

# CHANGES IN THE BACTERIAL COMMUNITY STRUCTURE AND DIVERSITY OF CHAGAN LAKE SEDIMENTS, NORTHEASTERN CHINA

DU, X.<sup>1,2#</sup> – LI, M. S.<sup>3#</sup> – SONG, D.<sup>1,2</sup> – YANG, J. S.<sup>4</sup> – LIU, H.<sup>1,2</sup> – SUI, X.<sup>5</sup> – HUO, T. B.<sup>1,2\*</sup>

<sup>1</sup>*Heilongjiang River Fisheries Research Institute, Chinese Academy of Fishery Sciences, 150076 Harbin, PR China*

<sup>2</sup>*Heilongjiang River Basin Fishery Ecological Environment Monitoring Center, Ministry of Agriculture and Rural Affairs, 150076 Harbin, PR China*

<sup>3</sup>*Institute of Nature and Ecology, Heilongjiang Academy of Sciences, 150040 Harbin, PR China*

<sup>4</sup>*Jilin Chagan Lake National Nature Reserve Administration, 138099 Songyuan, PR China*

<sup>5</sup>*School of Life Sciences, Heilongjiang University, Harbin, PR China*

<sup>#</sup>*Xue Du and Mengsha Li contributed equally to this work*

<sup>\*</sup>*Corresponding author  
e-mail: tbhuo@163.com*

(Received 16<sup>th</sup> Mar 2022; accepted 26<sup>th</sup> Jul 2022)

**Abstract.** This study employed Illumina MiSeq high-throughput sequencing to explore the composition of the bacterial community of Chagan Lake sediments and its response to soil physicochemical properties. Our findings indicated that bacterial abundance and diversity are significantly correlated with water depth. Particularly, the bacterial alpha diversity and phyla relative abundance increased with water depth. Furthermore, the five dominant bacterial phyla in the bacterial community according to all plots were Proteobacteria, Chloroflexi, Acidobacteriota, and Actinobacteriota. Moreover, our findings indicated that electrical conductivity (EC), pH, and total carbon (TC) in sediments are important factors that affect the bacterial community structure and diversity of sediments. In summary, the bacterial community structure and diversity varied significantly in different plot sediments of Chagan Lake, which were regulated by soil nutrients and physical properties. The results of this study can be used to further explore the potential relationship between bacterial communities and the environment, and provide a scientific basis for the prediction of ecosystem structure and function of alpine inland wetlands.

**Keywords:** *soil environmental factors, soil physicochemical properties, bacterial composition, water depth, functional prediction*

## Introduction

Microbial community and diversity in sediments are crucial for lake ecosystems. Particularly, sediment microbes drive the morphological transformation and geochemical cycle of most bioactive elements, regulate the environmental quality of water bodies, and contribute to water purification (Wan et al., 2017; Li et al., 2017). Furthermore, the distribution of sediment microbial communities is also affected by environmental factors such as temperature, pH, dissolved oxygen, electrical conductivity and nutrients (Chen et al., 2010; Fermani et al., 2013; Shao et al., 2013; Zhang et al., 2019). Therefore, studying the diversity, community composition, and environmental factors that shape sediment microbial communities is critical for the conservation of lake ecosystems.

Bacteria are a major component of lake microbial communities and are the main decomposers of organic compounds. Several studies have evaluated the microbial community structure of lake sediments and have reported that the microbial community composition of sediments varies depending on location, season, and sediment depth. Huang et al. (2015) studied the composition of bacterial communities in the sediments of Meiliang Bay, Xuhu Lake, and East Taihu Lake in summer, and found that the dominant bacterial phyla in different lake areas varied depending on the region. Chen et al. (2010) found that the composition of eukaryotic microbial communities in Meiliang Bay and the lake center of Taihu Lake exhibited obvious seasonal changes, and different lake areas responded differently to environmental factors. Meiliang Bay and the lake center were affected by total phosphorus (TP), total nitrogen (TN), and electrical conductivity (EC). However, Wan et al. (2017) found that, rather than lake location, season was the most important determinant of microbial community structure in sediments. Ye et al. (2009) found that although the vertical distribution of bacterial communities in the sediments of Meiliang Bay in Taihu Lake was similar, the composition of archaeal communities varied significantly depending on water depth.

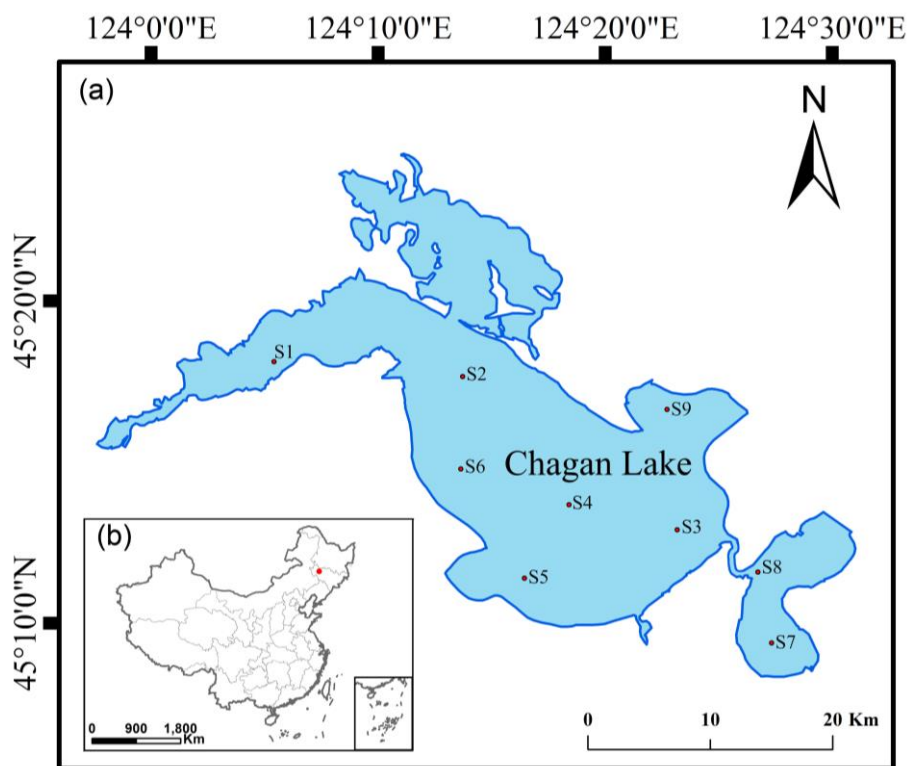
Chagan Lake is the largest inland lake in Jilin Province and is located within a large water network between the Nenjiang and the Huolin rivers. It is an important fishery base in Jilin Province and the largest lake in the Songliao Plain. Research on Chagan Lake has largely focused on characterizing the levels of organic matter in its sediments (Qu et al., 2021), its benthic community structure (Du et al., 2020), and the elemental composition of its sediments (Bu et al., 2009). However, very few studies have explored the microbial community composition of Chagan Lake sediments. Therefore, our study collected sediments from a 10–15 cm depth in the coastal areas of Chagan Lake and the center of the lake in 2017. The bacterial community structure of the sediments was then characterized via high-throughput sequencing technology to explore its relationship with different sediment properties. Collectively, our findings provide insights into the formation mechanism of sediment bacterial communities in Chagan Lake, which can serve as a theoretical basis for maintaining the stability of the Chagan Lake ecosystem.

