

Original Research

Bacterial Community Structure and Diversity in the Surface Water of a Plateau Lake, Yangzonghai, China

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Abstract

To guide the ecological management of lake water resources, this study aimed to investigate the bacterial community structure in the surface water of different zones of Lake Yangzonghai and its correlation with physicochemical factors. Water samples were collected from various sampling points, and SPSS (Statistical Package for the Social Sciences) was used to analyze the spatial differences in physicochemical parameters. Simultaneously, 16S rRNA gene high-throughput sequencing was employed to analyze bacterial diversity and community structure. The results showed that the physicochemical factors of the water body exhibited significant spatial heterogeneity, with the Oxidation-Reduction Potential (ORP) gradient being the most prominent (Yangzong River > South Yangzonghai > Central Yangzonghai > North Yangzonghai). Bacterial diversity indices reached the highest levels in the Central Yangzonghai zone. The dominant bacterial phyla in the surface water were Actinobacteriota (34.63%), Bacteroidota (33.79%), and Proteobacteria (27.29%). Correlation analysis revealed that Campylobacterota (at the phylum level) and *Flavobacterium*, *Limnohabitans*, and *Pseudarcicella* (at the genus level) were all highly significantly correlated with Dissolved Oxygen (DO) and Total Phosphorus (TP). Overall, the environmental factors (ORP, DO, and TP) in the different water zones of Lake Yangzonghai exerted a significant selective driving effect on the bacterial community structure and diversity.

Keywords: plateau lake, Yangzonghai lake, bacteria, community structure, diversity

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Introduction

Global research in lake microbial ecology now focuses on functional analysis and biogeographical integration, aiming to accurately elucidate bacterial community structure and the underlying mechanisms driven by environmental factors. Currently, international studies primarily utilize 16S rRNA gene high-throughput sequencing to profile community composition. However, technological advances now include metagenomics and metatranscriptomics, enabling the investigation of microbial metabolic functions and gene expression activity in the carbon, nitrogen, and phosphorus cycles [1, 2]. Regarding environmental driving mechanisms, research focuses on the selective pressure exerted by key physicochemical factors, such as Dissolved Oxygen (DO), Total Phosphorus (TP), and Oxidation-Reduction Potential (ORP), on bacterial communities. These factors directly determine microbial niche partitioning and significantly influence the distribution of anaerobic and aerobic respiratory groups [3, 4]. For instance, Actinobacteriota, Bacteroidota, and Proteobacteria are widely recognized as core dominant phyla; the genus *Flavobacterium* often serves as an indicator of organic matter degradation, and certain Campylobacterota groups may signal specific water quality anomalies [5]. Furthermore, current research transcends simple correlation by integrating microbial biogeography principles and GIS technology. This approach aims to quantify the relative contributions of environmental heterogeneity and dispersal limitation to spatial variation in lake bacterial communities, enabling the construction of accurate predictive models linking environment, microbial communities, and ecological function [6]. However, due to the high regional specificity of lake microbial communities, the universality of international conclusions – despite providing valuable theoretical frameworks – requires validation and refinement in lakes with unique physicochemical and hydrological characteristics, such as Lake Yangzonghai. As an important freshwater lake in China, Lake Yangzonghai is significantly impacted by regional human activities. Moreover, the considerable gradient differences in ORP, DO, and TP across its various zones (e.g., lake center, nearshore, river mouth) present a complex selective effect on microbial communities. Therefore, in-depth quantitative research focusing on the bacterial community structure and its association with spatially heterogeneous physicochemical factors in the surface water of Lake Yangzonghai is fundamentally necessary. This research will define the lake's ecological health status, trace pollution sources, and provide a scientific and precise theoretical basis for local water resource management.

The Nine Plateau Lakes (>30 km²) in Yunnan Province are a crucial ecological functional area in Southwest China, playing a significant role in regional economic and social development [7]. Lake Yangzonghai, one of these nine plateau lakes, is a deep

freshwater lake within the Nanpan River system of the Pearl River Basin, featuring an average annual temperature of 14.5°C and average annual precipitation of 963.5 mm. At an average water level of 1,770.6 m, the lake covers an area of 31.7 km², spanning 12 km (N-S) and 2.7 km (E-W). Its maximum depth is 30 m, with a storage capacity of 6.04×10⁸ m³ and a watershed area of 192 km² [2]. The main inflows are the Yangzong River and the Qili River in the south, supplemented by intermittent streams on the east and west sides. The sole outlet is Tangchi, located in the northeast [8], and it is primarily recharged by groundwater [9]. As a vital component of the upper Pearl River, Lake Yangzonghai plays a crucial role in preserving biodiversity and maintaining the ecological security pattern of the region [10]. However, increased human activity has compromised Lake Yangzonghai's water quality, notably due to the 2008 arsenic contamination incident, which severely impacted the ecological security of the lake basin [11]. While extensive research has focused on microbial community structure variations in the sediments of Lake Yangzonghai, reports detailing these characteristics in the surface water are sparse [12, 13]. Therefore, this study aims to analyze the physicochemical factors, bacterial diversity, and community structure of the surface water. Specifically, the goals are to determine the distribution characteristics of the bacterial community, identify dominant taxa, and clarify the main environmental factors influencing the community structure. The results will provide valuable reference and guidance for the protection and management of the Lake Yangzonghai ecosystem.

