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Original Research

Sediment DOM Fluorescence Characteristics in Lake Wetlands: Effects of Vegetation and Relationships with Bacterial Communities

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Abstract

To elucidate the fluorescence characteristics of sediment dissolved organic matter (DOM), the structural and functional features of bacterial communities, and their coupling relationships under different vegetation coverage levels, sediment samples from distinct water depth zones of Baiyu Lake in Harbin, China, were analyzed using three–dimensional fluorescence spectroscopy and high–throughput sequencing. The results showed that sediment DOM had mixed allochthonous and autochthonous sources. Zones with helophytes and emergent plants exhibited a higher degree of DOM humification, higher humic–like fluorescence intensity, and elevated bacterial diversity, relative abundance of taxa, and OTU numbers associated with C, N, and S cycling. The Mantel test revealed significant correlations between allochthonous humic–like substances and bacterial community diversity, composition, and functions, whereas protein–like substances showed no such correlations. The variance partitioning analysis indicated that humic–like and protein–like substances explained 56.90% and 6.95% of the variance in the bacterial community, respectively. Collectively, vegetation variations driven by water depth modulate the complex interactions between sediment DOM and bacterial communities in lake wetlands.

Keywords: dissolved organic matter, sediment, bacteria, fluorescence spectroscopy

Introduction

Wetland sediments, as a key component of wetland soil–water interfaces, consist of organic matter, minerals, and pollutants, and can exert varying impacts on wetland ecosystems through their distinct physicochemical properties and microbial community characteristics [1, 2]. Different water depths in wetlands can lead to variations in vegetation types and growth density, and consequently affect the properties and stability of sediments [3, 4]. Indeed, Stoorvogel et al. [5] highlighted higher sediment shear strengths in areas

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with densely growing *Spartina anglica* than those in unvegetated tidal flats and areas with sparsely growing *Scirpus maritimus*.

DOM refers to water–soluble organic matter that can pass through a 0.45 μm pore–size filter membrane. It is a key substance with unique physicochemical and biological properties in ecosystems, and is widely present in various spheres of the Earth in a molecular or colloidal form, including rivers, lakes, seas, soils, and the atmosphere [6, 7]. In addition, DOM is considered an important carrier of key elements involved in the global biogeochemical cycling system [8]. Due to its high reactivity and rapid turnover characteristics, DOM is regarded as the most active and mobile component within the carbon (C) pools of both terrestrial and aquatic ecosystems. It plays an indispensable role in regulating the processes of C fixation and release, and significantly influences biogeochemical processes such as the global C budget and greenhouse gas emissions [9, 10]. Furthermore, DOM promotes the cycling of essential nutrient elements, including nitrogen (N), phosphorus (P), and sulfur (S), by facilitating their mobilization, complexation, and transport through interactions with soil minerals, pollutants, and microbial communities [10, 11]. The sources of DOM in aquatic ecosystems exhibit significant spatiotemporal variability: allochthonous DOM includes terrestrial inputs (e.g., higher plant biomass and soil), atmospheric deposition (e.g., aerosols and precipitation), and inputs from other ecosystems, while autochthonous DOM is derived from microbial activities, in situ biological production processes, and the growth and metabolism of organisms (e.g., algae) [12, 13].

Microorganisms act as both producers and consumers of DOM: on the one hand, microbial communities can affect the sources, properties, and contents of DOM, and interspecific interactions (e.g., cooperation, competition, and mutualism) play a key role in the synthesis and decomposition of DOM; on the other hand, DOM with distinct chemical components (e.g., humic–like and protein–like substances) shapes the composition, structure, and diversity of microbial communities by providing heterogeneous ecological niches and energy substrates, thereby forming complex bidirectional interaction networks [14-16]. Existing studies have revealed a close covariation between DOM chemodiversity and microbial assembly in aquatic ecosystems; however, in relatively stable lake ecosystems, despite the dynamic equilibrium between microbial communities and DOM transformation processes, the key regulatory mechanisms underlying these interactions remain poorly elucidated [17].

Three–dimensional fluorescence spectroscopy has been widely used for DOM characterization due to its simplicity and high efficiency [18, 19]. This technique can, in fact, sensitively and accurately identify the sources and compositions of DOM via excitation (Ex)–emission (Em) matrices and parallel factor (PARAFAC) analysis [20, 21].

The humification index (HI), fluorescence index (FI), and biological index (BI) are calculated to characterize the degree of DOM humification, the microbial contribution to and dominant source of DOM, and the ratio of autochthonous to allochthonous organic matter, as well as the microbial degradation potential of DOM, respectively [22, 23]. The positions and intensities of fluorescence spectral peaks are of great importance for revealing the types and contents of DOM components [24]. For instance, an Ex/Em of 250 nm/450 nm (480 nm) corresponds to UV humic–like substances, which are commonly found in forests and wetlands, whereas an Ex/Em of 280 nm / 330 nm corresponds to tryptophan–like substances, mostly present in industrial wastewater and domestic sewage [25]. These findings provide a useful reference for an in–depth understanding of the role of DOM in ecosystems.

In summary, water depth drives vegetation differentiation in lake wetlands, and vegetation–mediated DOM–microbial interactions regulate DOM stability. However, the quantitative mechanisms remain unclear. This study followed the "water depth → vegetation → DOM–bacteria" pathway to determine how vegetation affected DOM properties and bacterial community structure, diversity, and function, and to quantify the responses of DOM fluorescence components to bacterial parameters, thereby advancing the understanding of DOM stability mechanisms in lake wetland sediments.

Materials and Methods

Sediment Sample Collection

Sediment samples were collected in August 2022 (the high–water period) from different water depth zones (Supplementary Table 1S) of Harbin Baiyu Lake National Wetland Park (45°53′18.28″-45°54′15.84″N, 126°52′30.70″-126°54′09.65″E), Heilongjiang Province, China. The emergent plant zone (S3) had significantly (p<0.05) higher plant biomass dry weight and higher plant density than the other zones. A 1 m × 1 m quadrat was established in each zone, and sediment samples were collected from the 0-5 cm surface layer using a piston–type sediment sampler with a 5 cm inner diameter. Specifically, three replicate sediment samples were collected from the four vertices and the center of each quadrat, and then thoroughly mixed to form a 200 g composite sediment sample per quadrat. All sampling procedures were performed in triplicate.

Determination of Three–Dimensional Fluorescence Spectroscopy

A 5 g aliquot of air–dried sediment was mixed with 50 mL of ultrapure water, shaken at 200 r/min for 24 h at room temperature, and centrifuged at 3500 r/min for 10 min at 4ºC. The resulting supernatant was filtered

through a 0.45 μm cellulose acetate filter membrane to obtain the sediment DOM extract. The dissolved organic carbon (DOC) concentration in the sediment DOM extract was determined using a total organic carbon analyzer (Multi N/C 2100, Jena, Germany). Ultrapure water was added to adjust the DOC concentration of all extracts to a uniform 15 mg/L.

