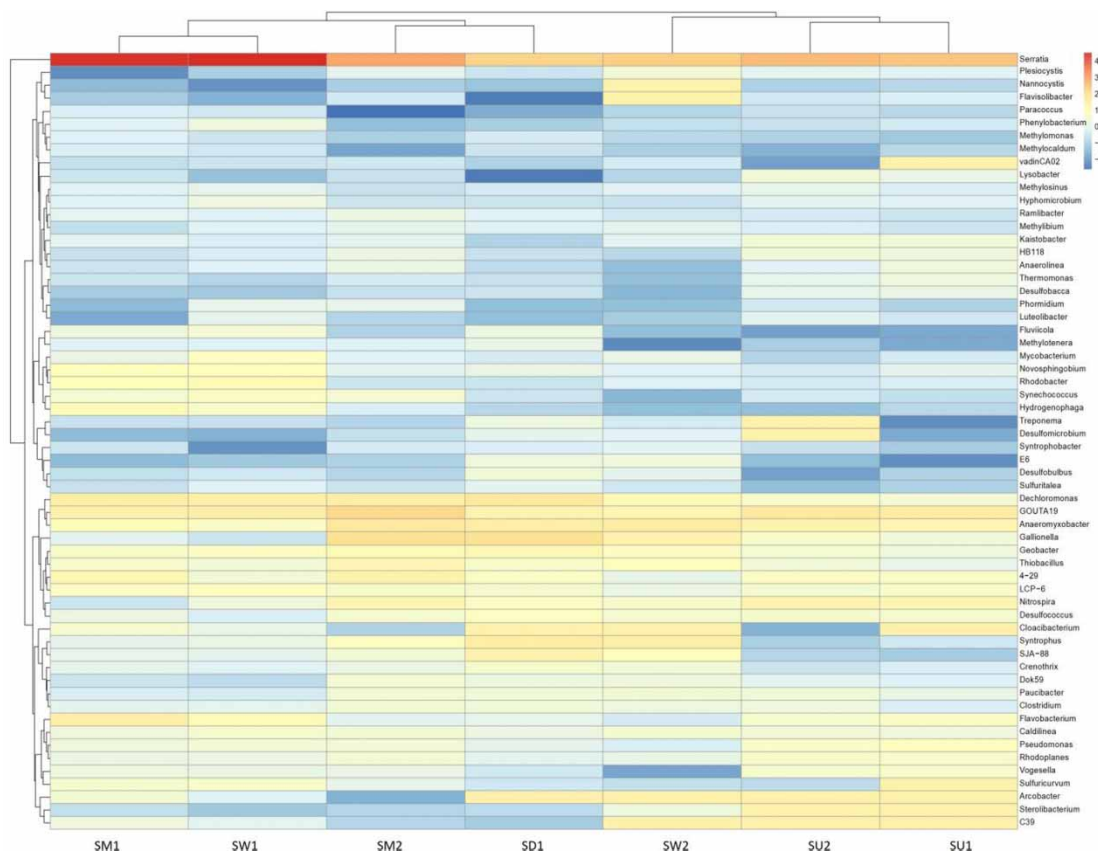


Figure 5 | The heatmap cluster analysis of bacteria assemblage at the genus level (relative abundance >1%) in sediments.

($2.22 \pm 0.13\%$) ($p < 0.0001$), together with the enriched abundance of the bacterial genus from *Syntrophaceae* family indicate a high potential of hydrocarbon biodegradation. *Thermodesulfovibrionaceae*, a kind of sulphate-reducing bacteria (SRB) belonging to class *Nitrospirae*, can reduce sulphates to sulphides under anaerobic conditions (Jankowska *et al.* 2015). The largest amount of ES at site SM2 (119.9 ± 2.92 mg/kg) ($p < 0.0001$) may contribute to the prevalence of SRB.

3.4. Influence of environmental parameters on bacterial communities

The influence of physiochemical parameters on bacterial communities was investigated by RDA. As shown in Figure 7, OM, TN, $\text{NH}_4^+\text{-N}$, $\text{NO}_3^-\text{-N}$, pH, and ES were identified to be important drivers for the bacterial community distribution of sites. The first two axes of the RDA explained 49.18 and 24.94% of the variations. Studies have illustrated that the bacterial community composition in sediments was influenced by heterogeneity of physiochemical parameters (Bai *et al.* 2009; Almeida *et al.* 2013). Similarly, bacterial communities found at sites SU1 and SU2 were highly correlated with $\text{NO}_3^-\text{-N}$ and TN. The pH and ES greatly affected bacterial communities at site SM2, which was also affected by $\text{NO}_3^-\text{-N}$, TN, and $\text{NH}_4^+\text{-N}$. The two sites SW1 and SM1 formed a separate cluster, which is distinct from other sites.