Materials and Methods

Study Site

The study site is located in the Yangzonghai Scenic Area, Yiliang County, Kunming, Yunnan Province, 24°01'–24°58' N, 102°59'–103°02' E.

Sample Collection and Processing

A total of four sampling sites were established for this study: YZN, YZM, YZS, and YZDH (coordinates listed in Table 1). Sampling was conducted on August 15, 2025. This period corresponds to the wet season of the Yunnan-Guizhou Plateau, characterized by high precipitation and relatively high water temperatures, during which the lake typically exhibits thermal stratification. Sampling was carried out from north to south, commencing at site YZN. At each site, three replicate samples were collected. The surface water samples from each site were mixed to form a composite sample, transferred into 10 L white plastic buckets, stored in a portable cooler box at low temperature, and transported to the laboratory within 1 hour for the determination of physicochemical factors.

Table 1. Coordinates of sampling sites.

Sampling Site	Central Longitude	Central Latitude
YZN	103.01298204	24.94576633
YZM	103.00040769	24.89029096
YZS	102.99118104	24.86705819
YZDH	102.99359101	24.86032686

Note: YZN: Yangzong Lake North, YZM: Yangzong Lake Middle, YZS: Yangzong Lake South, YZDH: Yangzong DAHE.

In-situ measurements for water pH, Oxidation-Reduction Potential (ORP), and Dissolved Oxygen (DO) were conducted using a portable water quality analyzer (DREL1900). Ammonia nitrogen ($\text{NH}_3\text{-N}$) concentration was determined via Nessler's reagent spectrophotometry (HJ 535-2009). Total Phosphorus (TP) concentration was determined using ammonium molybdate spectrophotometry (GB/T 11893-89). Total Nitrogen (TN) concentration was measured by alkaline potassium persulfate digestion UV spectrophotometry (HJ 636-2012). The concentration of Arsenic (As) was determined using Inductively Coupled Plasma Mass Spectrometry (ICP-MS).

Microbial Sequencing

Surface water samples were collected from four sites to determine bacterial abundance and diversity, with three replicates per site. High-throughput sequencing was conducted by Guangdong Giduo Biotechnology Co., Ltd. (Guangzhou, China). Genomic DNA was extracted, and the V3-V4 regions of the 16S rRNA gene were amplified using barcoded primers. Sequencing libraries were constructed following standard Illumina protocols. Sequencing was performed on an Illumina HiSeq 2500 platform (PE250 mode) to analyze the bacterial community structure.

Data Analysis

Data were processed using Microsoft Excel 2021 (Microsoft Corp., USA). Results are presented as

mean $\pm$ standard deviation (SD). Spearman correlation analysis and significance testing were performed using SPSS (Statistical Package for the Social Sciences) 25.0 (SPSS Inc., Chicago, IL, USA). Figures were generated using Origin 2019 (OriginLab Corp., Northampton, MA, USA). Total Nitrogen (TN) concentration was measured by alkaline potassium persulfate digestion UV spectrophotometry (HJ 636-2012). For Arsenic (As) determination, water samples were filtered through a 0.45 μm membrane and acidified with nitric acid (HNO_3) to pH<2 for preservation. The concentration of As was then determined using Inductively Coupled Plasma Mass Spectrometry (ICP-MS).

Results

Physicochemical Properties of Surface Water

Surface water pH values followed the order: YZN > YZS > YZDH > YZM, with no significant differences among sites ($P>0.05$). Concentrations of Dissolved Oxygen (DO), Total Nitrogen (TN), and Total Phosphorus (TP), as well as temperature, were highest at site YZDH. Conversely, the lowest values for DO, temperature, and TP were recorded at site YZM. Site YZN exhibited the lowest TN concentration but the highest Ammonia Nitrogen ($\text{NH}_3\text{-N}$) concentration.

Arsenic (As) concentrations were highest at YZM and lowest at YZN, following the trend: YZM > YZDH > YZS > YZN. The Oxidation-Reduction Potential (ORP) peaked at site YZDH, showing significantly higher values compared to YZM, YZS, and YZN ($P<0.05$). The lowest ORP was observed at site YZN (Table 2).

Bacterial Community Structure and Composition in the Overlying Water of Lake Yangzonghai

A total of 1,937,340 high-quality sequences were obtained from the water samples, with an average of 80,722 sequences per sample. The total number of Operational Taxonomic Units (OTUs) detected was 18,352. Venn diagram analysis (Fig. 1) showed that 743 OTUs were shared among all sampling sites. The number of unique OTUs identified at sites YZN, YZM, YZS,

Table 2. Analysis of differences in physicochemical properties of the samples.