Following the method of He et al. [26], three–dimensional fluorescence spectra were recorded using a fluorescence spectrophotometer (F–7000, Hitachi, Japan) equipped with a 450 W xenon lamp and a 700 V photomultiplier tube; the Ex and Em wavelengths ranged from 200 to 600 nm with a 2 nm interval, a 5 nm slit width, and a scanning speed of 2400 nm/min. Ultrapure water was used as a blank control to eliminate Rayleigh and Raman scattering interference.

DNA Extraction, PCR Amplification, and Sequencing

Genomic DNA was extracted from 0.5 g of air–dried sediment using the PowerSoil® DNA Isolation Kit (MoBio Laboratories, CA, USA) according to the manufacturer's protocol. The concentration and purity of the extracted genomic DNA were determined using a NanoDrop™ 2000 UV–Vis spectrophotometer (Thermo Fisher Scientific, MA, USA), and DNA quality was further verified via 1% agarose gel electrophoresis.

The V3-V4 hypervariable region of the bacterial 16S rRNA gene was amplified with the 338F/806R primer pair [27] using a PCR thermal cycler (GeneAmp® 9700, ABI, CA, USA). The 20 μL PCR reaction mixture contained 4 μL of 5×Fast*Pfu* buffer, 2 μL of 2.5 mM dNTPs, 0.8 μL each of the forward and reverse primers, 0.4 μL of Fast*Pfu* polymerase, 0.2 μL of bovine serum albumin, 10 ng of template DNA, and nuclease–free ddH_2O to bring the final volume to 20 μL. The PCR cycling program was as follows: initial denaturation at 95ºC for 3 min; 35 cycles of denaturation at 95ºC for 30 s, annealing at 55ºC for 30 s, and extension at 72ºC for 45 s; and a final extension at 72ºC for 10 min.

After electrophoresis, purification, and quantification, all PCR amplicons were subjected to paired–end 2×300 bp sequencing on the Illumina MiSeq high–throughput sequencing platform (Illumina, CA, USA). All PCR amplifications and sequencing reactions were performed in triplicate for each sample.

Data Analysis

Fluorescence spectral data were acquired using FL WinLab software (PerkinElmer, MA, USA), and scatter correction was performed via the DOMFluor V1.7 toolbox (MATLAB R2021b, MathWorks, MA, USA); PARAFAC analysis was then applied to identify fluorescent components and generate fluorescence spectra [28]. Origin 2021 software (OriginLab, MA, USA) was used to calculate the HI, FI, and BI values [22, 23].

Raw sequencing reads were quality–filtered and clustered into operational taxonomic units (OTUs) at a 97% sequence similarity threshold using UPARSE (v11) and VSEARCH (v2.28.1); the relative abundance of each OTU was then calculated using the QIIME 2 pipeline (https://qiime2.org/). Bioinformatic analyses (including diversity analysis, community composition analysis, and FAPROTAX functional prediction) and statistical analyses (Mantel's test, redundancy analysis (RDA), and variance partitioning analysis (VPA)) were performed using the Majorbio Cloud Platform (https://www.majorbio.com, Shanghai, China) [29]. Statistical significance tests for intra– or inter–group differences were performed using the SPSSAU online platform (https://spssau.com).

Results and Discussion

Analysis of the Fluorescence Spectral Indices

The FI values obtained in this study ranged from 1.4 to 1.9 (Supplementary Table 2S), which were consistent with the findings of Ma et al. [22]. These results indicated that the sediment DOM exhibited mixed allochthonous and autochthonous characteristics, derived from the combined inputs of plant litter and microbial metabolites [23], and thus its sources showed a diversified pattern during the wet season (August) [30]. The FI values in the S2 zone were significantly lower than those in the other sampling zones ($p<0.05$), followed by the S3 zone. Although no significant differences in FI values were observed between S3 and S1, S4, or S5 ($p>0.05$), the large plant biomass in the S3 zone contributed substantial litter inputs, which served as an important allochthonous source of sediment DOM.

The BI values of S2, S3, and S4 ranged from 0.6 to 0.8, indicating a dominant allochthonous origin of DOM in these zones [27]. In contrast, S1 and S5 had significantly higher BI values (greater than 0.8, $p<0.05$), suggesting a relatively high proportion of newly generated autochthonous DOM derived from microbial metabolism and other biogenic processes [23]. The S1 zone was located in the shallow water area, where humic components in sediment DOM were prone to photodegradation and transformation into low–molecular–weight substances (e.g., protein–like compounds), thereby enhancing the bioavailability of DOM [31]. Additionally, this zone was susceptible to the impacts of surrounding agricultural activities, which further increased the input of low–molecular–weight DOM [32]. For the S5 zone, situated in the deep water area with limited plant litter input, the relatively high proportion of autochthonous DOM was mainly attributed to in situ microbial and biological activities.

The HI values of sediment DOM varied from 1.677 to 5.085 across all sampling zones. The HI values of S1, S4, and S5 were all below four, with no statistically significant differences among them ($p>0.05$), which

indicated a low humification degree and weak stability of DOM in these zones [23]. In comparison, the HI values of S2 and S3 exceeded four, and no significant difference was found between these two zones (p>0.05). Notably, the HI values of S2 were significantly higher than those of S1, S4, and S5 (p<0.05). These results demonstrated that the high plant biomass in S2 and S3 zones increased the input of plant litter, which not only promoted the humification process of sediment DOM but also facilitated the formation of high–molecular–weight aromatic compounds, thus improving the stability of DOM [22].

Analysis of the Fluorescent Components

Five fluorescent components were identified in the sediment DOM via PARAFAC analysis (Fig. 1), with their Ex/Em maxima assigned as follows: C1 (275 nm/445 nm) as visible fulvic acid–like substances, C2 (240 nm/400 nm) as UV fulvic acid–like substances, C3 (230 nm/340 nm, 280 nm/340 nm) as tryptophan–like substances, C4 (280 nm/500 nm) as humic acid–like substances, and C5 (200 nm/295 nm) as tyrosine–like substances [25, 33]. Among these components, C1, C2, and C4 were categorized as allochthonous humic–like substances, predominantly derived from terrestrial inputs such as plant litter and surface runoff; in contrast, C3 and C5 were defined as autochthonous protein–like substances, closely associated with phytoplankton metabolism and microbial activity in situ. These fluorescent components of DOM have also been detected in sediments and overlying waters of other wetland types [16, 33-35], indicating their universal distribution in wetland aquatic environments.

Overall, the total content of the five fluorescent components in the S5 (non–vegetated zone) was significantly lower than that in all vegetated zones (p<0.05, Supplementary Table 3S), which directly confirmed that plant litter input is the primary source of sediment DOM in lake wetlands. Among all detected components, C4 (humic acid–like substances) had the lowest content across all sediment samples, suggesting a relatively low proportion of high–molecular–weight organic substances in the study area. This finding is consistent with the report by Zhang et al. [36], implying a generally low humification degree and poor intrinsic stability of sediment DOM in Baiyu Lake wetland. In line with the conclusion of Chen et al. [37] that protein–like substances are abundant in seasonally flooded lake wetland areas while humic acid–like components are scarce, our results showed a relatively high content of protein–like substances (C3 and C5) in S1, S4, and S5 zones, which was closely linked to their low sediment DOM humification degree. On the contrary, the high content of humic–like substances (C1, C2, and C4) in S2 and S3 zones further verified the relatively high humification degree of DOM in these two vegetated zones.

