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# Bacterial community composition of the sediment in Sayram Lake, an alpine lake in the arid northwest of China

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## Abstract

Sediment bacterial communities play a critical role in biogeochemical cycling in alpine lake ecosystems. However, little is known about the sediment microbial communities in these lakes. In this study, the bacterial community composition (BCC) and their relationships with environmental factors of the sediment in Sayram Lake, the largest alpine and cold-water inland lake, China was analyzed using Illumina MiSeq sequencing. In total, we obtained 618,271 high quality sequences. The results showed that the bacterial communities with 30 phyla and 546 genera, were spread out among the 5 surface sediment samples, respectively. The communities were dominated by Proteobacteria, Acidobacteria, Planctomycetes, Gemmatimonadetes, Chloroflexi, Actinobacteria, Verrucomicrobia and Bacteroidetes, accounting for  $48.15 \pm 8.10\%$ ,  $11.23 \pm 3.10\%$ ,  $8.42 \pm 2.15\%$ ,  $8.37 \pm 2.26\%$ ,  $7.40 \pm 3.05\%$ ,  $5.62 \pm 1.25\%$ ,  $4.18 \pm 2.12\%$  and  $2.24 \pm 1.10\%$  of the total reads, respectively. At the genus level, the communities were dominated by *Aquabacterium*, *Pseudomonas*, *Woeseia*, *MND1*, *Ignavibacterium* and *Truepera*, accounting for  $7.89\% \pm 8.24\%$ ,  $2.32\% \pm 1.05\%$ ,  $2.14\% \pm 0.94\%$ ,  $2\% \pm 1.22\%$ ,  $0.94\% \pm 0.14\%$  and  $0.80\% \pm 0.14\%$  of the total reads, respectively. Statistical analyses showed the similarity of the sediment bacterial communities at our field sites was considerably low, far below 35%, and total organic carbon (TOC) was the dominant environmental factor affecting the spatial changes of BCC in the sediment. Thus, this study greatly improving our understanding of the microbial ecology of alpine lake in the arid and semi-arid ecosystems today so seriously threatened.

**Keywords** Sayram Lake, Surface sediment, BCC, TOC, Illumina Miseq sequencing

## Introduction

Sediment bacterial communities are a major constituent of lake ecosystems, where they play a critical role in in decomposition of organic matter and mineralization of nutrients [1]. Recently, lakes, especially those lakes in arid and semi-arid regions, have been described as early indicators of both regional and global environmental change, and bacteria are thought to be a sensitive sentinel to those environmental changes [2–4]. Therefore, within lake environments, investigation of the sediment bacterial community can provide important clues to understanding ecosystem processes.

Determining the bacterial diversity and community composition in different ecotype lakes is one of the

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necessary steps in understanding aquatic microbial ecology. The 16S ribosomal ribonucleic acid (rRNA) gene-based high-throughput sequencing now provide us with unprecedented access to the diversity and composition of lake bacterial community, and have enabled us to identify the numerically dominant species in these ecosystems and learn much about their distributions in time and space [5–7]. Most of our knowledge about lake BCC originates from investigations of lowland freshwater lake systems [8–12]. Only recently have similar studies from saline and hypersaline habitats been reported [13–16]. Indeed, very few studies of microbial ecology have been performed in alpine lakes, especially those in arid and semi-arid regions.

Arid and semi-arid regions compose around 33% of the world's land area, and in China the percentage is considerably higher, 52.5%. Lakes in these regions provide sparse, but valuable, water resources for human beings [17]. The Tianshan Mountains lie in Central Asia and extend over Xinjiang Uygur autonomous region, China, Kazakhstan, and Kirghizstan, with a total length of 2500 km, running east–west and a width ranging from 250 to 400 km [18]. Sayram Lake, in the arid northwest of China, is an alpine lake in the center of the Tianshan Mountains. Although there are detailed studies on water quality and paleolimnology of Sayram Lake, very little is known about the sediment bacterial communities inhabiting in the lake.

The present study is the first to use Illumina MiSeq sequencing of 16S rRNA for the sediment microbial

communities in Sayram Lake. Our aims were to: (i) characterize the BCC of the surface sediment in this alpine lake, (ii) determine which major environmental factor control the spatial changes of the sediment BCC.