4. DISCUSSION

The hierarchical cluster analysis (Figure 5) has illustrated that genus *Serratia* (3.76–56.8%) was the most abundant taxon that existed in all sediment samples. Furthermore, the histogram of Figure 8 displays the top 10 genera with the highest proportions in the sediment samples. *Serratia*, *Nitrospira*, and *GOUTA19* existed in all samples, while other genera that occurred in specific samples like *Gallionella* were not found at sites SM1 and SW1. In many previous studies, the *Proteobacteria* as the dominant group was also found among the microbiota populated in sediments (Zhang *et al.* 2014a; Du *et al.* 2016). *Serratia*, belonging to the family *Enterobacteriaceae* and class *Gamaproteobacteria*, is commonly found in the



Figure 6 | Phylogenetic relation diagram of microbial communities in sediments. Branches of different colors represent different phyla (see the legend in the upper right corner for specific representative colors). The circles with gray letters indicate the 15 families with the highest proportions in this study. The outer circle is a heat map drawn according to abundance, and the histogram drawing of the outermost circle is the abundance and sample color (consistent with the color of the sample name at the bottom of the circle) of the sample with the highest proportion of the genus.

environment, and possesses the ability to colonize a variety of niches, like soil, water, plants, and animals (Hugouvieux-Cotte-Pattat *et al.* 2019). The abilities of resisting attack, responding appropriately to environmental conditions, and releasing numbers of compounds into the environment make *Serratia* highly successful in almost any niche and mutualistic symbiosis with other organisms (Petersen & Tisa 2013; Chen *et al.* 2017). *Serratia* can ferment OM, and remove ammonia nitrogen, and have the advantage of sulfide resistance (Huang *et al.* 2016; Newsome *et al.* 2015). Jian *et al.* (2014) proved the ability of a strain from *Serratia* to remove phenol and ammonium, and the high tolerance to phenol toxicity. Although *Serratia* was detected in all sampling sites in our study, the abundance of *Serratia* was negatively related to the increasing pollution level among the sites (Figure 8 and Table 3). It may be concluded that *Serratia* can be used as an indicator to evaluate sediment quality to a certain extent.

At the genus level, a large proportion of OTUs was related to the known nitrifiers and denitrifiers (Figure 8). *Nitrospira* belongs to nitrifiers, and *Anaeromyxobacter*, *GOUTA19*, *Gallionella*, *Dechloromonas*, *Geobacter*, and *Flavobacterium*

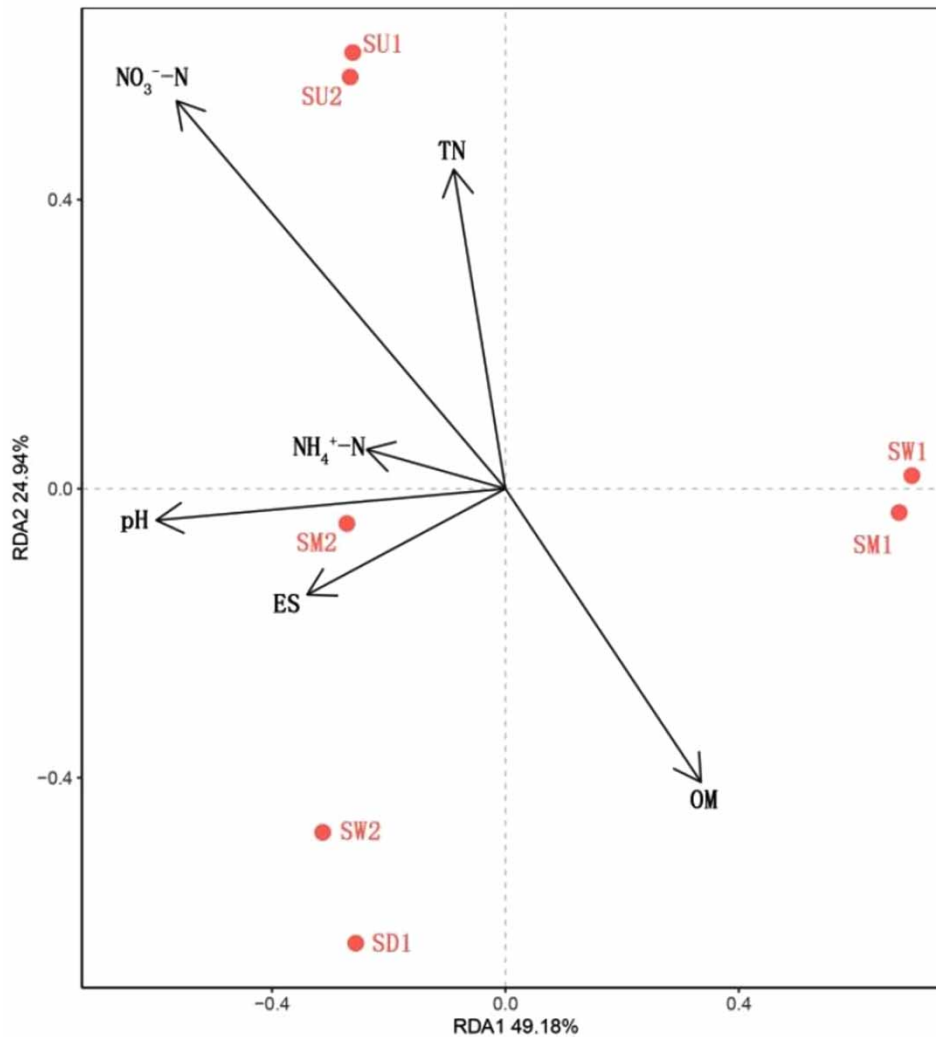


Figure 7 | Plot of two axes in RDA results correlating physicochemical parameters and bacterial community compositions in sediment samples.

