

Spatiotemporal Variations in Water Quality and Bacterial Communities in the Jiaoxi River After Reservoir Impoundment and Their Driving Factors

Peng Zhang, Hao Gong, Xiuyu Zong

Shaanxi Modern Architectural Design and Research Institute Co, Ltd, Xi'an, Shaanxi, China

Abstract: Reservoir impoundment alters the hydrodynamic conditions and nutrient distribution in rivers, thereby affecting bacterial community composition and ecosystem function. Investigating the spatiotemporal response patterns of river water quality and bacterial communities following reservoir impoundment is crucial for assessing the ecological impacts of water conservancy projects. To evaluate the water quality status and bacterial community response characteristics of the Jiaoxi River upstream of the Sanhekou Reservoir following its impoundment as part of the Han-Wei Water Diversion Project, we collected water samples at various cross-sections, measured physicochemical parameters, and conducted a comprehensive assessment of water quality using the Single-Factor Method, principal component analysis, and the cloud model. Additionally, 16S rDNA amplicons were sequenced to examine bacterial community composition and diversity. The RDA and Pearson correlation tests, meanwhile, helped identify the primary environmental factors. Our findings indicate that the water quality of the Jiaoxi River is generally very good. However, the commercial service area is a weak link in the aquatic environment of the study section of the river; at this location, total nitrogen (TN) met Class III standards, while key indicators at the remaining sampling sections all met Class II or higher standards. In the aquatic bacterial community, a total of 45 phyla, 121 classes, 326 orders, 576 families, and 1,375 genera were identified, with the dominant phyla being Proteobacteria, Bacteroidetes, Firmicutes, and Actinobacteria. Community composition exhibited distinct spatiotemporal variations and was jointly influenced by seasonal changes and local hydrodynamic conditions. RDA and correlation analyses indicated that WT, COD, and $\text{NH}_4^+\text{-N}$ were generally

negatively correlated with changes in community structure, while DO and pH were positively correlated with multiple dominant phyla. This study can serve as a reference for ecological conservation and pollution risk identification at the water source areas of the Han-Wei River Water Diversion Project.

Keywords: Jiaoxi River; Reservoir Impoundment; Water Quality Assessment; Bacterial Community; Spatiotemporal Variation; Environmental Drivers.

1. Introduction

Rivers are among the most important freshwater resources on Earth. Their water quality is not only closely linked to human production and daily life, but also intimately connected to ecological security and sustainable development [1]. In recent decades, the construction of water infrastructure—such as hydropower stations and reservoirs—has altered natural hydrological processes by reducing flow velocity and changing flow patterns, thereby affecting river water quality [2]. Therefore, systematically assessing water quality following the operation of large-scale water projects and identifying the key factors and primary sources affecting water quality are crucial for ensuring water security, preventing pollution, and supporting ecological conservation.

Inter-basin water transfer projects play a crucial role in alleviating spatial and temporal imbalances in regional water resources and ensuring the security of water supply within river basins [3]. At the same time, balancing the benefits of water transfers with their impacts on water quality and public health has become a key issue in environmental management and engineering practice [4]. Reservoir impoundment generates a backwater effect that significantly reduces the hydraulic gradient of tributaries, thereby altering nutrient retention and sedimentation processes. Previous studies have

demonstrated that backwater conditions can transform tributaries into phosphorus sinks and reshape material exchange between tributaries and reservoir systems [5]. Reservoir impoundment generates a backwater effect that significantly reduces the hydraulic gradient in tributaries, thereby altering the retention and deposition processes of nutrients. Previous studies have shown that backwater conditions can transform tributaries into phosphorus sinks and reshape material exchange between tributaries and reservoir systems [5]. Under the combined effects of water diversion and reservoir impoundment, dissolved organic matter (DOM) and microorganisms exhibit strong metabolic coupling and complex interaction networks. Changes in DOM sources and molecular characteristics can further modulate bacterial community structure and its potential functions through substrate supply–community selection mechanisms [6–8]. Therefore, a comprehensive understanding of changes in river water quality and microbial communities following reservoir impoundment is crucial for effective water environment management and ecological restoration [9].

