INTRODUCTION

Sediments are distinct components of basin ecosystems (Wang et al., 2012), and species and microbial diversity in sediments are considerably higher than those in water bodies (Zinger et al., 2011). As a main component of aquatic systems, sediment plays a critical role as nutrient provider, pool, and source (Huang et al., 2015). In a plain river network region, several types of sediment exist in different regions, such as lakes, wetlands, and estuaries. As sediment microbes from these regions affect entire aquatic systems (Shimeta & Cook, 2011; Shtarkman et al., 2013), understanding microbial communities in different basin regions is crucial.

Lakes, lake wetlands, and estuaries are the main components of a plain river network, and sediments in these regions are the media for...
matter transformation and migration. A lake wetland is a landform along the lake region and can be regarded as a filtration system of lake outflow. Bacterial communities in lake wetlands are ubiquitous and play key roles in ecosystem functions, including cycling of biologically active elements (Newton, Jones, Eiler, McMahon, & Bertilsson, 2011; Van der Gucht et al., 2007; Woese, Kandler, & Wheelis, 1990). Wetland ecosystems are the most biologically diverse around lake basins (Ding et al., 2015; Iasur-Kruh, Hadar, Milstein, Gasith, & Minz, 2010) and provide habitats for biota (Wu et al., 2015). As main components of lake basins, estuaries are buffer zones between rivers and lakes or oceans; runoff particles and suspended sediments are transported, stored, and modified in estuaries (Arzayus & Canuel, 2005; Sun, Wang, Wu, Wang, & Li, 2011). Inorganic and organic nutrients are usually stored by sedimentation and released back to the water column, and microbial communities in sediments play important roles in substance export, regeneration, and biochemical cycling in estuaries (Pinckney, Paerl, Tester, & Richardson, 2001; Yokokawa & Nagata, 2010).

Previous studies separately analyzed microbial communities in lake, wetland, and estuary sediments. In particular, the correlation between microbial communities in wetlands and environmental factors were mostly investigated under horizontal gradients, such as C or N availability (Lin et al., 2012; Mackelprang et al., 2011; Moseman-Valtierra, Armaiz-Nolla, & Levin, 2010), temperature (Redmond & Valentine, 2012), pH (Lindstrom, Kamst-Van Agterveld, & Zwart, 2005), and sediment structural characteristics (Liu, Ding, Jia, & Cai, 2012). The distribution of microbial communities in sediments, influence of microbial communities on nutrient or biogeochemical cycling in lakes (Cotner & Biddanda, 2002; Fang et al., 2015; Ligi et al., 2014; Song, Li, Du, Wang, & Ding, 2012), and interactions between microorganisms and sediment biogeochemistry in estuaries are researched independently (Freitag, Chang, & Prosser, 2006; Pimenov et al., 2010). Despite the importance of sediment microbes in distribution, substance cycling, and environmental influence in their respective regions, research on the overall distribution and differences in microbial community in sediments from a basin is limited. In response, the goal of this research was to expand the knowledge of microbial distribution in sediments from different basin regions of a plain river network. This would improve our understanding of microbial function in basin pollution control.

As one of the most densely populated regions in China, Taihu Basin (with a surface area of $1.58 \times 10^4$ km$^2$) is located in a typical plain river network in the middle-lower Yangtze River plain of eastern China. Rivers and lake wetlands typically exist in Taihu Basin. Approximately, 20 large-, medium-, and small-sized cities are located around Taihu Lake and have large inflow and outflow rivers, such as Taipu River, Wangyu River, and Dongtiao River, which are connected to Taihu Lake. The northwest part of Taihu Lake generally has small inflow rivers, and most of the pollutants from Yixing City and Changzhou City are discharged into Taihu Lake through these inflow rivers. Taihu Basin also has numerous lake wetlands, which are located in the eastern and southeast parts of Taihu Basin. Numerous lake wetlands exist around the Taipu River and influence the water quality in Jiaxing City. The location of Taihu Lake, the lake wetlands, and estuary rivers are shown in Figure 1.

In this study, we obtained millions of tags from the lake, lake wetland, and estuary sediments obtained from Taihu basin and compared the microbial communities in the sediments. We believe that this study can provide novel insights into basin pollution control in plain river networks.
2 | EXPERIMENTAL PROCEDURES