belong to denitrifiers. The genus *Nitrospira*, a kind of nitrite-oxidizing bacteria, was associated with nitrogen transformations ($r = 0.814$; $p < 0.05$) (Table 3). Previous study has shown that *Nitrospira* bacteria were capable of complete nitrification, i.e., the oxidation of ammonium and nitrite to nitrate directly (Daims *et al.* 2015). A high abundance of *Nitrospira* was found at sites SU1 and SU2 (Figure 8), and both sites were evidently influenced by the effluent from a fish farm, where nitrogen fertilizers were used to feed fish. This result matches a study that abundant *Nitrospira* was found in agricultural soil amended with nitrogen fertilizers (Li *et al.* 2019a). Qiu *et al.* (2021) found that NH₄⁺-N was negatively correlated with genus *Nitrospira*. Correlation analysis (Table 3) indicated that the genus *Nitrospira* was strongly and positively correlated with NO₃⁻-N ($r = 0.814$, $p < 0.05$), and which also demonstrated that *Nitrospira* might play an important role in ammonium removal. The genera 4-29 and *Nitrospira* were from the same order Nitrospirales. As shown in Table 3, the abundance of 4-29 was significantly positively correlated with ES ($r = 0.856$, $p < 0.05$), indicating that the presence of 4-29 may be related to the sulphur cycle.

It is well known that *Geobacter* is the clade of iron-reducing bacteria and is widely distributed in riverbank sediments. In the present study, according to the Pearson correlations analysis, the genus *Geobacter* was more positively related to NH₄⁺-N ($r = 0.910$, $p < 0.01$). Recently, more studies were reported that *Geobacter* could oxidize OM, participate in sulfite reduction and mediate the reduction of ammonium oxidation (Li *et al.* 2018, 2019b).

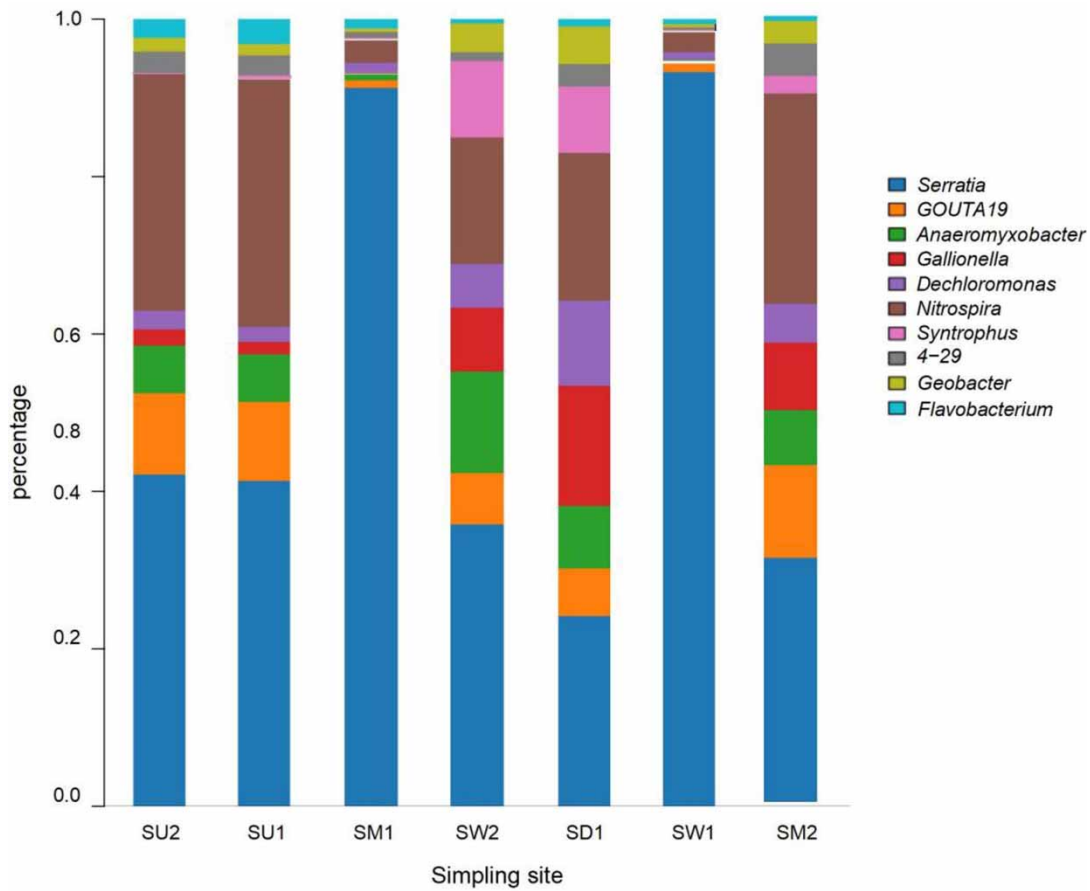


Figure 8 | Microbial community compositions in sediment samples at the genus level.