In research on aquatic environments in China's river basins, comprehensive water quality assessments based on multiple indicators have laid the foundation for water source management. Studies have shown that a Water Quality Index (WQI) model employing an improved weighting scheme and a comprehensive algorithm can enhance the robustness of comprehensive assessments and better characterize spatiotemporal heterogeneity [10]. Furthermore, methods such as cloud modeling and combined weighting techniques are commonly widely used to assess river water quality; they can characterize water quality evolution and identify key risk factors across multiple indicators and monitoring periods [11]. The construction and operation of reservoirs can also alter microbial habitats, thereby affecting community diversity and ecological functions. At the spatial scale of a river, environmental factors collectively shape the spatial distribution patterns of microbial communities, diffusion constraints, and stochastic processes, leading to significant differences in community composition across different river sections [12].

Taking the upper reaches of the Jiaxi River—specifically the section comprising the Hanjiang Water Diversion Project, following the filling of

the Sanhekou Reservoir—as the study area, a comprehensive water quality assessment was conducted using the single-factor evaluation method, principal component analysis (PCA), and the cloud plot model. Using high-throughput 16S rRNA gene sequencing technology, we analyzed the structure and diversity characteristics of the bacterial community in the study area; simultaneously, we employed redundancy analysis (RDA) and Pearson correlation analysis to identify the key environmental factors driving the spatial distribution of the bacterial community and changes in water quality.

2. Materials and Methods

2.1 Study Area and Sampling

The Jiaoxi River is located in Foping County, Hanzhong City, Shaanxi Province, China, and is one of the main tributaries supplying water to the Sanhekou Reservoir as part within the framework of the Hanjiang–Wei River Water Diversion Project. Based on the river's morphology and the intensity of human disturbance, five sampling sites were established along the riverbank: Guangoukou, Shiziba, the Commercial Service Station, the highway intersection, and the right bank of the bridge. The first sampling campaign was conducted on September 26, 2021 (Figure. 1), and the collected samples were designated F1–F5. The second sampling campaign was carried out on December 5, 2021, with samples designated S1–S5.

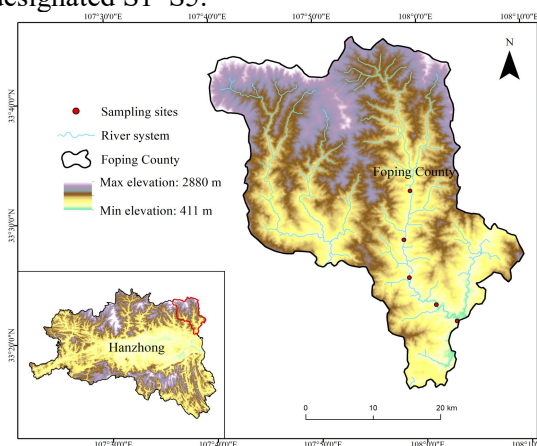


Figure 1. Study Area and Locations of Sampling Sites

2.2 Water Quality Analysis and Assessment

The water quality parameters were assessed in line with the Surface Water Environmental Quality Standard (GB 3838-2002). Specifically,

water temperature, pH, and used a portable multi-parameter water quality analyzer to measure dissolved oxygen in situ. In contrast, TN, $\text{NH}_4^+\text{-N}$, $\text{NO}_3^-\text{-N}$, TP, and COD were measured following the relevant national standard methods. Five core water quality parameters—dissolved oxygen, ammonia nitrogen, total nitrogen, total phosphorus, and chemical oxygen demand—were selected for a single-factor assessment, and the overall water quality category was determined based on the parameter with the most severe exceedance at each sampling site. To overcome the limitation associated with the single-factor assessment method in quantifying differences in the weights of individual indicators, Principal Component Analysis (PCA) was used to objectively calculate the weights of five key water quality parameters: dissolved oxygen (DO), ammonia nitrogen ($\text{NH}_4^+\text{-N}$), total nitrogen (TN), total phosphorus (TP), and chemical oxygen demand (COD) [13].

2.3 High-Throughput Sequencing for Analyzing Microbial Community Diversity Characteristics

After collecting the water samples, they were filtered using a 0.22 μm microporous filter membrane to concentrate the microbial cells in the samples. Using the V3–V4 hypervariable regions of the bacterial 16S rRNA gene as the amplification target, PCR amplification was performed using universal primer pairs; after purification of the amplification products, high-throughput sequencing was conducted on the Illumina MiSeq PE300 platform. Total genomic DNA was first extracted from the filter membranes using an environmental DNA extraction kit. High-quality, valid sequences were then clustered based on a 97% sequence similarity threshold to obtain operational taxonomic units (OTUs). Representative OTU sequences were aligned against public 16S rRNA databases for species annotation, thereby providing information on community composition at various taxonomic levels. To assess the species richness and diversity of bacterial communities in different samples, α -diversity indices such as Chao-1, Shannon, and Simpson were calculated based on standardized OTU tables, and dilution curves were plotted to verify the adequacy of sequencing depth.