Samples	pH	ORP	DO	T	$\text{NH}_3\text{-N}$	TP	TN	As
YZN	8.275 $\pm$ 0.26a	-83.06 $\pm$ 3.25c	0.86 $\pm$ 0.02a	18.06 $\pm$ 1.84a	0.58 $\pm$ 0.29a	0.04 $\pm$ 0.02a	0.84 $\pm$ 0.40a	23.44 $\pm$ 6.65a
YZM	8.075 $\pm$ 0.24a	137.8 $\pm$ 3.91b	0.85 $\pm$ 0.06a	17.60 $\pm$ 1.58a	0.44 $\pm$ 0.18a	0.03 $\pm$ 0.01a	0.87 $\pm$ 0.38a	27.34 $\pm$ 8.16a
YZS	8.093 $\pm$ 0.07a	112.4 $\pm$ 35.24b	0.87 $\pm$ 0.11a	18.20 $\pm$ 1.60a	0.48 $\pm$ 0.14a	0.04 $\pm$ 0.01a	0.97 $\pm$ 0.35a	25.06 $\pm$ 7.24a
YZDH	8.093 $\pm$ 0.15a	199 $\pm$ 5.86a	0.91 $\pm$ 0.12a	18.96 $\pm$ 1.41a	0.34 $\pm$ 0.06a	0.05 $\pm$ 0.01a	0.98 $\pm$ 0.27a	26.05 $\pm$ 7.06a

Note: YZN: Yangzong Lake North, YZM: Yangzong Lake Middle, YZS: Yangzong Lake South, YZDH: Yangzong DAHE, ORP: Oxidation-Reduction Potential, DO: Dissolved oxygen, T: Temperature, As: Arsenic, TP: Total phosphorus, $\text{NH}_3\text{-N}$: Ammonia nitrogen, TN: Total Nitrogen.

Table 3. Analysis of bacterial alpha diversity indices.

Group	Sobs	Chao	Shannon	Simpson
YZN	2054.5±329.67ab	2385.04±352.01ab	6.37±0.73a	0.916±0.04b
YZM	2386.83±468.14a	2609.46±542.66a	6.92±0.27a	0.956±0.01a
YZS	1800±253.02b	2021.75±279.41b	6.74±0.37a	0.951±0.01a
YZDH	2110.83±389.98ab	2414.59±433.39ab	6.49±0.33a	0.941±0.01ab

Note: YZN: Yangzong Lake North, YZM: Yangzong Lake Middle, YZS: Yangzong Lake South, YZDH: Yangzong DAHE.

and YZDH was 593, 1,575, 792, and 1,064, respectively. Alpha diversity was evaluated using the Sobs (observed species), Chao1, Shannon, and Simpson indices. The Sobs index represents the number of observed OTUs; a higher value indicates greater species richness. Species richness in the overlying water at YZM was the highest and was significantly higher than that at YZS ($P<0.05$). The Chao1 index reflects bacterial community richness, with higher values indicating greater richness. Community richness at YZM was the highest, exceeding that of YZN and YZDH, and was significantly higher than that of YZS ($P<0.05$). The Simpson and Shannon indices reflect both species richness and evenness. In this study, both indices followed the order: $YZM > YZS > YZDH > YZN$. However, no significant differences were observed among the sampling sites ($P>0.05$) (Table 3).

Analysis of Bacterial Community Structure in the Surface Water of Lake Yangzonghai

At the phylum level, the top 10 bacterial phyla by relative abundance in the surface water of Lake Yangzonghai (Fig. 2) were Actinobacteriota, Bacteroidota, Proteobacteria, Cyanobacteria, Verrucomicrobiota, Patescibacteria, Chloroflexi,

Campylobacterota, Planctomycetota, and Firmicutes.

Actinobacteriota was the most abundant phylum in the surface water at sites YZN, YZS, and YZDH, with relative abundances ranging from 33.56% to 37.71%. In contrast, Bacteroidota was the dominant phylum in the surface water at site YZM, reaching a relative abundance of 33.79%.

At the genus level, the top 10 bacterial genera by relative abundance (Fig. 3) were *hgclb_clade*, *CL500-29_marine_group*, *Flavobacterium*, *Acinetobacter*, *Terrimonas*, *Cylindrospermopsis*, *CRJ1*, *Sediminibacterium*, *Prochlorothrix* PCC-9006, *Limnohabitans*, and *Pseudarcicella*.

The most abundant genus in the surface water at sites YZN and YZS was *hgcl_clade*, reaching a relative abundance of 37.56%. At site YZM, the dominant genus was *Flavobacterium*, with a relative abundance of 42.02%. At site YZDH, *CL500-29_marine_group* was the most abundant genus in the surface water, reaching 28.57%.

Beta diversity analysis revealed that the bacterial community structure in the surface water at YZM was distinctly different from that at other sampling sites (Fig. 4). Furthermore, ANOSIM and ADONIS tests confirmed significant differences in bacterial community structure among the sampling groups ($P<0.05$).