Table 3 | Correlations analysis between physiochemical parameters and dominant genera in sediment samples

	TN ^a	NH ₄ ⁺ -N	NO ₃ ⁻ -N	ES ^b	OM ^c	pH	EC ^d	TDS ^e	T ^f
<i>Serratia</i>	-0.754	-0.523	-0.487	-0.278	-0.292	-0.335	-0.572	-0.594	0.032
<i>GOUTA19</i>	0.608	0.162	0.688	0.647	-0.087	0.016	0.571	0.451	0.201
<i>Anaeromyxobacter</i>	0.593	0.529	0.061	0.114	0.532	0.290	0.594	0.705	-0.336
<i>Gallionella</i>	0.632	0.943**	0.004	0.381	0.676	0.482	0.601	0.589	-0.476
<i>Dechloromonas</i>	0.281	0.821*	-0.251	0.175	0.586	0.361	0.227	0.195	-0.417
<i>Nitrospira</i>	0.549	0.161	0.814*	0.151	-0.266	0.274	0.161	0.104	0.494
<i>Syntrophus</i>	0.326	0.703	-0.335	-0.071	0.682	0.456	0.355	0.474	-0.573
4-29	0.730	0.450	0.553	0.856*	0.282	-0.325	0.625	0.438	0.127
<i>Geobacter</i>	0.497	0.910**	-0.145	0.276	0.653	0.511	0.511	0.515	-0.510
<i>Flavobacterium</i>	-0.326	-0.501	0.164	-0.204	-0.396	-0.576	-0.596	-0.674	0.576

^aTotal nitrogen.

^bEffective sulphur.

^cOrganic matter.

^dElectrical conductivity.

^eTotal dissolved solids.

^fTemperature.

* $p < 0.05$, ** $p < 0.01$; '/' represents values cannot be calculated.

The genera *GOUTA19* and *Gallionella* have been proven as a kind of microbes related to autotrophic denitrification (Wang *et al.* 2020b; Mai *et al.* 2021). *GOUTA19* (from the family Thermodesulfobionaceae) has been observed in diverse conditions previously, such as alfalfa-rice rotation systems, oil-storage cavities and groundwater contaminated with diesel/biodiesel blends (Watanabe *et al.* 2002; Lopes *et al.* 2014). As mentioned above, Thermodesulfobionaceae as SRB was often observed in sulphate reduction process. Previous study has indicated that *GOUTA19* might be responsible for the anaerobic biodegradation of benzene and naphthalene under iron and sulphate reduction (Müller *et al.* 2017). The high abundance of *GOUTA19* (Figure 8) and the highest concentration of ES at site SM2 (Table 1), suggest the importance of sulphate to SRB in the sediments. In addition, a high abundance of *GOUTA19* was observed at sites SU1 and SU2, which may be due to the relatively high concentrations of NO_3^- -N. Studies have indicated that NO_3^- -N not only serves as the essential nutrient for microbial physiological activities, but also acts as efficient electron acceptors which can oxidize sulfide to sulphate for the growth of SRB (Wang *et al.* 2018; Whw *et al.* 2019).

Dechloromonas as denitrifying bacteria can degrade various mono-aromatic compounds anaerobically. For example, *Dechloromonas* can mineralize benzene to carbon dioxide (CO_2) under anaerobic conditions with nitrate as an electron acceptor (Coates *et al.* 2001). A recent article has reported the ability of *Dechloromonas* to Sb(V) reduction and removal in the sediments (Yang *et al.* 2021). The abundance of *Dechloromonas* and *Gallionella* in sediment samples was significantly positively correlated with the NH_4^+ -N concentrations, and the corresponding r values were 0.821 ($p < 0.05$) and 0.943 ($p < 0.01$), respectively. Thus, the sites SM1 and SW1 with the lowest NH_4^+ -N concentrations did not detect the presence of *Gallionella* (Figure 8). Studies have indicated that ammonium or nitrate were nitrogen sources of *Gallionella* (Hallbeck *et al.* 1993). A lack of NH_4^+ -N would limit the growth of *Gallionella*.

Summing up the above, the contaminants discharged from different anthropogenic activities were the crucial factors shaping the bacterial community.

5. CONCLUSIONS

In conclusion, urban rivers are of prime importance to human survival and industrial development and are simultaneously subjected to human waste. The untreated and treated effluents containing nutrients and contaminants present negative consequences on river water and sediment quality and further shape the bacterial community compositions of aquatic ecosystems. We selected seven sites and measured the environmental variables, and the results displayed that the sediments immediately downstream of effluents were more influenced by wastewater, with higher bacterial abundance and biodiversity. Environmental factors, including NO_3^- -N, NH_4^+ -N, ES, and OM are important in shaping the bacterial community. Nitrifiers (e.g., *Nitrospira*) and denitrifiers (e.g., *Anaeromyxobacter*) at the genus level seem to be predominant bacteria at those sites impacted by effluents, while the genus *Serratia* was the most dominant bacteria at the sites non-impacted by effluents. In sediment sites, the physiochemical parameters and bacterial community structures were spatially different and were closely related to the different effluents they received.

AUTHOR CONTRIBUTIONS

Preparation of sediment samples and DNA extraction were performed by Y.G. and Z.L. Microbial community analysis was performed by L.H. and J.F. The manuscript was written by J.F. and Y.L.. The corresponding author was Y.L.