2.1 | Sediment collection and characterization

Taihu Lake is the third largest freshwater lake in China and located in the eastern plain of the country (30°55′40″–30°55′40″ N, 119°52′32″–120°36′10″ E) (Xu et al., 2015; Zhu et al., 2013). A total of 65 sediment samples were collected, 32 from the wetland in the southeast part of Taihu Lake (Group A), 27 from the main lake district (Group B), and six from the main river estuaries (Group C). Figure 1 shows the sampling sites in the three regions. The sediment samples were collected in July 2017, and the lake, lake wetland, and estuary sediments were assigned as T, W, and R, respectively. The weights of the collected samples were sufficient for DNA extraction and analysis of physicochemical parameters. After sampling, the sediment samples were placed in sealed plastic bags, stored in a portable ice box, transferred into the laboratory within 24 hr, and stored at –80°C before analysis. Each type of sediments was mixed with deionized water or 0.01 mol L\(^{-1}\) KCl solution in a 1:2.5 (w/v) mixture for pH measurement, and organic matter (OM) content in each sediment was calculated according to the loss on ignition to constant mass (4 hr) at 550°C (Huang et al., 2015). Total nitrogen (TN) and total phosphorus (TP) in sediments were measured with standardized methods and tests (Huang, Chen, Jiang, & Zheng, 2017). Physicochemical parameters are shown in Figure 2.

2.2 | Extraction of genomic DNA

Total genomic DNA was extracted from the sediment samples using a PowerSoil DNA Isolation Kit (Mbio Laboratories Inc., San Diego, CA, USA) according to the manufacturer’s protocol. DNA concentration and quality were determined using a NanoDrop Spectrophotometer (Thermo Scientific NanoDrop Lite, CA, USA). DNA was diluted to 10 ng \(\mu\text{l}^{-1}\) using sterile ultrapure water and stored at –80°C for further analysis.

2.3 | PCR amplification

The V4–V5 regions of bacterial 16SrRNA genes were amplified with universal primers 515F (GTGCCAGCMGCCGCGGTAA) and 926R (CCGTCAATTCMTTTRAGTTT). These primers were
selected because of their high coverage across phyla (Liu, DeSantis, Andersen, & Knight, 2008; Wang & Qian, 2009; Xiong et al., 2014). The PCR mixture (25 μl) contained 1 × PCR buffer, 1.5 mmol L\(^{-1}\) MgCl\(_2\), 0.4 μmol L\(^{-1}\) each of deoxynucleoside triphosphate, 1.0 μmol L\(^{-1}\) of each primer, 0.5 U of TaKaRa Ex Taq, and 10 μg of template DNA. The PCR amplification program was as follows: initial denaturation at 94°C for 1 min, followed by 30 cycles (denaturation at 94°C for 20 s, annealing at 56°C for 30 s, and elongation at 72°C for 45 s), and a final extension at 72°C for 5 min. Three replicates of PCR reactions for each sample were combined. A similar volume of 1× loading buffer (containing SYBR green) was mixed with PCR products and then subjected to electrophoresis on 2% agarose gel for detection of PCR product size. Samples showing a bright main strip of 300–500 bp were selected for further experiments. PCR products were purified with an OMEGA gel extraction kit (Omega Bio-Tek, USA), and equal molar amounts of the products from different samples (65 samples from three different regions) were pooled. Sequencing libraries were generated with TruSeq DNA PCR-free sample prep kit (Illumina) according to the manufacturer’s recommendations, and index codes were added. Library quality was assessed on a Qubit® 2.0 Fluorometer (Thermo Scientific, CA, USA) and Agilent Bioanalyzer 2100 system. The library was finally subjected to paired-end sequencing (2 × 250 bp) on an Illumina Miseq apparatus from TinyGene Biotech Co., Ltd. (Shanghai).

## 2.4 | Data analysis

The 16S sequences were analyzed using a combination of software mothur (version 1.33.3) (Schloss et al., 2009), UPARSE (Edgar, 2013), and R (version 3.2.3). The demultiplexed reads were clustered at 97% sequence identity into operational taxonomic units (OTUs) using the UPARSE pipeline (http://drive5.com/usearch/manual/uparsecmds.html). The OTU representative sequences were assignment for taxonomy against Silva 119 database with confidence score ≥0.8 by the “classify.seqs” command in mothur. OTU’s were named to the species level using SILVA taxonomic nomenclature.

Principal component analysis (PCA) was employed to explore and visualize the similarities between sediment samples obtained from three regions based on Bray–Curtis dissimilarity using package

**FIGURE 3** Diversity of the sediment samples from the three regions (a for the lake wetland, b for the lake, and c for the river estuary). *p < .05, **p < .01
Redundancy analysis (RDA) based on population abundance and environment factors was performed using Canoco4.5. LEfSe (Linear discriminant analysis Effect Size) (Segata et al., 2011) was used to find indicator bacterial groups specific to the sediment samples (p-value cutoffs .05). Independent t-test and permutational multivariate analysis of variance (ggpubr package of R, p-value .05) were used to identify the differences that exist among different groups.

3 | RESULTS

3.1 | Diversity indices of bacterial communities in the sediments from different regions

A total of 65 sediment samples were obtained, 32 from the lake wetland (Group A), 27 from the lake (Group B), and six from the estuary (Group C). After tag merge and quality control, 2,822,582 reads were obtained. Although the total number of errors were low, stringent quality controls were set because of the overestimation of numbers SRP133902 for samples from lake wetland (32 samples), lake (27 samples), and estuary (six samples).