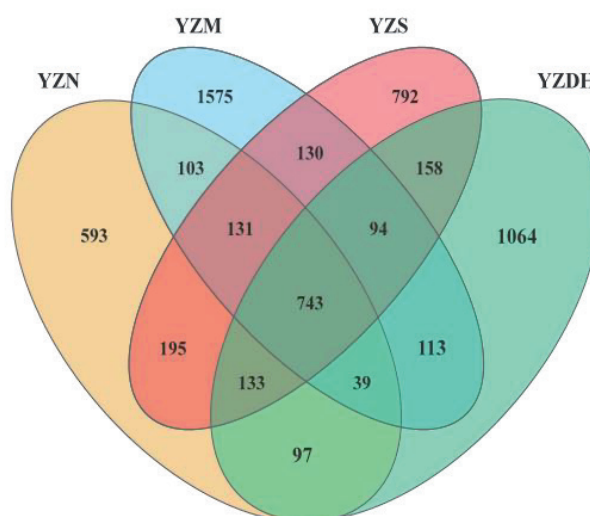


Fig. 1. Venn diagram of species distribution.

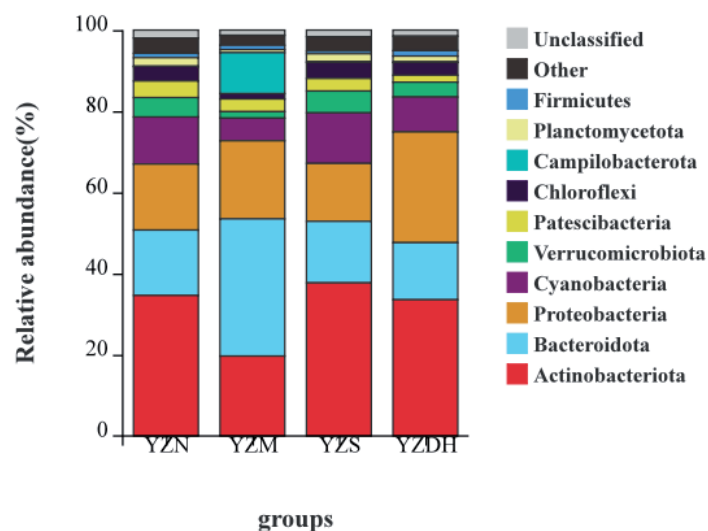


Fig. 2. Bacterial community composition at the phylum level in the surface water. Abbreviations: YZN, Yangzonghai North; YZM, Yangzonghai Middle; YZS, Yangzonghai South; YZDH, Yangzong River (Yangzong Dahe).

Correlation Analysis between Environmental Factors and Bacterial Diversity

Correlations were observed between environmental factors in the surface water and bacterial diversity indices (Fig. 5 and Fig. 6). Specifically, Arsenic (As) showed a significant positive correlation with the Sobs index. Total Phosphorus (TP) was negatively correlated with the Sobs, Chaol, Shannon, and Simpson indices. Ammonia Nitrogen $\text{NH}_3\text{-N}$ and Total Nitrogen (TN) were negatively correlated with the Sobs and Chaol indices but positively correlated with the Shannon and Simpson indices.

At the genus level (Fig. 7), *hgcI*_clade, *Cylindrospermopsis*_CRJ1, CL500-29_marine_group, *Terrimonas*, and *Prochlorothrix*_PCC-9006 were negatively correlated with pH, T, DO, and As, but positively correlated with ORP, $\text{NH}_3\text{-N}$, TN, and TP. *Sediminibacterium* showed negative correlations with pH, T, DO, As, and ORP, while showing positive correlations with $\text{NH}_3\text{-N}$, TN, and TP. *Acinetobacter* was negatively correlated with pH, T, DO, As, ORP, $\text{NH}_3\text{-N}$, and TN, but positively correlated with TP. In contrast, *Flavobacterium*, *Limnohabitans*, and *Pseudarcicella* were positively correlated with pH, T, DO, As, and ORP, but negatively correlated with $\text{NH}_3\text{-N}$, TN, and TP.