FUNDING

This study was supported by the Fundamental Research Funds for the Central Universities (226-2023-00077), National Natural Science Foundation of China (91851110), and Foundation for Outstanding Young Scientific and Technological Innovation Teams of Colleges and Universities in Hubei Province (T2022053).

DATA AVAILABILITY STATEMENT

All relevant data are included in the paper or its Supplementary Information.

CONFLICT OF INTEREST

The authors declare there is no conflict.

REFERENCES

- Almeida, R., Mucha, A. P., Teixeira, C., Bordalo, A. A. & Almeida, C. M. 2013 Biodegradation of petroleum hydrocarbons in estuarine sediments: Metal influence. *Biodegradation* **24**, 111–123. <https://doi.org/10.1007/s10532-012-9562-9>.
- Bai, J., Li, H. Y., Zhang, J. & Zhao, Y. G. 2009 Diversity of bacterial community in the sediments of the northern yellow sea. *China Environmental Science* **29**, 1277–1284.
- Bartlett, R. J. & Ross, D. S. 1988 Colorimetric determination of oxidizable carbon in acid soil solutions. *Soil Science Society of America Journal* **52**, 1191–1192. <https://doi.org/10.2136/sssaj1988.03615995005200040055x>.
- Berehanu, B., Lemma, B. & Tekle-Giorgis, Y. 2015 Chemical composition of industrial effluents and their effect on the survival of fish and eutrophication of Lake Hawassa, Southern Ethiopia. *Journal of Environmental Protection* **06**, 792–803. <https://doi.org/10.4236/jep.2015.68072>.
- Buckley, C., Hynes, S. & Mehan, S. 2012 Supply of an ecosystem service – Farmers' willingness to adopt riparian buffer zones in agricultural catchments. *Environmental Science and Policy* **24**, 101–109. <https://doi.org/10.1016/j.envsci.2012.07.022>.
- Chen, X., Hitchings, M. D., Mendoza, J. E., Balanza, V., Facey, P. D., Dyson, P. J., Bielza, P. & Del Sol, R. 2017 Comparative genomics of facultative bacterial symbionts isolated from European Orius species reveals an ancestral symbiotic association. *Frontiers in Microbiology* **8**, 1969. <https://doi.org/10.3389/fmicb.2017.01969>.
- Chonova, T., Keck, F., Labanowski, J., Montuelle, B., Rimet, F. & Bouchez, A. 2016 Separate treatment of hospital and urban wastewaters: A real scale comparison of effluents and their effect on microbial communities. *Science of the Total Environment* **542** (A), 965–975. <https://doi.org/10.1016/j.scitotenv.2015.10.161>.
- Coates, J. D., Chakraborty, R., Lack, J. G., O'Connor, S. M., Cole, K. A., Bender, K. S. & Achenbach, L. A. 2001 Anaerobic benzene oxidation coupled to nitrate reduction in pure culture by two strains of *Dechloromonas*. *Nature* **411** (6841), 1039–1043. <https://doi.org/10.1038/35082545>.
- Daims, H., Lebedeva, E. V., Pjevac, P., Han, P., Herbold, C., Albertsen, M., Jehmlich, N., Palatinszky, M., Vierheilig, J., Bulaev, A., Kirkegaard, R. H., von Bergen, M., Rattei, T., Bendinger, B., Nielsen, P. H. & Wagner, M. 2015 Complete nitrification by *Nitrospira* bacteria. *Nature* **528** (7583), 504–509. <https://doi.org/10.1038/nature16461>.
- Das, B. K. 2005 Environmental pollution impact on water and sediments of Kumaun lakes, lesser Himalaya, India: A comparative study. *Environmental Geology* **49**, 230–239. <https://doi.org/10.1007/s00254-005-0077-0>.
- Du, R., Cao, S., Li, B., Niu, M., Wang, S. & Peng, Y. 2017 Performance and microbial community analysis of a novel DEAMOX based on partial-denitrification and anammox treating ammonia and nitrate wastewaters. *Water Research* **108**, 46–56. <https://doi.org/10.1016/j.watres.2016.10.051>.
- Fu, J., Zhao, C., Luo, Y., Liu, C., Kyzas, G. Z., Luo, Y., Zhao, D., An, S. & Zhu, H. 2014 Heavy metals in surface sediments of the Jialu river, China: Their relations to environmental factors. *Journal of Hazardous Materials* **270**, 102–109. <https://doi.org/10.1016/j.jhazmat.2014.01.044>.
- Gray, N. D., Sherry, A., Grant, R. J., Rowan, A. K., Hubert, C. R. J., Callbeck, C. M., Aitken, C. M., Jones, D. M., Adams, J. J., Larter, S. R. & Head, I. M. 2011 The quantitative significance of Syntrophaceae and syntrophic partnerships in methanogenic degradation of crude oil alkanes. *Environmental Microbiology* **13** (11), 2957–2975. <https://doi.org/10.1111/j.1462-2920.2011.02570.x>.
- Grob, C., Ostrowski, M., Holland, R. J., Heldal, M., Norland, S., Erichsen, E. S., Blindauer, C., Martin, A. P., Zubkov, M. V. & Scanlan, D. J. 2013 Elemental composition of natural populations of key microbial groups in Atlantic waters. *Environmental Microbiology* **15** (11), 3054–3064. <https://doi.org/10.1111/1462-2920.12145>.
- Guilpart, A., Roussel, J.-M., Aubin, J., Caquet, T., Marle, M. & Le Bris, H. 2012 The use of benthic invertebrate community and water quality analyses to assess ecological consequences of fish farm effluents in rivers. *Ecological Indicators* **23**, 356–365. <https://doi.org/10.1016/j.ecolind.2012.04.019>.
- Hallbeck, L., Stahl, F. & Pedersen, K. 1993 Phylogeny and phenotypic characterization of the stalk-forming and iron-oxidizing bacterium *Gallionella ferruginea*. *Journal of General Microbiology* **139**, 1531–1535. <https://doi.org/10.1099/00221287-139-7-1531>.
- Huang, G., Fan, G. & Liu, G. 2016 Enhanced treatment of tannery wastewater in an integrated multistage bioreactor (IMBR) by the predominant bacterial strains enriched from marine sediments. *Water Science and Technology* **73**, 807–817. <https://doi.org/10.2166/wst.2015.548>.
- Hugouvieux-Cotte-Pattat, N., Jacot-des-Combes, C. & Briolay, J. 2019 Genomic characterization of a pectinolytic isolate of *Serratia oryzae* isolated from lake water. *Journal of Genomics* **7**, 64–72. <https://doi.org/10.7150/jgen.38365>.
- Jankowska, E., Jankowska, K. & Włodarska-Kowalczyk, M. 2015 Seagrass vegetation and meiofauna enhance the bacterial abundance in the Baltic sea sediments (puck bay). *Environmental Science and Pollution Research International* **22** (18), 14372–14378. <https://doi.org/10.1007/s11356-015-5049-7>.
- Jian, L., Qiang, J., He, Y., Xia, H. & Zhao, J. 2014 Simultaneous removal of phenol and ammonium using *Serratia* sp. *Lj-1* capable of heterotrophic nitrification-aerobic denitrification. *Water, Air, and Soil Pollution* **225**, 2125.
- Johnston, G. P. & Leff, L. G. 2015 Bacterial community composition and biogeochemical heterogeneity in pah-contaminated riverbank sediments. *Journal of Soils and Sediments* **15**, 225–239. <https://doi.org/10.1007/s11368-014-1005-2>.
- Kelemen, P., Fierer, N. & Matter, J. M. 2016 Modern water/rock reactions in Oman hyperalkaline peridotite aquifers and implications for microbial habitability. *Geochimica et Cosmochimica Acta*.

