Spatiotemporal correlations between water quality and microbial community of typical inflow river into Taihu Lake, China

Yajie Zhang · Ye Zhang · Lecheng Wei · Mengyan Li · Weitang Zhu · Liang Zhu

Received: 12 October 2021 / Accepted: 29 January 2022 / Published online: 23 April 2022
© The Author(s), under exclusive licence to Springer-Verlag GmbH Germany, part of Springer Nature 2022

Abstract
Changxing River, which is a typical inflow river into Taihu Lake and occurs severe algae invasion, is selected to study the effect of different pollution sources on the water quality and ecological system. Four types of pollution sources, including the estuary of Taihu Lake, discharge outlets of urban wastewater treatment plants, stormwater outlets, and nonpoint source agricultural drainage areas, were chosen, and next-generation sequencing and multivariate statistical analyses were used to characterize the microbial communities and reveal their relationship with water physicochemical properties. The results showed that ammonia nitrogen (NH$_4^+$-N), total nitrogen (TN), and total phosphorus (TP) were the main pollutants in Changxing River, especially at stormwater outlets. At the same time, the diversity of microbial communities was the highest in the summer, and dominant microbes included Proteobacteria (40.9%), Bacteroidetes (21.0%), and Euryarchaeota (6.1%). The results of BIOENV analysis showed that the major seasonal differences in the diversity of microbial community of Changxing river were explained by the combination of water temperature (T), air pressure (P), TP, and COD$_{Mn}$. From the perspective of different pollution types, relative abundances of Microcystis and Nostocaceae at the estuary of Taihu Lake were correlated positively with dissolved oxygen (DO) and pH, and relative abundances of Pseudomonas and Arcobacter were correlated positively with concentrations of TN and nitrate nitrogen (NO$_3^-$-N) at stormwater outlets. This study provided a reference for the impact of pollution types on river microbial ecosystem under complex hydrological conditions and guidance for the selection of restoration techniques for polluted rivers entering the important lake.

Keywords Taihu Lake · Changxing River · Water quality characteristics · Microbial community · Spatial–temporal distribution

Introduction
Over the past decades, rapid industrialization and urbanization around the Taihu Lake Basin in China have caused severe water pollution issues, attracting considerable attention (Yang et al., 2013; Zhang et al., 2019c). According to the Health Status Report of Taihu Lake (2018), the average concentration of chlorophyll a was 31.5 mg/m$^3$, and the average comprehensive trophic level index (TLI) was 60.3, indicating its moderate eutrophication. The annual total nitrogen concentration in the most polluted area of Taihu Lake was above 2.0 mg/L, while the total nitrogen concentration of the class III environmental quality standard for surface water in China (GB3838-2002) is less than 1.0 mg/L. The input and retention of high-load pollutants have caused eutrophication and frequent algae outbreaks in Taihu Lake.

Based on the statistics of Taihu Lake Basin and Southeast Rivers Water Resources Bulletin (2018), 10 of 22 major
inflow rivers around Taihu Lake were contaminated, with COD above 20 mg/L and TN above 1.0 mg/L. Previous studies (Wang et al., 2007; Rodriguez-Mozaz et al., 2015; Zhou et al., 2016a; Du et al., 2017; Zhang et al., 2019c) showed that inflow rivers were one of the sources that contribute to eutrophication and algae bloom in downstream receiving lakes (reservoirs), especially for Taihu Lake. Wang et al. (2011) calculated that more than 90% of the total nutrient load of COD, ammonia nitrogen, total nitrogen, and total phosphorus in Taihu Lake were attributed to the rivers in the Changxing County and Huzhou Urban Area. The highest concentration of NO$_3^-$-N in Changxing River reached 14 mg/L (Yang et al., 2013). Since natural water was diverted from the Yangtze River to Taihu Lake in 2002, the water level of Taihu Lake has risen each year. At the same time, it was exacerbated by the overexploitation and utilization of water resources and meteorological factors, such as precipitation, wind velocity, and wind direction (Liu et al., 2013). Over the past years, the water quality of the section of Changxing River has remained unstable, without meeting the environmental quality standard for surface water in China (GB3838-2002). Therefore, the development of efficient polluted river restoration technology is needed to prevent and control the eutrophication of Taihu Lake.