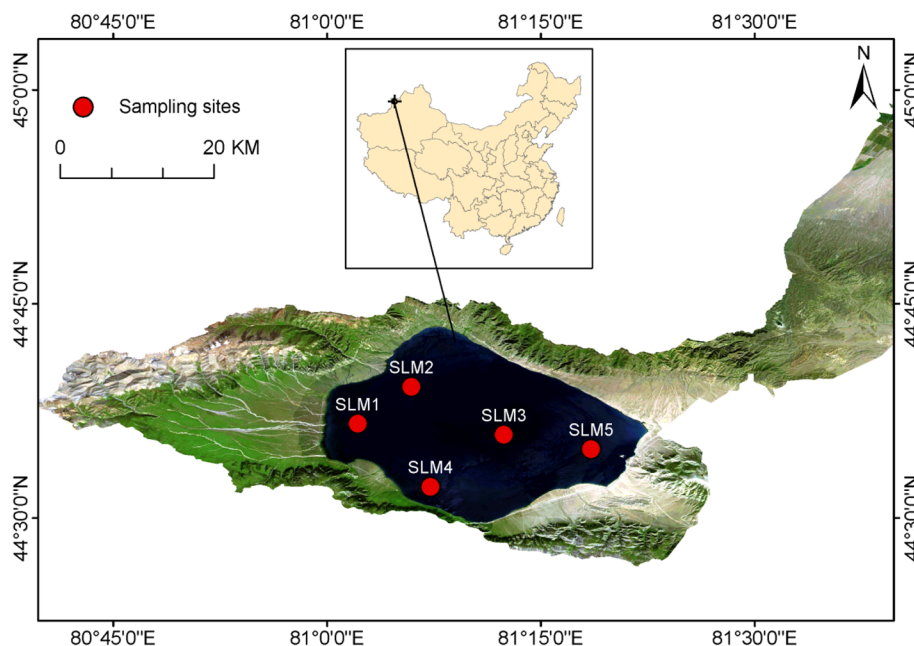
## Materials and methods

### Study area

Sayram Lake, is the largest alpine lake and the highest (2073 m above mean sea level) cold water inland lake in Xinjiang Uygur autonomous region, China (Fig. 1). The surface area of lake is 458 km<sup>2</sup>, water mean temperature is 1.1 °C and highest temperature is about 19 °C. Only a few small rivers flows into Sayram Lake and water input mainly originate from groundwater recharge [18]. Within the lake, we worked at 5 sampling sites — SLM1, SLM2, SLM3, SLM4, SLM5 (Fig. 1).

### Sampling and geochemistry measurements

Three surface sediment (0–2 cm), was collected with peterson sediment sampler, from each sampling sites on 16 August 2018. The pH was measured in situ with specific electrodes (REX, PHB-5, INESA, China). The salinity was measured on location by soil electrical conductivity meter (HI98331, HANNA, China). The sediment samples were immediately transferred into sterile plastic containers, and dried with a freeze dryer (LABCONCO, USA) in the laboratory. Total nitrogen (TN) was determined by the micro-Kjeldahl method and total phosphorus (TP) was measured by Mo-Sb colorimetric method. TOC



**Fig. 1** Map of Sayram Lake basin, China, showing the location of 5 sampling sites (SLM1, SLM2, SLM3, SLM4, SLM5)

content and C/N ratios were analyzed using an elemental analyzer (Vario EL III, Germany).

#### DNA extraction and Illumina Miseq sequencing

Sediment DNA was extracted from 0.5 g sample (dry weight) using the MoBio PowerSoil™ DNA isolation kit (MoBio Laboratories Inc, Carlsbad, CA, USA) following the instructions of the manufacturer. The V3-V4 hypervariable regions of the bacterial 16S rRNA genes were polymerase chain reaction (PCR) amplified using the primer set 338F (5'-ACTCCTACGGGAGGCAGCAG-3') and 806R (5'-GGACTACHVGGGTWTCTAAT-3') [19]. Equimolar amounts of barcoded amplicons for each sample were sequenced using the Illumina MiSeq platform by the Shanghai Personal Biotechnology (Co. Ltd.), China.

#### Sequences processing and analysis

The bioinformatic analysis was performed using the Microbial Genomics Module on CLC Genomics Workbench 20.0 (Qiagen, Aarhus C, Denmark). After importing raw reads, a standard quality control process was implemented, comprising merger paired reads (minimum overlap of 200 bp), trim off adapters and the primer sequences. Microbial phylotypes were assigned to operational taxonomic units (OTUs, 97% similarity). The low abundance OTUs (<10 reads) was filtered out for minimizing the random sequencing error. Taxonomic classification of the sequences was conducted using the SILVA small subunit rRNA (SSU) database v132 [20]. Sequences related with chimeras and chloroplast was excluded from subsequent analysis. The  $\alpha$ -diversity, including Shannon, Simpson, Chao1 and ACE indexes was analysed using the Mothur software (version 1.31.2).