- Kowalchuk, G. A., van Os, G. J., van Aartrijk, J. & van Veen, J. A. 2003 Microbial community responses to disease management soil treatments used in flower bulb cultivation. *Biology and Fertility of Soils* **37**, 55–63. <https://doi.org/10.1007/s00374-002-0561-6>.
- Li, C. H., Zhou, H. W., Wong, Y. S. & Tam, N. F. 2009 Vertical distribution and anaerobic biodegradation of polycyclic aromatic hydrocarbons in mangrove sediments in Hong Kong, south China. *Science of the Total Environment* **407** (21), 5772–5779. <https://doi.org/10.1016/j.scitotenv.2009.07.034>.
- Li, Y., Yang, N., Qian, B., Yang, Z., Liu, D., Niu, L. & Zhang, W. 2018 Development of a bacteria-based index of biotic integrity (ba-ibi) for assessing ecological health of the Three Gorges reservoir in different operation periods. *Science of the Total Environment* **640–641**, 255–263. <https://doi.org/10.1016/j.scitotenv.2018.05.291>.
- Li, C., Hu, H. W., Chen, Q. L., Chen, D. & He, J. Z. 2019a Comammox *Nitrospira* play an active role in nitrification of agricultural soils amended with nitrogen fertilizers. *Soil Biology and Biochemistry* **138**, 107609. <https://doi.org/10.1016/j.soilbio.2019.107609>.
- Li, H., Su, J. Q., Yang, X. R., Zhou, G. W., Lassen, S. B. & Zhu, Y. G. 2019b RNA stable isotope probing of potential feammox population in paddy soil. *Environmental Science and Technology* **53**, 4841–4849. <https://doi.org/10.1021/acs.est.8b05016>.
- Lopes, A. R., Manaia, C. M. & Nunes, O. C. 2014 Bacterial community variations in an alfalfa-rice rotation system revealed by 16S rRNA gene 454-pyrosequencing. *FEMS Microbiology Ecology* **87**, 650–663. <https://doi.org/10.1111/1574-6941.12253>.
- Lors, C., Ryngaert, A., Périé, F., Diels, L. & Damidot, D. 2010 Evolution of bacterial community during bioremediation of PAHS in a coal tar contaminated soil. *Chemosphere* **81** (10), 1263–1271. <https://doi.org/10.1016/j.chemosphere.2010.09.021>.
- Lu, J. Y., Wang, X. M., Liu, H. Q., Yu, H. Q. & Li, W. W. 2019 Optimizing operation of municipal wastewater treatment plants in China: The remaining barriers and future implications. *Environment International* **129**, 273–278. <https://doi.org/10.1016/j.envint.2019.05.057>.
- Lynch, S. F. L., Batty, L. C. & Byrne, P. 2018 Environmental risk of severely Pb-contaminated riverbank sediment as a consequence of hydrometeorological perturbation. *Science of the Total Environment* **636**, 1428–1441. <https://doi.org/10.1016/j.scitotenv.2018.04.368>.
- Machado, A., Magalhães, C., Mucha, A. P., Almeida, C. M. R. & Bordalo, A. A. 2012 Microbial communities within saltmarsh sediments: Composition, abundance and pollution constraints. *Estuarine, Coastal and Shelf Science* **99**, 145–152. <https://doi.org/10.1016/j.ecss.2011.12.028>.
- Mai, Y., Liang, Y., Cheng, M., He, Z. & Yu, G. 2021 Coupling oxidation of acid volatile sulfide, ferrous iron, and ammonia nitrogen from black-odorous sediment via autotrophic denitrification-anammox by nitrate addition. *Science of the Total Environment* **790**, 147972. <https://doi.org/10.1016/j.scitotenv.2021.147972>.
- Martínez-Santos, M., Lanzén, A., Unda-Calvo, J., Martín, I., Garbisu, C. & Ruiz-Romera, E. 2018 Treated and untreated wastewater effluents alter river sediment bacterial communities involved in nitrogen and sulphur cycling. *Science of the Total Environment* **633**, 1051–1061. <https://doi.org/10.1016/j.scitotenv.2018.03.229>.