2.5 | Accession numbers

All of the sequencing data analyzed in this study can be downloaded from the NCBI's Sequence Read Archive using the accession numbers SRP133902 for samples from lake wetland (32 samples), lake (27 samples), and estuary (six samples).
ties in the sediments are shown in Figure 4. A total of 34 phyla in sediment samples |
Bacterial community composition in 3.2 alpha-diversity (Fang et al., 2015; Wang et al., 2012). Figure 3 shows the average values of the diversity indices (Chao, ACE, Shannon, and Simpson) and the results of variance analysis in the sediments from the three regions. The bacterial community in lake sediment had higher diversity than the lake wetland and estuary sediments. The Chao, ACE, and Shannon indices of the bacterial communities in all the sediments exhibited similar variation trend. The bacterial community from the lake had the highest Chao (4864.2 on average), ACE (4975.0 on average), and Shannon (6.69 on average) values, and lowest Simpson value (0.005 on average). The analysis of variance results indicated that the Chao, ACE, and Shannon values of the samples from the three groups varied significantly (p < .05) among each other. The Simpson index of sediment from the estuary showed the highest average value (0.016), and significant differences (p<0.01) existed between the samples from the lake and the lake wetland or the estuary.

3.2 Bacterial community composition in sediment samples
The phylum and class level distributions of bacterial communities in the sediments are shown in Figure 4. A total of 34 phyla were detected in the sediment samples obtained from the three regions. Proteobacteria represented more than 30% of all phyla in sediments (Figure 4a), and Proteobacteria classes, such as Gammaproteobacteria, Betaproteobacteria, and Deltaproteobacteria, were the main classes in the sediments (Figure 4b). The relative abundance of Nitrospira in the lake sediments was greater than those from the lake and estuary (8.53% ± 2.27% vs. 1.81% ± 1.42% or 0.24% ± 0.14%, respectively). Acidobacteria in the lake sediments had higher abundance than those in the lake wetland and inflow river (3.46%–10.21% vs. 1.49%–8.12% or 2.42%–8.73%, respectively). Firmicutes was more abundant (mean value of 22.30%) in estuary sediments than in lake (mean value of 1.32%) and wetland (mean value of 5.59%) sediments. Bacteroidetes (10.85%), Chloroflexi (11.09%), Cyanobacteria (0.62%), and Actinobacteria (1.94%) were the other highly abundant phyla in the sediment samples.

Figure 4b shows the changes in the bacterial community composition at the class level. Gammaproteobacteria, Betaproteobacteria, Nitrospira, Flavobacteriia, Deltaproteobacteria, and Holophagae were abundant in the three regions. Gammaproteobacteria was more abundant in the sediment from the lake wetland (14.27%) than in the sediments from the lake and the estuary (8.35% and 7.89%, respectively). Clostridia was more abundant in the wetland and estuary sediments (4.30% and 11.23%, respectively) than in lake sediments (1.13%). The lake sediments had more Nitrospira (8.53%) than lake wetland and estuary sediments (1.81% and 1.53%, respectively). Nitrospira and Deltaproteobacteria were more abundant in the lake sediments than in the wetland and estuary sediments (p < .01). Bacilli, Epsilonproteobacteria, Gemmatimonadetes, Ignavibacteria, Chlorobia, and Phycisphaerae were the other classes detected in the sediment samples from the three regions.

The taxonomic composition at the genus level of the bacterial communities in sediment samples from the three regions is shown in Figure 5. Nitrospira, Thiothrix, and Sulfuritalea were the most dominant genera in most of the sediment samples from the lake region with relative abundance of more than 4%. The bacterial communities in the wetland sediments had relatively higher abundance of Flavobacterium and Acinetobacter than those in the lake and estuary sediments. The relative abundance of Bacillus, Fusibacter, Lactococcus, and Pseudomonas in the sediment samples from the estuary was more than 6%, which was higher than those in the sediment samples from the other two regions (lower than 1%). Thiothrix, Anaerolinea, Desulfobulbus, Rhodobacter, and Novosphingobium were the other dominant genera with relatively high abundance in the sediment samples from the three regions.

3.3 Principal component analysis
Figure 6 shows the groupings of the sediment samples according to their bacterial community structure. Two PCAs explained 78.3% of the total variation in the microbial community structure. The result indicated that the sediments obtained from the three regions had significantly different bacterial phyla. Acidobacteria (7.53%), Gemmatimonadetes (1.56%), Chlorobi (3.39%), Nitrospirae (8.53%), and Planctomycetes (4.18%) were abundant in the lake sediments, while Firmicutes (5.59% and 2.23%), Actinobacteria (2.65% and 2.58%), Bacteroidetes (13.29% and 13.91%), and two Proteobacteria groups, Gammaproteobacteria (14.27% and 7.89%) and Betaproteobacteria (14.81% and 14.11%), were abundant in the wetland and estuary sediments. The sediments from R5 and R6 had more Cyanobacteria and Verrucomicrobia abundance than the sediments from other parts of the estuary.