## Material and Methods

### *Research area*

Chagan Lake (124°03'–124°34', 45°09'–45°30') is located in the boundary of the northwestern Jilin Province, Inner Mongolia Autonomous Region, Heilongjiang Province, and Jilin Province in China, and acts as a weir at the end of the Huolin River. Sai Lake is among the top ten freshwater lakes in China, the largest natural lake, and the largest fishery production base in Jilin Province at the confluence of the Songhua River, the southern source of Songhua River, and the Nen River (*Figure 1*). The lake has an area of 420 km<sup>2</sup> and an average water depth of 2.5 m. Furthermore, the lake integrates with the Xindianpao and Mayingpao lakes when the water level reaches 130 m. Chagan Lake is primarily replenished through natural precipitation, water diversion from the Songhua River, and return water from irrigation areas. The lake is surrounded by farmlands and is therefore severely affected by agricultural non-point source pollution. Saline-alkali land and sandy terrain are widely distributed around the lake and serve as a runoff collection area. Furthermore, the rapid development of tourism and catering services in the surrounding area threatens the water quality of Chagan Lake. In this study, nine sampling points were established across Chagan Lake based on its habitat

characteristics (Figure 1). According the water depth, we divided 9 soil point into three categories: low water depth (S7 and S9)  $\leq 2$  m, medium water depth (S1 and S8) between 2 m and 3 m and high water depth (S2, S3, S4, S5 and S6)  $\geq 3$  m.



**Figure 1.** Distribution of sampling sites in Chagan Lake. (a) the map of China and the red point is the research site; (b) research site and S1-S9 indicated the locations of sediment samples taken

### ***Sediment samples***

On October 10, 2017, sediment samples were collected from a 10–15 cm depth from the surface of the lake bottom using a stainless steel grab. In each plot, the five sediment soils (each sediment soil were  $\sim 100$  g) were taken and then mixed one sediment soil. The samples were then placed in sterilized self-sealing bags, stored at 4 °C, and quickly transported to the laboratory. Microbial DNA was immediately extracted from a portion of the fresh sediment samples, whereas the other portion was freeze-dried, ground, passed through a 125  $\mu\text{m}$  sieve, and stored at -20 °C to characterize the physicochemical properties of the sediment samples within one week.

### ***Analysis of physical and chemical indicators***

The soil-water pH ratio of the sediment (1:2.5) was determined using a pH meter, the EC value of the sediment was determined using a soil EC value tester, and the total carbon (TC), total nitrogen (TN), and total phosphorus (TP) in the sediment were determined via ammonium molybdate spectrophotometry.

### ***DNA extraction and sequencing of sediment microorganisms***

The total DNA of the microorganisms in the sediment samples was extracted using the FastDNA SPIN kit (MP Biomedical, USA). PCR amplification was performed on the V3-V4 region of the 16S rRNA of the DNA samples using the 338F (5'- ACT CCT ACG GGA GGC AGC AG-3') and 806R (5'- GGA CTA CHV GGG TWT CTA AT-3') primer pair. Each 30 µl reaction contained 100 ng of template DNA, 15 µl 2x EasyTaq PCR SuperMix, and 10 µM of primers. All reactions were conducted in triplicate in a Veriti 96-well fast thermocycler (ABI, USA) and the reagents used in our experiments were purchased from Beijing Quanshijin Company. The PCR amplification conditions were the following: pre-denaturation at 95 °C for 2 min, followed by 30 cycles of denaturation at 95 °C for 20 s, annealing at 52 °C for 60 s, extension at 72 °C for 60 s, and a final extension at 72 °C for 10 min.

### ***Bioinformatics and statistical analyses***

The purified sediment PCR products were sequenced on the Illumina MiSeq platform (Illumina, USA) (2 × 300 bp paired-end sequencing). Quality control measures were taken to ensure the quality of the reads, and the original sequences were filtered and spliced, after which chimeric sequences were removed using the QIIME2 software (Bolyen et al., 2019) and the sequence length was screened. The clean reads were then assigned to different operational taxonomic units (OTUs) at a 97% similarity threshold using QIIME. Annotation of taxonomic information from the phylum to genus level was performed by aligning the sequences with those in the SILVA database using RDP Classifier. The OTUs were analyzed based on abundance and diversity indices, including the Chao1 and ACE indices of community richness, as well as the Shannon and Simpson indices of community evenness.

Multiple comparisons between groups were conducted through one-way analysis of variance (ANOVA) using the SPSS 26.0 software and differences were considered statistically significant at  $P < 0.05$ . Pearson correlation was used to analyze the correlation between the physicochemical properties of the sediment and the alpha diversity of the sediment, and correlations were considered statistically significant at  $P < 0.05$  and  $P < 0.01$ . The top 50 bacterial phyla with the highest abundances and soil physicochemical properties were visualized in heatmaps using the 'vegan' package in R (R Development Core Team, 2017). Canonical association analysis was performed using Canoco5.0. Principal co-ordinates analysis (PCoA) was also conducted based on OTU-level composition profiles using the 'vegan' package in R. Dilution profiles were also analyzed using the 'vegan' package. Functional predictive analysis (Functional Annotation of Prokaryotic Taxa, FAPROTAX) was used to predict the microbial functions in the sediments. Permutational Multivariate Analysis of Variance (PERMANOVA) performed by R software using the 'vegan' package.

