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Pattern changes of microbial communities in urban river affected by anthropogenic activities and their environmental driving mechanisms

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Abstract

The microbial community structure of sediments in the Bahe River Basin, China was studied using a high-throughput sequencing platform and PCR amplification to investigate the pattern changes in microbial communities in urban rivers affected by anthropogenic activities and their environmental driving mechanisms. The results demonstrated that the average total nitrogen and total phosphorus in the sediments were 524 and 734 mg/kg, respectively. The T, COD and NH_4^+-N of the water and the moisture content of the sediments has significantly impacted on the microbial community structure. Twenty microbial species with a relative abundance > 1% in the sediments of the river were observed, accounting for 95–99% of the total microbial community. The primary species were Proteobacteria (13.86–69.14%), Firmicutes (1.45–58.33%), Chloroflexi (3.68–26.18%), Actinobacteria (2.7–21.51%), Acidobacteria (0.73–16.36%), Bacteroides (1.53–14.11%), and Thermodesulfobacteria (0.1–8.9%), accounting for over 90% of the total microbial community. At the class level, the primary species were γ-proteobacteria, Alphaproteobacteria, Anaerolineae, Bacillus, Bacteroidota, Actinobacteriota, and Clostridia, accounting for over 70% of the total microbial community. Our results provide direct evidence for a link between microbial community structure and environment factors. This evidence demonstrates that sediment microorganisms can be applied to evaluate urban rivers pollution levels, which can provide a scientific basis for pollution control and management in the urban river affected by human activities.

Keywords: High-throughput sequencing, Bacteria, Environmental factors, Water quality parameter, Sediment

Introduction

Microorganism is a crucial part of ecosystems, patterns of microbial distribution represent the integrated effects of historical and biological processes, which play a significant role in biogeochemical cycles [17, 40, 47, 53]. Sediments are significant habitat for microbial community, and they provide valuable ecological information. The characteristics of sediment microbial populations can be used as biological indicators to reveal the biodiversity and health status of ecosystems, which is of great significance to solving problems related to aquatic environment [14, 56]. The rapid advancement of high-throughput sequencing technology provides an essential technical means for studying the complexity and diversity of microbial communities, particularly for microorganisms that are difficult to cultivate and those that represent a minority of the population [4, 49]. Some scholars used 16S rRNA sequencing to investigate both planktonic and benthic bacterial communities in the Jiulong River Watershed. They found that nutrient concentrations were the main factors of both α- and β-diversity patterns of bacterioplankton communities. Betaproteobacteria, Actinobacteria and Firmicutes were significantly more abundant in

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planktonic than in benthic communities, whereas the relative abundances of Acidobacteria, Delta-, Gammaproteobacteria, Chloroflexi and Nitrospira were higher in sediment than in water samples [14].

In recent years, rapid economic development has predominantly increased urbanization and industrialization [15]. As a result, high pollution loads are discharged to the water bodies, which has eventually caused water pollution to be of major concern. Pollutants deposited in river sediments are gradually released into the river water, thus deteriorating the water quality. They can serve as both a source and pool of water pollutants, the pollutants can bioaccumulate in sediments through various mechanisms and further re-release into the water body under favourable conditions, causing secondary pollution. Some studies suggest that pollutants can harm the aquatic ecosystem when the concentration of pollutants in the sediments is 2–3 times higher than the background concentrations [44]. The redundancy analysis (RDA) showed a positive correlation between population, industrial wastewater, domestic sewage, livestock and nitrogen pollution concentrations in the river [33]. Pollutants generated from anthropogenic sources have been causing changes in microbial community [42]. Some researchers showed consistent shifts in sediment bacterial communities in response to nitrogen pollution gradient in the east China sea [47]. Firmicutes were found most abundantly in disturbed zone, highlighting the impacts of anthropogenic activities [35]. Firmicutes were also found to be related to human impact in an urban river in Mexico [12]. Meanwhile, environmental factors are also key factors affecting the abundance of sediment microbial community. For example, Sediment total phosphorus was most influential on the bacterial community structures in coastal area [35]. Research in Pune River, a typical urban river in India, showed that ammonium came from agricultural runoffs significantly shaped the microbial community in the river, especially ammonium oxidizing archaea group [51]. And another research in Peru proved that high BOD_5 can make aerobic microorganisms flourish, then lead to decrease in DO [8]. Some scientists also studied the changes in water quality and land use in the Yangtze River basin from multiple temporal and spatial perspectives, the results showed that the correlation between DO and land use is low, while that between NH_4^+-N and land use is high [45].

It has been widely investigated about the human health risks from water quality deterioration around the world, including India [2], South Africa [10], Sudan [19] and Nigeria [5]. These researches emphasized that ecosystem in river, especially urban river, is of great importance on human health. However, in urban rivers heavily affected by human activities, the correlation of environmental factors in water and sediment on microbial community structure of sediments and the coupling effect of microbial diversity and water pollution in urban rivers are not clear. Therefore, we investigated the following research problems: (1) whether microbial biodiversity in urban river sediments undergo significant changes under the influences of anthropogenic activities, (2) the possible patterns and influencing mechanisms of these changes, (3) the correlationship between physicochemical parameters and microbial community structures and (4) to evaluate how sediment bacterial communities respond to pollution water in the urban cities. The limitation of this study is that the scope focused in the current status of microbial community and the distribution pattern along the river, as well as the effect of environmental factors. For the study, the 16s RNA microbial gene was used as the target for high-throughput sequencing to reveal the relationship between the changes in microbial community structure and environmental factors in urban river sediments and to provide a scientific basis for the management of urban river ecosystems and protection of biodiversity.