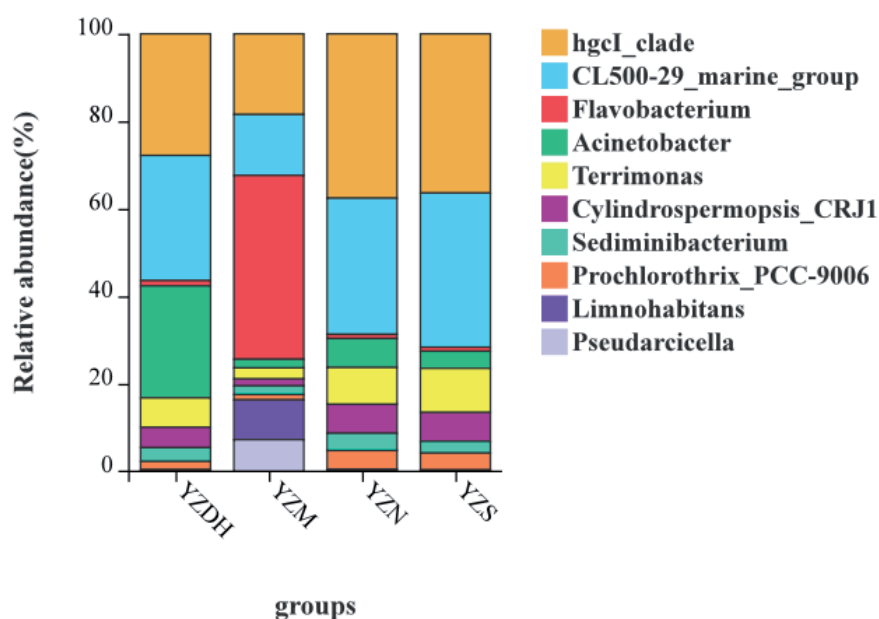


Fig. 3. Stacked bar chart of bacterial community composition at the genus level in the surface water. Abbreviations: YZN, Yangzonghai North; YZM, Yangzonghai Middle; YZS, Yangzonghai South; YZDH, Yangzong River (Yangzong Dahe).

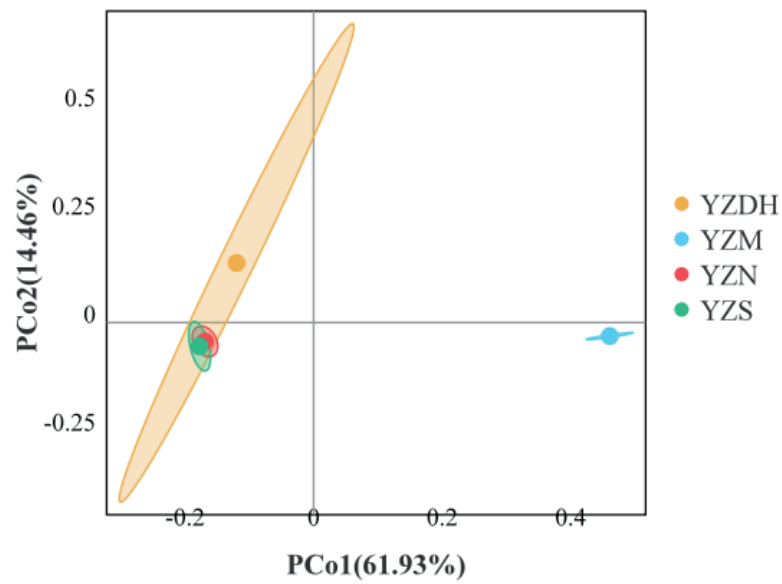


Fig. 4. Principal Component Analysis (PCA) of bacterial community structure in the samples. Abbreviations: YZN, Yangzonghai North; YZM, Yangzonghai Middle; YZS, Yangzonghai South; YZDH, Yangzong River (Yangzong Dahe).

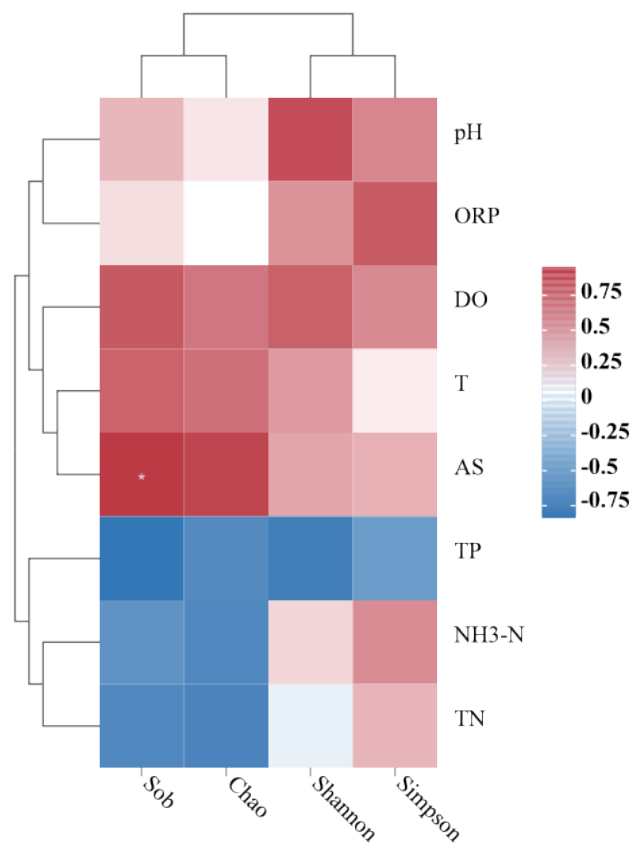


Fig. 5. Correlation analysis between environmental factors and bacterial alpha diversity. Abbreviations: ORP, Oxidation-Reduction Potential; DO, Dissolved Oxygen; T, Temperature; AS, Arsenic; TP, Total Phosphorus; NH₃-N, Ammonia Nitrogen; TN, Total Nitrogen. Asterisks indicate statistical significance: *P<0.05, **P<0.01.