Microorganisms exist in river ecosystems either in the suspended phase or attached to biofilms (Battin et al., 2016). The composition and structure of microorganisms in river ecosystems are highly dynamic. They can reflect different ecological functions and show a high degree of sensitivity to changes in environmental conditions (Lundgaard et al., 2017) and are recognized as one of the important indicators for the stability of aquatic ecosystems (Liao et al., 2018; Sharuddin et al., 2018; Santos et al., 2019). A number of studies noted that the effects of seasons on microbial communities in rivers were greater than locations (Zhang et al., 2019a, b; Zhu et al., 2019). Microbial community changes generally follow a pattern of periodic recurrence and exhibit a predictable temporal pattern in a simple habitat (Gilbert et al., 2012; Portillo et al., 2012). Zhang et al. (2012) found that there was a significant difference in microbial community compositions between samples collected in the low-temperature months (December to February of the following year) and the high-temperature months (June to October) ($R = 0.102, p < 0.005$). Further, the relative abundance of Cyanobacteria during the rainy season in Dongjiang River was about 10 times higher than that in the dry season, and the abundance of actinomycetes in the dry season was much higher than that in the rainy season (Sun et al., 2017). However, other studies have found that bacterial communities varied across the sites, while seasonal effects were not significant (Ouyang et al., 2020). For instance, a significant positive correlation was reported between the Gammaproteobacteria and TN in Chaohu Lake, China, which suggested their roles in nitrogen transformation in aquatic ecosystems (Zhang et al., 2020). Studies have also shown that small phytoplankton with low nutrient requirements for nitrogen and phosphorus become dominant species in oligotrophic waters (Jiang et al., 2015).

Therefore, correlating physiochemical characteristics with microbial communities can provide the reference for the prediction of ecological functions of the river and the strategies for restoration. In this study, Changxing River was selected as a typical inflow river located at South Taihu Lake Basin. We collected samples from four pollution types of sites over four seasons, including the estuary of Taihu Lake, discharge outlets of urban wastewater treatment plants, stormwater outlets, and nonpoint source agricultural drainage areas. The microbial communities, water physicochemical properties, and their spatiotemporal correlation were investigated. This study could provide the reference for the impact of pollution types on river microbial ecosystem under complex hydrological conditions and direct the selection of restoration techniques for polluted rivers entering an important lake.

Materials and methods

Study area and sampling sites

Changxing River is one of the main inflow rivers in the south Taihu Basin. It plays a vital role in water supply, irrigation, tourism, and fishery and is one of the major navigable rivers in Zhejiang Province (Liu et al., 2011; Wu et al., 2018). However, there are many sources of pollution along the river, such as crop production, human living, effluent of industry, and urban wastewater treatment plants.

Based on pollution sources along the Changxing River, the pollution types were divided into four categories: the estuary of Taihu Lake (I), discharge outlets of urban wastewater treatment plants (II), stormwater outlets (III), and nonpoint source agricultural drainage areas (IV). The cluster analysis of sampling sites was shown in Fig. S1. For each type, we selected 2–3 sites for water sample collection in the summer (August 2018), autumn (October 2018), winter (January 2019), and spring (March 2019), respectively. The geographic locations of the sampling sites were described in Table 1 and depicted in Fig. 1.

Water samples were collected using a plexiglass sampler. At each sampling site, three water samples were taken in 500-mL bottles. After acidification to pH < 2 with H$_2$SO$_4$, samples were stored at 4 °C prior to physicochemical analysis. 1 L of surface water at each sampling site was also collected into glass bottles for algae examination by microscopy. Another 1 L of surface water at each sampling site was sampled and filtered through 0.22-μm glass fiber filters.
(50-mm diameter, Shanghai) by vacuum filtration to collect the microorganisms. The filters were immediately stored at −80 °C in the laboratory prior to DNA extraction (Liao et al., 2018).

**Physicochemical analysis methods**

The water temperature (T), air pressure (P), dissolved oxygen (DO), electrical conductivity (EC), total dissolved solids (TDS), salinity (SAL), pH, and oxidation reduction potential (ORP) were measured in situ at each site by using a multiparameter water quality monitor (YSI Professional Plus, USA). Total organic carbon (TOC) and total nitrogen (TN) were measured by the TOC analyzer (TOC-VCPH, SHIMADZU). Nessler’s reagent spectrophotometry, N-(1-naphthyl) ethylenediamine dihydrochloride spectrophotometric, ultraviolet spectrophotometry, and ammonium molybdate spectrophotometric methods were used to determine the concentrations of ammonia nitrogen (NH$_4^+$-N), nitrate (NO$_3^-$-N), nitrite (NO$_2^-$-N), and total phosphorus (TP) in surface water, respectively (State Environmental Protection Administration of China., 2002). All physicochemical parameters were calculated as the average triplicate measurements.