Materials and methods

Study area

The Bahe River (33°50′ to 34°27′N and 109°00′ to 109°47′E), a typical urban river with significant human influence, is the primary tributary of the Weihe River in the Yellow River, China, flowing southeast to northwest. The study area is semi-arid and semi-humid continental monsoon climate of warm temperate zone, with distinct four seasons and mild climate. The river length is approximately 78 km (south to north) with a width of 50 km (east to west), basin area of 2,581 km^2 and an annual runoff of 718 million m^3 [20]. The annual average temperature (T) is 13.1–14.3 °C, and the annual precipitation is 528.3–716.5 mm [15]. The dominant wind direction is northeast, and the maximum wind speed is 2.4 m/min. Annual average humidity is 69.6%, annual sunshine is 2058.2 h. The annual average evaporation is 852.7 mm, with the largest evaporation from June to August, accounting for 43.5% of the annual evaporation [13]. Bahe River provides a rainwater discharge in the monsoon and is primarily used for farmland irrigation, and landscape channel development.

Sample collection and pre-treatment

Sediment samples were collected from 24 to 29 September 2020. The river is the raining season on September, the average daily temperature ranges from 15 ℃ to 24 ℃. Most of the precipitation occurs in July and September, accounting for 45–60% of the annual rainfall. Researches have proved that comparing to dry season,

rivers in raining season have higher river connectivity, which provides better understanding of longitudinal pattern of microbial distribution and surrounding pollution effect [18, 36]. Considering the natural attributes such as surface width, water depth, riverbed geotechnical properties, and the water pollution distribution in Bahe River, the sampling points were distributed at intervals of 1–1.5 km. A total of 18 sampling points, including points B1–B6 in the upper reach, points B7–B12 in the middle reach, and points B13–B18 in the lower reach were considered for the study (Fig. 1). Four litres of water were collected per sampling point and placed in the Teflon sampling bottles. Additionally, 500 g of surface sediment was collected per sample by use of a Peterson grab sampler. All the samples were collected with three replicates for later testing. Sediments were transported to the laboratory in sterile plastic bags and frozen in a freezer at − 80 °C. Ten percent of the sediment sample was subjected to high-throughput sequencing, while the remaining sample was cold-dried, ground, and screened for later use [26, 50]. According to other research about high-throughput sequencing of sediments, samples could be grouped to carry out statistical analysis [6, 25, 27, 37, 48]. However, to ensure the samples are homogenized, three replicates were mixed and pressed for the later 16s-RNA analysis [7, 22, 28, 38, 46].

Analysis of physical and chemical properties of water and sediments

The T, pH, dissolved oxygen (DO), oxidation–reduction potential (ORP), electrical conductivity (EC), turbidity (measured in nephelometric turbidity units, NTU), and total dissolved solids (TDS) of the water samples were measured using a Hash portable multi-parameter detector (HASH SL-1000, Suzhou city, Jiangsu province, China), chemical oxygen demand (COD) of the water samples was determined through the microwave heating method (GB11914-89). Ammonia nitrogen (NH_4^+-N) of the water samples was determined using salicylic acid spectrophotometry (HJ 535-2009). In the sediments, total nitrogen (TN) was determined using alkaline potassium persulfate digestion ultraviolet spectrophotometry (HJ 636-2012), total phosphorus (TP) was determined using ammonium molybdate spectrophotometry (GB 11893-89), moisture content (MC) was determined gravimetrically, and organic matter (OM) was determined through loss on ignition [16, 41, 52]. See Table 1 for the physical and chemical parameters of the Bahe River Basin.

DNA extraction and polymerase chain reaction (PCR) amplification analysis of microorganisms in sediments

One percent agarose gel electrophoresis was used to detect and extract DNA from sediments in the Chanba River Basin. The, 338F_806R primer was used for PCR amplification and product purification. Each sample was amplified in triplicate in a 50 μL reaction mixture under the conditions: 30 cycles of denaturation at 94 ℃ for 30 s, annealing at 55 ℃ for 30 s, and extension at 72 ℃ for 30 s, with a final extension at 72 ℃ for 10 min [47]. The sediment DNA was stored in a freezer at − 80 °C for later use [43, 55, 59].

High-throughput sequencing analysis

The PCR products were detected and quantified using the QuantiFluor™-ST blue fluorescence quantitative system and were mixed according to the sequencing amount of each sample. Each sample was amplified in triplicate, pooled and purified using the QIA quick PCR purification kit (Qiagen, Valencia, CA, USA) [14]. Then all amplicons were mixed in equimolar concentration. A paired-end library was constructed for Illumina sequencing [57]. The sediments were tested, the average sequence