Notably, *Flavobacterium*, *Limnohabitans*, and *Pseudarcicella* exhibited a highly significant positive correlation with DO (P<0.001) and a highly significant

negative correlation with TP (P<0.001).

Discussion

Physicochemical Variations in the Surface Water of Lake Yangzonghai

Oxidation-Reduction Potential (ORP) serves as a key indicator of the redox status in media such as water and soil [14, 15]. Generally, an ORP > 0 mV indicates an

oxidative environment, while an ORP < 0 mV indicates a reductive one [16]. In this study, the surface water at site YZN exhibited an ORP of <0 mV, indicating a reductive environment. This is primarily attributed to iron release from sediments, a process known to lower ORP values [17]. Additionally, ORP is influenced by factors such as water temperature, pH, and dissolved oxygen (DO) [18]; specifically, increases in pH or temperature can lead to

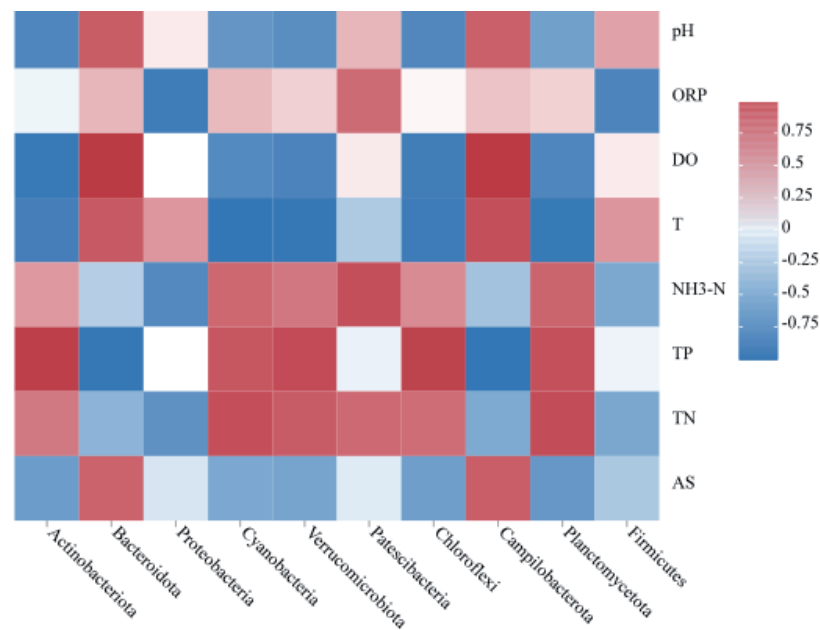


Fig. 6. Correlation analysis between environmental factors and bacterial community structure at the phylum level in water samples. Abbreviations: ORP, Oxidation-Reduction Potential; DO, Dissolved Oxygen; T, Temperature; As, Arsenic; TP, Total Phosphorus; NH₃-N, Ammonia Nitrogen; TN, Total Nitrogen. Statistical significance is indicated by asterisks: *P<0.05, **P<0.01.

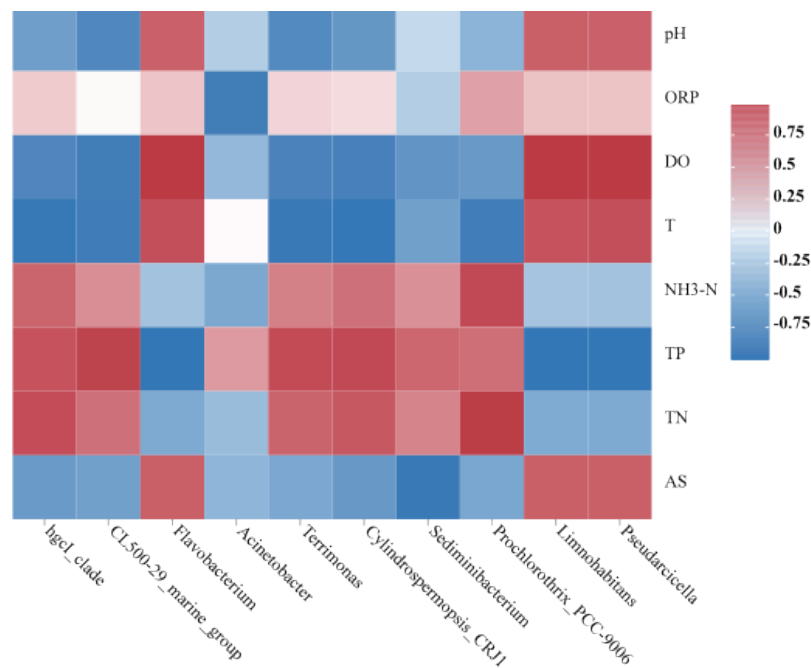


Fig. 7. Analysis of environmental factors and bacterial community structure at the genus level in water samples. Abbreviations: ORP, Oxidation-Reduction Potential; DO, Dissolved Oxygen; T, Temperature; As, Arsenic; TP, Total Phosphorus; NH₃-N, Ammonia Nitrogen; TN, Total Nitrogen. Statistical significance is indicated by asterisks: *P<0.05, **P<0.01.