**Analysis of microbial community**

The PowerSoil DNA extraction kit (MoBio Laboratories, CA, USA) was used to extract the DNA of microorganisms filtered on water filtration membranes. The V3–V4 region of 16S rRNA was amplified using universal primers 515F (5ʹ-GTGCCAGCMGCGGTAA-3ʹ) and 806R (5ʹ-GGACTACA CHVGGGTWTCTAAAT-3ʹ) (Liao et al., 2018). The PCR systems with a total volume of 25 μL contained two primers (2.5μL for each), genomic DNA (25 ng), PCR Premix (12.5 μL), and PCR-grade water. All PCR reactions were performed in Phusion® high-fidelity PCR Master Mix (New
Environmental Science and Pollution Research (2022) 29:63722–63734

Statistical analysis

Principal component analysis (PCA) was analyzed using the IBM SPSS Statistics 20 software to preprocess the data. Spearman’s rank correlation after the Shapiro–Wilk test was used to analyze the correlation of water quality physicochemical indicators. One-way ANOVA, Kruskal–Wallis test, and ANOSIM were used to determine the significance of differences in physicochemical indicators of water quality and relative microbial abundance in different seasons and pollution types with SPSS, GraphPad Prism, and R (Version 3.5.2). Canoco 4.5 redundancy analysis (RDA) was used to determine the relationship between the environment variables and microbial community structures. The ward.D was used to perform clustering analysis (CA) based on the relative abundance of microbial communities. BIOENV correlation analysis was used to study the relationship between microbial community structure and the environment variables in different seasonal and identify the best combination of environmental variables.

Results and discussion

Spatial and temporal variations of water quality characteristics

As shown in Fig. 2, the changing trend of the average water temperature (T) in Changxing River was summer (31.3 °C) > autumn (22.6 °C) > spring (14 °C) > winter (7.6 °C). pH was neutral to slightly alkalescent (7.0–7.9), which may be related to the properties of upstream soil or affected by the surface runoff of irrigation from farmland (Feng et al., 2017). The concentrations of DO in summer and autumn were 3.98 mg/L and 3.49 mg/L, respectively. They were both lower than the limit of Class III environmental quality standard for surface water in China (≥ 5 mg/L) (GB3838-2002) and significantly (p < 0.0001) lower than those in winter (9.50 mg/L) and spring (7.77 mg/L). There was a significant negative correlation between DO and T (r = −0.790, p < 0.01). Studies have shown that DO was affected by rainfall and temperature and was generally higher in the dry season like winter and spring (Tanaka et al., 2017; Shi et al., 2017).

The concentration of TN in autumn was the highest (4.99 mg/L), followed by spring (4.50 mg/L), winter (4.31 mg/L), and summer (3.22 mg/L). The concentration of NH₄⁺-N in autumn was also the highest (1.92 mg/L). In other seasons, NH₄⁺-N concentrations also exceeded the limit of class III environmental quality standard for surface water in China (≤ 1 mg/L) (GB3838-2002). NO₃⁻-N was the main form of inorganic nitrogen in the water body of Changxing River (58%). The concentrations of NO₃⁻-N in summer (1.65 mg/L) and autumn (1.96 mg/L) were significantly lower than those in winter (2.74 mg/L) and spring (3.06 mg/L). The concentrations of TP in summer (0.39 mg/L) and autumn (0.44 mg/L) were higher than those in winter (0.16 mg/L) and spring (0.18 mg/L).

ANOVA analysis found that T, P, pH, ORP, NO₂⁻-N, and NO₃⁻-N didn’t change significantly among the four pollution types (p > 0.05). As shown in Fig. 3, the average concentrations of TDS, EC, and SAL in water samples from the discharge outlets of urban wastewater treatment plants (II) were 307 mg/L, 422 μS/cm, and 0.24 ng/L, respectively, which were higher than other pollution types. It was mainly related to the effluent composition of the sewage treatment plant. The concentrations of TN, NH₄⁺-N, TP, TOC, and CODₘₙ were the highest at the monitoring points of the stormwater outlets (III), indicating that the sewage from the stormwater outlets (III) had a greater contribution to the pollution of Changxing River sections. The average concentrations of TN, NH₄⁺-N, and TP in water samples from the stormwater outlets (III) were 5.30, 2.19, and 0.55 mg/L, respectively, which were significantly higher than those in other pollution types (p < 0.01). According to the statistical analysis, the NH₄⁺-N emissions of domestic sewage (597 tons) accounted for 89.6% of the total NH₄⁺-N emissions in Changxing County in 2018, indicating that the rain sewage discharge at the stormwater outlets (III) had a significant impact on the concentration increase of TN and NH₄⁺-N in Changxing River.