## **Results**

### ***Analysis of physicochemical properties of the bottom sediments in Chagan Lake***

As summarized in *Table 1*, the water depths of the nine points in Chagan Lake ranged from 1.4 m (S7) to 3.6 m (S6). Soil TP in sediments ranged from 0.34 to 1.07 g/kg, TC ranged from 3.23 to 47.96 g/kg, TN ranged from 0.26 to 3.03 g/kg, pH ranged from 8.2 to 9.0, conductivity ranged from 519 to 1082, and the C/N variation

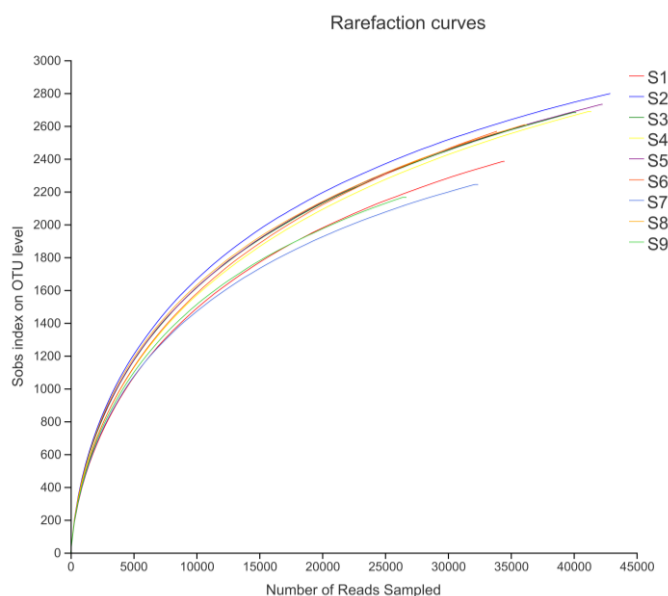
ranged from 0.4 to 6.69. Among the sampling points, S4 had the highest TP, TC, TN, and EC, reaching values of 1.07 g/kg, 47.96 g/kg, 3.03 g/kg, and 1082, respectively. In contrast, S1 had the lowest TP and TN levels (0.34 and 0.71 g/kg, respectively).

**Table 1.** Soil physicochemical properties at different points across Chagan Lake

Plots	TP	TC	TN	C/N	pH	EC	Water depth	Categories
S1	0.34	9.46	0.71	0.55	8.62	1049	2.3	medium
S2	0.83	33.81	1.97	0.44	8.83	1002	3.6	high
S3	0.18	3.23	0.26	0.48	8.86	1069	3	high
S4	1.07	47.96	3.03	0.57	8.7	1082	3.5	high
S5	0.50	15.02	0.86	0.54	8.84	980	3.1	high
S6	0.82	29.71	1.67	0.4	9.00	1030	3.6	high
S7	0.65	26.60	1.75	0.58	8.27	552	1.4	low
S8	0.39	10.20	0.76	6.69	8.84	985	2.1	medium
S9	0.62	36.03	2.4	6.13	8.2	519	1.9	low

### Rarefaction curve of bacterial communities in the bottom sediment of Chagan Lake

The rarefaction curve reflects the sampling depth of the sample and can be used to evaluate whether the sequencing volume is sufficient to cover all taxa. *Figure 2* illustrates the rarefaction curve of all samples in this experiment under a 97% similarity threshold. As illustrated in *Figure 2*, the dilution curves of all soil samples tended to be flat, indicating that the read numbers were high enough to accurately reflect the bacterial community structure of the soil samples.



**Figure 2.** Rarefaction curves of different sample points in Chagan Lake

### Alpha diversity of the bacterial community of Chagan Lake sediment

As summarized in *Table 2*, the coverage of each sample library ranged from 97% to 98%, indicating that the sequencing results accurately reflected the structure of the bacterial communities in the sediments. The abundance of bacterial communities

reflected by the Chao1 and Ace indices exhibited the same order: low water depth (S7 and S9) < medium water depth (S1 and S8) < high water depth (S2, S3, S4, S5, S6). In other words, the water level increased proportionally with flooding degree, and bacterial abundance was affected by the water level. Bacterial abundance was highest at the S2, S3, and S4 sample points (where the water level was high), but the results at low water depths did not change significantly ( $P < 0.05$ ). In contrast, the bacterial Shannon indices at medium water depths were significantly different but exhibited no consistent trend ( $P < 0.05$ ). Therefore, these findings demonstrated that the water depth significantly affected the bacterial abundance in the sediments, but the difference in the uniformity was not significant.

**Table 2.** Bacterial alpha diversity in Chagan Lake sediments

Plots	Sobs	Shannon	Simpson	Ace	Chao1	Coverage (%)	PD
S1	2384.00	6.05	0.01	3129.86	3063.26	98	238.59
S2	2797.00	6.46	0.00	3483.69	3473.16	98	276.22
S3	2683.00	6.36	0.00	3451.95	3470.29	98	258.66
S4	2688.00	6.30	0.01	3524.26	3466.48	98	262.85
S5	2731.00	6.41	0.00	3497.31	3481.71	98	269.15
S6	2567.00	6.06	0.01	3528.15	3510.47	97	257.76
S7	2243.00	6.11	0.01	2864.26	2854.29	98	217.81
S8	2607.00	6.35	0.01	3405.81	3398.09	98	250.17
S9	2165.00	6.11	0.01	2832.75	2850.00	97	211.01
One-way ANOVA (Water depth)	$P < 0.05$	$P < 0.05$	$P > 0.05$	$P < 0.05$	$P < 0.05$	$P > 0.05$	$P < 0.05$

### Beta diversity of the bacterial community in Chagan Lake sediment

According to the principal coordinate analysis of the Pearson distance algorithm at the OTU level, the correlations and differences of the bacterial communities in the sediments of the nine sampling points were compared. As shown in *Figure 3*, the cumulative explained variation of the first axis and the second axis reached 41.93% and 21.42%, respectively. The bacterial communities at different sampling points in Chagan Lake did not overlap significantly with each other and could thus be easily distinguished. From the perspective of bacterial community similarity, there were similarities in the bacterial community structure of the subsoil of the S7 and S9, S1, S5, and S2, and S1, S3, S6, and S8 sampling points, and therefore these sampling sites formed three distinct clusters (*Figure 3*). Overall, the community structure of bacteria in the sediments of different water depths was significantly different (PERMANOVA  $P < 0.05$ ), which indicated that the water depths had a significant effect on the bacterial community structure of the sediments.