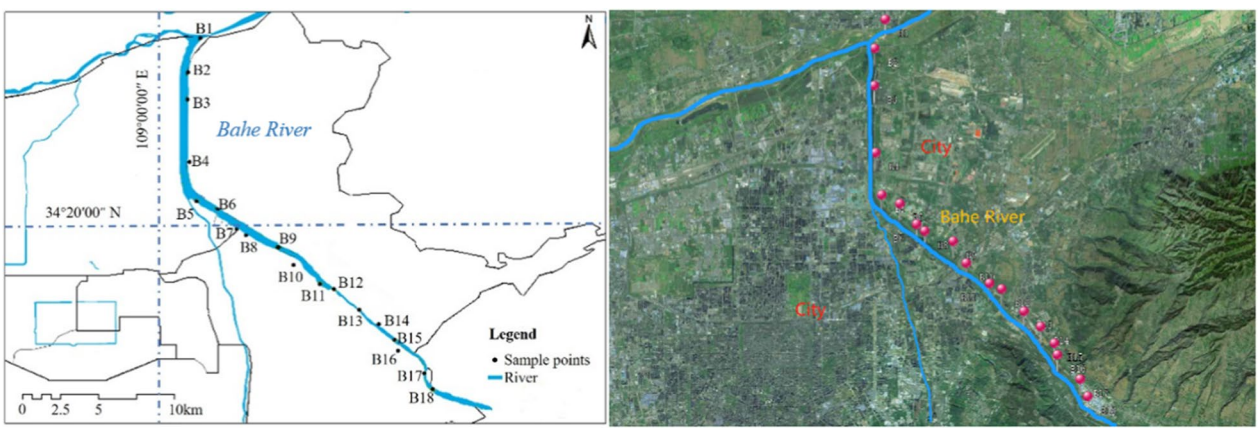

Fig. 1 Distribution of sampling points

Table 1 Physical and chemical parameters of Bahe River Basin

Type	Parameter	Mean	Standard deviation	Standard error	Minimum	Maximum	Range
Water	pH	8.47	0.57	0.13	7.05	9.12	2.07
	DO (mg/L)	9.06	1.70	0.40	6.13	12.21	6.08
	T (°C)	28.88	2.50	0.59	23.00	32.00	9.00
	COD (mg/L)	45.49	11.41	2.69	26.10	68.27	42.17
	ORP (mV)	179.40	31.84	8.22	103.00	222.00	119.00
	EC (mS/cm)	0.46	0.11	0.03	0.33	0.67	0.34
	NTU	91.43	81.38	21.01	14.40	323.00	308.60
	TDS (g/L)	0.30	0.07	0.02	0.22	0.43	0.21
	TN (mg/L)	2.84	0.64	0.15	1.94	4.12	2.18
	NH_4^+-N (mg/L)	0.40	0.36	0.08	0.15	1.05	0.90
	TP (mg/L)	0.01	0.02	0.00	0.00	0.06	0.06
Sediment	MC (%)	24.49	11.42	11.09	5.75	45.82	40.06
	OM (%)	3.75	1.51	1.47	0.80	6.27	5.47
	TN (mg/kg)	523.76	514.87	500.37	24.06	1812.13	1788.07
	TP (mg/kg)	734.43	225.90	219.54	215.91	1177.27	961.36

number was 42,651, the average basic sequence number was 17,863,794, and the average sequence length was 418.92.

Data processing and analysis

QIIME1.9.0 analysis software was used for filtering, splicing, and chimera removal of the original FASTQ files. Operational taxonomic units (OTUs) at a similarity level of 97% were statistically analyzed for biological information [24]. According to the species' taxonomy information corresponding to each OTU, the representative sequences of OTUs at a similarity level of 97% were subjected to taxonomic analysis using the Ribosomal Database Project Bayesian classifier algorithm, and the community species composition in each sample was counted.

QIIME software was used to calculate the diversity indices (Sobs, Chao, Ace, and Shannon indices). R software was used to perform redundancy analysis (RDA) on the environmental factors and bacterial community structure. The method of least significant difference was used to conduct significance comparisons ($\alpha = 0.05$). A Kruskal–Wallis H test was used to study the significance of inter-group differences. Based on the community abundance data of the samples, statistical methods were used to detect species with abundance differences in the microbial communities in the various samples, and hypothetical tests were conducted to evaluate the significance of the observed differences. A Venn diagram was used to count the number of common and unique species in the samples and to visually represent the composition similarity and overlap of the environmental samples at different OTU classification levels. To study the similarities or differences in the microbial community structures of the sediments in the Bahe River Basin, a distance matrix of the microbial community was analyzed using clustering, and a hierarchical cluster tree of samples was constructed. Data analysis was performed using an Illumina MiSeq sequencing platform of the Shanghai Majorbio Biotesting Center.

Results and discussion

Nutrient analysis of sediments in Bahe River Basin

The TN contents in the sediments of Bahe River ranged from 24 to 1,812 mg/kg, with an average of 524 mg/kg (Table 1). The TN contents at B2, B5, B8, B16 and B18 ranged from 1000 to 2000 mg/kg (Additional file 1: Fig. S1), indicating moderate pollution according to the Environmental Protection Agency (EPA) classification and grading standard for the sediments, while those at the remaining points were lower than 1000 mg/kg, indicating mild pollution (Additional file 1: Fig. S1; Table 1). The TP contents in the sediments ranged from 216 to 1177 mg/kg, with an average of 734 mg/kg (Table 1). The TP contents at B1 and B3 were less than 420 mg/kg, indicating mild pollution according to the EPA classification and grading standard for sediments; while that at points B6 and B14 were 420–650 mg/kg, indicating moderate pollution; and at the remaining points were greater than 650 mg/kg, indicating severe pollution (Additional file 1: Fig. S1). Compared with the TN and TP contents in the sediments of rural rivers, the nutrients were higher, while the pollution level was lower compared to other urban rivers [21].

The water quality at points B1–B4 belongs to that of a Class IV water body and at points B5–B18 to that of a Class III water body according to the Environmental Quality Standards for Surface Water (GB 3838-2002). The primary reason for this result is that a rubber dam downstream has slowed the water flow and decreased the DO concentration. The OM content in the sediments in the lower reaches of the river ranged from 2.37 to 50.58 $g{\cdot}kg^{-1}$, with an average of 9.85 $g{\cdot}kg^{-1}$(Additional file 1: Fig. S1; Table 1). This result is primarily due to the anthropogenic interferences in the lower reaches of the river, which has affected the soil mass in the long term and frequently disturbed the sediments. The TN contents in the lower reaches of the river ranged from 0.05 to 2.78 $g{\cdot}kg^{-1}$, with an average of 0.64 $g{\cdot}kg^{-1}$ (Additional file 1: Fig. S1). The TP contents in the lower reaches of the river ranged from 0.40 to 3.06 $g{\cdot}kg^{-1}$, with an average of 2.10 $g{\cdot}kg^{-1}$ (Additional file 1: Fig. S1). The TP contents are at a moderate-to-high level due to phosphorus enrichment from urban construction, domestic waste discharge and irrigation using sewage [54]. Since microbial community is significantly influenced by environmental factors, especially nutrient content, these physiochemical properties could be more meaningful in the following RDA analysis.

Analysis of species diversity of sediment microbial communities in Bahe River Basin

Pan/core species analyses

According to the high-throughput sequencing technique, there are 63 phyla, 201 classes, 464 orders, 770 families, 1590 genera, 3477 species, and 10,127 OTUs in the sediments of the Bahe River Basin. Using pan-OTU, we observed an increase in the total OTU number as the number of samples increased. It was used to observe the decrease in the number of common OTUs as the number of samples increased. As illustrated in Additional file 1: Fig. S2, for the 18 sequenced samples obtained from the pan/core species analyses, the curves gradually flatten out, indicating that the sample size is sufficient and can be used to determine the abundance of the sediment microbial communities of the Bahe River Basin and for the subsequent evaluation and analysis of the number of core species.