At the individual component level, C3 exhibited the highest content in S1 and S4 zones, while C5 showed relatively higher contents in S3 and S4 zones. This distinct distribution pattern suggested that C3 and C5 had different autochthonous source pathways in the sediment DOM. Combined with the findings of Long et al. [31], the high content of C3 in the S1 zone may be additionally affected by anthropogenic inputs (e.g., agricultural non–point source pollution), in addition to in situ microbial metabolism. This observation also corresponds to the aforementioned analysis of BI and FI indices in the S1 zone, further reflecting the combined effects of natural biological processes and human activities on the composition of sediment DOM in shallow water areas of lake wetlands.

Diversity of the Sediment Bacterial Community

No significant differences in DNA copy numbers were observed between the S2 and S3 zones (p>0.05, Supplementary Table 4S). In contrast, the S3 zone had significantly higher DNA copy numbers while the S5 zone had markedly lower ones compared with the S1 and S4 zones (p<0.05), which directly indicated that vegetation cover could significantly promote the increase in sediment bacterial abundance. A total of 1,668,679 high–quality sequencing reads were obtained from the sediment samples of the five zones, with an average sequence length of 417 bp. These reads were clustered into 24,389 OTUs, which were affiliated with 65 phyla, 201 classes, 482 orders, 795 families, 1578 genera, and 4009 species, reflecting a rich bacterial taxonomic diversity in the study area.

At the OTU level, the phylogenetic diversity (PD), Chao1, and Shannon indices of the S2 and S3 zones were all higher than those of the other sampling zones, whereas the corresponding diversity indices of the S1 and S5 zones were relatively low. This result was consistent with the conclusion of Li et al. [38], demonstrating that the high sediment DOM content in the non–seasonally waterlogged zones of lake wetlands can provide more diverse ecological niches and sufficient carbon sources for bacterial growth, which is conducive to improving the richness and diversity of the sediment bacterial community. Although the total content of fluorescent components in the S1 zone was relatively high (Supplementary Table 3S), this zone was affected by seasonal waterlogging and had sparse vegetation cover, with its sediment DOM exhibiting prominent autochthonous characteristics. In contrast, the S2 and S3 zones featured high plant density and large biomass, and their sediment DOM had obvious allochthonous characteristics derived from abundant plant litter input, which ultimately supported a higher diversity of the bacterial community. This finding was also in line with the suggestion of Stadler et al. [39], confirming that aquatic environments dominated by terrigenous allochthonous DOM have a stronger potential for bacterial growth and community diversification.

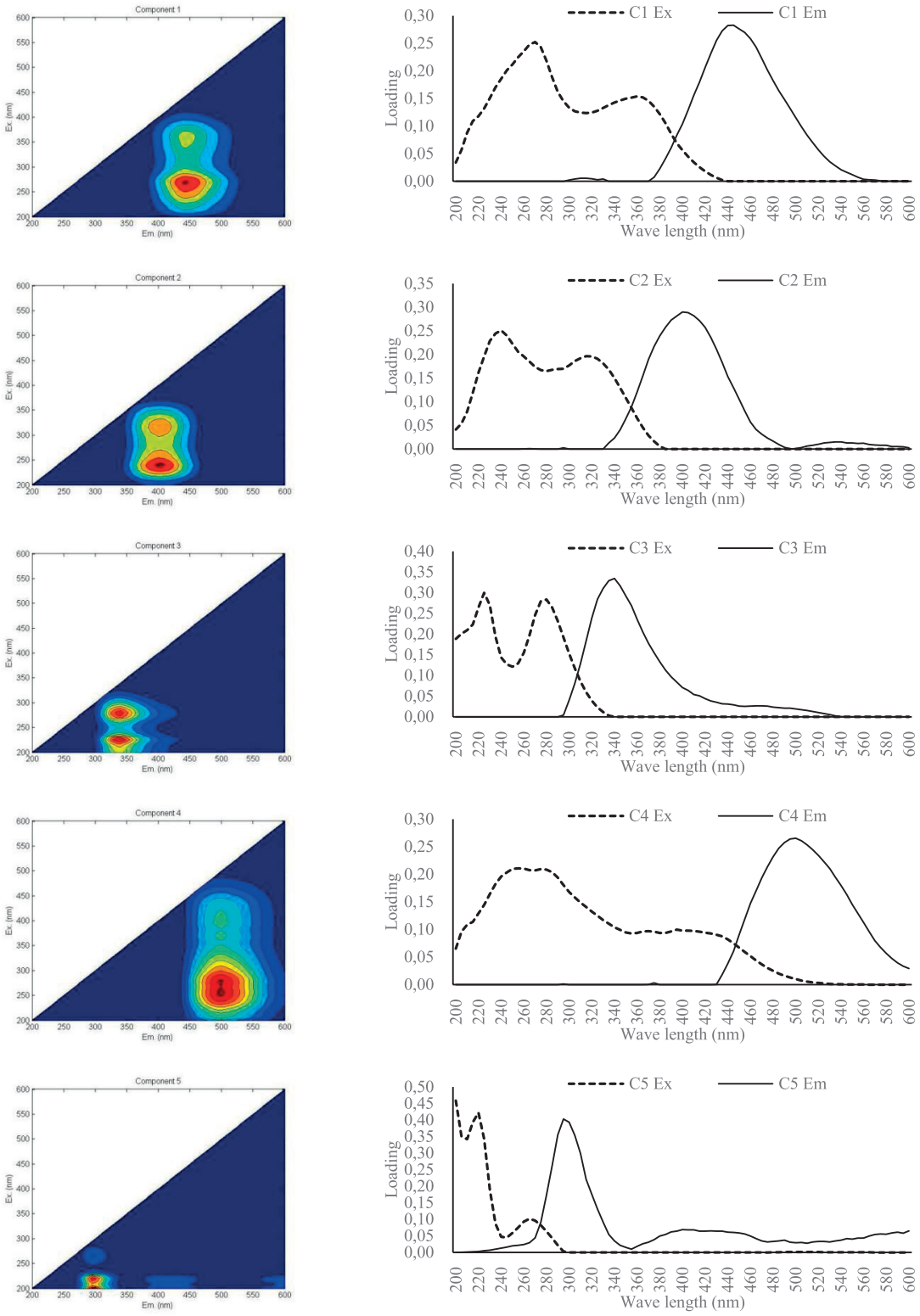

Fig. 1. Fluorescence components of lake wetland sediment DOM and their Ex/Em loadings.