### Analysis of bacterial community structure in Chagan Lake sediments

A total of 5,362 OTUs were identified in the nine sampling points using high-throughput sequencing, which encompassed 60 bacterial phyla (*Figure 4(a)*) and 1,077 bacterial genera (*Figure 4(b)*). As illustrated in *Figure 4(a)*, the main phyla in the soil samples included Proteobacteria (26%), Chloroflexi (14%), Acidobacteriota (10%), Actinobacteriota (9%), Desulfobacterota (8%), Bacteroidota (8%), and Cyanobacteria (7%).

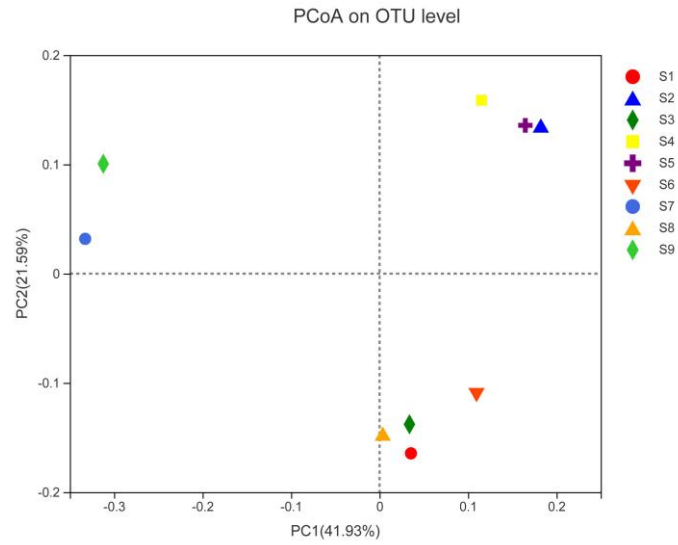


Figure 3. Bacterial beta diversity in the sediments of Chagan Lake

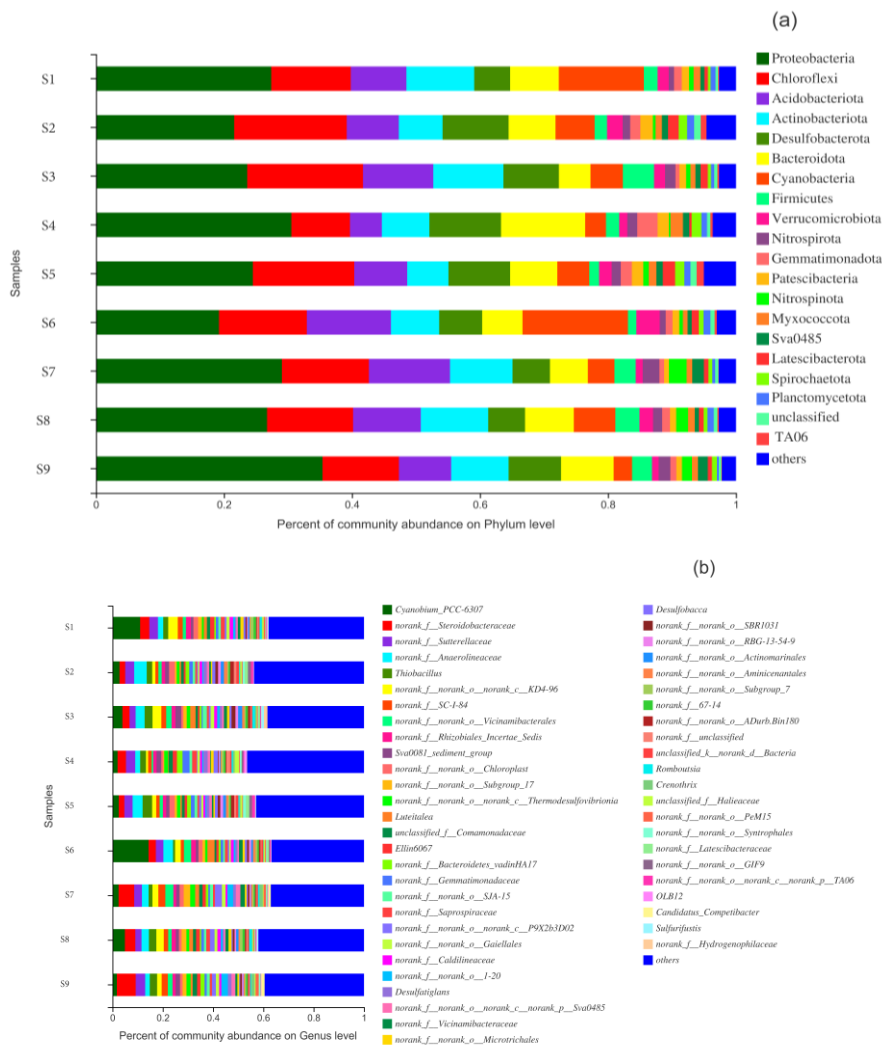
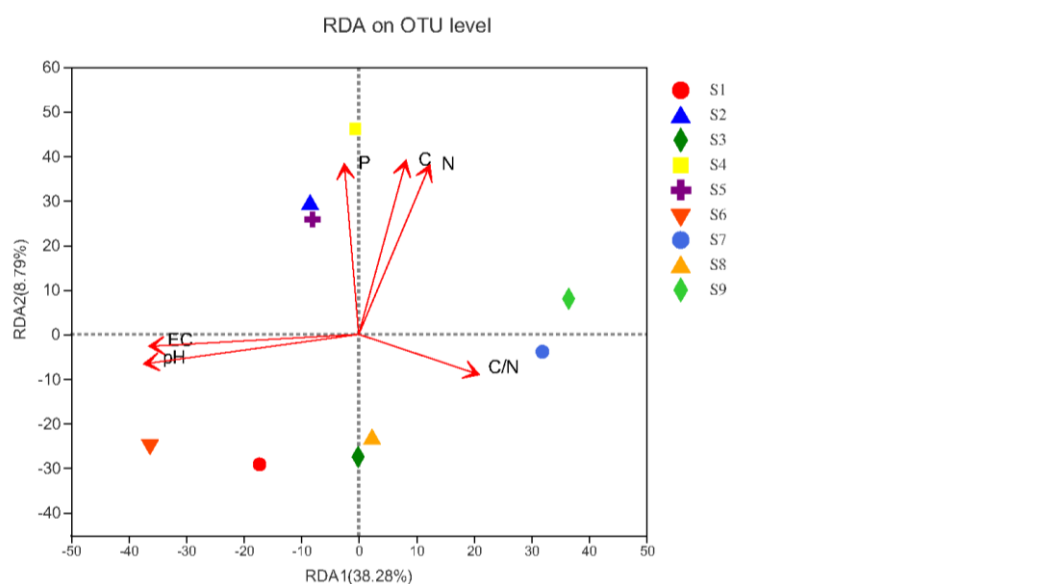