Alpha diversity analysis

The species richness in the sediment microbial communities of the Bahe River Basin was obtained using diversity index analysis and was expressed using statistical analysis indices (Sobs, Chao, and Ace), which can also reflect the biotic and microbiological activities. The Sobs index represents the actual observed abundance, and the Chao and Ace indices represent the species richness. As displayed in Fig. 2a–c, the average values of the three indices at the OTU classification level were higher than 2000, indicating that the selected sequencing samples reflect the species richness of the sediment microbial communities of the Bahe River Basin. The Shannon index primarily reflects the diversity of microbial communities with a higher Shannon value indicating high community diversity. As illustrated in Fig. 2d, the Shannon index of the Bahe River Basin was higher than the average value of 6, indicating that the microbial community diversity in the sediments of the Bahe River Basin is high.

Microbial community composition analysis in sediments of Bahe River Basin

Venn diagram analysis of microbial species in sediments of Bahe River Basin

Ten dominant microbial populations, including Proteobacteria, Firmicutes, Chloroflexi, Actinobacteria, and Bacteroidota, were tested for their differences. The microbial community characteristics of Bacteroidota in the upper, middle and lower reaches of the Bahe River Basin were significantly different ($P<0.05$) (Fig. 3). Some literatures showed that many species of bacteroidetes live in the intestines of humans and animals and sometimes become pathogens, in feces, Bacteroides is the main microorganism in terms of the number of cells, flavobacteriaceae exist mainly in aquatic environments, which can degrade cellulose [56, 13, 41]. Bacteroidota were all detected in the upper, middle and lower reaches of the Bahe River Basin, it showed that domestic sewage or aquaculture wastewater (such as feces) was the important source in the Bahe River Basin. Venn diagram can be seen in Additional file 1: Fig. S3 that the river is divided into the upper (points B1–B6), middle (points B7–B12), and lower reaches (points B13–B18). There were 3259 common species of microorganisms in the Bahe River Basin sediments. The unique microbial sequences in the sediments of the upper, middle, and lower reaches of the Bahe River Basin included 963 species, 800 species, and 1150 species, respectively. The microbial diversity of the sediments in the Bahe River Basin was in the following order: lower reaches > middle reaches > upper reaches (Additional file 1: Fig. S3).

Analysis of community composition in sediments of Ba river basin

The community composition histogram visually presents two types of information: (1) the dominant species contained in each sample at a certain taxonomic level and (2) the relative abundance of each dominant species in the sample (Fig. 4). As can be seen from Fig. 4a, at the phylum level, the dominant species of the sediment microbial communities in the river basin are Proteobacteria,

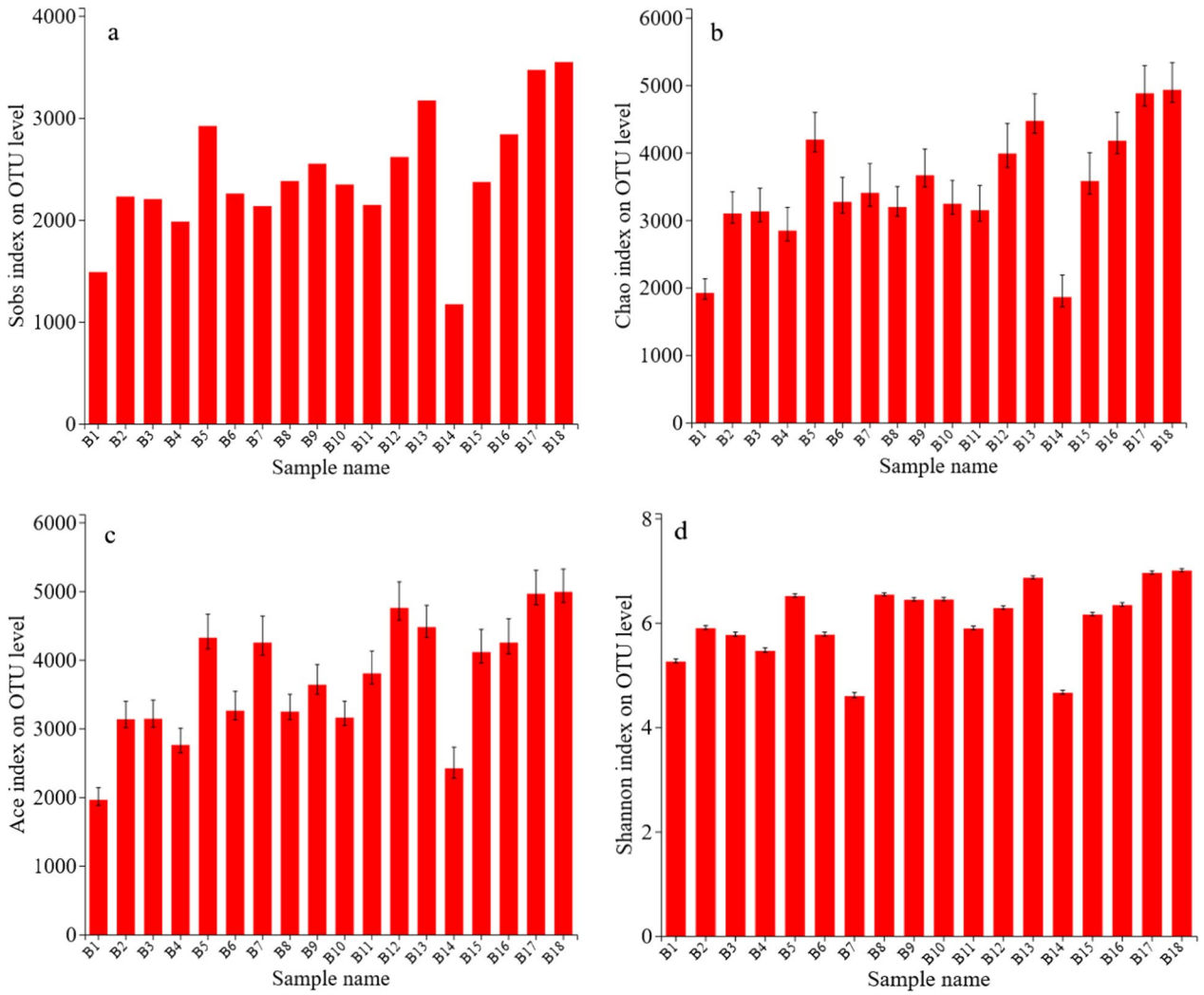

Fig. 2 Index histograms of sediments in Bahe River Basin at OTU level: **a** Sobs, **b** Chao, **c** Ace, and **d** Shannon