3.4 Redundancy analysis
RDA was performed on the basis of the abundance at the phylum level and environmental factors (physicochemical parameters). Figure 7 shows the relationship between bacterial community composition and physicochemical parameters. The first axis explained 67.6% of the bacterial diversity, whereas the second axis explained 19.8% of the variation. Few physicochemical parameters influenced the bacterial community in the sediment from the lake, and TN influenced the bacterial community in the sediment to a certain extent. The bacterial communities in the sediments from the lake wetland and estuary were associated with physicochemical parameters, such as OM, pH, DO, and TP content. The bacterial communities in the sediments from several parts of the lake wetland and the river estuary were positively correlated with TP and OM (0.894, p < .05).

3.5 LEfSe analysis based on community abundance
Figure 8 shows that the bacterial communities dominant in the lake wetland were Flavobacteria (the class and order of Flavobacteriales), Anaerolineae (the class and order of Anaerolineales), and...
Gammaproteobacteria (the class and orders of Xanthomonadales and Pseudomonadales). The lake wetland had LDA values greater than 3.0 for Flavobacterium, Pseudomonadales, Anaerolineaceae, Acinetobacter, and Xanthomonadales (Figure 9).

Five bacterial taxa were abundant in the lake sediments (Figure 8), namely, Nitrospirae (from phylum to family), Acidobacteria (from phylum to order), Chlorobi (from phylum to family), Deltaproteobacteria, and Betaproteobacteria (the class and orders of Hydrogenophilales and Nitrosomonadales). The lake sediment only had Nitrospiraceae, Acidobacteria, Hydrogenophilaceae, and Ignavibacteriales taxa exceeding LDA values greater than 3.0 (Figure 9).

The Firmicutes and Bacteroidetes phyla were abundant in the estuary sediments (Figures 8 and 9), particularly Bacilli, Clostridia, and Bacteroidia. The bacterial communities abundant in the estuary were Rhodocyclales (an order within Betaproteobacteria) and Epsilonproteobacteria. Among these bacterial communities, several fine communities, namely, Bacillus, Clostridiales, Bacillaceae, Rhodocyclaceae, Rhodocyclales, Campylobacterales, Helicobacteraceae, Geobacter, and Fusibacter, had an LDA value of 3.0 or higher.
4 | DISCUSSION

Different regions, such as wetland, estuary, and lake side zone, exist in the Taihu Basin. The sediments in these regions are critical to pollutant release and can influence the water quality in Taihu Lake. The sediment samples from the lake wetland, lake, and river estuary were collected, and the differences among the microbial communities in the three regions were studied.

The diversity indices revealed that the Chao, ACE, Shannon, and Simpson values of the samples from the three regions varied significantly. This result indicated that the bacterial communities in the sediments from the three regions had significant regional differences. Numerous inflow and outflow rivers exist in Taihu Basin. Rivers 1–4 (Figure 1) are the main inflow rivers of Taihu Lake, and Rivers 5 and 6 are the outflow rivers. Pollutants entered the lake region through the inflow rivers and were discharged through the outflow rivers. Large pollutants deposition occurred in lake region, which caused the bacterial communities in the sediment from lake region to have higher diversity than those in the sediments from the two other regions (Deng, Cui, Hernandez, & Dumont, 2014; Liu et al., 2009). The bacterial community in the sediment from the lake wetland also had relatively high diversity because of the high amount of pollutant discharge from cities such as Suzhou and Jiaxing (Figure 1).

Although the pollution source exists around the inflow and outflow rivers, most of the pollutants do not easily deposit because of the high-flow velocity. The bacterial diversity in the sediments from the four inflow rivers (Rivers 1–4) was therefore lower than those in sediments from the two other regions (Beardsley, Moss, Malfatti, & Azam, 2011; Wu et al., 2017). In addition, as shown in Figure 2, the sediments from the outflow rivers had low pollutant concentrations, and the sediments from outflow rivers also had the lowest bacterial diversity.

Proteobacteria, a phylum that commonly exists in sediment, is nearly the most abundant phylum detected in samples among the three regions and plays a critical role in degradation and metabolism (Bai et al., 2012; Chaudhry, Rehman, Mishra, Chauhan, & Nautiyal, 2012; Huang & Jiang, 2016). Studies revealed that abundance of Acidobacteria is significantly correlated with pH, and Acidobacteria prefers an environment with low pH of ~5.5 (Jones et al., 2009). The sediment from the lake had the relatively lowest pH, and Acidobacteria was abundant in the sediment samples from the lake.