In addition, the lowest DO (2.20 mg/L) was found at the estuary of Taihu Lake (I) during the algae bloom in autumn in Fig. 4. Simultaneously, compared with other seasons and pollution types, the concentrations of NH₄⁺-N (3.62 mg/L) and TP (0.99 mg/L) were particularly prominent at the stormwater outlets (III) in autumn. The issue of commingling discharge of stormwater and municipal sewage at the stormwater outlets (III) in autumn had a particularly significant impact on the nutrient level in Changxing River.

Comprehensive analysis showed that in all seasons, the average concentrations of NH₄⁺-N (1.92 mg/L), TN (4.99 mg/L), and TP (0.44 mg/L) in autumn were the highest. Among the different pollution types, the highest concentrations of nutrient pollution occurred in the stormwater outlets (III). The average concentrations of nutrient pollution occurred in the stormwater outlets (III) were significantly higher than those in other pollution types (p < 0.05).
outlets (III). The concentrations of NH$_4^+$-N, TN, and TP were 2.19, 5.30, and 0.55 mg/L, respectively. The results of two-way ANOVA in Table S1 showed that seasonal variation was the main factor affecting the water quality characteristics (all values of $p$ were less than 0.05).

Analysis of microbial community in Changxing River

The Shannon index characterizes the diversity of microbial community, whereas the Chao1 index represents the species richness in microbial communities (Ren et al., 2018). The results showed that seasonal variation was the main factor affecting the diversity of microbial community (Fig. 5 and Table S2). The diversity of aquatic microbial communities in summer was the highest, with Shannon and Chao1 indexes of 9.4 and 3,278, respectively. In summer, high temperature can improve the activity of microorganisms, and surface runoff from rainfall can carry nutrients and different microorganisms from the upstream (Feng et al., 2016), contributing to the highest diversity.

Compared with other pollution types, the highest diversity (Shannon) of microbial community occurred in the estuary of Taihu Lake (I), while the highest species richness (Chao1) occurred in the discharge outlets of urban wastewater treatment plants (II). The lowest Shannon index (7.1) and Chao1 index (1,502) both occurred in the nonpoint source agricultural drainage areas (IV). Combined with previous researches, the geographic location of the estuary of Taihu Lake (I) and the effluent sludge of the urban wastewater treatment plants (II) both affected the diversity of microbial community in Changxing River (Lu et al., 2016; Tang et al., 2016). In general, the diversity of microbial community was not significantly different between the monitoring points of different pollution types. This stability of diversity against environmental perturbations may be related to the high functional redundancy with respect to a multitude of functions that the microbial community usually exhibits.
The diversity of aquatic and sediment-attached microbiota was also affected by shear stress, water flow velocity, and water residence time. The flowing water clearly acts to transport microbial community relatively quickly (Zeglin, 2015) (Fig. 6).

Proteobacteria was the dominant phylum across all monitoring sites (accounting for 45.8% on average), followed by Bacteroidetes (18.9%), Cyanobacteria (12.8%), Firmicutes (4.6%), Actinobacteria (4.0%), Euryarchaeota (1.7%), Chloroflexi (1.6%), Acidobacteria (1.5%), Verrucomicrobia (1.0%), and Nitrospirae (0.9%). According to the Kruskal–Wallis test, the dominant phyla in summer included Proteobacteria (40.9%), Bacteroidetes (21.0%), and Euryarchaeota (6.1%). The dominant microbes in autumn and winter included Proteobacteria (45.0–48.7%), Bacteroidetes (19.3–20.5%) and Cyanobacteria (10.1–17.8%), and the dominant phyla in spring included Proteobacteria (48.8%), Cyanobacteria (20.6%), and Bacteroidetes (17.6%). Further, the relative abundance of Euryarchaeota (6.12%, p < 0.001) and Nitrospirae (3.13%, p < 0.001) in summer was significantly higher than in other seasons. The analysis of similarities (ANOSIM) revealed significant differences in the relative abundance of dominant microbial community (R = 0.62, p = 0.001) between different seasons.

The dominant microbes of monitoring points at the estuary of Taihu Lake (I), the discharge outlets of urban wastewater treatment plants (II), stormwater outlets (III), and nonpoint source agricultural drainage areas (IV) are shown in Fig. 3.
wastewater treatment plants (II), and the stormwater outlets (III) were Proteobacteria (39.1–55.2%), Bacteroidetes (16.7–21.0%), and Cyanobacteria (4.4–13.4%), while the dominant microbes at the nonpoint source agricultural drainage areas (IV) were Cyanobacteria (32.3%), Proteobacteria (30.5%), and Bacteroidetes (18.3%). There are significant differences in the abundance of Cyanobacteria between different pollution types (Fig. 7).