Composition of the Sediment Bacterial Community

A total of 17 bacterial phyla were identified in all sediment samples after excluding taxa with a relative abundance of less than 1% and unclassified taxa (Fig. 2). The cumulative relative abundance of the top 10 dominant phyla exceeded 85%, indicating a relatively concentrated distribution of the bacterial community at the phylum level. Chloroflexi, Actinobacteriota, and Acidobacteriota were the most dominant phyla, with a total relative abundance approaching 50%, followed by Proteobacteria, Firmicutes, and Bacteroidetes. This dominant phylum composition differed from the findings

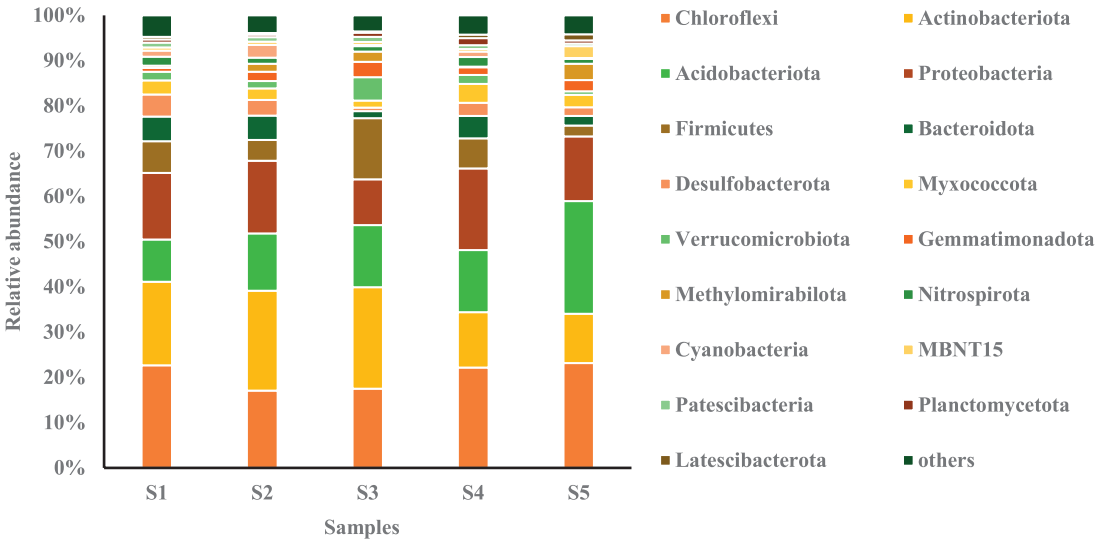

Fig. 2. Relative abundances of lake wetland sediment bacterial phyla (excluding taxa with relative abundance < 1% and unclassified groups).

of Li et al. [14] and Wang et al. [27], who reported Proteobacteria as the most abundant phylum in wetland sediments, and this discrepancy may be attributed to the unique hydrological conditions, vegetation cover characteristics, and sediment physicochemical properties of the Baiyu Lake wetland study area.

At the phylum level, the relative abundances of Chloroflexi in S1 (22.70%), S4 (22.15%), and S5 (23.18%) showed no significant differences (p>0.05), but were significantly higher than those in S2 (17.05%) and S3 (17.49%) (p<0.05). For Actinobacteriota, its relative abundances in S2 (22.13%) and S3 (22.46%) were not significantly different (p>0.05), yet both were significantly higher than that in S1 (18.44%) (p<0.05); in turn, the relative abundance of Actinobacteriota in S1 was significantly higher than those in S4 (12.24%) and S5 (10.89%) (p<0.05). The relative abundance of Acidobacteriota in S1 (9.30%) was the lowest among all zones (p<0.05), while that in S5 (24.86%) was the highest (p<0.05), with the values in S2 (12.65%) and S3 (13.72%) falling in the middle and showing no significant difference from S4 (13.76%) (p>0.05). In summary, the relative abundances of Chloroflexi and Acidobacteriota exhibited a decreasing trend with the increase in plant biomass in the sampling zones, whereas the relative abundance of Actinobacteriota showed the opposite increasing trend. Notably, the dominant taxa within Actinobacteriota possess strong organic matter utilization capabilities and are specialized in degrading refractory DOM components (e.g., aromatic compounds), especially allochthonous humic–like substances [40]. The composition of microbial dominant taxa is largely dependent on the utilization efficiency and substrate preference of microorganisms for sediment DOM [17], which further indicates that water depth–driven changes in vegetation distribution and biomass can alter sediment DOM characteristics, and thereby reshape the structure and ecological interactions of the sediment bacterial community.

At the genus level, among the 1578 identified genera, unclassified taxa accounted for 46.45% of the total relative abundance, reflecting a high degree of unknown bacterial diversity in the lake wetland sediments. The cumulative relative abundance of the top 10 classified genera in S3 reached 18.33% (Fig. 3), which was significantly higher than those in the other sampling zones (p<0.01); by contrast, the corresponding value in S5 was only 3.43%, the lowest among all zones (p<0.01). This distinct distribution pattern indicated that emergent plant cover could significantly enhance the dominance of specific bacterial genera and shape a more concentrated and structured bacterial community at the genus level in lake wetland sediments.

Pseudarthrobacter (phylum Actinobacteriota) has strong environmental adaptability and plays a key role in the degradation of polycyclic aromatic hydrocarbon pollutants in cold regions [41]. Its relative abundance showed no significant difference between S1 (3.98%) and S2 (5.02%) (p>0.05), but was significantly higher in these two zones than in the remaining sampling zones (p<0.01), which implied that the shallow water zones of the wetland were subject to adverse impacts of anthropogenic activities, and these disturbances drove the selective enrichment of *Pseudarthrobacter* in the sediment bacterial community. The relative abundances of *Bacillus* (phylum Firmicutes) and *Gaiella* (phylum Actinobacteriota) in S3 reached 5.23% and 3.40%, respectively, which were the highest among all zones. These two genera are well–documented to play critical roles in terrestrial and aquatic nitrogen and carbon biogeochemical cycling [42-43], and their high relative abundance in the emergent plant zone (S3) was closely associated with the high content of allochthonous humic–like DOM in this zone; meanwhile, their strong

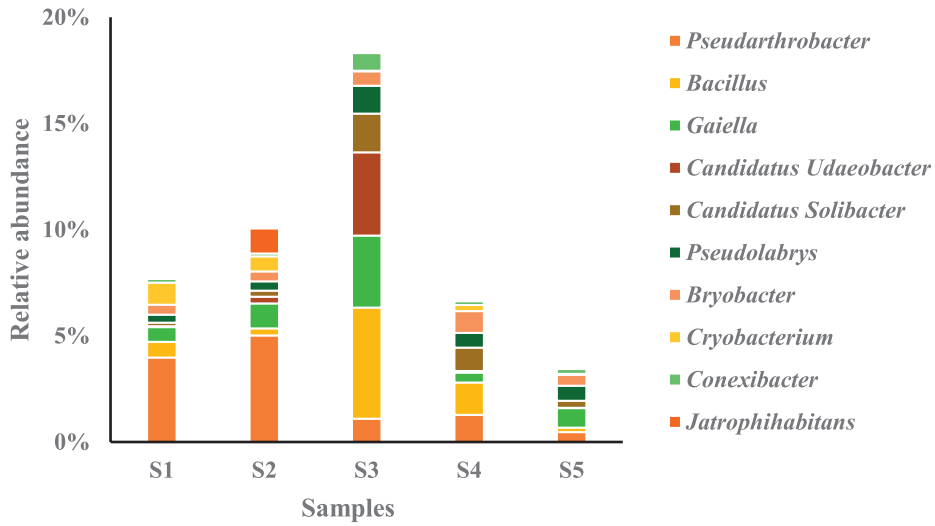

Fig. 3. Relative abundances of the top 10 genera in lake wetland sediment bacterial communities (excluding unclassified taxa).

metabolic activity further indicated that the sediment bacterial community in vegetated zones exhibited higher nutrient cycling and organic matter decomposition activity.