3. Results

3.1 Water physicochemical characteristics

The statistical characteristics of the water quality parameters obtained from the two sampling events on the Jiaoxi River are shown in Table 1. To clarify the current water quality status of this watershed and evaluate its compliance with standards, this study evaluated the measured water quality parameters based on the Class III water body limits specified in the Surface Water Environmental Quality Standards (GB 3838–2002).

During the two sampling periods, the pH of the river ranged from 7.6 to 8.4, indicating that the water was slightly alkaline. Dissolved oxygen (DO) in the study section generally remained at a high level, with concentrations ≥ 8.43 mg/L, exceeding the Class III standard limit of 5.0 mg/L. Concentrations of ammonia nitrogen ($\text{NH}_4^+\text{-N}$) and total phosphorus (TP) in the area are on the low side, and both meet the Class II surface water quality standards. The average total nitrogen (TN) concentrations from the two sampling occasions were 0.82 mg/L and 0.79 mg/L, respectively; however, the maximum concentration exceeded 1.0 mg/L. The coefficients of variation were 0.24 and 0.18, respectively, indicating significant differences among the sampling sites. Therefore, total nitrogen was identified as the primary sensitive indicator for the study river section. The average concentration of chemical oxygen demand (COD) ranged from 7.65 to 8.27 mg/L, remaining at a relatively low level overall.

The physicochemical parameters of water quality exhibited distinct spatial patterns at each sampling site. Between the two sampling periods, water temperature (WT) showed a gradual increase from upstream to downstream; overall, Water temperatures in September were significantly higher than in December, consistent with seasonal variations and patterns in hydrodynamic conditions. Dissolved oxygen (DO) concentrations at the Gangoukou and Shiziba sites were generally higher than those at downstream sampling sites, while DO concentrations near the Business Service Station showed slight fluctuations. Between the two sampling periods, the $\text{NH}_4^+\text{-N}$ concentration generally increased from upstream to downstream. Under the combined effects of cumulative transport from upstream and water retention at the reservoir tail, the highest $\text{NH}_4^+\text{-N}$ concentration (0.07 mg/L) was observed in the downstream reach. The $\text{NO}_3^-\text{-N}$ concentration varied relatively little along the river, although

localized increases were observed. The TN concentration reached its maximum value (1.15 mg/L) at the Business Service Station. The spatial distribution pattern is characterized by higher concentrations in the middle reaches and

lower concentrations in the upper and lower reaches. The highest COD concentration (12.18 mg/L) was observed at the Right Bank of the Bridge.

Table 1. Statistical Description Results of Basic Water Quality Parameters in the Study Area

Parameter	ID	Min	Max	Mean	SD	CV	Class III Standard (GB 3838–2002)
WT	first sampling campaign	18.6	26.8	21.44	3.58	0.17	–
DO		9.03	9.87	9.41	0.35	0.04	≥ 5.0
pH		8.1	8.40	8.30	0.12	0.01	6–9
NH ₄ -N		0.03	0.07	0.05	0.02	0.38	≤ 1.0
NO ₃ -N		0.25	0.35	0.30	0.04	0.14	≤ 10.0
TN		0.69	1.15	0.82	0.20	0.24	≤ 1.0
TP		0.01	0.01	0.01	0.00	0.00	≤ 0.20
COD		6.15	12.18	8.27	2.55	0.31	≤ 20.0
WT	Second sampling campaign	5.60	14.10	8.06	3.52	0.44	–
DO		8.43	9.32	8.89	0.37	0.04	≥ 5.0
pH		7.60	8.2	7.90	0.22	0.03	6–9
NH ₄ -N		0.03	0.08	0.05	0.02	0.47	≤ 1.0
NO ₃ -N		0.23	0.33	0.28	0.04	0.15	≤ 10.0
TN		0.66	1.04	0.79	0.15	0.18	≤ 1.0
TP		0.01	0.01	0.01	0.00	0.00	≤ 0.20
COD		4.61	11.83	7.65	2.77	0.36	≤ 20.0

3.2 Spatiotemporal Patterns and Comprehensive Assessment of Water Quality

Based on the functional requirements for surface water environments and the Class III standard for rivers in the Surface Water Environmental Quality Standards (GB 3838–2002), the water quality indicators at each sampling site were evaluated using the single-factor assessment method. As demonstrated by the single-factor assessment, during both sampling campaigns, Dissolved oxygen (DO), NH₄⁺-N, TP, and COD met Class II or higher water quality standards at all sampling sites; total nitrogen (TN) at the Business Service Station cross-section met the Class III standard limits in both sampling rounds, whereas the remaining sampling sites met the Class II standard. These results were generally consistent with those obtained from the cloud model-based comprehensive assessment, indicating that the Business Service Station was the most sensitive sampling site with relatively high water quality risk in the study reach.