Firmicutes, Chloroflexi, Actinobacteria, Acidobacterota, Bacteroidota and Desulfobacterota, accounting for over 90% of the total microbial community. Of these, Desulfobacterota can oxidise reduced sulphides (e.g. H_2S, $S_2O_3^{2-}$, etc.) and elemental sulphur. The existence of Desulfobacterota reduces the content of sulphides in the river water and thus reduces the risk of polluted water, which is of significance in improving the river water quality [29–31].

As can be seen from Fig. 4a, the microbial population in the sediments of the Bahe River Basin is primarily composed of Proteobacteria (13.86–69.14%), Firmicutes (1.45–58.33%), Chloroflexi (3.68–26.18%), Actinobacteriota (2.7–21.51%), Acidobacterota (0.73–16.36%), Bacteroidea (1.53–14.11%), and Thermodesulfobacteria (0.1–8.9%). Such community composition is consistent with other urban rivers, indicating Baha River is a typical urban river [1, 9]. Some researchers found that benthic bacterial communities were clearly more diverse and uniform than surface bacterioplankton communities [14]. The relative abundances of Acidobacteria, proteobacteria and Chloroflexi were higher in sediment than in water samples [35]. In particular, several sewer- and fecal-pollution bacterial indicators were observed in sediment samples, implying that the water bodies of Bahe river were contaminated by sewer- and fecal-pollution.

The average abundance of the Proteobacteria population in the Bahe River Basin is high, particularly at points B1, B2, and B14, accounting for over 50% of the microbial population, and it is one of the dominant species at the other points. Figure 4a, the analysis of the species distribution and proportions at the phylum level demonstrated that the phyla in the microbial community at point B1 in

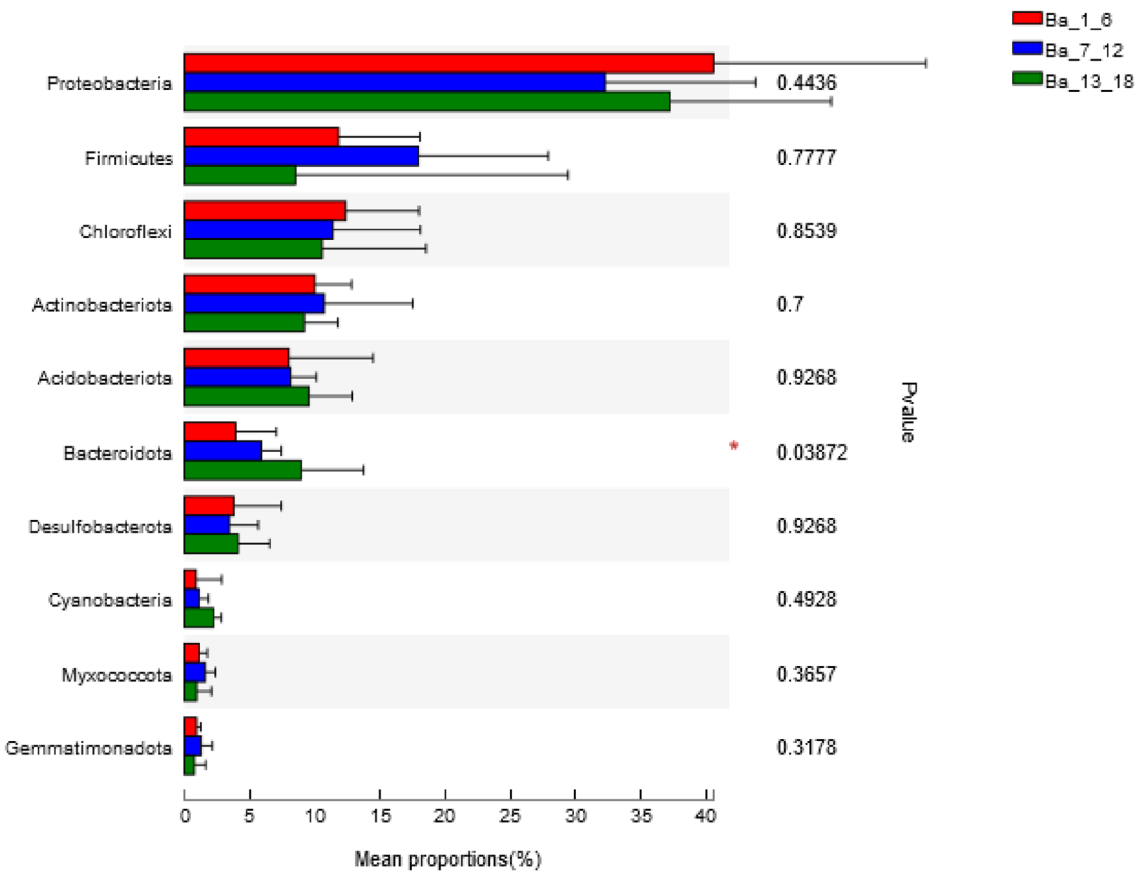

Fig. 3 The relative abundance of dominant bacterial groups in sediment samples obtained from Bahe River Basin. Bars denote standard error of the mean