#### Statistical analyses

The statistical analyses and the visualization were performed by Microsoft Excel. To evaluate the  $\beta$ -diversity (variation of community structures) among the 5 surface sediment samples, we performed cluster analysis and non-metric multidimensional scaling (NMDS) by using Bray–Curtis similarity based on distance matrix of bacterial community [21, 22]. To analyze the significant environmental variable associated with BCC, we carried out Canonical correspondence analysis (CCA) using CANOCO 5.0 (Microcomputer Power, Ithaca NY, USA).

## Results

### Physicochemical characteristics

The longitude and latitude of sampling sites, and the value for physicochemical parameters of the surface sediment in Sayram Lake is summarized in Table S1. The pH values for sediment ranged from 9.11 (SLM2) to 9.13

(SLM5), and salinity ranged from 2.538 ms/cm (SLM1) to 2.548 ms/cm ((SLM4). The contents of TN and TP for sediment ranged from 0.513% to 0.546%, 0.069% to 0.071%, respectively, with the lowest value found in site SLM2, and the highest in site SLM5. Sediment TOC content, and C/N ratio varied from 4.854 (SLM1) to 5.014% (SLM4), and 8.859 (SLM1) to 9.045 (SLM2), respectively.

### Bacterial $\alpha$ -diversity and $\beta$ -diversity

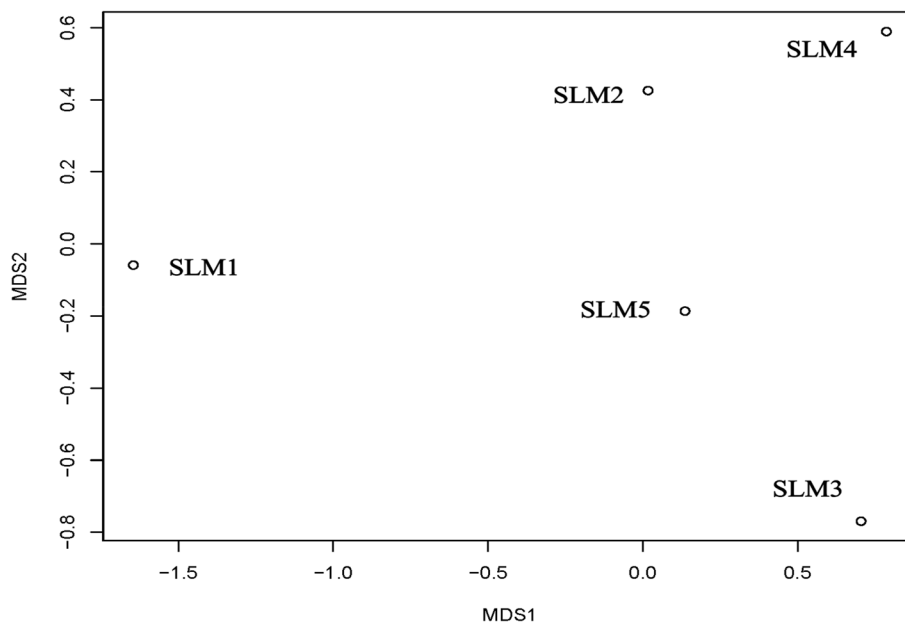
We generated 618,271 high-quality reads with a mean of 123,654 reads per sample. Across the 5 different surface sediment samples, the reads were classified into 2,486 OTUs. The rarefaction curves of Shannon index approached an asymptote after 1,500 reads (Fig. S1), indicating enough sequencing depth for further analysis. This was confirmed by the high Good's coverage, ranging from 98.90% to 99.53% (Table S2).

The bacterial  $\alpha$ -diversity patterns, including the Shannon, Simpson, Chao1 and ACE indexes were distinct among the 5 surface sediments, with the lowest value found in site SLM4, and the highest in site SLM1 (Table S2). For the Shannon and Simpson indices,  $\alpha$ -diversity (community diversity) ranged from 6.4535 to 7.5702, and 0.9516 to 0.9874, respectively. For the Chao-1 and ACE indices,  $\alpha$ -diversity (community richness) ranged from 732 to 904, and 495 to 634, respectively.