Functional Prediction of the Sediment Bacterial Community

Based on the FAPROTAX functional prediction results, the number of OTUs associated with P cycling accounted for less than 1% of the total; thus, only the functional prediction results related to C, N, and S cycling were focused on and reported in Supplementary Table 5S. In this study, the number of bacterial OTUs linked to N cycling was relatively high across all sampling zones, which was consistent with the research findings of Wang et al. [27] and reflected the important role of sediment bacterial communities in the N biogeochemical cycle of lake wetlands.

Previous studies have suggested a close intrinsic link between sediment DOM composition and bacterial metabolic functions [44]. Landa et al. [45] proposed that variations in DOM sources may alter the structural composition of bacterial communities but have no significant effect on their functional diversity. In contrast, Yu et al. [46] demonstrated that N–containing (CHON) and S–containing (CHOS) molecular components in DOM can provide key nutrient elements (e.g., N and S) for bacterial growth and metabolism, thereby regulating the distribution and abundance of functional bacterial groups involved in corresponding biogeochemical cycles. The results of this study showed that the number of OTUs related to aromatic compound degradation in S1, S2, and S3 was significantly higher than that in S4 and S5 (p<0.05), which indicated that a larger number of functional bacteria were involved in the degradation of refractory humic–like substances in the shallow water zones (depth<80 cm) of the lake wetland, and the metabolic process of aromatic compound decomposition was more active in these areas. Notably, the number of OTUs associated with cellulolysis in the emergent plant zone (S3) was significantly higher than in the other sampling zones (p<0.05), which was closely related to the large input of plant litter driven by high plant biomass in this zone; the abundant cellulose substrates further enriched the functional bacterial groups with cellulolytic metabolic capacity, forming a clear substrate–driven functional differentiation of the bacterial community.

Humic–like substances in sediment DOM have been confirmed to enhance the resource utilization capacity of bacterial communities by providing stable carbon sources and energy substrates [40], and this finding was also verified in the present study. The number of OTUs related to C, N and S cycling in the S5 (non–vegetated zone) was the lowest among all sampling zones, which was consistent with the low content of allochthonous humic–like substances in the sediment of this zone; the lack of sufficient organic carbon and nutrient substrates further led to the weak metabolic activity of bacterial communities, resulting in a minor contribution to the biogeochemical cycling of key elements. In contrast, the high contents of humic–like substances in S2 and S3 significantly enriched the functional bacterial groups associated with C, N, and S cycling and enhanced their metabolic activities. Specifically, the S3 zone had significantly more OTUs related to methanotrophy, respiration of S compounds, sulfite respiration, nitrate reduction, N respiration, ureolysis, hydrocarbon degradation, dark thiosulfate oxidation, S respiration, and thiosulfate respiration than the other zones (p<0.05). This indicated that the emergent plant zone, with high plant biomass and abundant allochthonous DOM input, had the most active bacterial metabolic functions and played a core role in the biogeochemical cycling of C, N, and S in the lake wetland sediment ecosystem.

Correlations between the Sediment DOM Fluorescent Components and Bacterial Community

A significant positive correlation was observed between the contents of the two fulvic acid–like components (C1 and C2) in sediment DOM (p<0.01, Fig. 4), and the humic acid–like component C4 also showed significant positive correlations with both C1 and C2 (p<0.05). These results confirmed that the three humic–like components (C1, C2, and C4) shared similar material sources, which were predominantly derived from allochthonous inputs such as plant litter and terrestrial surface runoff [33]. In contrast, the two protein–like components (C3 and C5) exhibited a positive but statistically insignificant correlation in their content distribution (p>0.05), suggesting that the formation of protein–like substances in the study area was jointly driven by autochthonous microbial metabolism and partial exogenous anthropogenic inputs, which also explained the relatively complex source characteristics of low–molecular–weight protein–like DOM in lake wetland sediments [31].

Previous studies have proposed inconsistent views on the correlation between DOM composition and microbial community structure. Zhang et al. [47] pointed out that microbial metabolism is a key driver of DOM compositional dynamics, and bacteria and fungi exhibit distinct sensitivities to different DOM components. Li et al. [14] emphasized that the chemodiversity of sediment DOM is mainly regulated by eukaryotic and fungal community composition, with no obvious correlation with bacterial and archaeal communities. However, Li et al. [44] observed a significant positive correlation between DOM chemodiversity and bacterial community diversity in aquatic ecosystems, and Wang et al. [34] confirmed that bacterial communities can affect sediment DOM content through catabolic and anabolic processes, thereby further regulating the biogeochemical cycling of C, N, and S. In this study, Mantel's test was used to further explore the correlations between the contents of five DOM fluorescent components and bacterial community diversity indices, phylum–level relative abundances, and the number of OTUs involved in C, N, and S cycling. The results showed that the bacterial community diversity and composition were significantly correlated with fulvic acid–like substances (C1 and C2) (p<0.05), and the bacterial community composition was significantly correlated with humic–like substances (C1, C2, and C4) (p<0.05 or p<0.01). In contrast, no statistically significant correlations were found between bacterial community characteristics and protein–like substance contents (p>0.05). Meanwhile, the number of bacterial OTUs involved in C, N, and S biogeochemical cycling also showed significant positive correlations with humic–like substance contents (p<0.05 or p<0.01). This phenomenon may be attributed to the diverse source pathways of protein–like substances and the differential utilization preferences and response patterns of different bacterial taxa to sediment DOM components [15], which was consistent with the research conclusions of Wang et al. [34] and Li et al. [44]. Combined with the results of our previously published study [35], it can be definitively confirmed that allochthonous humic–like substances in lake wetland sediments have significant coupling correlations with both bacterial and fungal communities, and are the key DOM components regulating the structure and function of sediment microbial communities.