Figure 4. Bacterial phyla (a) and genera (b) level classification in sediments of Chagan Lake

### ***Redundancy analysis of bacterial community and physicochemical properties in sediments of Chagan Lake***

The key environmental factors affecting the sediment bacterial community of Chagan Lake were further analyzed, and the soil fungal community structure and soil physicochemical properties were explored via redundancy analysis (*Fig. 5*). Our findings indicated that the cumulative explained variation of the two axes reached 47.07%, and could thus reflect nearly 50% of the variation characteristics of soil bacterial communities and their influencing factors. Particularly, pH was the key environmental factor that dominated the bacterial community changes ( $R^2 = 0.75$ ,  $P = 0.01$ ).



***Figure 5. Redundancy analysis of bacterial community and physicochemical properties in sediments of Chagan Lake***

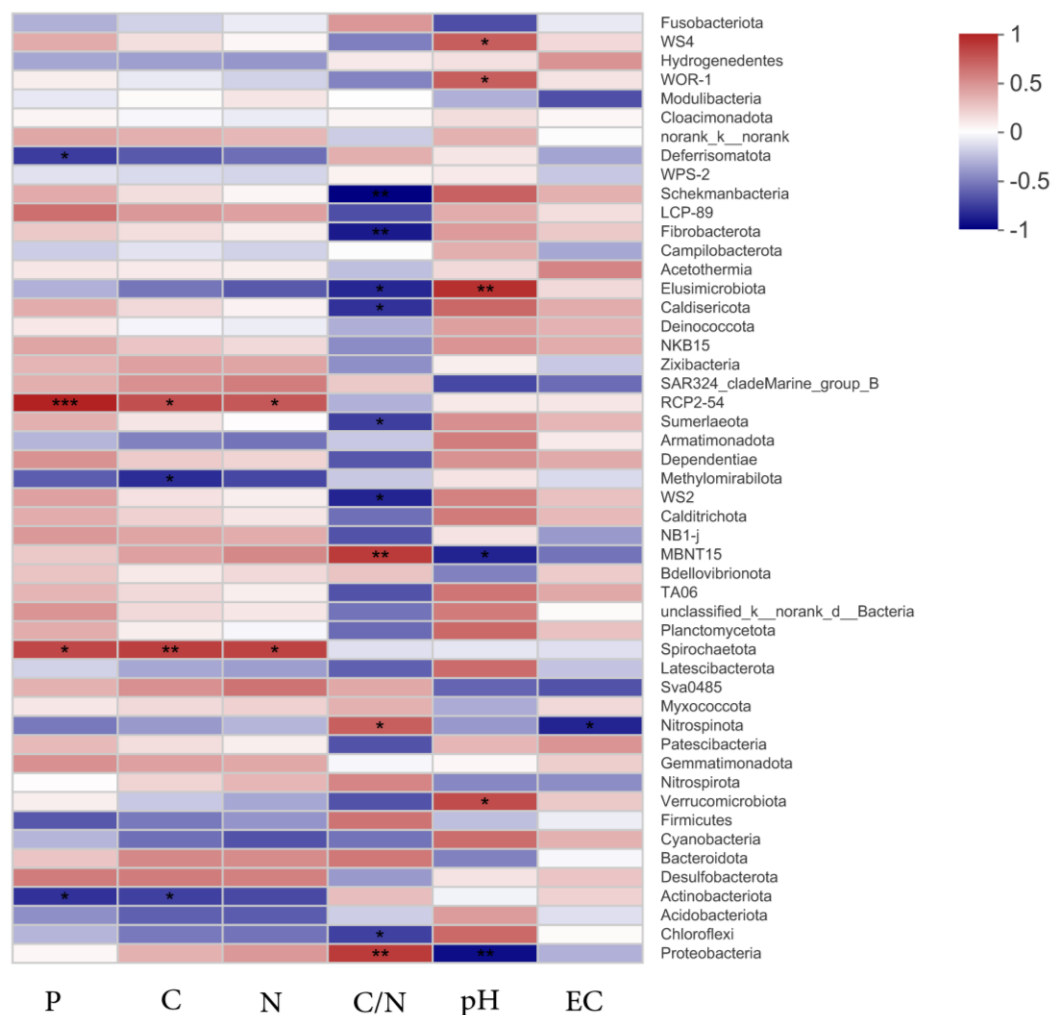
The key environmental factors affecting the abundance of soil bacteria in the bottom of Chagan Lake were further analyzed, and the correlation between the horizontal abundance of soil fungi and soil physicochemical properties was determined (*Fig. 6*). Our findings indicated that the abundance of different bacterial phyla was affected by different environmental factors, among which WS4, WOR-1, Elusimicrobiota, Verrucomicrobiota, and Proteobacteria were significantly correlated with soil pH; Nitrospinta was significantly correlated with soil EC; Proteobacteria, Chloroflexi, Nitrospinta, MBNT15, WS2, Sumerlaeota, Caldisericota, Elusimicrobes, and Fibrobacteria were significantly correlated with C/N; Spirochaetota was significantly correlated with C, N, P; and Actinobacteriota was significantly correlated with soil C and P.

### ***Relationships between soil physicochemical properties and soil bacterial alpha diversity***

As summarized in *Table 3*, the correlation analysis between soil physicochemical properties and the alpha diversity of soil bacteria in the sediments indicated that the



Sobs index, Shannon index, Ace index, and Chao1 index were significantly positively correlated with the soil organic carbon in the sediments ( $P < 0.05$ ). However, there was no significant correlation between other indices and the physicochemical properties of the sediment.