The sediment from the lake also had higher Nitrospirae content than those in the sediments from the two other regions. In Taihu Basin, the lake region had high nitrogen concentration (2.62 ± 1.46 mg L⁻¹, 2013–2014) (Wu, Qin, Yu, Deng, & Zhou, 2016), and the nitrogen release in sediment contributed to the high nitrogen concentration in the lake. Nitrospirae participates in nitrogen cycling and may be one of the main reasons for the high nitrate concentration in the sediments (Huang et al., 2017). The result also indicated that nitrogen might be the factor limiting eutrophication, and our previous study obtained similar results (Huang et al., 2017). The bacterial distribution at the genus level also indicated that the NO₃⁻N concentration was higher in the lake than in lake wetland and river estuary because of the participation of Thiobacillus in NO₃⁻N metabolism (Bruckner et al., 2013; Li, Zhao, & Wang, 2011). In the sediment from the estuary regions, the bacterial community from outflow river (R5 and R6) had higher abundance of Chloroflexi than that in other sediments.
from the inflow rivers. Chloroflexi, a photoautotrophic microbe, may have participated in organic pollutant degradation, thereby possibly causing the low OM content in the outflow rivers. The lake wetlands, located in the southeast part of Taihu basin, are polluted with agricultural pollutants and industrial pollution discharge (Beardsley et al., 2011; Bissett, Bowman, & Burke, 2006) from Jiaxing City (Figure 1). The region has more organic pollutants than the lake and estuary, especially in sediments. As a result, the lake wetland sediments had high abundance of Gammaproteobacteria, which are usually present in organic-rich sediments (Figure 4b) (Song et al., 2012).

Taihu Lake is an algae-dominated area, and algal blooms typically occur in summer. The algal growth and metabolism are significantly related to the sediment. Previous studies revealed that P is a major limiting factor of eutrophication in Taihu Lake, and the sediments of the algae-dominated area is dominated by Microcystis (Huang et al., 2017; Shao et al., 2011; Wu, Chen, Xu, Liu, & Hahn, 2007). The results of this study revealed that TN concentration in water and sediment significantly influences bacterial community, and Nitrospira (phylum Nitrospirae) and Thiobacillus (phylum Proteobacteria) are significantly related to TN concentration. These two genera were also abundant in the lake sediments (Figure 5). N forms and concentrations were affected by Nitrospira, and Thiobacillus directly participated in NO$_3^-$ metabolism and subsequently influenced TN concentration in the lake (Bruckner et al., 2013; Li et al., 2011). Therefore, TN concentration in sediment is possibly one of the main factors limiting eutrophication, and the limiting factor of eutrophication in Taihu Lake may be changed from P to N.

In the lake wetland around Taihu Lake, a large amount of pollutants from the towns and cities entered the rivers, which are connected with wetlands, and organic matters were deposited into

**FIGURE 8** Cladogram showing the phylogenetic distribution of microbial communities associated with the sediments from the three regions; lineages with LDA values of 3.0 or higher as determined by LEfSe are shown. Differences are represented by the color of the most abundant class. Red (a) indicates lake wetland region, green (b) lake region, and blue (c) river estuary region; yellow represents insignificant difference. The diameter of each circle is proportional to a taxon's abundance. Circles from inner region to outer region represent the phylogenetic levels from domain to genus.
Figure 9: Indicator microbial groups in the three groups of sediment samples with LDA values higher than 3.0
this region, which caused the high OM content in the lake wetland region. Nutrients in this region are frequently transformed from inorganic to organic forms, and may explain the association between Desulfarculaceae (phyllum Proteobacteria and class Deltaproteobacteria) and OM. The results indicated that the bacterial communities in sediments from parts of the lake wetland were influenced by TP and OM, and Proteobacteria was significantly positively correlated with TP and OM (p < .05). The inorganic P might therefore transform to organic P, and Desulfarculaceae might be one of the main OM indicators in the lake wetland (Jorgensen, 1982; Pallud & Van Cappellen, 2006).

The sediment samples from R1 to R4 are located in the estuary of inflow rivers. Large amounts of pollutants mixed, and parts of the pollutants were deposited into the surface sediments (Liu et al., 2009). The bacterial communities were influenced by the OM, TP, pH, and DO, indicating that the environmental conditions in this region were complex, and the bacterial communities were affected by these factors. In addition, R5 and R6 are the estuaries of outflow rivers. In these regions, flow velocities are high, and pollutants frequently migrated and transformed (Bai et al., 2009). Pollutants, such as inorganic and organic matters, are hardly deposited into the sediments. OM, DO, and pH, are not the main environmental factors that influence bacterial communities in this region.