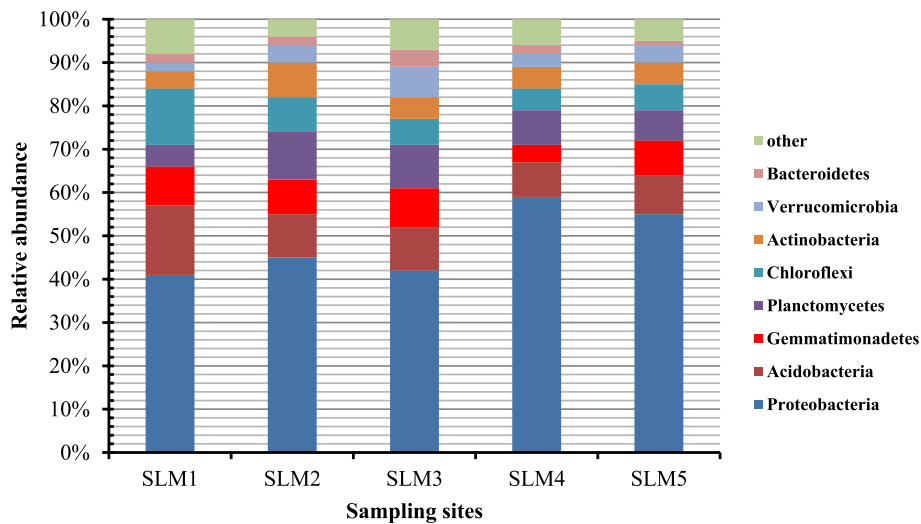
We investigated the spatial  $\beta$ -diversity patterns of the sediment bacterial communities by using NMDS. Notably, the sediment samples were scattered on the NMDS plot, suggesting low similarity of the sediment BCC among the 5 different sampling sites (Fig. 2).

### Bacterial taxonomy and community structure

In the Sayram lake sediment habitats, we detected a total of 30 different phyla: the dominant phyla (mean relative abundance  $\geq 2\%$ ) were Proteobacteria, Acidobacteria, Planctomycetes, Gemmatimonadetes, Chloroflexi, Actinobacteria, Verrucomicrobia and Bacteroidetes, accounting for  $48.15 \pm 8.10\%$ ,  $11.23 \pm 3.10\%$ ,  $8.42 \pm 2.15\%$ ,  $8.37 \pm 2.26\%$ ,  $7.40 \pm 3.05\%$ ,  $5.62 \pm 1.25\%$ ,  $4.18 \pm 2.12\%$  and  $2.24 \pm 1.10\%$  of the total reads, respectively (Fig. 3). At the genus level, we detected a total of 546 different genus: the 6 dominant genus (mean relative abundance  $\geq 0.8\%$ ) were *Aquabacterium*, *Pseudomonas*, *Woeseia*, *MND1*, *Ignavibacterium* and *Truepera*, accounting for  $7.89 \pm 8.24\%$ ,  $2.32 \pm 1.05\%$ ,  $2.14 \pm 0.94\%$ ,  $2\% \pm 1.22\%$ ,  $0.94 \pm 0.14\%$  and  $0.80 \pm 0.14\%$  of the total reads, respectively (Fig. 4). To determine in more detail the similarities of the bacterial communities in surface sediment, cluster analysis was carried out. The resulting dendrograms indicated the BCC among 5 different sediment samples is of low similarity, only with the similarities 20–35% (Fig. S2).



**Fig. 2** The NMDS plot based on the UniFrac weighted distance calculated from read numbers among the 5 sampling sites in Sayram Lake