the Bahe River Basin from high to low are Proteobacteria (51.8%), Actinobacteriota (22.3%), Acidobacterota (7.68%), Chloroflexi (5.55%), Firmicutes (4.83%) and others. Proteobacteria was the main component of microorganisms, which was consistent with previous research results [23, 30, 34]. At point B7, the population of Firmicutes accounts for over 50% of the microbial community, indicating that more OM is decomposed at this point. Firmicutes is important biological resources for degrading carbohydrates [34]. The distribution proportions of phyla in the microbial community at point B18 in the Bahe River Basin are Proteobacteria (28.5%) > Chloroflexi (15.1%) > Acidobacteriota (13.9%) > Actinobacteriota (12.0%) > Firmicutes (7.5%) > Desulfobaacteria and others. The relative abundance of the other predominate phyla is lower than that of Proteobacteria and Firmicutes, indicating that the relative contents of organic carbon and nitrates may be lower at these points. As can be seen from Fig. 4b, the dominant species in the sediment microbial communities of the Bahe River Basin are Gammaproteobacteria, Alphaproteobacteria, Anaerolineae, Bacilli, Bacteroidota, Actinobacteriota, Clostridia, and Vicinamibacteria, accounting for over 70% of the total microbial community. Similar results were also observed by a prior field research of microbial community in sediments by 16S rRNA sequences [24, 14].

Hierarchical clustering analysis of sediments in Bahe River Basin

Figure 5 displays the hierarchical clustering analysis of the sediment microbial communities in the Bahe River Basin at the phylum, class, family, and genus classification levels. From Fig. 5, it can be seen that there are significant differences between point B7 and the microbial communities at the other sampling points at all classification levels. The population of Firmicutes accounts for over 50% of the microbial community (Fig. 5a), Some reports showed that Firmicutes and Bacteroidetes communities are important biological resources for degrading carbohydrates such as rice straw and dietary fiber [34]. Under anaerobic conditions, Firmicutes and

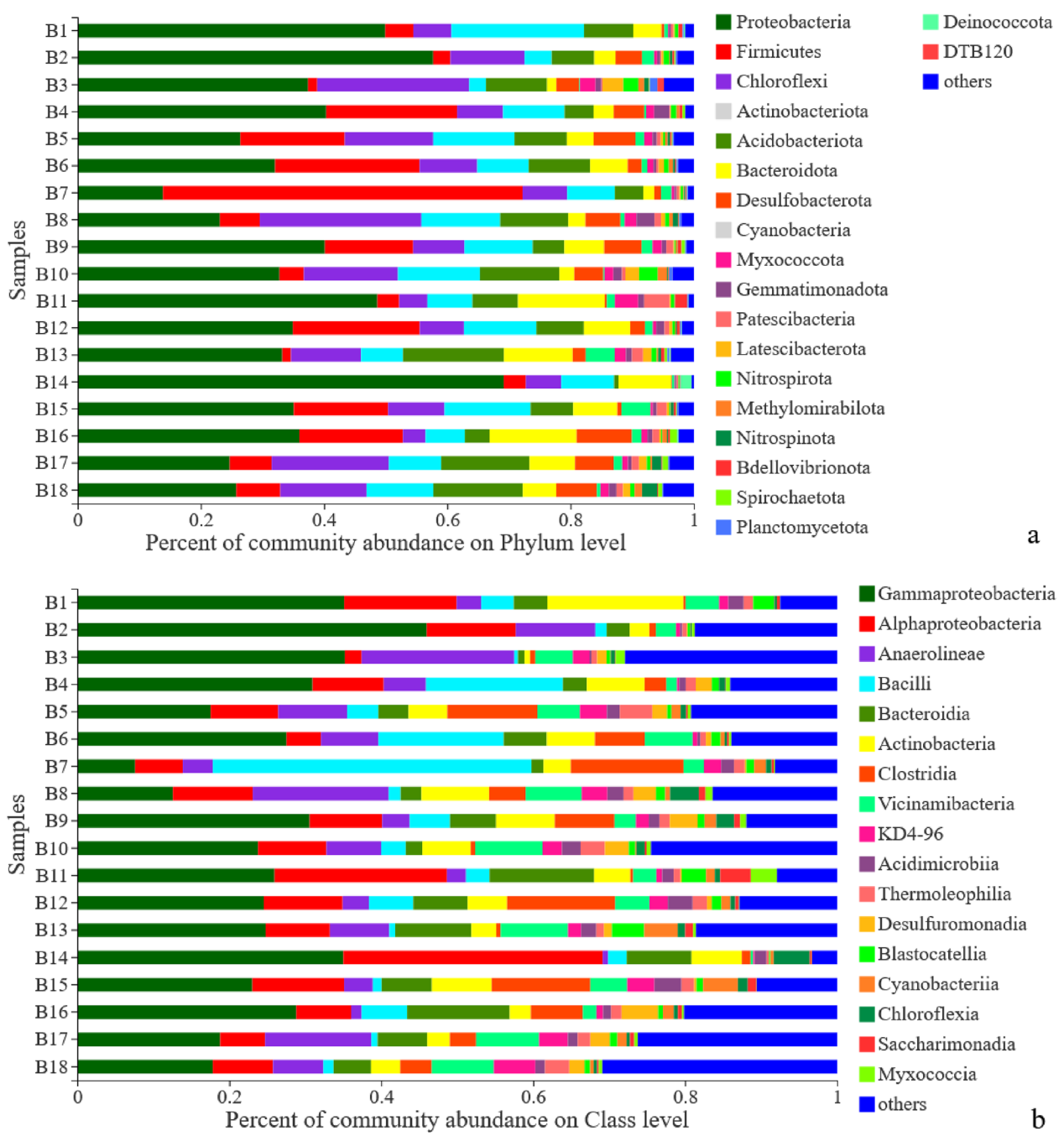

Fig. 4 Histograms of microbial community diversity in the sediments of Bahe River Basin at (**a**) phylum and (**b**) class levels

Bacteroidetes communities can degrade simple or complex organics (such as cellulose, hemicellulose and lactic acid) into pyruvate and acetyl coenzyme A, and then produce metabolites such as ethanol and methane [3].