decreased ORP [19, 20]. Thermal discharge from the power plant on the northern shore may also contribute to the observed ORP variations [21]. Site YZM exhibited the lowest DO content and water temperature, likely because Lake Yangzonghai reaches its maximum depth at this location, a finding consistent with vertical physicochemical variations reported in Lake Fuxian and Lake Zurich [22, 23].

Bacterial Diversity and Community Structure

Bacterial alpha-diversity reflects both species abundance and community complexity. In this study, diversity indices at YZM were significantly higher than at other sites, suggesting a richer and more complex community structure [4]. Bacterial alpha-diversity is closely linked to anthropogenic impact; for instance, Wang et al. found that tourism development in wetland parks can reduce diversity indices [24, 25]. Located in the lake center, site YZM is subject to less anthropogenic disturbance. Furthermore, as the deep-water zone, YZM is characterized by a larger water volume and greater environmental stability compared to littoral areas. This hydrological stability buffers against rapid fluctuations in environmental factors, which, combined with reduced human interference, likely accounts for its higher diversity.

At the phylum level, the dominant bacterial taxa included Actinobacteriota, Bacteroidota, Proteobacteria, and Cyanobacteria, which are also predominant in arsenic-contaminated water bodies [26, 27]. The relative abundance of Actinobacteriota is typically higher in deep lakes [28]; its prevalence in Lake Yangzonghai may be attributed to its small cell size and high efficiency in utilizing low-concentration nutrients [29]. The phylum Proteobacteria comprises numerous ubiquitous autotrophic and heterotrophic bacteria, and both Proteobacteria and Bacteroidota are widely distributed in lacustrine environments [30]. Cyanobacteria, capable of photosynthesis and nitrogen fixation, were also frequently detected, aligning with previous findings in reservoirs and lakes [31, 32].

At the genus level, *hgcI*_clade, CL500-29_marine_group, and *Flavobacterium* exhibited relatively high abundances. *hgcI*_clade contributes to carbon (C) and nitrogen (N) cycling, thereby improving water quality, and is considered a persistent microorganism in global oligotrophic aquatic ecosystems [33, 34]. Consistent with our results, *hgcI*_clade has been identified as a dominant genus in diverse aquatic environments [35, 36]. The CL500-29_marine_group, also belonging to Actinobacteriota, plays a dominant role in water quality evolution and shares similar spatiotemporal trends with *hgcI*_clade [37-40]. *Flavobacterium* is a denitrifying bacterium capable of degrading high-molecular-weight compounds (e.g., proteins, carbohydrates, lipids) [41], facilitating nitrogen and phosphorus removal. This pattern mirrors findings in Lake Taihu and Lake Liangzi [42, 43].

Environmental Drivers of Community Structure: Insights from Niche Theory

Actinobacteriota and Chloroflexi were positively correlated with $\text{NH}_3\text{-N}$, TP, and TN. Since phosphorus (P) and nitrogen (N) are essential nutrients for bacterial metabolism, the availability of these nutrients is a prerequisite for growth [44]. Conversely, these phyla showed a negative correlation with Arsenic (As), likely because heavy metals induce reactive oxygen species (ROS) production, causing bacterial toxicity [45].

Environmental factors, including pH, ORP, temperature, DO, TN, TP, and heavy metals, are primary drivers of bacterial community variation in lake ecosystems [46-48]. In this study, *Flavobacterium*, *Limnohabitans*, and *Pseudarcicella* showed highly significant correlations with DO and TP ($P < 0.001$). As dominant genera within Proteobacteria and Bacteroidota, they are significantly affected by TP [49, 50]. Furthermore, these genera participate in organic matter decomposition and nutrient cycling [51, 52]. Given that these aerobic heterotrophs consume oxygen during decomposition, their abundance is tightly coupled with DO levels, explaining the observed significant correlation.

PCoA results indicated significant differences in bacterial community structure between YZM and other sites. This divergence is likely driven by variations in hydrological conditions and environmental factors, such as the significantly lower DO and water temperature at YZM [53, 54].