**Fig. 3** The relative abundance of BCC at the phylum level in the surface sediment of Sayram Lake

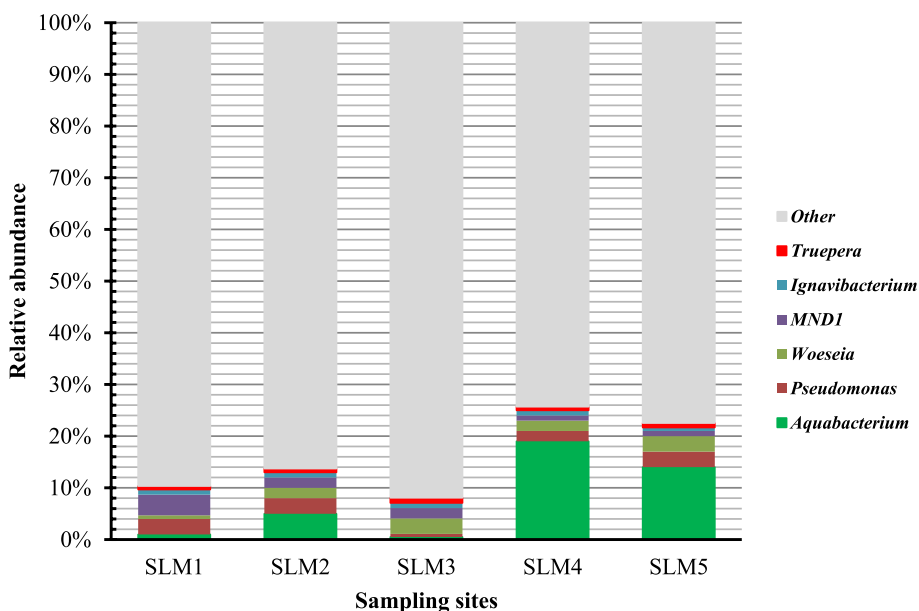
**Relationships of environmental factors and sediment bacterial communities**

We prepared a CCA biplot of the sediment BCC and the 6 environmental variables (TN, TP, pH, C/N, TOC and Salinity) for Sayram Lake (Fig. 5). The plot showed that TOC was the significant environmental variable affecting the spatial changes of BCC in the sediment. The eigenvalues of the first and second axis were 0.049 and 0.01, respectively, and these 2 axes explained 74.6% of the spatial variation in the BCC of the sediment.

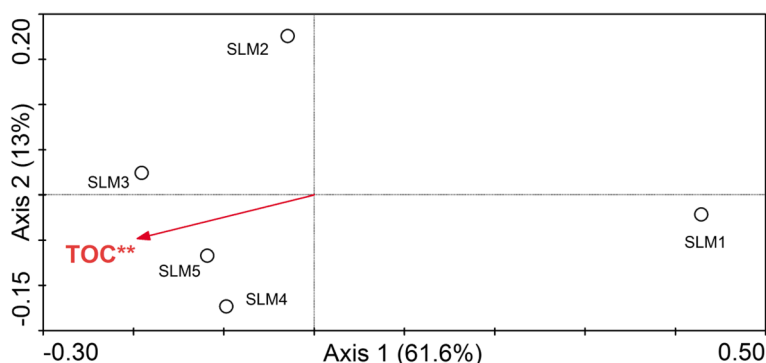
**Discussion**

**Sediment BCC in Sayram Lake**

In this study, we have shown that the dominant bacterial phylum in the Sayram Lake sediment habitats were Proteobacteria, Acidobacteria, Planctomycetes, Gemmatimonadetes, Chloroflexi, Actinobacteria, Verrucomicrobia, Bacteroidetes, and these phyla are found in the waters and sediments of other various lakes. It is known that Proteobacteria is the largest phylum of bacteria, and they might be involved in the functioning and



**Fig. 4** The relative abundance of BCC at the genus level in the surface sediment of Sayram Lake



**Fig. 5** The CCA biplot showed the relationship between environmental factors and sediment bacterial community. The statistically significant variable is marked with an asterisk (\*\*) according to a Monte Carlo permutation test ( $P < 0.01$ ). Abbreviations: TOC, Total organic carbon

processes of lake ecosystems [23, 24]. Proteobacteria was commonly observed in waters and sediments from other saline and alkaline lakes [25–28] and marine coastal waters [29]. Acidobacteria have the ability of their resistance to antibiotics, and can utilize a wide variety of simple and complex carbohydrates as substrates, and play important roles in the C, N and S biogeochemical cycles [30]. They were not only found in the saline and alkaline Qinghai Lake, China [31], but also dominated in 13 freshwater lakes sediment on the Yunnan Plateau, China [32]. Planctomycetes have the ability to degrade complex sulfated polysaccharides of algal origin [33, 34]. They are mainly characterized by an attached lifestyle, adhering to surfaces in the various environments include aquatic, extreme and polluted habitats [34]. Gemmatimonadetes

is a new phylum, is defined on a phylogenetic basis by comparative 16S rDNA sequence analysis of one isolated strain and uncultured representatives from multiple terrestrial and aquatic habitats [24]. They were found as the major components of sediment bacterial communities in 13 freshwater lakes on the Yunnan Plateau, China [32]. Chloroflexi was ubiquitous in the environment, and they were found in sediments of lakes [32, 35–37], and the hot springs in the Tibetan Plateau, China [38]. Actinobacteria was commonly a minor bacterial group or was even absent in lake sediment ecosystems [23, 35, 39, 40]. But Actinobacteria was also identified as the major components of sediment bacterial communities in 13 freshwater lakes on the Yunnan Plateau, China [32]. Verrucomicrobia are capable of degrading diverse polysaccharides [41]



and fixing nitrogen [42, 43]. They were also the major components of sediment bacterial communities in 13 freshwater lakes on the Yunnan Plateau, China [32]. Bacteroidetes was reported to be associated with nutrient conversion in lake sediments [44]. So far, previous studies reported the dominance of Bacteroidetes in freshwater lake sediment [36, 39], inland lakes [14, 16, 44] and estuaries [43, 45–47].