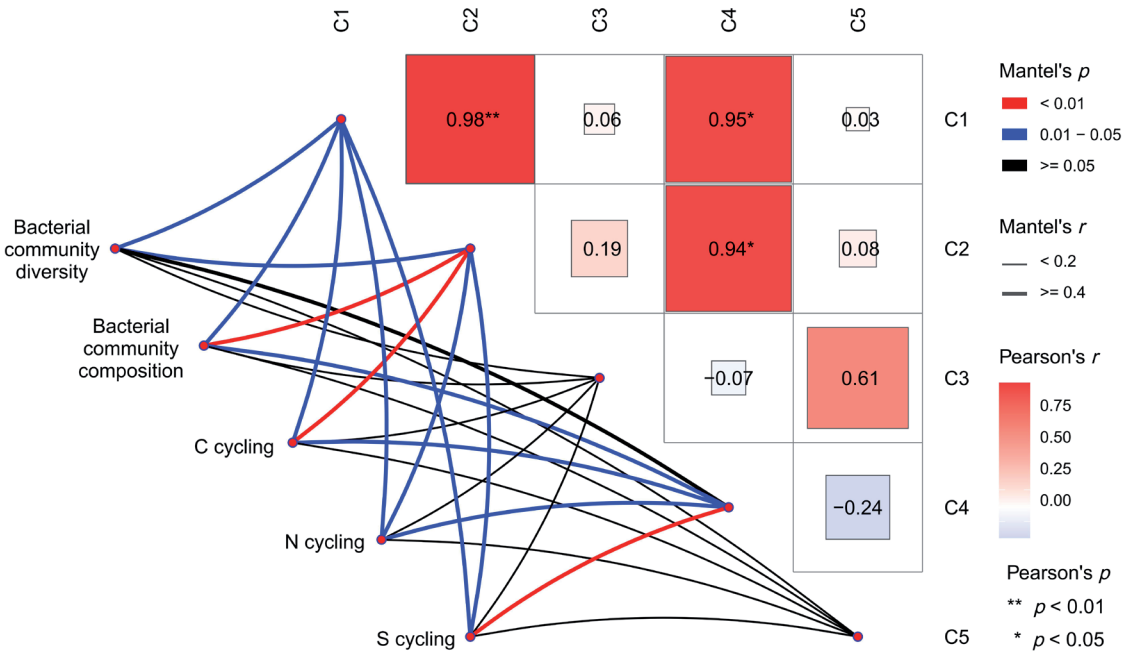

Fig. 4. Correlation between DOM fluorescent components and bacterial community structure in lake wetland sediment.

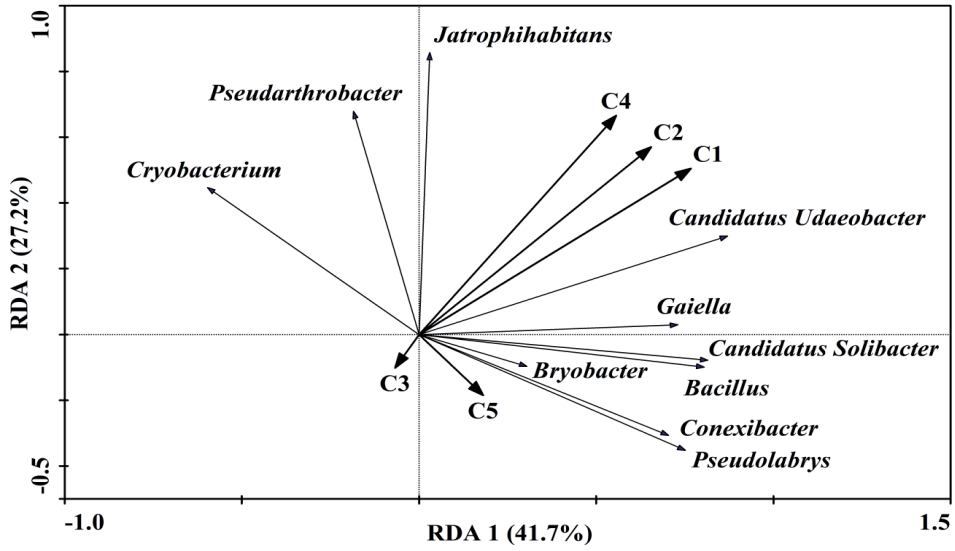

Fig. 5. RDA of the DOM fluorescent components and the top 10 genera of bacterial communities (excluding unclassified taxa) in lake wetland sediment.

RDA was further conducted to explore the correlations between the contents of the five DOM fluorescent components and the relative abundances of the top 10 dominant bacterial genera (Fig. 5). The results showed that the three humic–like components (C1, C2, and C4) were positively correlated with *Pseudarthrobacter*, *Bacillus,* and *Gaiella*, indicating that the increase in humic–like substance contents could promote the enrichment of these three genera in the sediment bacterial community. In contrast, these three dominant genera showed a negative correlation with the tryptophan–like component C3, and *Pseudarthrobacter* was also negatively correlated with the tyrosine–like component C5, while *Bacillus* and *Gaiella* exhibited a positive correlation with C5. These findings confirmed the specific roles of different bacterial taxa in the transformation and decomposition of DOM components [46] and indicated that specific bacterial genera could selectively utilize different DOM fluorescent components, thereby affecting the synthesis and degradation processes of sediment DOM [38, 44]. In particular, the positive correlation between humic–like substances and C5 suggested that the tyrosine–like component C5 in the study area was more likely to be a by–product generated during the bacterial degradation of allochthonous humic–like substances, whereas C3 was mainly derived from autochthonous microbial metabolism and exogenous anthropogenic inputs, which further explained the insignificant correlation between C3 and C5 contents.

The VPA results showed that humic–like substances independently explained 56.90% of the bacterial community variance, while protein–like substances only explained 6.95% of the variance, and the two types of DOM components jointly explained 1.80% of the total variance. These quantitative results further demonstrated that humic–like substances had a far stronger regulatory effect on the composition of the sediment bacterial community than protein–like substances, and were the core DOM components driving the enrichment and differentiation of bacterial communities in lake wetland sediments. This result also verified the previous finding [40] that humic–like substances can significantly enhance the resource utilization capacity of sediment bacterial communities.

Conclusions

Differences in water depth in lake wetlands can affect vegetation distribution patterns. Particularly in zones covered by helophytes and emergent plants, high plant biomass produces more plant residues, which not only increases the sediment DOM content but also elevates the proportion of allochthonous substances, thereby enhancing the humification degree of sediment DOM. This, in turn, increases the diversity and metabolic activity of sediment bacterial communities. Sediment bacterial communities regulate the stability of sediment DOM primarily by participating in the synthesis and decomposition of humic–like substances. These results provide a scientific basis for exploring the regulatory mechanisms underlying DOM stability in lake wetland sediments. Future research will employ high–precision techniques, spatiotemporal multi–scale observations, and multi–omics integration to elucidate DOM's molecular transformation pathways and microbial regulatory mechanisms, thereby providing scientific support for assessing wetland DOM stability and carbon pool dynamics.

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AI Usage Declaration Statement

The authors used DeepSeek for English native-language polishing of this manuscript.

Conflict of Interest

The authors declare no conflict of interest.