Principal Component Analysis (PCA) was used to analyze the data collected during the two sampling periods, with the aim of identifying the dominant factors influenced by multiple water quality parameters. The cumulative variance contribution rates of the first two principal components both exceeded 80%, indicating that they could adequately represent the overall variation characteristics of water quality. For the

first sampling campaign, the first principal component was mainly dominated by WT, pH, DO, and NH₄⁺-N, reflecting the temperature–oxygen conditions and the basic physicochemical properties of the water body. The second principal component was mainly dominated by TN, COD, TP, and NO₃[–]-N, indicating the nutrient and organic pollution levels of the river water. During both sampling campaigns, NH₄⁺-N, TN, and COD played the largest role in determining the overall water quality classification.

To address the fuzziness and randomness of water quality classification boundaries, the normal cloud model based on the digital characteristic inversion method was employed to construct the standard clouds for DO, NH₄⁺-N, TN, TP, and COD, respectively. Determine the expected value (EX), entropy (EN), and hyperentropy (HE) corresponding to each water quality standard. Using the digital characteristics of the standard clouds as parameters, the X-condition cloud generator was applied to calculate the membership degree of each water quality indicator to the five water quality classes. Combined with the weights extracted by principal component analysis (PCA), the comprehensive membership vector and characteristic grade value of each sampling site were obtained, thereby providing a comprehensive cloud model-based assessment of water quality in the study reach.

The comprehensive membership vectors and characteristic grade values of the cloud model for each sampling site are presented in Table 2. Cloud modeling assessments confirm that water quality in the study section of the river is primarily Class I and Class II. At most sampling sites, the membership degrees for Class I and Class II water quality were higher than those for Class III–V. Guangoukou and Shiziba, located in the upstream reach, exhibited relatively better water quality. In contrast, the Business Service Station showed a relatively higher characteristic grade value and a relatively poorer final evaluation grade, indicating that this sampling site represented a section with relatively prominent water quality risk in the study reach. Evaluation Results Combining Single-Factor Analysis, Principal Component Analysis (PCA), and Cloud Modeling, The study found that the overall water quality in the target section of the Jiaoxi River exceeds the Class III water quality standards. The water quality at the upstream and downstream sampling sites remained stable at the Class II level. In contrast, the Business Service Station in the middle reach was affected by domestic sewage discharge and anthropogenic activities along the riverbanks, resulting in significantly increased concentrations of TN and COD, which played a dominant role in determining the water quality classification and its spatiotemporal variations.

Table 2. Comprehensive Membership Degrees, Grade Characteristic Values of Water Quality at Sampling Sites in the Jiaoxi River

Sampling Site	Class I	Class II	Class III	Class IV	Class V	Characteristic Value
F1	0.513	0.248	0.209	0.002	0	1.720
F2	0.526	0.258	0.213	0.001	0	1.688
F3	0.595	0.247	0.014	0.182	0.001	1.792
F4	0.743	0.257	0.213	0.001	0	1.565
F5	0.664	0.189	0.191	0.013	0	1.576
S1	0.734	0.259	0.19	0.001	0	1.543
S2	0.713	0.251	0.193	0.004	0	1.558
S3	0.654	0.26	0.044	0.082	0	1.569
S4	0.703	0.238	0.169	0.001	0	1.520
S5	0.57	0.204	0.194	0.004	0	1.621

Note: The values are unnormalized comprehensive membership degrees calculated by weighting the membership degrees of individual indicators with the PCA-derived weights.

3.3 Bacterial Community Composition and Spatiotemporal Variations

3.3.1 Community Composition and Dominant Taxa

Based on the results of high-throughput sequencing of the 16S rRNA gene, the planktonic bacterial community composition of the Jiaoxi River water samples was analyzed after quality control, chimera removal, OTU clustering, and taxonomic annotation. The OTU annotation results covered 45 phyla, 121 classes, 316 orders, 576 families, and 1,365 genera, indicating a high level of taxonomic diversity in the bacterial communities of the study river section.