The dominant genus of Sayram Lake sediment were *Aquabacterium*, *Pseudomonas*, *Woeseia*, *MND1*, *Ignavibacterium*, and *Truepera*, and these genera also existed in other various environments. Previous study have showed that *Aquabacterium* dominated in the high arsenic groundwater, and *Pseudomonas* dominated in the high arsenic sediments of Hetao Plain of Inner Mongolia, China [48]. *Pseudomonas* was also found in sediments of saline Qinghai Lake [31], and Lake Chaka, a hypersaline lake on Tibetan plateau, China [49]. *Woeseia* has previously been reported to existed in offshore sediments from Shenzhen, China [50]. *Woeseia* and *Ignavibacterium* were also greatly enriched in saline–sodic soils, Northeast China [51]. Ya et al. [52] have indicated that *Ignavibacterium* was the putative keystone species, could be responsible for the deterioration of nitrogen removal under high salinity condition in wastewater treatment system. Furthermore, Shen et al. [53] have reported that the *MND1* was existed in petroleum-contaminated soils. In addition, *Truepera* has been found in environments as diverse as stone ruins at historic sites in Tamil Nadu, India [54], an iron tailing pond in northwest China [55] and composting distilled grain waste [56].

### Environmental factors governing sediment bacterial communities

Our CCA results suggested that TOC significantly influenced the bacterial community structure of the sediment in Sayram Lake, which is in agreement with previous studies of various environments. In Lake Chaohu, China, TOC has a significant effect on the BCC of two estuaries of this lake [57]. In Lake Bosten, China, TOC was the main environmental factor influencing the sediment bacterial community [38]. TOC was also the most important driving factor that determined the bacterial community in urban river sediments [57]. Furthermore, TOC concentration statistically explained the differences in the bacterial diversity and community composition within different sampling sites in the coastal aquaculture area [58]. Zhang et al. [59] have indicated that TOC plays an important role in shaping the microbial community structure in these groundwater systems in Qiji County, Yuncheng City, China. In addition, TOC was also the major factor in the open areas driving bacterial communities in water of the Xixi National Wetland Park, China [60]. Numerous

studies have shown that carbon, either organic carbon or inorganic carbon, is a necessary nutrient element for microorganisms and is one of the fundamental factors that structures microbial communities by controlling the growth and distribution of microorganism [59].

### Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s12866-023-02793-1>.

**Additional file 1: Table S1.** The longitude and latitude of sampling sites, and the value for physicochemical parameters of 5 surface sediments in Sayram Lake. **Table S2.** The OTU-based species diversity represented by 4  $\alpha$ -diversity indices and Goods coverage of 5 sediment samples in Sayram Lake. **Fig. S1.** Rarefaction curves for the different sediment samples analyzed using the Shannon diversity. **Fig. S2.** Sediment bacterial communities clustering generated from the 16S ribosomal ribonucleic acid (rRNA) gene-based Illumina MiSeq sequencing of 16S rDNA OTUs data (97% similarity).

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Not applicable.

### Authors' contributions

K.S. and J.C. conceived and designed the experiments, T.B. sampled sediments, L.Z. analyzed the data and prepared figures, K.S. wrote the main manuscript text, J.C. and G.G. revised the manuscript. All authors reviewed the manuscript. The author(s) read and approved the final manuscript.

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### Availability of data and materials

The raw sequencing data in our study have been deposited at the Sequence Read Archive database of the National Center for Biotechnology Information (NCBI) with the BioProject accession number PRJNA888417 (GenBank BioSample identifier; SLM1, SAMN31217440; SLM2, SAMN31217441; SLM3, SAMN31217442; SLM4, SAMN31217443; SLM5, SAMN31217444).

### Declarations

#### Ethics approval and consent to participate

Not applicable.

#### Consent for publication

Not applicable.

#### Competing interests

The authors declare no competing interests.

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