- Meier, K., Kuusemets, V., Luig, J. & Mander, Ü. 2005 Riparian buffer zones as elements of ecological networks: Case study on Parnassius Mnemosyne distribution in Estonia. *Ecological Engineering* **24**, 531–537. <https://doi.org/10.1016/j.ecoleng.2005.01.017>.
- Müller, J. B., Ramos, D. T., Larose, C., Fernandes, M., Lazzarin, H. S. C., Vogel, T. M. & Corseuil, H. X. 2017 Combined iron and sulfate reduction biostimulation as a novel approach to enhance BTEX and PAH source-zone biodegradation in biodiesel blend-contaminated groundwater. *Journal of Hazardous Materials* **326**, 229–236. <https://doi.org/10.1016/j.jhazmat.2016.12.005>.
- Mulvaney, R. L. 1996 Nitrogen-inorganic forms: In: Sparks, D., Page, A., Helmke, P., Loeppert, R. H., Soltanpour, P. N., Tabatabai, M. A., Johnston, C. T. & Sumner, M. E. (eds) 1996 Methods of Soil Analysis: Part 3 – Chemical Methods. Wiley.
- Newsome, L., Morris, K. & Lloyd, J. R. 2015 Uranium biominerals precipitated by an environmental isolate of *Serratia* under anaerobic conditions. *PLOS ONE* **10**, e0132392. <https://doi.org/10.1371/journal.pone.0132392>.
- Niu, Z. S., Pan, H., Guo, X. P., Lu, D. P., Feng, J. N., Chen, Y. R., Tou, F. Y., Liu, M. & Yang, Y. 2018 Sulphate-reducing bacteria (SRB) in the Yangtze estuary sediments: Abundance, distribution and implications for the bioavailability of metals. *Science of the Total Environment* **634**, 296–304. <https://doi.org/10.1016/j.scitotenv.2018.03.345>.
- Petersen, L. M. & Tisa, L. S. 2013 Friend or foe? A review of the mechanisms that drive *Serratia* towards diverse lifestyles. *Canadian Journal of Microbiology* **59**, 627–640. <https://doi.org/10.1139/cjm-2013-0343>.
- Qiu, Z., Zhang, S., Ding, Y., Zhang, W., Gong, L., Yuan, Q., Mu, X. & Fu, D. 2021 Comparison of *Myriophyllum spicatum* and artificial plants on nutrients removal and microbial community in constructed wetlands receiving WWTPs effluents. *Bioresour Technol* **321**, 124469. <https://doi.org/10.1016/j.biortech.2020.124469>.
- Ran, J., Wang, D., Wang, C., Zhang, G. & Zhang, H. 2016 Heavy metal contents, distribution, and prediction in a regional soil–wheat system. *Science of the Total Environment* **544**, 422–431. <https://doi.org/10.1016/j.scitotenv.2015.11.105>.
- Rice, J., Wutich, A. & Westerhoff, P. 2013 Assessment of de facto wastewater reuse across the US: Trends between 1980 and 2008. *Environmental Science and Technology* **47**(19), 11099–11105. <https://doi.org/10.1021/es402792s>.
- Shi, J., Zhang, B., Wang, Y. & Fu, J. 2020 Effects of hydropower dam construction on sulfur distribution and sulfate-reducing prokaryotes assemblage. *Science of the Total Environment* **705**, 135819. <https://doi.org/10.1016/j.scitotenv.2019.135819>.
- Tang, X., Li, R., Wu, M., Zhao, W., Zhao, L., Zhou, Y. & Bowes, M. J. 2019 Influence of turbid flood water release on sediment deposition and phosphorus distribution in the bed sediment of the Three Gorges Reservoir, China. *Science of the Total Environment* **657**, 36–45. <https://doi.org/10.1016/j.scitotenv.2018.12.011>.
- Thomsen, T. R., Kong, Y. & Nielsen, P. H. 2007 Ecophysiology of abundant denitrifying bacteria in activated sludge. *FEMS Microbiology Ecology* **60**, 370–382. <https://doi.org/10.1111/j.1574-6941.2007.00309.x>.