Proteobacteria were relatively abundant in water samples collected at the discharge outlets of urban wastewater treatment plants (II, 53.8%) and the stormwater outlets (III, 55.2%), which may be related to their roles in nitrification and denitrification. Proteobacteria can play an important role in COD depletion and nitrogen transformation (Yu et al., 2021). Studies have found that the relative abundance of Proteobacteria is positively correlated with TN (Ouyang et al., 2020). In this study, the concentration of TN was also the highest at the discharge outlets of urban wastewater treatment plants (II) and the stormwater outlets (III).

At the genus level, more taxa showed significant differences in their relative abundances among different seasons or pollution types. The heatmap in Fig. 8 showed the genera with the top 80 relative abundance in Changxing River. Dominant microbes included Microcystaceae (19.3%), Flavobacterium (9.6%), and Pseudomonas (8.9%).

Microcystis in the genera of Microcystaceae is one of the most dominant cyanobacteria found in the algae bloom at Taihu Lake, which has attracted great attention since it is a culprit that secrets highly toxic and persistent microcystin (Shi et al., 2015). The microbial community

Fig. 4 The concentration of DO, NH₄⁺-N, TN, and TP in water samples collected in Changxing River in different pollution types and seasons (I, estuary of Taihu Lake; II, discharge outlets of urban wastewater treatment plants; III, stormwater outlets; IV, nonpoint source agricultural drainage areas)
analysis results showed that the relative abundances of Microcystaceae in spring and autumn (19.8% and 14.3%, respectively) were higher than that in summer and winter (2.4% and 9.7%, respectively). The highest relative abundances were observed at the nonpoint source agricultural drainage areas (IV, 47.7%) in autumn and the estuary of Taihu Lake (I, 41.9%) in spring. Microcystaceae was relatively high in general at the nonpoint source agricultural drainage areas (IV) due to the input of agricultural nonpoint source nitrogen load (Paerl et al., 2016). Previous studies have shown the heaviest algae bloom in Taihu Lake occurred in March (Hampel et al., 2018). During the dry season or the flat-water period, backflow stagnation occurred frequently at the river channels around the lake. This likely explains why the Microcystaceae was highly enriched in Taihu Lake in spring. Besides, the optimal TN/TP ratio in water to promote algae bloom is between 13 and 35. When this ratio is below 13, an algae bloom
can rarely occur. According to Fig. 4, the TN/TP ratios in spring, autumn, and winter at the estuary of Taihu Lake (I) were between 20 and 35, but there were no algae bloom in winter at the estuary of Taihu Lake (I). It indicated that the main reason for the relatively higher abundance of Microcystaceae at the estuary of Taihu Lake (I) in spring and autumn may be the reflux of algae, rather than the nutrient content.

The relative abundance of Flavobacterium was relatively high in winter (11.0%), which may be related to the psychrophilic nature of several species in Flavobacterium (Lopes et al., 2016). In addition, Flavobacterium exhibited
the highest relative abundance (15.6–19.0%) at the discharge outlets of urban wastewater treatment plants (II) and the stormwater outlets (III). Studies have shown that *Flavobacterium* can participate in denitrification, although this genus also contains fish pathogens (Liu et al., 2017b).

The relative abundances of *Pseudomonas* in winter and spring (7.5–8.3%) were higher than in summer and autumn (0.5–1.6%). Bacteria belonging to *Pseudomonas* were highly enriched at the discharge outlets of urban wastewater treatment plants (II, 12.6–17.6%) and the stormwater outlets (III, 12.0–12.4%). *Pseudomonas* contains a diversity of heterotrophic bacteria, some of which can perform denitrification at low temperatures (Yang et al., 2018). In addition to *Flavobacterium* and *Pseudomonas*, there were other denitrifying bacteria like *Acinetobacter*, *Rhodobacter*, *Dechloromonas*, *Thiobacillus*, *Hydrogenophaga*, *Aeromonas*, *Stenotrophomonas*, *Comamonas*, etc. (Zhang et al., 2011; Zhou et al., 2016b, 2019; Kim et al., 2018; Li et al., 2018; Martinez-Santos et al., 2018) in Changxing River. Among them, *Acinetobacter* showed high relative abundance in autumn and significant enrichment at the stormwater outlets (III). Microorganisms that can participate in ammonia oxidation independently, such as *Sphingomonas* and *Nitrospirae* (Fitzgerald et al., 2015), showed relatively low abundance (0.1% and 0.9%).