The bacterial community composition at each sampling point within the phylum level showed a high degree of overall similarity, with Proteobacteria, Bacteroidetes, Firmicutes, and Actinobacteria being the shared dominant phyla, accounting for the majority of the microbial community (Figure. 2), whereas the remaining phyla exhibited relatively low abundances. Compared with the upstream sites, Guangoukou and Shiziba, The proportions of Proteobacteria and Bacteroidota were slightly greater in the samples collected from the Business Service Station and the Right Bank of the Bridge, while the relative abundance of Actinobacteriota decreased. However, the bacterial community still exhibited the typical freshwater community characteristic of coexistence between a few dominant phyla and numerous rare phyla.

At the genus level, the spatial variation in the planktonic bacterial community was more pronounced (Figure. 3). In the upstream samples collected from Guangoukou (F1/S1) and Shiziba (F2/S2), freshwater-associated genera, including *Flavobacterium*, *Rhodospirillum rubrum*, *Hydrogenophaga*, and the *hgcI* clade, were relatively abundant. In contrast, the relative abundances of *Limnochlamydomonas*, the abundances of *hgcI* clade and *CL500-29_marine_group* were markedly higher in the samples collected from the Business Service Station (F3/S3) and the Right Bank of the Bridge (F5/S5). In addition, several genera associated with organic matter accumulation or eutrophic waters exhibited increased occurrence frequency and relative abundance at the middle and downstream sampling sites.

The planktonic bacterial community in the Jiaoxi River exhibited a stable composition at the phylum level and was dominated by a few common freshwater phyla. In contrast, obvious spatial heterogeneity was observed at the genus level, with substantial differences in the dominant genera between the upstream and

downstream sampling sites and those located near the residential area in the middle reach.

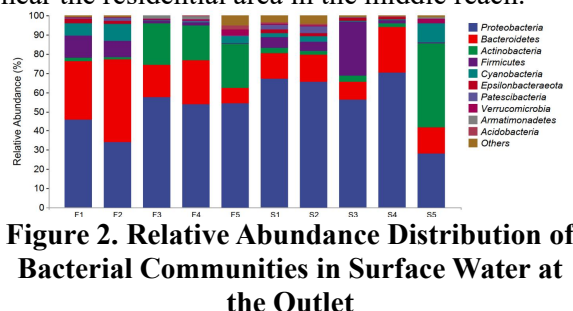


Figure 2. Relative Abundance Distribution of Bacterial Communities in Surface Water at the Outlet

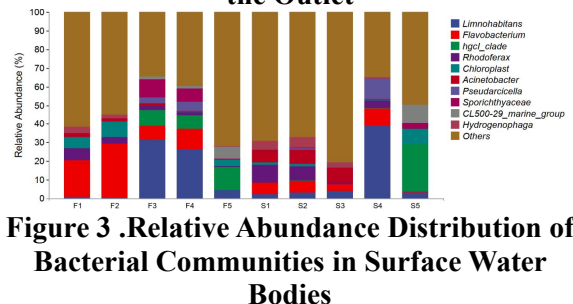


Figure 3. Relative Abundance Distribution of Bacterial Communities in Surface Water Bodies

3.3.2 Community Diversity and Spatiotemporal Variations

The α diversity index of the bacterial community was worked out with the OTU abundance matrix, and the results appear in Table 3. Overall, the bacterial communities at all sampling sites in the Jiaoxi River exhibited relatively high α -diversity. The Species and Chao1 indices ranged from 1,943 to 5,480 and 2,089.65 to 5,816.63, respectively. The Shannon index ranged from 7.34 to 10.09, the Simpson index was greater than 0.96 for all samples, and the Coverage values exceeded 0.98, indicating that the sequencing results adequately reflected the characteristics of the bacterial groups in the samples.

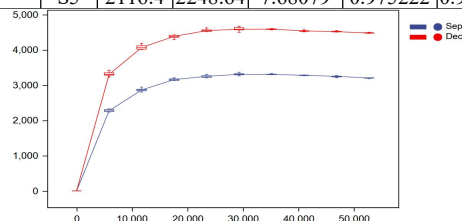
Spatially, the diversity of the bacterial communities exhibited local variations among the sampling sites. In the samples collected in September, species richness and community diversity were relatively higher at Guangoukou and Shiziba, lower at the Business Service Station and Highway Junction, and intermediate at the Right Bank of the Bridge. In the samples collected in December, the diversity indices were generally higher at Guangoukou, Shiziba, and the Business Service Station.