Hierarchical clustering analysis of microbial communities in the sediments of the Bahe River Basin at the family level (Fig. 5d) revealed that Sphingomonadaceae, Xanthomonadaceae, Camobacteriaceae, Rhodobacteraceae of alpha-3-Proteobacteria, Comamonadaceae, and Clostridlaceae are the dominant species in the sediment microbial communities of the Bahe River Basin at the family level, and the other microbial communities account for over 50% of the total microbial community. Of these, the sediment

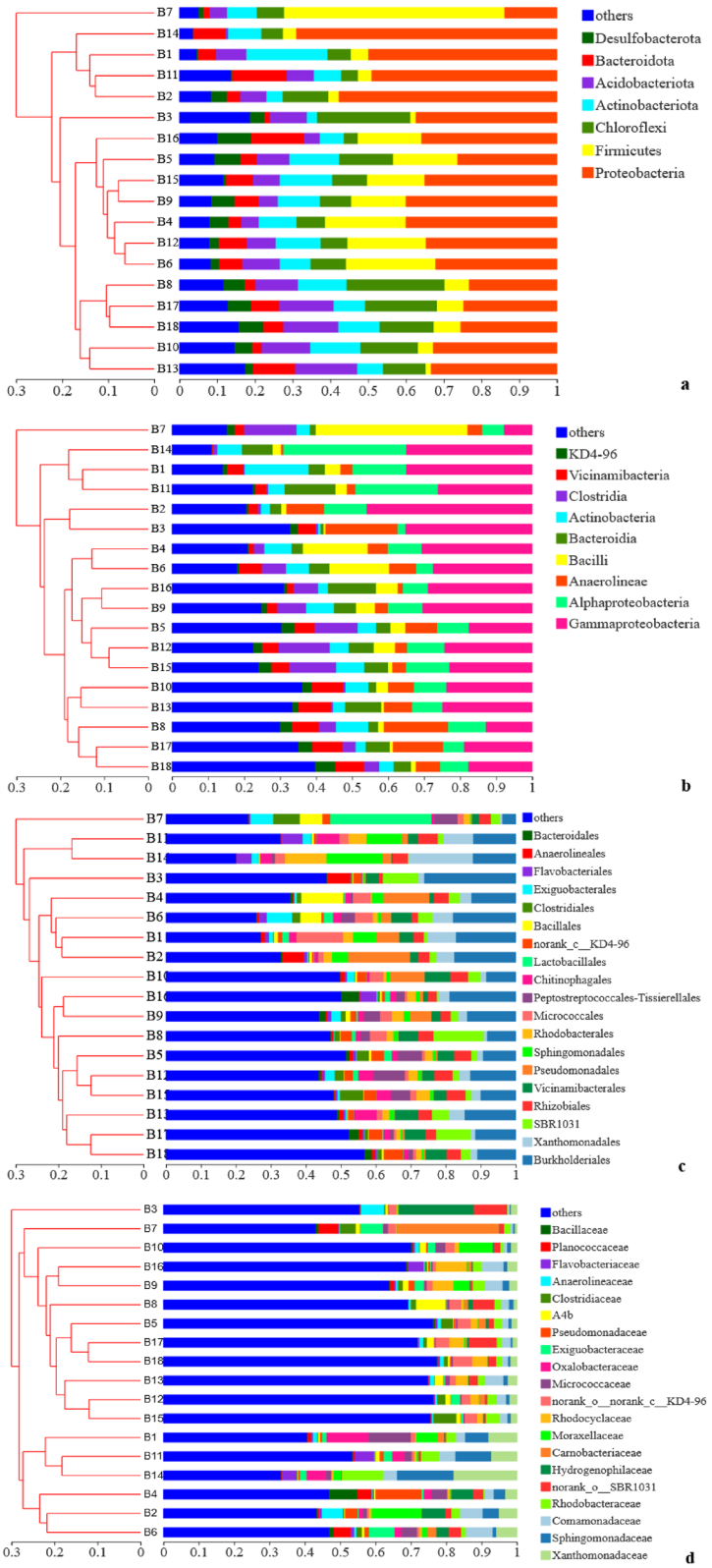

Fig. 5 Hierarchical clustering analysis diagram of sediment microbial communities in Bahe River Basin at the different levels (**a** phylum level, **b** class level, **c** order level, **d** family level)

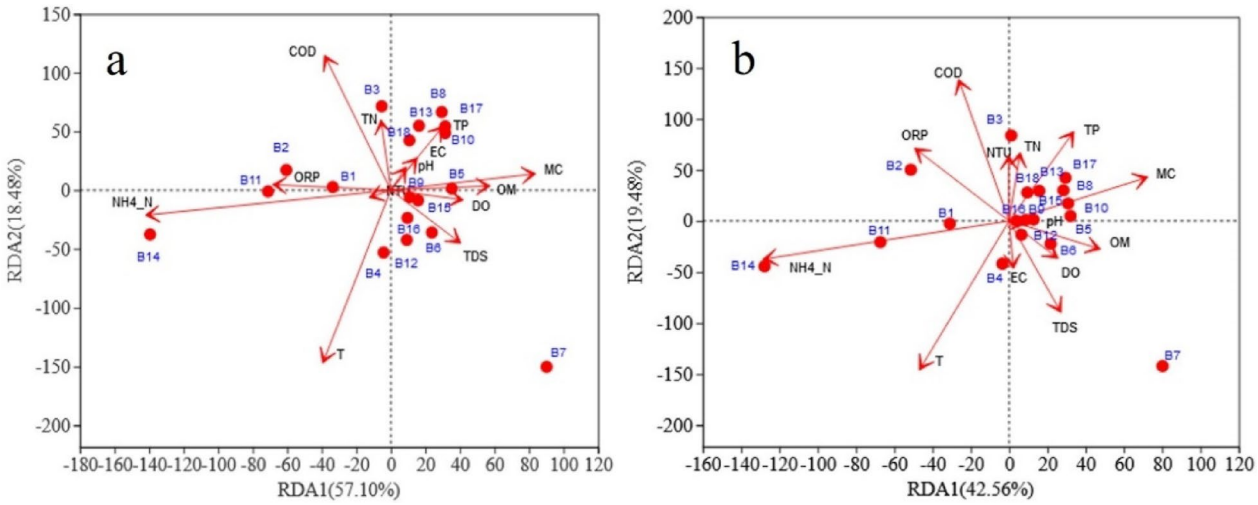

Fig. 6 Redundancy analysis of environmental factors and the abundance of microbial community (**a** at the phylum level, **b** at the class level. T, pH, DO, ORP, COD, EC, TDS, TN, TP, NH_4^+-N were the parameters of the water samples. MC, OM were the parameters of the sediment samples)

microbial communities at points B11 and B14 of the Bahe River Basin show similarity, and those at points B2, B4, and B6 show similarity.