**Correlation between microbial communities and environmental variables**

Redundancy analysis (RDA) was conducted to evaluate relationships between the relative abundance of dominant genera and environmental variables detected in the water samples. As shown in Fig. 9a, T, COD$_{Mn}$, DO, P, and NO$_2$^−-N had a relatively large impact on the seasonal differences in the diversity of microbial community in Changxing River. The concentration of DO had a positive effect on the microbial community in winter, and the microbial community in summer positively correlated with COD$_{Mn}$. The results of BIOENV analysis were used to select environmental variables “best explaining” the seasonal differences in the diversity of microbial community, by the relation analysis (Almagro-Pastor et al., 2015). The results showed that 78.3% of the variance shown by the seasonal differences in the diversity of microbial community were due to the combination of T, P, TP, and COD$_{Mn}$. Although the environmental variables had little influence on the distribution of microbial community in different pollution types in Changxing River, the microbial community structure at the stormwater outlets (III) was still significantly affected by TP, T, and COD$_{Mn}$ in summer and affected by NH$_4$^+-N in autumn (Fig. 9b).

As shown in Fig. 10a, *Proteobacteria* and *Bacteroidetes* positively correlated with TN and NH$_4$^+-N. *Proteobacteria* can promote the degradation of COD and participate in the transformation of nitrogen (Yu et al., 2021). *Bacteroidetes* can play an important role in the denitrification process (Li et al., 2020). It also degrades organic matters with high molecular weight and promotes the mineralization of hydrocarbons and the decomposition of carbonates (Eiler and Bertilsson, 2007; Zhang et al., 2021). *Actinobacteria* and *Cyanobacteria* were positively correlated with DO and NO$_3$^−-N. Studies have shown that *Actinobacteria* has a higher relative abundance with lower nutrient concentration (Pascault et al., 2014; Mao et al., 2019). At the same time, *Acidobacteria*, *Euryarchaeota*, *Chloroflexi*, and *Nitrospirae* were positively correlated with COD$_{Mn}$, T, and ORP. Thereinto, *Chloroflexi* can participate in the metabolism of organic matters in sediments (Feng et al., 2009; Yamada and Sekiguchi, 2009) and pollutant conversion (Hug et al., 2013) and can convert carbon dioxide into nutrients to provide energy for heterotrophic bacteria (Wang et al., 2020).

*Microcystis* and *Nostocaceae* were highly abundant in Taihu Lake, and their relative abundances were positively correlated with pH. Previous studies revealed that higher pH of the water body can promote the growth and reproduction...
of Cyanobacteria (Unrein et al., 2010; Wood et al., 2015). Microcystis was also positively correlated to DO (Fig. 10b). In addition, Microcystis is more competitive for NH$_4^+$-N than most of nitrifying bacteria (Paerl et al., 2014; Hampel et al., 2018), and serious accumulation of Microcystis may inhibit the nitrogen cycle of aquatic ecosystems.

**Suggestion for remediation of Changxing River**

According to the above results, restoration of the estuary of Taihu Lake (I) should focus on addressing the accumulation problem of cyanobacterial bloom caused by the backflow of cyanobacteria from Taihu Lake and enhancing the colonization of nitrifiers and denitrifiers. In the autumn, the DO level is low, and the NH$_4^+$-N concentration is high due to the eutrophication at the nonpoint source agricultural drainage areas (IV). Reoxygenation and addition of zeolite or clay materials can be used to enhance the colonization of ammonia-oxidizing bacteria (Chen et al., 2018).

This study found that the DO level at the stormwater outlets (III) was low, especially in summer and autumn. Effective nitrification requires a high DO level. At a low DO level (less than 3 mg/L), the removal efficiency of ammonia nitrogen can be greatly hindered. Biological processes can be integrated to maintain the DO level in the natural water. Two successful cases include a novel biofilm pretreatment process with reed addition (Feng et al., 2013) and bioactive thin layer coverage that enhances the in situ microbial growth and enrichment (Zhou et al., 2016b).

**Conclusions**

Changxing River is an important inflow river into Taihu Lake, but human activities, such as the discharge of domestic sewage and agricultural drainage, affected the diversity of microbial community and the ability for natural water to self-purify. T, TP, and COD$_{\text{Mn}}$ were the important environmental variables affecting the seasonal differences in the diversity of microbial community in Changxing River. This study provided the reference for the impact of pollution types on river microbial ecosystem under complex hydrological conditions and guidance for the ecological recovery of algae-polluted rivers.

**Supplementary Information** The online version contains supplementary material available at https://doi.org/10.1007/s11356-022-19023-2.