Temporally, the species richness and Shannon index of most samples collected in December were higher than those of the samples collected in September, suggesting that seasonal variation had an important influence on bacterial community diversity. However, the degree of this response varied among the different sampling sites.

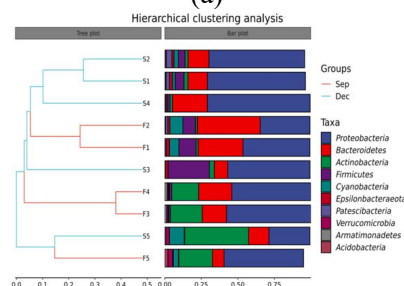
The rarefaction curves gradually approached a plateau with the increase in sequencing reads, this indicates that the sequencing depth was sufficient to cover the major bacterial groups present in the samples (Figure 4a). Cluster analysis further revealed the spatiotemporal variation in bacterial community structure (Figure 4b). At the temporal scale, samples collected during the same sampling campaign exhibited a clear clustering pattern, whereas samples collected in different seasons were distinctly separated, seasonal variation was an important factor influencing the bacterial community structure in the Jiaoxi River. At the spatial scale, the samples from Guangoukou and Shiziba clustered together, the Business Service Station formed a relatively independent cluster, and the Highway Junction and the Right Bank of the Bridge were grouped more closely, showing that anthropogenic activities and differences in hydrodynamic conditions jointly shaped the spatial variation pattern of planktonic bacteria in the Jiaoxi River.

Table 3. Statistical results of alpha diversity

Sample	Name	species	Chao1	Shannon	Simpson	Coverage
water	F1	4115.9	4393.77	9.13143	0.990036	0.984357
	F2	4183.5	4499.87	8.78824	0.979643	0.983129
	F3	2013.7	2120.59	7.35983	0.97658	0.993254
	F4	1943	2089.65	7.33645	0.976459	0.992915
	F5	2675.3	2901.31	8.32976	0.987666	0.988925
	S1	5256.4	5669.42	9.89657	0.990404	0.980237
	S2	5480	5816.63	10.0897	0.99308	0.981562
	S3	5028.1	5059.59	10.0125	0.9956	0.993235
	S4	3310.9	3588.76	7.50405	0.963893	0.986501
	S5	2116.4	2248.64	7.68079	0.975222	0.992815



(a)



(b)

Figure 4. Rarefaction Curves and Cluster Analysis of Microbial Diversity (a. Rarefaction Curves of Sample Richness Index; b. Cluster Analysis of Different Samples)

3.4 Environmental Drivers of Bacterial Community Variation

To elucidate the response of bacterial communities in the Jiaoxi River basin to environmental factors and the patterns of interaction between them, the seven dominant phyla (relative abundance >1%) and water quality parameters (WT, pH, DO, $\text{NH}_4^+\text{-N}$, $\text{NO}_3^-\text{-N}$, TN, TP, and COD) were selected for redundancy analysis (RDA) to characterize the community structure of the two sampling campaigns. Associations of the α -diversity indices with environmental variables were evaluated using Pearson's correlation coefficients.

The RDA results are shown in Figure 5. WT, $\text{NH}_4^+\text{-N}$, TN, and COD exhibited relatively long vectors and were oriented opposite to the dominant bacterial phyla, which demonstrates that rising water temperature as well as increased nitrogen and COD contents restrain the formation of bacterial community structure. In contrast, DO, pH, and $\text{NO}_3^-\text{-N}$ were generally distributed in the same direction as the dominant bacterial phyla, suggesting that these factors positively influenced community succession. During the first sampling campaign, the WT vector was opposite to the distribution of most bacterial phyla, indicating that the relatively high water temperature was an important factor limiting bacterial diversity, whereas the positive effects of pH and DO were relatively weak. During the second sampling campaign, the vector lengths and contributions of DO, pH, and $\text{NO}_3^-\text{-N}$ increased markedly and were generally consistent with the distribution of most dominant bacterial phyla. The results of Pearson correlation analysis are generally consistent with those of redundancy analysis (RDA). The number of phyla and genus horizontal species taxonomic units, as well as the Chao1 index and Shannon index, are generally positively correlated with pH and dissolved oxygen (DO), Water temperature (WT), ammonia nitrogen ($\text{NH}_4^+\text{-N}$), and total nitrogen (TN) show a negative correlation with it. This indicates that nutrient load, Water temperature and dissolved oxygen jointly govern the spatial differentiation and seasonal succession patterns of bacterial communities in the Jiaoxi River.