In summary, the bacterial communities in the lake, wetland, and estuary sediments varied significantly, and the bacterial community varied according to region. In this study, we compared the three regions (i.e., lake, wetland, and estuary) in a plain river network. The lake sediments had the most diverse bacterial communities, followed by the wetland sediments. Proteobacteria was the most abundant of all phyla in the sediments from the three regions. Nitrospirae, Acidobacteria, and Firmicutes were the most abundant phyla in the lake, lake wetland, and estuary sediments, respectively. TN affected the bacterial community in sediments from the lake region, and physicochemical parameters, such as OM, pH, DO, and TP concentrations, influenced the bacterial community in the wetland sediments. TP and OM contents were positively correlated (p < .05) to the distinct bacterial communities in sediments from several parts of the estuary regions.

ACKNOWLEDGMENT

This study was supported by the Major Science and Technology Program for Water Pollution Control and Treatment (No. 2017ZX07206), Beijing Natural Science Foundation (B1740080), and the project was funded by China Postdoctoral Science Foundation (2017M610968).

CONFLICT OF INTEREST

None declared.

ORCID

Wei Huang http://orcid.org/0000-0003-4069-7343

REFERENCES

Arzayus, K. M., & Canuel, E. A. (2005). Organic matter degradation in sediments of the York River estuary: Effects of biological vs. physical mixing. Geochimica et Cosmochimica Acta, 69, 455–464. https://doi.org/10.1016/j.gca.2004.06.029

Bai, X. L., Ding, S. M., Fan, C. X., Liu, T., Shi, D., & Zhang, L. (2009). Organic phosphorus species in surface sediments of a large, shallow, eutrophic lake, Lake Taihu, China. Environmental Pollution, 157, 2507–2513. https://doi.org/10.1016/j.envpol.2009.03.018

Bai, Y., Shi, Q., Wen, D., Li, Z., Jefferson, W. A., Feng, C., & Tang, X. (2012). Bacterial communities in the sediments of Diaochi Lake, a partitioned eutrophic waterbody in China. PLoS ONE, 7, e37796. https://doi.org/10.1371/journal.pone.0037796

Beardsley, C., Moss, S., Malfatti, F., & Azam, F. (2011). Quantitative role of shrimp fecal bacteria in organic matter fluxes in a recirculating shrimp aquaculture system. FEMS Microbiology Ecology, 77, 134–145. https://doi.org/10.1111/j.1574-6941.2011.01094.x

Bissett, A., Bowman, J., & Burke, C. (2006). Bacterial diversity in organically-enriched fish farm sediments. FEMS Microbiology Ecology, 55, 48–56. https://doi.org/10.1111/j.1574-6941.2005.00012.x

Bruckner, C. G., Mammitzsch, K., Jost, G., Wendt, J., Labrenz, M., & Jurgens, K. (2013). Chemolithoautotrophic denitrification of epsilonproteobacteria in marine pelagic redox gradients. Environmental Microbiology, 15, 1505–1513. https://doi.org/10.1111/j.1462-2920.2012.02880.x

Chaudhry, V., Rehman, A., Mishra, A., Chauhan, P. S., & Nautiyal, C. S. (2012). Changes in bacterial community structure of agricultural land due to long-term organic and chemical amendments. Microbial Ecology, 64, 450–460. https://doi.org/10.1007/s00248-012-0025-y

Cotner, J. B., & Biddanda, B. A. (2002). Small players, large role: Microbial influence on biogeochemical processes in pelagic aquatic ecosystems. Ecosystems, 5, 105–121. https://doi.org/10.1007/s10021-001-0059-3

Deng, Y., Cui, X., Hernandez, M., & Dumont, M. G. (2014). Microbial diversity in hummock and hollow soils of three wetlands on the Qinghai-Tibetan Plateau revealed by 16S rRNA pyrosequencing. PLoS ONE, 9, e103115. https://doi.org/10.1371/journal.pone.0103115

Ding, X., Peng, X.-J., Jin, B.-S., Xiao, M., Chen, J.-K., Li, B., ... Nie, M. (2015). Spatial distribution of bacterial communities driven by multiple environmental factors in a beach wetland of the largest freshwater lake in China. Frontiers in Microbiology, 6, 129.

Edgar, R. C. (2013). UPARSE: Highly accurate OTU sequences from microbial amplicon reads. Nature Methods, 10, 996. https://doi.org/10.1038/nmeth.2604

Fang, L., Chen, L., Liu, Y., Tao, W., Zhang, Z., Liu, H., & Tang, Y. (2015). Planktonic and sedimentary bacterial diversity of Lake Sayram in summer. MicrobiologyOpen, 4, 814–825. https://doi.org/10.1002/mbo3.281

Freitag, T. E., Chang, L., & Prosser, J. I. (2006). Changes in the community structure and activity of betaproteobacterial ammonia-oxidizing sediment bacteria along a freshwater-marine gradient. Environmental Microbiology, 8, 684–696. https://doi.org/10.1111/j.1462-2920.2005.00947.x