**Author contribution** Conceptualization, Yajie Zhang; methodology, Yajie Zhang, Ye Zhang, Lecheng Wei, Mengyan Li; formal analysis and investigation, Yajie Zhang, Ye Zhang, Lecheng Wei, Mengyan Li, Weitang Zhu; writing—original draft preparation, Yajie Zhang, Ye Zhang; writing—review and editing, Yajie Zhang, Mengyan Li, Liang Zhu; funding acquisition, Liang Zhu; resources, Liang Zhu; supervision, Liang Zhu.

**Funding** This work was financially supported by the Major Science and Technology Program for Water Pollution Control and Treatment (2018ZX07208009) and the National Natural Science Foundation of China (No. 51961125101).

**Data availability** All data generated or analyzed during this study are included in this published article [and its supplementary information files].

**Declarations**

**Ethics approval and consent to participate** Not applicable.

**Consent for publication** Not applicable.

**Competing interests** The authors declare no competing interests.

**References**

Almagro-Pastor V, Conradi M, DelValls TA, Riba I (2015) Alterations in the macrobenthic fauna from Guadarranque River (Southern...
Spain) associated with sediment–seawater acidification deriving from CO₂ leakage. Mar Pollut Bull 96:65–75
Battin TJ, Besemer K, Bengtsson MM, Romani AM, Packmann AI (2016) The ecology and biogeochemistry of stream biofilms. Nat Rev Microbiol 14:251–263
Chen CY, Pan G, Shi WQ, Xu F, Techtmann SM, Pfiffner SM, Hazen TC (2018) Clay flocculation effect on microbial community composition in water and sediment. Front Environ Sci 6:60
Du CG, Li YM, Wang Q, Liu G, Zheng ZB, Mu M, Li Y (2017) Temporal-spatio dynamics of water quality and its response to river flow in estuary of Taihu Lake based on GOCI imagery. Environ Sci Pollut Res 24:28079–28101
Eiler A, Bertilsson S (2007) Flavobacteria blooms in four eutrophic lakes: Linking population dynamics of freshwater bacterioplankton to resource availability. Appl Environ Microbiol 73:3511–3518
Feng BW, Li XR, Wang JH, Hu ZY, Meng H, Xiang LY, Quan ZX (2009) Bacterial diversity of water and sediment in the Changjiang estuary and coastal area of the East China Sea. FEMS Microbiol Ecol 70:236–248
Feng JJ, Zhu L, Yang Q, Yang GF, Xu J, Xu XY (2013) Simultaneous enhancement of organics and nitrogen removal in drinking water biofilm pretreatment system with reed addition. Bioresour Technol 129:274–280
Feng QQ, Han L, Tan X, Zhang YL, Meng TY, Lu J, Lv J (2016) Bacterial and archaeal diversities in Maotai Section of the Chishui River, China. Curr Microbiol 73:924–929
Feng ZB, Su B, Xiao DD, Ye LY (2017) Study on pH value and its variation characteristics of the main rivers into Dianchi lake under the anthropogenic and natural processes, Yunnan, China. J Inf Optim Sci 38:1197–1210
Gilbert JA, Steele JA, Caporaso JG, Steinbrück L, Knight R, Joint I, Somerfield P, Huhman E (2012) Defining seasonal marine microbial community dynamics. ISME J 6:298–308
Hampel JJ, McCarthy MJ, Gardner WS, Zhang L, Xu H, Zhu GW, Newell SE (2018) Nitrification and ammonium dynamics in Taihu Lake, China: seasonal competition for ammonium between nitrifiers and cyanobacteria. Biogeosciences 15:733–748
Health Status Report of Taihu Lake (2018). Taihu basin authority of ministry of water resources. http://www.tba.gov.cn/slbthlylj/sj/sj.html. Accessed 9 December 2021
Hug LA, Castelle CJ, Wrighton KC, Thomas BC, Sharon I, Frischkorn KR, Williams KH, Tinge SG, Banfield JF (2013) Community genomic analyses constrain the distribution of metabolic traits across the Chloroflexi phylum and indicate roles in sediment carbon cycling. Microbiome 1:22
Jiang ZB, Zhou FZ, Zhou L, Chen QZ, Tao BY, Yan XJ, Wang K (2015) Controlling factors of summer phytoplankton community in the Changjiang (Yangtze River) Estuary and adjacent East China Sea shelf. Cont Shelf Res 101:71–84
Kim H, Kaown D, Mayer B, Lee JK, Lee KK (2018) Combining pyrosequencing and isotopic approaches to assess denitrification in a hyporheic zone. Sci Total Environ 631–632:755–764