**Figure 6.** Correlation heatmap between soil physicochemical properties and soil bacterial phyla. Asterisk indicates significantly different at  $P < 0.05$  and  $P < 0.01$

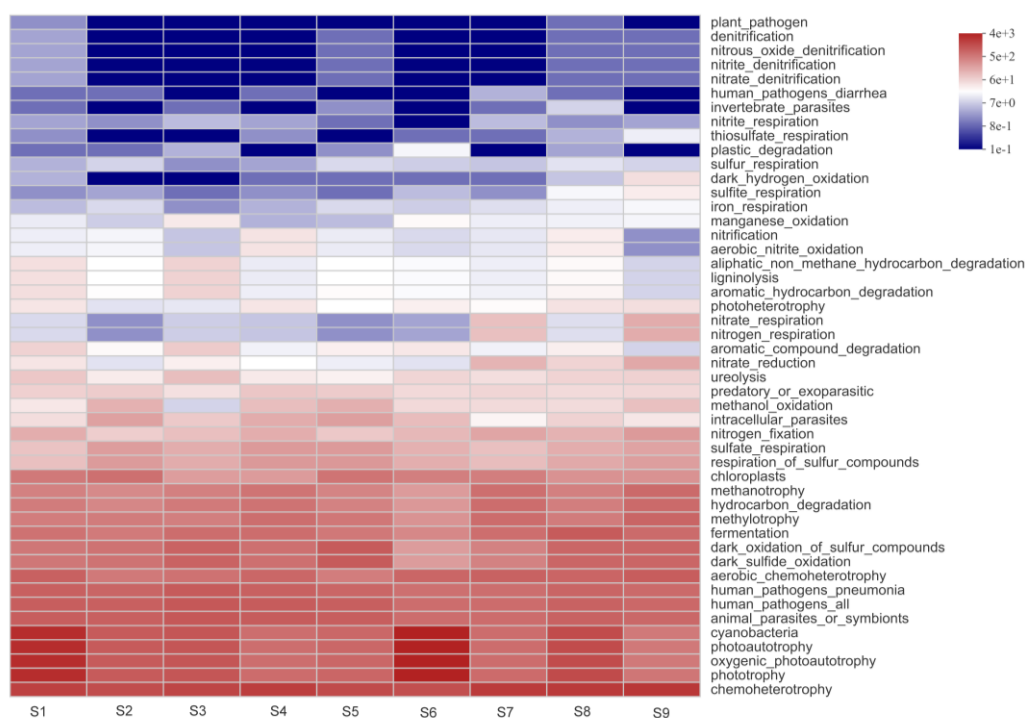
**Table 3.** Correlation coefficients between the soil physicochemical properties and soil bacterial  $\alpha$ -diversity

Alpha diversity	TP	TC	TN	C/N	pH	EC
Sobs	0.441	0.985**	0.119	-0.090	-0.175	-0.371
Shannon	0.563	0.720*	-0.030	-0.108	-0.148	-0.037
Simpson	-0.378	-0.630	0.259	0.313	0.380	0.384
Ace	0.242	0.955**	0.165	-0.065	-0.155	-0.347
Chao1	0.212	0.948**	0.134	-0.085	-0.176	-0.310

\* $P < 0.05$ ; \*\* $P < 0.01$

### Functional annotation space of sediment bacteria

Different types of sediment bacterial communities were predicted and analyzed by the FAPROTAX function prediction software to analyze the changes in the microbial function of the subsoil as shown in *Figure 7*. A total of 48 types of metabolic function-related pathways were identified in all samples, among which 18 types of sediment bacteria were the main functional microorganisms in the nine sampling points (the relative abundance of functional gene sequences was >1%). As shown in *Fig. 7*, the functions with abundance rates greater than 10% among all samples included chemoheterotrophy, phototrophy, cyanobacteria, oxygenic\_photoautotrophy, and photoautotrophy. Additionally, the functional structures of S1 and S8, S7 and S9, and S2, S3, S5, and S6 were similar.



**Figure 7.** Prediction of FAPROTAX functions of soil bacteria in sediments of Chagan Lake at different locations

### Discussion

Lake sediment is a unique biological environment that is characterized by the participation of various microorganisms, frequent exchange of substances, and high biological activity (Yang et al., 2018). Soil microbes possess complex metabolisms and reproduce rapidly and are thus considered a key component of soil ecology. However, these microbial communities are highly sensitive to external environmental disturbances. Water depth is a key factor affecting the ecological processes of lakes (Gutknecht et al., 2006), and many studies have demonstrated that changes in flooding degree can significantly affect soil microbial communities (Rees et al., 2006; Mentzer et al., 2006). Wang Peng et al. studied the characteristics of soil bacterial communities in the vegetation zone of Poyang Lake with different water levels and found that the soil

under the medium water level had a higher bacterial community abundance. Through the study of soil microorganisms in coastal reed wetlands under different flooding conditions, Zhang et al. (2017) reported that soil archaea and bacterial diversity were higher under flooding conditions. Zhang et al. (2016) studied the bacterial diversity in plant roots at different water level depths and found that the bacterial diversity in the plant roots decreased as water depth increased. Liu (2017) also demonstrated that water depth has a significant effect on bacterial community structures. Our findings indicated that different water depths had a significant impact on the bacterial community diversity in the sediment, which was consistent with the findings of Zhang et al. (2017) and Wang et al. (2016a). In this study, the bacterial diversity in the bottom sediment of Chagan Lake exhibited the following order: low water depth < medium water depth < high water depth. In other words, bacterial diversity was higher in deeper waters. The potential mechanisms that drive this phenomenon will be described below.

Changes in water level conditions can directly change the living environment of the bacterial community in the sediment. Our findings indicated that the soil TP, TC, and TN contents in the deeper sampling points were significantly higher than those in the low- and medium-water levels. High nutrient conditions provide abundant carbon and nitrogen sources, thus promoting microorganism growth. From the perspective of the beta diversity of sediment bacteria, the bacterial community structure of sediments at different water levels was also significantly different. The bacterial community structure in the sediments of the S7 and S9, S1, S5, and S2, and S1, S3, S6, and S8 samples was similar. This was consistent with our bacterial alpha diversity results. That is, the soil richness, uniformity, and community structure of different sample sites varied significantly depending on the water level. Our findings demonstrated that the changes in microbial community abundance, diversity, and community structure composition in response to different water level conditions were largely the same. Deeper waters were associated with greater bacterial community abundance and diversity indices, and therefore water depth could be used as a predictor of bacterial diversity and abundance in Chagan Lake. Understanding the environmental changes caused by different water depths and submerged periods would provide a basis for the development of better management practices for the conservation of Chagan Lake.