The Decoupling of ORP and DO at Site YZN

Typically, surface water exhibits positive ORP values due to direct atmospheric reaeration. However, site YZN presented a distinct anomaly with a negative ORP (-83.06 mV) despite maintaining a detectable, albeit hypoxic, DO level (0.86 mg/L). This “mismatch” between DO and ORP indicates a non-equilibrium redox state driven by specific local pollution sources. The primary driver is likely the thermal discharge from the adjacent power plant. Beyond merely elevating temperature, the discharge effluent may introduce reductive chemical constituents or induce localized hydraulic scouring that resuspends reduced compounds (e.g., sulfides, ferrous iron) from the sediment. These strong reducing agents can drastically lower the redox potential even when trace dissolved oxygen is still present, effectively overriding the oxidizing potential of oxygen and creating a localized reductive environment in the surface layer.

Environmental Drivers of Spatial Variation in Microbial Community Structure

PCoA results revealed a distinct spatial separation in bacterial community structure between YZM and other sites. This variation stems largely from environmental

gradients (e.g., lower DO and temperature at YZM) [53, 54], highlighting the dominance of deterministic environmental filtering in shaping community assembly. In this study, spatial heterogeneity in ORP and TP exerted strong environmental selection pressure. For instance, the low-ORP, reductive environment at YZN likely selected for taxa with facultative anaerobic or reductive metabolic potential. Conversely, high-TP zones favored taxa capable of efficient phosphate utilization and organic matter decomposition, such as *Flavobacterium*. This environmental heterogeneity drives the structural divergence between YZM and nearshore sites. Rather than stochastic dispersal, the distinct physicochemical properties of the deep-water zone (YZM) compared to the river-influenced nearshore areas create unique ecological niches, suggesting that environmental filtering acts as the primary mechanism governing the observed biogeographical patterns in Lake Yangzonghai.

Correlation between Arsenic and Bacterial Richness

Unexpectedly, a significant positive correlation was observed between As concentration and bacterial richness (Sobs index), with site YZM exhibiting the highest levels of both. While heavy metal accumulation is typically associated with reduced microbial diversity due to toxicity, this finding may be explained by the Intermediate Disturbance Hypothesis (IDH). The As concentrations at YZM, while elevated relative to other sites, likely represent a moderate environmental pressure rather than a lethal threshold. According to IDH, such moderate disturbance can prevent competitive exclusion by dominant species, thereby allowing a wider range of taxa – including both As-tolerant and generalist species – to coexist. Furthermore, the high diversity at YZM is likely reinforced by its hydrological stability; as the deep-water center of the lake, YZM experiences fewer physical fluctuations (e.g., temperature changes or turbulence) compared to littoral zones. This environmental stability may act as a buffer against chemical stress, providing a stable niche that supports a complex and diverse planktonic community despite the presence of Arsenic.

Conclusions

Through multidimensional analysis, this study systematically characterized the ecological features and environmental drivers of the bacterial community in the surface water of Lake Yangzonghai, a plateau lake. Results revealed significant spatial heterogeneity in the lake's physicochemical environment. Notably, Oxidation-Reduction Potential (ORP) exhibited distinct spatial gradients. Low ORP in nearshore areas was linked to sediment iron release, thermal discharge-

induced warming, and pH variations, highlighting complex biochemical reduction processes.

Regarding microbial diversity, the lake center (YZM) exhibited the highest alpha-diversity due to minimal anthropogenic disturbance, underscoring the negative impact of human activities on the micro-ecosystem's health. Community composition analysis identified Actinobacteriota, Bacteroidota, and Proteobacteria as core dominant taxa, forming the backbone of the microbial community. Further analysis at the genus level identified freshwater-specific dominant taxa such as *hgcl_clade* and *CL500-29_marine_group*. These taxa contribute to the material cycling stability under oligotrophic conditions by efficiently utilizing low-concentration nutrients. Concurrently, the high abundance of denitrifying bacteria, such as *Flavobacterium*, indicates an active potential for nitrogen and phosphorus degradation.

Crucially, this study identified Dissolved Oxygen (DO) and Total Phosphorus (TP) as the core environmental drivers of bacterial community structure. Correlation analysis revealed that indicator taxa – including *Campylobacterota* (phylum) and *Flavobacterium*, *Limnohabitans*, and *Pseudarcicella* (genera) – were highly sensitive to DO and TP variations. This confirms the strong selective pressure exerted by nutrient loading and redox status, while suggesting the pivotal role of these taxa in organic matter decomposition and oxygen consumption.

In conclusion, this study elucidates the environmental filtering mechanisms governing bacterial community assembly in Lake Yangzonghai. It provides critical scientific support for water quality assessment, eutrophication warning systems, and the development of regionalized, targeted ecological management strategies.

Acknowledgments

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AI Usage Disclosure Statement

During the preparation of this work, the authors used OpenAI ChatGPT using the GPT-5.5 model solely to translate portions of the authors' original text into English and to improve English grammar, clarity, readability, and linguistic flow. The AI tool was not used to generate research ideas, data, analyses, results, references, figures, tables, scientific interpretations,

or conclusions. All AI-assisted text was critically reviewed, edited, and verified by the authors, who take full responsibility for the content of the publication.

Conflict of Interest

The authors declare no conflict of interest.

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