4. Discussion

Reservoir construction can significantly alter the

hydrodynamic conditions and material transport processes of upstream inflows, thereby changing the spatiotemporal distribution patterns of nutrients and organic matter [14]. Water quality monitoring results from the two sampling periods indicate that, After the Sanhekou Reservoir began storing water, the overall water quality of the Jiaoxi River remained at a good level; however, total nitrogen (TN) concentrations were relatively high at the Business Service Station site, and chemical oxygen demand (COD) levels were elevated at the Right Bank of the Bridge site, reflecting significant spatial variations in water quality within the study river section. Previous studies have indicated that water retention in reservoir bays can exacerbate the sedimentation and accumulation of nutrients [15]. In the present study, Compared with December, the overall concentrations of total nitrogen (TN) and chemical oxygen demand (COD) were higher in September; this phenomenon reflects the impact of seasonal hydrological conditions on the dilution and transport of pollutants. Previous studies have shown that, along a gradient of anthropogenic pollution, the α -diversity and community structure of riparian bacterial communities undergo significant changes [16]. In eutrophic lakes, deterioration of water quality is often accompanied by the restructuring of microbial communities, and changes in key functional taxa can reflect the spatial variation in nitrogen and phosphorus loading as well as the potential risk of eutrophication.

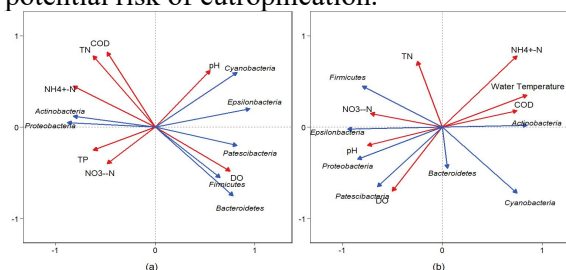


Figure 5. RDA analysis of microbial communities and environmental factors (Figure a. First sampling; Figure b. Second sampling)

The TN concentration at the Business Service Station was higher than that at the other sampling sites during both sampling campaigns, and the COD concentration at this site also remained relatively high. In addition, the community composition at the genus level differed markedly from that of the upstream and downstream sampling sites, indicating that local domestic sewage inputs had affected the bacterial

community. This site was enriched with taxa associated with organic matter degradation and pollution tolerance, suggesting that changes in water quality had already been reflected in bacterial community assemblages.

The diversity and structural distribution of bacterial communities in rivers are jointly influenced by environmental factors such as WT, nutrients, organic matter (OM), dissolved oxygen (DO), and hydrodynamic conditions. Variations in these environmental gradients can significantly influence the patterns of both α -diversity and β -diversity [17]. In the present study, the elevated TN and COD concentrations at the Business Service Station were consistent with the pronounced differentiation of the bacterial community structure at this site, indicating that nutrient and organic matter loading were the key factors driving bacterial community differentiation in the study reach. Meanwhile, DO explained a relatively large proportion of the variation in community structure, which is consistent with previous watershed studies reporting that dissolved oxygen plays an important role in shaping bacterial community distribution [18–19]. Therefore, in the reaches of the Sanhekou Reservoir that are more strongly affected by anthropogenic activities, water temperature, nutrients, and organic matter jointly shaped the spatiotemporal distribution patterns of the bacterial community.

5. Conclusions

(1) After the impoundment of the Sanhekou Reservoir, the overall water quality of the Jiaoxi River study reach remained good and was mainly classified as Class I–II. Except for the Business Service Station, where TN reached the Class III standard, the major water quality parameters at the remaining sampling sites met the Class I–II standards. The Business Service Station was identified as the most vulnerable section of the aquatic environment in the study reach.

(2) Analysis based on high-throughput sequencing shows that the bacterial communities in the waters of the Jiao Xi River exhibit high species richness, with the phyla Proteobacteria, Bacteroidetes, Firmicutes, and Actinobacteria being the dominant phyla. Significant spatiotemporal variations in community structure were observed at the genus taxonomic level, and the relative proportions of potential pollution indicator bacteria were higher in samples

collected at the business service area and on the right bank of the bridge.

(3) Bacterial diversity exhibited localized spatial fluctuations; species richness and diversity indices in December samples were generally higher than those in September, indicating that seasonal variations and hydrodynamic conditions jointly influence the pattern of community diversity.

(4) RDA and Pearson correlation analyses showed that WT, COD, and $\text{NH}_4^+\text{-N}$ were generally negatively correlated with bacterial community structure, while DO and pH were positively correlated with multiple dominant phyla. Among these, DO played a particularly prominent role in explaining community structure and is a key environmental factor influencing the distribution of bacterial communities in the Jiaoxi River.