Response relationship between environmental factors and microbial communities

The RDA results reflect the relationship between the sediment bacterial population and environmental factors. The principal components in Fig. 6a explained 57.1% and 18.4% of the variation in the sediment bacterial communities at the phylum level while the principal components in Fig. 6b explain 42.56% and 19.48% of the variation in the sediment bacterial communities at the class level. Of these, the environmental factors pH, EC, MC, OM, TP, DO were positively correlated each other, and these environmental factors controlled the abundance of microbial community at the phylum level at points B5, B8, B9, B10, B13, B15, B17, and B18 of sediments in the Bahe River, while these environmental factors were negatively correlated with ORP, NH_4^+-N, T, and they limited the abundance of microbial community at the phylum level at points B1, B2, B11, B14 of sediments in the Bahe River (Fig. 6a). Analysis based on Additional file 1: Fig. S4, the concentration of TN was significant positive correlation with part of microbial community (i.e., Dependentiae, Nitrospirota, Planctomycetota and DTN120) at the phylum level in the Bahe River Basin. The RDA indicated that population, industrial wastewater, domestic sewage, livestock production were positively correlated with nitrogen pollution of river waters [33]. It was speculated that the concentration of nitrogen maybe impact on the structure of microbial community. Some researchers found that nutrients (e.g., nitrogen and phosphorus) was influential on the bacterial community structures [35]. Meanwhile, microbial community structure was related to land type and source, namely the human influence in Bahe basin. The previous reports shown that forestlands and grasslands were negatively correlated with nitrogen pollution of river water [33]. It was reported that in Turag River, pollution from factories along the river significantly changed the environmental conditions such as DO, COD and BOD_5 nearby, which could be the key factors determining the longitudinal distribution pattern of the microbial community [32]. The strength of stressor inflow, namely the volume, also had crucial influence on the distribution of nutrient and microorganisms [61]. However, that habitat probably have more influence than pollution on microorganisms [1]. It can be seen from the land type around sampling points in Fig. 1 that B17 and B18 were close to forestlands, while sampling points B3, B5, B8 and B10 were close to grasslands, which was similar to the results presented by Shi et al. [33].

The environmental factors pH, MC, OM, and TP are positively correlated with each other, and these environmental factors controlled the abundance of microbial community at the class level at points B5-6, B8-10, B12-13, B15-18 of sediments in the Bahe River, while these environmental factors were negatively correlated with COD, ORP, NH_4^+-N, T, and they limited the abundance of microbial community at the class level at points B1, B2, B11, B14 of sediments in the Bahe River (Fig. 6b). Microbial abundance and diversity are particularly critical to the control of the denitrification rate [59]. The bacterial communities in the sediments of the Bahe River Basin exhibit high diversity, and the seven primary bacterial families

discovered in the present study are consistent with previous reports [58, 60]. Researches have proved that environmental factors could be changeable in different season, which could significantly influence the microbial community [39]. Therefore, future research about seasonal transformation of dynamics between environmental factors and microbial community is highly recommended.

Management measures for water quality improvement in the urban river

The nitrogen and phosphorus in the upper and lower reaches of the Bahe river mainly came from domestic sewage treatment plant. The nutrients pollution was considerably affected by human activities in the Bahe river. The water quality of the Bahe river at the downstream of B5 point and the upstream of B8 point were better than other sample points, and were less affected by the tail water of the sewage treatment plant. The inlet water of the sewage treatment plant should control the mixing of external water (i.e., rainwater, groundwater and river water) into the sewage pipe network. It is necessary to continue to rectify the mixing and misconnecting of the pipe network and improve the efficiency of the sewage transmission system. Meanwhile, optimizing chemical fertilizer application rates and employing deep fertilizing techniques will improve fertilizer use efficiency.

Conclusion

(1) The microbial composition in the Bahe River Basin is rich and typical in urban rivers, with some of the key taxa, among which Proteobacteria is an indicator organism of river water pollution, these bacteria play a vital role in organic pollutant degradation, maintaining the carbon cycle and biogeochemical cycles in the ecosystem.
(2) Both environmental factors and spatial distribution of habitat shaped the microbial community in Bahe River, indicating the land use and pollution input could be the key anthropogenic activity input influencing the ecology of urban rivers.
(3) To develop the management measures, rectifying the mixing and misconnecting of the pipe network and improving the efficiency of the sewage transmission system are extremely necessary in the future.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12302-022-00669-1.

Additional file 1: Fig. S1. Physicochemical parameters of sediments in the Bahe River Basin. (MC: moisture content, OM: organic matter, TN: total nitrogen, TP: total phosphorus). **Fig. S2**. Pan and core species analysis curves. **Fig. S3** Venn diagram of microbial community species in the sediments of Bahe River Basin. **Fig. S4**. Pearson correlation heatmap between environmental factors and the abundance of microbial community at the phylum level in the Bahe River Basin.

Author contributions

WF: Data analysis, Methodology, Writing—original draft and Writing Reviewing; JG: Test data and analysis; YW: Writing-Reviewing and Editing; DL: Resources; FY: Writing-original draft; QZ: Visualization; YB: Investigation, Data curation and Supervision. All authors read and approved the final manuscript.

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Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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