Huang, W., Chen, X., Jiang, X., & Zheng, B. H. (2017). Characterization of sediment bacterial communities in plain lakes with different trophic statuses. MicrobiologyOpen, 6, e503.
Huang, W., & Jiang, X. (2016). Profiling of sediment microbial community in dongting lake before and after impoundment of the three gorges dam. *International Journal of Environmental Research and Public Health*, 13, 617. https://doi.org/10.3390/ijerph13060617

Huang, W., Lu, Y., Li, J. H., Zheng, Z., Zhang, J. B., & Jiang, X. (2015). Effect of ionic strength on phosphorus sorption in different sediments from a eutrophic plateau lake. *RSC Advances*, 5, 79607–79615. https://doi.org/10.1039/C5RA12568D

Lasur-Kruh, L., Hadar, Y., Milstein, D., Gasith, A., & Minz, D. (2010). Microbial population and activity in wetland microcosms constructed for improving treated municipal wastewater. *Microbial Ecology*, 59, 700–709. https://doi.org/10.1007/s00248-009-9611-z

Jones, R. T., Robeson, M. S., Lauber, C. L., Hamady, M., Knight, R., & Newton, R. J., Jones, S. E., Eiler, A., McMahon, K. D., & Bertilsson, S. (2011). A guide to the natural history of freshwater lake bacteria. *Microbiology and Molecular Biology Reviews*, 75, 14–49. https://doi.org/10.1128/MMBR.00028-10

Pallud, C., & Van Cappellen, P. (2006). Kinetics of microbial sulfate reduction in estuarine sediments. *Geochimica et Cosmochimica Acta*, 70, 1148–1162. https://doi.org/10.1016/j.gca.2005.11.002

Paradis, E., Claude, J., & Strimmer, K. (2004). APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, 20, 289–290. https://doi.org/10.1093/bioinformatics/btg412

Pimenov, N. V., Ulyanova, M. O., Kanapatsky, T. A., Veslopolova, E. F., Sigalevich, P. A., & Sikov, V. V. (2010). Microbially mediated methane and sulfur cycling in pockmark sediments of the Gdansk Basin, Baltic Sea. *Geo-Marine Letters*, 30, 439–448. https://doi.org/10.1007/s00367-010-0200-4

Pincney, J. L., Paerl, H. W., Tester, P., & Richardson, T. L. (2001). The role of nutrient loading and eutrophication in estuarine ecology. *Environmental Health Perspectives*, 109, 699–706. https://doi.org/10.1289/ehp.10109569

Redmond, M. C., & Valentine, D. L. (2012). Natural gas and temperature structured a microbial community response to the Deepwater Horizon oil spill. *Proceedings of the National Academy of Science of the United States of America*, 109, 20292–20297. https://doi.org/10.1073/pnas.1108756108

Schloss, P. D., Westcott, S. L., Ryabin, T., Hall, J. R., Hartmann, M., Hollister, E. B., ... Weber, C. F. (2009). Introducing mothur: Open-source, platform-independent, community-supported software for describing and comparing microbial communities. *Applied and Environmental Microbiology*, 75, 7537–7541. https://doi.org/10.1128/AEM.01541-09

Segata, N., Izard, J., Waldron, L., Gevers, D., Miropolsky, L., Garrett, W. S., & Huttenhower, C. (2011). Metagenomic biomarker discovery and explanation. *Genome Biology*, 12, R60. https://doi.org/10.1186/gb-2011-12-6-r60

Shao, K. Q., Gao, G., Qin, B. Q., Tang, X. M., Wang, Y. P., Chi, K. X., & Dai, J. Y. (2011). Comparing sediment bacterial communities in the macrophyte-dominated and algae-dominated areas of eutrophic Lake Taihu, China. *Canadian Journal of Microbiology*, 57, 263–272. https://doi.org/10.1139/w11-003

Shimeta, J., & Cook, P. L. M. (2011). Testing assumptions of the eukaryotic inhibitor method for investigating interactions between aquatic protozoa and bacteria, applied to marine sediment. *Limnology and Oceanography-Methods*, 9, 288–295. https://doi.org/10.4319/loom.2011.9.288

Shtarkman, Y. M., Kocer, Z. A., Edgar, R., Veerapaneni, R. S., D’Elia, T., Morris, P. F., & Rogers, S. O. (2013). Subglacial Lake Vostok (Antarctica) accretion ice contains a diverse set of sequences from aquatic, marine and sediment-inhabiting bacteria and eukarya. *PLoS ONE*, 8, e67221. https://doi.org/10.1371/journal.pone.0067221

Song, H., Li, Z., Du, B., Wang, G., & Ding, Y. (2012). Bacterial communities in sediments of the shallow Lake Dongping in China. *Journal of Applied Microbiology*, 112, 79–89. https://doi.org/10.1111/j.1365-2672.2011.05187.x

Sun, F.-L., Wang, Y.-S., Wu, M.-L., Wang, Y.-T., & Li, Q. P. (2011). Spatial heterogeneity of bacterial community structure in the sediments of the Pearl River estuary. *Biologia*, 66, 574–584.