References

1. DAS B.K., SAHA A., DAS A.K., CHANDRA P., MONDAL K., KAYAL T., CHAKRABORTY S., BHATTACHARYA S., SAHOO B.K., JANA C. Assessment of the physicochemical properties of the sediment from the Gangetic floodplain wetlands of West Bengal, India, with GIS and a statistical approach. Frontiers in Environmental Science. **12**, 1397715, **2024**.
2. HE D.M., LI L.W., ZHOU R.Y., QIU S.M., XING W., YUAN Y.D. Urban wetland sediments in Yangzhou: physicochemical properties, microbial communities, and functional associations. Microorganisms. **13** (8), 1843, **2025**.
3. BAI X., CHEN K.N., CHEN X.M. Short–time response in growth and sediment properties of *Zizania latifolia* to water depth. Environmental Earth Sciences, **70**, 2847, **2013**.
4. WANG Y.K., DAI J.F., JIANG F., WAN Z.P., ZHANG S.P. Coupled effects of water depth, vegetation, and soil properties on soil organic carbon components in the Huixian wetland of the Li river basin. Land, **14** (3), 584, **2025**.
5. STOORVOGEL M.M., DE SMIT J.C., WIESEBRON L.E., VAN BELZEN J., VAN DE KOPPEL J., TEMMERMAN S., BOUMA T.J. Plant species, inundation, and sediment grain size control the development of sediment stability in tidal marshes. Ecological Applications, **35** (1), e3078, **2025**.
6. GUO B.X., LIU Y.Q., WANG J.J., ZHENG Q., SHI Q., HE C., JIAO N.Z. Environmental and microbial factors shape dissolved organic matter across multiple ecosystems. Communications Earth & Environment, **6** (1), 917, **2025**.
7. HAN L., HU A., MZUKA H.L., CHEN X.T., SHEN J., WANG J.J. Molecular properties of dissolved organic matter across earth systems: a meta–analysis. Journal of Earth Science, **36** (6), 2674, **2025**.
8. CHEN M., HUR J. Pre–treatments, characteristics, and biogeochemical dynamics of dissolved organic matter in sediments: A review. Water Research, **79**, 10, **2015**.
9. ZHANG H.Z., CHENG D.D., SONG J.X., ZHANG Y.X. Spatiotemporal fate of dissolved organic matter (DOM) in aquatic systems: drivers, patterns and global implications. Journal of Hydrology, **661** (Part B), 133637, **2025**.
10. ZHAO J., YUAN Q.S., LEI X., LIEKE T., LIU Y., STEINBERG C.E.W., PAN B., XING B.S. The double–edged environmental effect of dissolved organic matter in global climate change. Environmental and Biogeochemical Processes, **1**, e009, **2025**.
11. AMRUTHA K.K., BEENA V.I. Environmental significance of dissolved organic matter in soils: A review. The Pharma Innovation Journal, **11** (11S), 95, **2022**.
12. D'ANDRILLI J., SILVERMAN V., BUCKLEY S., ROSARIO–ORTIZ F.L. Inferring ecosystem function from dissolved organic matter optical properties: a critical review. Environmental Science & Technology, **56** (16), 11146, **2022**.
13. ZHANG X.Y., ZHU S.H., LAN X., TIAN S.Y., LU J., TANG J.H., CHEN X.L., GAO L., LV J.T., YIN Y.G., YANG G.L., JIANG T., TANG Z.W., WANG D.Y. Influence of duckweed (Lemnaceae) on the characteristics of dissolved organic matter (DOM) in urban ponds. Hydrobiologia, **853** (5), 1433, **2026**.
14. LI W., LIU N., LI J., WANG B.L., SHI X.J., LIANG X., YANG M.L., XU S., LIU C.Q. Chemodiversity of dissolved organic matter is governed by microbial biogeography in inland waters. Environmental Science & Technology, **57** (20), 7753, **2023**.
15. WANG S.Z., HEAL K.V., ZHANG Q., YU Y.C., TIGABU M., HUANG S.D., ZHOU C.F. Soil microbial community, dissolved organic matter and nutrient cycling interactions change along an elevation gradient in subtropical China. Journal of Environmental Management, **345**, 118793, **2023**.
16. ZHOU L., WU Y.H., ZHOU Y.Q., ZHANG Y.L., XU H., JANG K.S., DOLFING J., SPENCER R.G.M., JEPPESEN E. Terrestrial dissolved organic matter inputs drive the temporal dynamics of riverine bacterial ecological networks and assembly processes. Water Research, **249**, 120955, **2024**.
17. ZHANG P.L., ZHANG H.X., HUO S.L., ZHANG J.T., WENG N.Y., LI Y., MA C.Z. Research frontiers of interaction between microbes and dissolved organic matter in lakes. Environmental Monitoring in China, **40** (5), 171, **2024** [In Chinese].
18. MURPHY K.R., STEDMON C.A., GRAEBER D., BRO R. Fluorescence spectroscopy and multi–way techniques. PARAFAC. Analytical Methods, **5** (23), 6557, **2013**.
19. XU X.G., WU C., XIE D.Y., MA J. Sources, migration, transformation, and environmental effects of organic carbon in eutrophic lakes: A critical review. International Journal of Environmental Research and Public Health, **20** (1), 860, **2023**.
20. HUAN J., ZHENG Y.C., XU X.G., ZHANG H., YUAN J.L., LI X.C., ZHOU L.F. Characterization of DOM sources and distribution in Changdang Lake based on 3D fluorescence combined with PARAFAC approach. Spectroscopy and Spectral Analysis, **45** (2), 591, **2025** [In Chinese].
21. LI L., WANG Y., ZHANG W.J., YU S.L., WANG X.Y., GAO N.Y. New advances in fluorescence excitation–emission matrix spectroscopy for the characterization of dissolved organic matter in drinking water treatment: A review. Chemical Engineering Journal, **381**, 122676, **2020**.