- Wang, X., Wang, C., Wang, P., Chen, J., Miao, L., Feng, T., Yuan, Q. & Liu, S. 2018 How bacterioplankton community can go with cascade damming in the highly regulated Lancang–Mekong River basin. *Molecular Ecology* **27** (22), 4444–4458. <https://doi.org/10.1111/mec.14870>.
- Wang, S., Zhang, B., Li, T., Li, Z. & Fu, J. 2020a Soil vanadium(V)-reducing related bacteria drive community response to vanadium pollution from a smelting plant over multiple gradients. *Environment International* **138**, 105630. <https://doi.org/10.1016/j.envint.2020.105630>.
- Wang, Y., Shen, L., Wu, J., Zhong, F. & Cheng, S. 2020b Step-feeding ratios affect nitrogen removal and related microbial communities in multi-stage vertical flow constructed wetlands. *Science of the Total Environment* **721**, 137689. <https://doi.org/10.1016/j.scitotenv.2020.137689>.
- Watanabe, K., Kodama, Y. & Kaku, N. 2002 Diversity and abundance of bacteria in an underground oil-storage cavity. *BMC Microbiology* **2**, 23. <https://doi.org/10.1186/1471-2180-2-23>.
- Weisener, C., Lee, J., Chaganti, S. R., Reid, T., Falk, N. & Drouillard, K. 2017 Investigating sources and sinks of N₂O expression from freshwater microbial communities in urban watershed sediments. *Chemosphere* **188**, 697–705. <https://doi.org/10.1016/j.chemosphere.2017.09.036>.
- Wu, Q., Du, Y., Huang, Z., Gu, J., Leung, J. Y. S., Mai, B., Xiao, T., Liu, W. & Fu, J. 2019 Vertical profile of soil/sediment pollution and microbial community change by e-waste recycling operation. *Science of the Total Environment* **669**, 1001–1010. <https://doi.org/10.1016/j.scitotenv.2019.03.178>.
- Yang, Z., Hosokawa, H., Kuroda, M., Inoue, D. & Ike, M. 2021 Microbial antimonate reduction and removal potentials in river sediments. *Chemosphere* **266**, 129192. <https://doi.org/10.1016/j.chemosphere.2020.129192>.
- Yu, S. X., Pang, Y. L., Wang, Y. C., Li, J. L. & Qin, S. 2017 Spatial variation of microbial communities in sediments along the environmental gradients from Xiaoqing River to Laizhou Bay. *Marine Pollution Bulletin* **120** (1–2), 90–98. <https://doi.org/10.1016/j.marpolbul.2017.04.059>.
- Yu, M., Liu, S., Li, G., Zhang, H., Xi, B., Tian, Z., Zhang, Y. & He, X. 2020 Municipal wastewater effluent influences dissolved organic matter quality and microbial community composition in an urbanized stream. *Science of the Total Environment* **705**, 135952. <https://doi.org/10.1016/j.scitotenv.2019.135952>.
- Zhang, Y., Chen, L., Sun, R., Dai, T., Tian, J., Liu, R. & Wen, D. 2014a Effect of wastewater disposal on the bacterial and archaeal community of sea sediment in an industrial area in China. *FEMS Microbiology Ecology* **88**, 320–332. <https://doi.org/10.1111/1574-6941.12298>.
- Zhang, X., Qin, L., Qu, R., Feng, M., Wei, Z., Wang, L. & Wang, Z. 2014b Occurrence of polychlorinated diphenyl sulfides (PCDPSs) in surface sediments and surface water from the Nanjing section of the Yangtze River. *Environmental Science and Technology* **48**(19), 11429–11436. <https://doi.org/10.1021/es502197b>.
- Zhang, M., Luo, Y., Lin, L., Lin, X., Hetharua, B., Zhao, W., Zhou, M., Zhan, Q., Xu, H., Zheng, T. & Tian, Y. 2018 Molecular and stable isotopic evidence for the occurrence of nitrite-dependent anaerobic methane-oxidizing bacteria in the mangrove sediment of Zhangjiang Estuary, China. *Applied Microbiology and Biotechnology* **102**, 2441–2454. <https://doi.org/10.1007/s00253-017-8718-2>.
- Zhang, M., Wang, Z. J., Huang, J. C., Sun, S., Cui, X., Zhou, W. & He, S. 2021 Salinity-driven nitrogen removal and its quantitative molecular mechanisms in artificial tidal wetlands. *Water Research* **202**, 117446. <https://doi.org/10.1016/j.watres.2021.117446>.
- Zivic, I., Markovic, Z., Filipovic-Rojka, Z. & Zivic, M. 2010 Influence of a trout farm on water quality and macrozoobenthos communities of the receiving stream (Trenjica river). *Serbia International Revue of Hydrobiology* **94**, 673–687.

First received 7 January 2023; accepted in revised form 8 May 2023. Available online 19 May 2023