Louca S, Polz MF, Mazel F, Albright MBN, Huber JA, O’Connor MI, Ackermann M, Hahn AS, Srivastava DS, Crowe SA, Doebeli M, Parfrey LW (2018) Function and functional redundancy in microbial systems. Nature Ecol Evol 2:936–943
Lopes FAC, Catão ECP, Santana RH, Cabral AAds, Paranhos R, Rangel TP, Rezende CEd, Edwards RA, Thompson CC, Thompson FL, Kruger RH (2016) Microbial community profile and water quality in a protected area of the caatinga biome. PLOS ONE 11:e0148296
Li SJ, Luo ZX, Ji GD (2018) Seasonal function succession and biogeographic zonation of assimilatory and dissimilatory nitrate-reducing bacterioplankton. Sci Total Environ 637:1518–1525
Li X, Li YY, Lv DQ, Li Y, Wu JH (2020) Nitrogen and phosphorus removal performance and bacterial communities in a multi-stage surface flow constructed wetland treating rural domestic sewage. Sci Total Environ 709:136235
Liao KLL, Bai YH, Huo Y, Jian ZY, Zhou F, Zhao C, Ji JH (2018) Integrating microbial biomass, composition and function to discern the level of anthropogenic activity in a river ecosystem. Environ Int 116:147–155
Liu J, Liang XQ, Yang JJ, Ye YS, Su MM, Nie ZY, Chen YX (2011) Size distribution and composition of phosphorus in the East Tiao River, China: the significant role of colloids. J Environ Monit 13:2844–2850
Liu L, Xu ZX, Reynard NS, Hu CW, Jones RG (2013) Hydrological analysis for water level projections in Taihu Lake, China. J Flood Risk Manag 6:14–22
Liu HY, Zhu LY, Tian XY, Yin YS (2017) Seasonal variation of bacterial community in biological aerated filter for ammonia removal in drinking water treatment. Water Res 123:668–677
Lu SD, Sun YJ, Zhao X, Wang L, Ding AZ, Zhao XH (2016) Sequencing insights into microbial communities in the water and sediments of Fenghe River, China. Arch Environ Contam Toxicol 71:122–132
Lundgaard ASB, Treusch AH, Stief P, Thamdrup B, Glud RN (2017) Nitrogen cycling and bacterial community structure of sinking and aging diatom aggregates. Aquat Microb Ecol 79:85–99
Mao YF, Liu Y, Li H, He Q, Ai HH, Gu WK, Yang GF (2019) Distinct responses of planktonic and sedimentary bacterial communities to anthropogenic activities: case study of a tributary of the Three Gorges Reservoir, China. Sci Total Environ 682:324–332
Martínez-Santos M, Lanzen 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. Sci Total Environ 633:1051–1061
Ouyang L, Chen HR, Liu XY, Kong MH, Xu FF, Yang XW, Xu W, Zeng QH, Wang WM, Li SF (2020) Characteristics of spatial and seasonal bacterial community structures in a river under anthropogenic disturbances. Environ Pollut 264:114818
Paerl HW, Gardner WS, Havens KE, Joyner AR, McCarthy MJ, Newell SE, Qin B, Scott JT (2016) Mitigating cyanobacterial harmful algal blooms in aquatic ecosystems impacted by climate change and anthropogenic nutrients. Harmful Algae 54:213–222
Paerl HW, Xu H, Hall NS, Zhu GW, Qin B, Scott JT (2016) Mitigating cyanobacterial harmful algal blooms in aquatic ecosystems impacted by climate change and anthropogenic nutrients. Harmful Algae 54:213–222
Pascualt N, Roux S, Artigas J, Pesce S, Leloup J, Tadonleke RD, Martinez-Santos M, Lanzen A, Unda-Calvo J, Artigas J, Roux S, Leloup J, Tadonleke RD, Martinez-Santos M, Lanzen A, Unda-Calvo J, Martin I, Garbisu C, Ruiz-Romera E (2018) Treated and untreated wastewater effluents alter river sediment bacterial communities involved in nitrogen and sulphur cycling. Sci Total Environ 633:1051–1061
Portillo MC, Anderson SP, Fierer N (2012) Temporal variability in the diversity and composition of stream bacterioplankton communities. Environ Microbiol 14:2417–2428
Ren W, Wang Y, Yan J, Liu G, Zhong B, Hussain T, Peng C, Yin J, Li T, Wei H, Zhu G, Reiter RJ, Tan B, Yin Y (2018) Melatonin alleviates weaning stress in mice: involvement of intestinal microbiota. J Pineal Res 64:e12448
Rodriguez-Mozaz S, Chamorro S, Marti E, Huerta B, Glos M, Sanchez-Melsio A, Borrego CM, Barcelo D, Balcazar JL (2015) Occurrence of antibiotics and antibiotic resistance genes in...