22. MA Z.N., GUO C.Z., ZHANG H., SONG S., GONG Y. Q., SHOU C.Y., YUE F.J. Analysis the source and spatiotemporal variation of dissolved organic matter in the Chaohe river watershed. Environmental Science, **46** (3), 1395, **2025** [In Chinese].
23. AO J., WANG T., CHANG R.Y. Application of the Three–dmensional excitation–emission matrix fluorescence spectroscopy in the analysis of soil dissolved organic matter components. Chinese Journal of Soil Science, **53** (3), 738, **2022** [In Chinese].
24. TU S.Q., LI Q.Q., NIE L., GAO H.J., YU H.B. Applying fluorescence spectroscopy with absolute principal component coefficient to explore dynamic migration of DOM fractions from an urbanized river during torrential rainfall. Spectrochimica Acta, Part A. Molecular and Biomolecular Spectroscopy, **314**, 124206, **2024**.
25. LIU L., FANG Y.C., SUN X.L. Research progress of organic matter based on three–dimensional fluorescence spectroscopy–parallel factor analysis (EEM–PARAFAC). Water Purification Technology, **41** (10), 7, **2022** [In Chinese]
26. HE J., WU X., ZHI G.Q., YANG Y., WU L.F., ZHANG Y., ZHENG B.H., QADEER A., ZHENG J.L., DENG W.M., ZHOU H.B., SHAO Z. Fluorescence characteristics of DOM and its influence on water quality of rivers and lakes in the Dianchi Lake basin. Ecological Indicators, **142**, 109088, **2022**.
27. WANG J.L., LI C., WU W., REN L., DONG Y.H. Fluorescence spectral characteristics of DOM and its effects on the bacterial community structure in Bosten Lake, China. Journal of Freshwater Ecology, **40** (1), 2501976, **2025**.
28. GUO T.B., XU H.C. Molecular weight–and type–dependent heterogeneity in dissolved organic matter binding with heavy metals in natural waters. Polish Journal of Environmental Studies, **2025**.
29. REN Y., YU G., SHI C.P., LIU L.M., GUO Q., HAN C., ZHANG D., ZHANG L., LIU B.X., GAO H., ZENG J., ZHOU Y., QIU Y.H., WEI J., LUO Y.C., ZHU F.J., LI X.J., WU Q., LI B., FU W.Y., TONG Y.L., MENG J., FANG Y.H., DONG J., FENG Y.T., XIE S.C., YANG Q.Q., YANG H., WANG Y., ZHANG J.B., GU H.D., XUAN H.D., ZOU G.Q., LUO C., HUANG L., YANG B., DONG Y.C., ZHAO J.H., HAN J.C., ZHANG X.L., HUANG H.S. Majorbio Cloud: A one–stop, comprehensive bioinformatic platform for multiomics analyses. iMeta, **1** (2), e12, **2022**.
30. HUANG Y.Y., LIU T.T., WANG G.Y., CHU Z.S., GAO S.J., PAN Y.F., ZHENG B.H. Composition characteristics and source tracing of dissolved organic matter of lacustrine sediment in northeastern China: A case study of Lake Kulipao. Journal of Lake Sciences, **36** (1), 165, **2024**.
31. LONG Y.C., WANG L.Y., HU J., JIANG J. Spatial and temporal distribution characteristics of DOM in sediments from Guizhou Caohai based on UV–Vis and EEM–PARAFAC. Research of Environmental Sciences, **37** (12), 2698, **2024** [In Chinese].
32. LÜ Y., SONG H.Y., PAN X.J., JIANG J.Y., TAN W., LI Y.J., SHI D.N. Source apportionment of dissolved organic matter in the Yiluo River using the positive matrix factorization model. Research of Environmental Sciences, **38** (11), 2394, **2025** [In Chinese].
33. LIU D.P., GAO H.J., CUI B., YU H.B., YANG F. Fluorescence spectra and multivariate statistical model characterization of DOM composition structure of Baitapu River sediment. Journal of Environmental Engineering Technology, **11** (2), 249, **2021** [In Chinese].
34. WANG X.D., LI H.M., ZHANG R.K., LIU X.D., NAN F.R., LIU Q., LV J.P., FENG J., XIE S.L., LIU Y. Bacterial community and dissolved organic matter networks in urban river: The role of human influence. Environmental Research, **263**, 120021, **2024**.
35. SHI C.Q., LI Y., MENG L.B., HU Y., JIN L. Characteristics of dissolved organic matter fluorescence components in wetland surface sediment and their correlation with fungal communities. Spectroscopy and Spectral Analysis, **45** (1), 191, **2025** [In Chinese]
36. ZHANG J., TAN J.J., WANG Y.J. Spatial differences of dissolved organic matter composition and humification in an artificial lake. Water Science & Technology, **90** (3), 995, **2024**.
37. CHEN J., LI Z.W., JIN C.S., WEN J.J., NIE X.D., WANG L. Characteristics and sources of DOM in lake sediments under different inundation environments. Environmental Science, **43** (9), 4566, **2022** [In Chinese]
38. LI S.D., FANG J., ZHU X.S., SPENCER R.G.M., ÁLVAREZ–SALGADO X.A., DENG YC., HUANG T., YANG H., HUANG C.C. Properties of sediment dissolved organic matter respond to eutrophication and interact with bacterial communities in a plateau lake. Environmental Pollution, **301**, 118996, **2022**.
39. STADLER M., EJARQUE E., KAINZ M. J. In–lake transformations of dissolved organic matter composition in a subalpine lake do not change its biodegradability. Limnology and Oceanography, **65** (7), 1554, **2020**.
40. ZHANG N., LIU J.Y., ZHANG T.Y., TENG Y.M., MENG Z.Y., LIU F.D. Sources and composition of sediment dissolved organic matter determine the ecological strategies of bacteria in rivers: evidence, mechanism, and implications. Journal of Soils and Sediments, **23** (6), 2613, **2023**.
41. NALOKA K., KUNTAVEESUK A., MUANGCHINDA C., CHAVANICH S., VIYAKARN V., CHEN B., PINYAKONG O. *Pseudomonas* and *Pseudarthrobacter* are the key players in synergistic phenanthrene biodegradation at low temperatures. Scientific Reports, **14** (1), 11976, **2024**.
42. HE H.H., LI Y.R., ZHANG L., DING Z.Y., SHI G.Y. Understanding and application of *Bacillus* nitrogen regulation: A synthetic biology perspective. Journal of Advanced Research, **49**, 1, **2023**.
43. WEI L., WANG Y., LI N., ZHAO N., XU S.X. Bacteria–like *Gaiella* accelerate soil carbon loss by decomposing organic matter of grazing soils in alpine meadows on the Qinghai–Tibet plateau. Microbial Ecology, **87** (1), 104, **2024**.
44. LI H.Y., WANG H., WANG H.T., XIN P.Y., XU X.H., MA Y., LIU W.P., TENG C.Y., JIANG C.L., LOU L.P., AMOLD W., CRALLE L., ZHU Y.G., CHU J.F., GLIBERT J.A., ZHANG Z.J. The chemodiversity of paddy soil dissolved organic matter correlates with microbial community at continental scales. Microbiome, **6** (1), 187, **2018**.
45. LANDA M., COTTRELL M.T., KIRCHMAN D.L., KAISER K., MEDEIROS P.M., TREMBLAY L., BATAILLER N., CAPARROS J., CATALA P., ESCOUBEYROU K., ORIOL L., BLAIN S., OBERNOSTERER I. Phylogenetic and structural response of heterotrophic bacteria to dissolved organic matter of different chemical composition in a continuous

culture study. Environmental Microbiology, **16** (6), 1668, **2013**.
46. YU S.Y., LV J.T., JIANG L., GENG P.Y., CAO D., WANG Y.W. Changes of soil dissolved organic matter and its relationship with microbial community along the Hailuogou Glacier forefield chronosequence. Environmental Science & Technology, **57** (9), 4027, **2023**.
47. ZHANG S.Q., YOU J.H., ZHU X.F., JI G.D. Response of microbe–DOM interactions to bioavailability in heterogeneous water diversion systems. Water Research, **291**, 125254, **2026**.

Supplementary Material

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