As the most important inland lake in Jilin Province, Chagan Lake is the largest lake in the Songliao Plain and an important fishery base in Jilin Province. The water quality of Chagan Lake is directly affected by the quality of its recharge sources (particularly the recharge water in the Qianguo Irrigation Area), as well as the water dynamics in the Songnen Plain and the lake area (Sun et al., 2011). The water quality of Chagan Lake has been steadily deteriorating each year, with decreases in dissolved oxygen concentrations and increases in pH and pollutant concentrations including nitrogen and phosphorus (Du et al., 2020). Recent studies have demonstrated that the water quality of Chagan Lake is close to the Class III standard and is in a state of mild eutrophication (Du et al., 2020). Water pollution leads to increased nutrient fluxes in river waters, destroys water ecosystems, and affects bacterial community compositions (Xue et al., 2018). This study showed that the abundance of Proteobacteria in the bottom sediments of Lake Chagan was the highest (26%), followed by Chloroflexi (14%) and Actinobacteria (10%). This is consistent with a study by Wang et al. (2016b), where sediment bacteria from the bottom of the Hunhe river was dominated by Proteobacteria, as well as other bacterial taxa including Cyanobacteria and Bacteroidetes. Zhang et al. (2016) reported similar results in a study of lake sediments in Finland. Many studies

have shown that Proteobacteria have a high proportion in lake sediments (Yu et al., 2020; Hu et al., 2021), and also have strong tolerance to polluted soils, so they are the dominant bacterial community in different lake sediments. Addition, there are a large number of aerobic or facultative bacteria in Proteobacteria, and the lake sediment has been in a state of high water level for a long time, and the relative abundance of Proteobacteria is less under the high water level conditions (*Figure 4a*); Chloroflexi is another dominant bacterial phylum, and the response of Chloroflexi to different water level conditions presents the characteristics of diversity. In our study, it was found that the largest abundance appeared at low water level (*Figure 4a*), this is due to the Chloroflexi are facultative anaerobic bacteria, relying on light energy for photosynthesis and anaerobic respiration under anaerobic conditions (Yu et al., 2020), so under low water level, the environment is more suitable for the growth of Chloroflexi. Actinobacteria is also one of the phyla with higher distribution in this study (*Figure 4a*). The reason may be the surface source pollution in Chagan Lake. Because Actinomycetes belong to Saprophytic bacteria can exist in polluted environments, so we speculate that the increase of Actinomycetes may be due to the influence of farmland and human activities around Chagan Lake, and a large amount of agricultural sewage and pesticides injected into the water body. Particularly, the sediments were mainly dominated by Proteobacteria, as well as Acidobacteria and Actinobacteria. However, different sites can have specific bacterial compositions. In this study, Desulfobacterota and Bacteroidota in S9 were more abundant than in other sampling points. S9 is located at the confluence of Chagan Lake and the Nenjiang River. The research site is seriously polluted by agricultural non-point sources and it is close to the saline-alkali area in western Heilongjiang. Therefore, the study area is affected by high saline-alkali water and water eutrophication, which might explain the high abundance of Desulfobacterota and Bacteroidota at this site. Different soil physicochemical properties can affect the bacterial community structure in sediments (Wang et al., 2016a). Our study demonstrated that EC, TC, and TN, as well as pH and C/N, were the main environmental factors that shaped the bacterial community structure of the Chagan Lake sediments at the phylum level (*Figure 6*). Wang et al. (2017) and Wang et al. (2018) studied the Poyang Lake estuary and found that the main environmental factor of microbial community structure was also pH. Previous studies of lake sediments in the United Kingdom (Wang et al., 2016b) and Qiantang River sediments in China (Liu et al., 2015) also reported that pH was the main factor that influenced bacterial community structure. Xue et al. (2021) also found that soil SOC, TN, and pH were the main factors affecting soil bacterial communities in Jialing River sediments. However, additional studies are needed to comprehensively explore the structure and diversity of bacterial communities at the genus level. Our study identified significant differences in the bacterial community structure of sediments depending on the sampling locations, suggesting that the structure of these bacterial assemblages responds to the environmental pressures of each location.

## Conclusion

This study evaluated the variations in the bacterial community structure and diversity of Chagan Lake sediments collected at different points. Our findings indicated that the bacterial community diversity in the sediments of different points of Chagan Lake varied depending on the water depth, with higher diversity occurring in deeper sites.

The five dominant phyla in the sediment samples were Proteobacteria, Chloroflexi, Acidobacteriota, Actinobacteriota, and Actinobacteriota. However, the proportions of these and other phyla varied depending on the sampling site, thus demonstrating the influence of environmental characteristics on bacterial communities. Among these environmental factors, EC, pH, and TC had the most significant effects on bacterial community composition and diversity. Taken together, our findings provide key insights into the response of sediment bacterial communities to environmental factors and how these responses affect the functions of lake ecosystems, which is of great significance for the rational utilization of water and biological resources.

**Acknowledgements.** This work was financially supported by the National Key Research and Development Program of China (2019YFD0900602 and 2019YFD0900605), National Natural Science Foundation of China (No. 31802298) and the Finance Special Fund of Ministry of Agriculture and Rural Affairs (Fisheries Resources and Environment Survey in the Key Water Areas of Northeast China). We also thank Scientific Paper Edit Co. Ltd for linguistic editing.