Acknowledgments

work was supported by the 2025 Corporate-level Scientific Research Project of Shaanxi Modern Architecture Design & Research Institute Co., Ltd. (Document No. [2025]32).

References

- [1] Zhang, R. N., Liu, Z., Zhang, S. H., et al. Effects of watershed land use types on river water quality: A case study of the Nanpan River in the Pearl River Basin (in Chinese). *Journal of Hydroecology*, pp. 1–13.
- [2] Yang, H. Y. Causes of urban water supply quality deterioration and preventive measures (in Chinese). *Urban Water Supply*, 2021, (2): 31–34.
- [3] Wu W, Chen H, Xu S, et al. Water environment characteristics and water quality assessment of water source of diversion system of project from Hanjiang to Weihe River. *International Journal of Environmental Research and Public Health*, 2023, 20(4): 2890.
- [4] Nong X, Luo K, Lin M, et al. Relationships between water quality of a long-distance inter-basin water diversion project and air pollution emissions along the canal: Distributions, lag effects, and nonlinear responses. *Environmental Pollution*, 2024, 361: 124813.
- [5] Cheng B, Zhang Y, Xia R, et al. Backwater makes the tributaries of large river becoming phosphorus “sink”. *Water Research*, 2024, 261: 122012.

- [6] Zhang L, Fang W, Li X, et al. Strong linkages between dissolved organic matter and the aquatic bacterial community in an urban river. *Water Research*, 2020, 184: 116089.
- [7] Wang X, Li H, Zhang R, et al. Bacterial community and dissolved organic matter networks in urban river: The role of human influence. *Environmental Research*, 2024, 263: 120021.
- [8] Shi K, Zhang J, Zhao Y, et al. Distinct co-succession of dissolved organic matter and bacterial generalists and specialists in inflow rivers of Baiyangdian Lake. *Environmental Research*, 2025: 121378.
- [9] Guo, N. N., Qi, Y. K., Meng, S. L., et al. Research progress in restoration technologies for eutrophic lakes (in Chinese). *Chinese Agricultural Science Bulletin*, 2019, 35(36), 72–79.
- [10] Ding F, Hao S, Zhang W, et al. Using multiple machine learning algorithms to optimize the water quality index model and their applicability. *Ecological Indicators*, 2025, 172: 113299.
- [11] Fan, Y. L., Hu, G. L., Bai, Y. R., et al. Water quality assessment and prediction of the Shiyang River Basin based on a secondary game cloud model (in Chinese). *Water Purification Technology*, 2025, 44(5), 44–56.
- [12] Zhu A, Liang Z, Gao L, et al. Dispersal limitation determines the ecological processes that regulate the seasonal assembly of bacterial communities in a subtropical river. *Frontiers in Microbiology*, 2024, 15: 1430073.
- [13] Yi, H. M. Research and application of a cloud model-based safety evaluation method for reservoir dams (in Chinese). *Hongshui River*, 2022, 41(6), 1–6.
- [14] Xiang R, Wang L, Li H, et al. Water quality variation in tributaries of the Three Gorges Reservoir from 2000 to 2015. *Water Research*, 2021, 195: 116993.
- [15] Liu X, Huang W, Qi Z, et al. Seasonal water storage of large reservoirs exacerbates eutrophication risk in the fluctuating backwater zone: A case study of Three Gorges Reservoir, China. *Ecological Indicators*, 2025, 171: 113100.
- [16] Lenart-Boroń A, Boroń P, Kulik K, et al. Anthropogenic pollution gradient along a mountain river affects bacterial community composition and genera with potential pathogenic species. *Scientific Reports*, 2022, 12: 18140.
- [17] Shi K, Zhang J, Zhao Y, et al. Spatiotemporal distribution, assembly processes, and key drivers of bacterial communities in a multi-terrain river basin of northern China. *Journal of Environmental Chemical Engineering*, 2025: 116756.
- [18] Xiao P, Wu Y, Zuo J, et al. Differential microbiome features in lake–river systems of Taihu basin in response to water flow disturbance. *Frontiers in Microbiology*, 2024, 15: 1479158.
- [19] Tan, Q. Y., Lü, J. Y., Bai, X. Y., et al. Vertical distribution and source tracking of bacterial community composition and nitrogen cycling functions in a typical urban inland river (in Chinese). *Environmental Science*, 2023, 44(3), 1497–1507