Van der Gucht, K., Cottenie, K., Muylaert, K., Vloemans, K., Cousin, S., Declerck, S., ... De Meester, L. (2007). The power of species sorting: Local factors drive bacterial community composition over a wide range of spatial scales. *Proceedings of the National Academy of Sciences of the United States of America*, 104, 20404–20409. https://doi.org/10.1073/pnas.0707200104

Wang, Y., & Qian, P. Y. (2009). Conservative fragments in bacterial 16S rRNA genes and primer design for 16S ribosomal DNA amplicons in metagenomic studies. *PLoS ONE*, 4, e7401. https://doi.org/10.1371/journal.pone.0007401
Wang, Y., Sheng, H. F., He, Y., Wu, J. Y., Jiang, Y. X., Tam, N. F., & Zhou, H. W. (2012). Comparison of the levels of bacterial diversity in freshwater, intertidal wetland, and marine sediments by using millions of illumina tags. *Applied and Environmental Microbiology*, 78, 8264–8271. https://doi.org/10.1128/AEM.01821-12

Woese, C. R., Kandler, O., & Wheelis, M. L. (1990). Towards a natural system of organisms-proposal for the domains Archaea, Bacterial, and Eucarya. *Proceedings of the National Academy of Sciences of the United States of America*, 87, 4576–4579. https://doi.org/10.1073/pnas.87.12.4576

Wu, Q. L. L., Chen, Y. W., Xu, K. D., Liu, Z. W., & Hahn, M. W. (2007). Intra-habitat heterogeneity of microbial food web structure under the regime of eutrophication and sediment resuspension in the large subtropical shallow Lake Taihu, China. *Hydrobiologia*, 581, 241–254.

Wu, H., Li, Y., Zhang, J., Niu, L., Zhang, W., Cai, W., & Zhu, X. (2017). Sediment bacterial communities in a eutrophic lake influenced by multiple inflow-rivers. *Environmental Science and Pollution Research*, 24, 19795–19806. https://doi.org/10.1007/s11356-017-9602-4

Wu, P., Qin, B. Q., Yu, G., Deng, J. M., & Zhou, J. (2016). Effects of nutrient on algae biomass during summer and winter in inflow rivers of Taihu Basin, China. *Water Environment Research*, 88, 665–672. https://doi.org/10.2175/106143016X14609975746767

Wu, H., Zeng, G., Liang, J., Guo, S., Dai, J., Lu, L., … He, X. (2015). Effect of early dry season induced by the Three Gorges Dam on the soil microbial biomass and bacterial community structure in the Dongting Lake wetland. *Ecological Indicators*, 53, 129–136. https://doi.org/10.1016/j.ecolind.2015.01.041

Xiong, J. B., Ye, X. S., Wang, K., Chen, H. P., Hu, C. J., Zhu, J. L., & Zhang, D. M. (2014). Biogeography of the sediment bacterial community responds to a nitrogen pollution gradient in the East China Sea. *Applied and Environmental Microbiology*, 80, 1919–1925. https://doi.org/10.1128/AEM.03731-13

Xu, H., Paerl, H. W., Qin, B., Zhu, G., Hall, N. S., & Wu, Y. (2015). Determining critical nutrient thresholds needed to control harmful cyanobacterial blooms in eutrophic Lake Taihu, China. *Environmental Science & Technology*, 49, 1051–1059. https://doi.org/10.1021/acs.est.5b03744q

Yokokawa, T., & Nagata, T. (2010). Linking bacterial community structure to carbon fluxes in marine environments. *Journal of Oceanography*, 66, 1–12. https://doi.org/10.1007/s10872-010-0001-4

Zhu, M. Y., Zhu, G. W., Li, W., Zhang, Y. L., Zhao, L. L., & Gu, Z. (2013). Estimation of the algal-available phosphorus pool in sediments of a large, shallow eutrophic lake (Taihu, China) using profiled SMT fractional analysis. *Environmental Pollution*, 173, 216–223. https://doi.org/10.1016/j.envpol.2012.10.016

Zinger, L., Amaral-Zettler, L. A., Fuhrman, J. A., Horner-Devine, M. C., Huse, S. M., Welch, D. B. M., … Ramette, A. (2011). Global patterns of bacterial beta-diversity in seafloor and seawater ecosystems. *PLoS ONE*, 6, e24570. https://doi.org/10.1371/journal.pone.0024570

How to cite this article: Huang W, Chen X, Wang K, Chen J, Zheng B, Jiang X. Comparison among the microbial communities in the lake, lake wetland, and estuary sediments of a plain river network. *MicrobiologyOpen*. 2019;8:e644. https://doi.org/10.1002/mbo3.644