## REFERENCES

- [1] Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Caporaso, J. G. (2019): Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. – *Nat Biotechnol* 37(8): 852-857.
- [2] Bu, X. J., Chai, S. L., Zhang, Q. W., Xu, X. C. (2009): The spatial distributions of elements in sediments of lake Chagan in west Jilin Province. – *J. Arid Land Resour. Environ* 23: 179-184.
- [3] Chen, M., Chen, F., Zhao, B., Wu, Q. L., Kong, F. (2010): Seasonal variation of microbial eukaryotic community composition in the large, shallow, subtropical Taihu Lake, China. – *Aqua Ecol* 44(1): 1-12.
- [4] Du, X., Yang, J. S., Song, D., Wang, H. B., Jin, X., Liu, H., Wang, L., Huo, T. B. (2020): Community structure of macroinvertebrate and its relationship with environmental factors in chagan lake. – *Chin J Fish* 33(6): 61-67.
- [5] Fermani, P., Diovisalvi, N., Torremorell, A., Lagomarsino, L., Zagarese, H. E., Unrein, F. (2013): The microbial food web structure of a hypertrophic warm-temperate shallow lake, as affected by contrasting zooplankton assemblages. – *Hydrobiologia* 714(1): 115-130.
- [6] Gutknecht, J. L., Goodman, R. M., Balser, T. C. (2006): Linking soil process and microbial ecology in freshwater wetland ecosystems. – *Plant Soil* 289(1): 17-34.
- [7] Hu, H., Li, D. L., Wang, Y. N., Liu, Y. G., Wang, Y. (2021): Response of bacterial community structure and diversity in sediment of arsenic-rich lakeside wetland to water level change. – *Environ Chem* 40(5): 1452-1463.
- [8] Huang, R., Zhao, D., Jiang, C., Wang, M. (2015): Heterogeneity of bacterial community compositions in surface sediments of three Lake zones in Lake Taihu. – *Proceedings of the National Academy of Sciences, India Section B: Biological Sciences* 85(2): 465-474.
- [9] Li, F., Li, M., Shi, W., Li, H., Sun, Z., Gao, Z. (2017): Distinct distribution patterns of proteobacterial nirK- and nirS-type denitrifiers in the Yellow River estuary, China. – *Can J Microbiol* 63(8): 708-718.
- [10] Liu, S., Ren, H., Shen, L., Lou, L., Hu, B. (2015): pH levels drive bacterial community structure in sediments of the Qiantang River as determined by 454 pyrosequencing. – *Front Microbiol* 6: 285.
- [11] Liu, Y. J. (2017): Response of soil microbial community structure and function to water condition change in Wetland. – Nanchang: Nanchang Univer.
- [12] Mentzer, J. L., Goodman, R. M., Balser, T. C. (2006): Microbial response over time to hydrologic and fertilization treatments in a simulated wet prairie. – *Plant Soil* 284(1): 85-100.

- [13] R Development Core Team (2017): R: A Language and Environment for Statistical Computing. – R Foundation for Statistical Computing: Vienna, Austria, 2017. Available online: <http://www.R-project.org/>.
- [14] Rees, G. N., Watson, G. O., Baldwin, D. S., Mitchell, A. M. (2006): Variability in sediment microbial communities in a semipermanent stream: impact of drought. – *J N Am Benthol Soc* 25(2): 370-378.
- [15] Shao, K., Gao, G., Wang, Y., Tang, X., Qin, B. (2013): Vertical diversity of sediment bacterial communities in two different trophic states of the eutrophic Lake Taihu, China. – *J Environ Sci* 25(6): 1186-1194.
- [16] Sun, X., Wang, Z., Zhao, C., Xu, L., Dong, Y. (2011): Impact assessment of saline-sodic agricultural drainage on water quality in vented area of Chagan Lake. – *Trans Chin Society Agricultu Eng* 27(9): 214-219.
- [17] Wan, Y., Bai, Y., He, J., Zhang, Y., Li, R., Ruan, X. (2017): Temporal and spatial variations of aquatic environmental characteristics and sediment bacterial community in five regions of Lake Taihu. – *Aqua Ecol* 51(3): 343-358.
- [18] Wang, N. F., Zhang, T., Yang, X., Wang, S., Yu, Y., Dong, L. L., Guo, Y. D., Ma, Y. X., Zang, J. Y. (2016a): Diversity and composition of bacterial community in soils and lake sediments from an arctic lake area. – *Front. Microbiol* 7. doi: 10.3389/fmicb.2016.01170.
- [19] Wang, J., Peng, J., Song, Y., Yuan, L., Shi, G. (2016b): Seasonal changes of microbial community distribution in sediments of hunhe river. – *Res Environ Sci* 29(2): 202-210.
- [20] Wang, P., Chen, B., Zhang, H. (2017): High throughput sequencing analysis of bacterial communities in soils of a typical Poyang lake wetland. – *Acta Ecologica Sin* 37(5): 1650-1658.
- [21] Wang, P., Xiao, H. Y., Zhang, H., Liu, J. Z. (2018): Bacterial communities in the estuarine sediment of Poyang Lake. – *China Environ Sci* 38(4): 1481-1489.
- [22] Xue, Y., Liu, F., Jiang, X., Geng, J., Teng, J., Xie, W., Chen, X. Y. (2018): The diversity of bacterial communities in the sediment of different lake zones of Lake Taihu in winter. – *China Environ. Sci* 38(2): 719-728.
- [23] Xue, Y. Q., Xu, F., Liu, K. H., Wang, J. Y., Zhu, L. P., Zhu, Z. H., Zhang, T. (2021): Non-point Source Pollution (NPSP) Induces Structural and Functional Variation of Bacterial Communities in Sediments of Jialing River. – *Environ Sci.* 43(5): 2595-2605.
- [24] Yang, H., Zhang, G. Z., Yang, X. N., Jian, L. I., Song, X. S., Wang, B. S. (2018): Microbial community of sediment in cellar water and its correlation with environmental factors. – *J Lanzhou Jiaotong Univer.* 37(3): 110-115.
- [25] Ye, W., Liu, X., Lin, S., Tan, J., Pan, J., Li, D., Yang, H. (2009): The vertical distribution of bacterial and archaeal communities in the water and sediment of Lake Taihu. – *FEMS Microbiol Ecol* 70(2): 263-276.
- [26] Yu, X., Zhang, P., Zhang, J., Chen, F., Yang, Y. (2020): Characteristics of distribution patterns of microbial biomass and community structures in the sediments from urban river. – *Acta Sci. Circumstantiae* 40: 585-596.
- [27] Zhang, X. (2016): Microbial community characteristics and microbial indicators evaluation study in fresh water sediment. – Shanghai: Shanghai Univer.
- [28] Zhang, Q. Q., Huang, X. R., Guo, X. Y. (2016): Analysis of the characteristics of rhizosphere bacterial diversity from plants with different water level gradients based on T-RFLP. – *Acta Ecologica Sin* 36: 4518-4530.
- [29] Zhang, H. X., Zheng, S. L., Wei, W. C., Wang, B. C., Wang, O. M., Liu, F. H. (2017): Effects of water conditions on the diversity of soil microbial communities in the coastal reed wetlands. – *Marine Sci* 41(5): 144-152.
- [30] Zhang, L., Zhao, T., Shen, T., Gao, G. (2019): Seasonal and spatial variation in the sediment bacterial community and diversity of Lake Bosten, China. – *J Basic Microbiol* 59(2): 224-233.