



Eutrophic levels and algae growth increase emissions of methane and volatile sulfur compounds from lakes[☆]

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ABSTRACT

Eutrophic lakes are hot spots of CH₄ and volatile sulfur compound (VSC) emissions, especially during algal blooms and decay. However, the response of CH₄ and VSC emissions to lake eutrophication and algae growth as well as the underlying mechanisms remain unclear. In this study, the emissions of CH₄ and VSCs from four regions of Lake Taihu with different eutrophic levels were investigated in four months (i.e., March, May, August and December). The CH₄ emissions ranged from 20.4 to 126.9 mg m⁻² d⁻¹ in the investigated sites and increased with eutrophic levels and temperature. H₂S and CS₂ were the dominant volatile sulfur compounds (VSCs) emitted from the lake. The CH₄ oxidation potential of water ranged from 2.1 to 14.9 μg h⁻¹ L⁻¹, which had positive correlations with trophic level index and the environmental variables except for the NH₄⁺-N concentration. Eutrophic levels could increase the abundances of bacteria and methanotrophs in lake water. *α-Proteobacteria* methanotroph *Methylocystis* was more abundant than *γ-Proteobacteria* methanotrophs in March and May, while the latter was more abundant in August and November. The relative abundance of *Cyanobacteria*, including *Microcystis*, *A. granulata* var. *angustissima* and *Cyanobium* had significantly positive correlations with temperature, turbidity, SO₄²⁻-S, and total sulfur. Partial least squares path modelling revealed that the algal growth could promote VSC emissions, which had a positive correlation with CH₄ oxidation potential, likely due to the positive correlation between the CH₄ and VSC emissions from lakes. These findings indicate that water eutrophication and algae growth could increase the emissions of CH₄ and VSCs from lakes. Controlling algae growth might be an effective way to mitigate the emissions of CH₄ and VSCs from freshwater lakes.

CRedit authorship statement

Jing Wang: Methodology, Data curation, Formal analysis, Writing - original draft, Investigation. **Zhi-Peng Wei:** Sampling, Methodology, Data curation; **Yi-Xuan Chu:** Data curation, Formal analysis, Investigation. **Guangming Tian:** Conceptualization, Resources, Supervision, Writing - review & editing. **Ruo He:** Conceptualization, Methodology, Resources, Supervision, Project administration, Writing - review & editing.

1. Introduction

Methane (CH₄) is the second most important greenhouse gas after CO₂, accounting for approximately 20% of the greenhouse effect of global warming (Wuebbles and Hayhoe, 2002). Lake is an important natural source of CH₄ emissions, accounting for ~3% of the Earth's continental surface area and is responsible for approximately 6%–16% (8–48 Tg yr⁻¹) of global CH₄ emissions (Bastviken et al., 2004; Bastviken et al., 2011; Downing et al., 2006). Recently, due to anthropogenic activities and agricultural inputs of nutrients, algae growth and decay in eutrophic lakes have led to a large amount of organic matter degradation (Perga et al., 2016; Xiao et al., 2020) and CH₄ release (West et al.,

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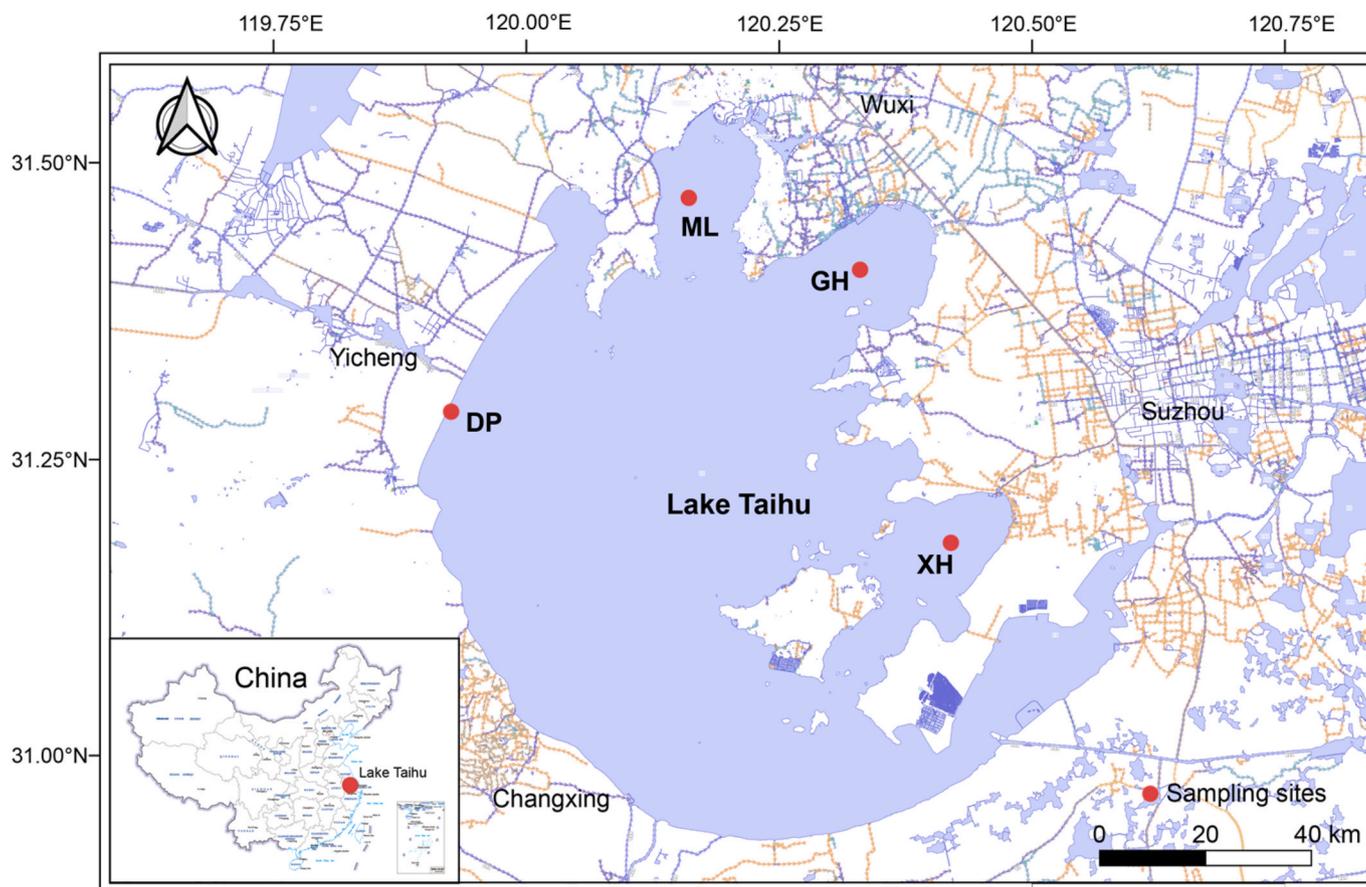


Fig. 1. Location of the four sampling positions, i.e., ML, DP, GH and XH, in Lake Taihu, China.

2016; Xiao et al., 2017). It is estimated that CH_4 emissions can be increased by 30%–90% with increase in eutrophication level from lakes and impoundments during the 21st century and can affect the C cycle and greenhouse effect in lacustrine ecosystems (West et al., 2016; Beaulieu et al., 2019).

Aerobic CH_4 oxidation is the major sink of CH_4 in freshwater lakes (Borrel et al., 2011). Methanotrophs are a unique group of bacteria that can use CH_4 as the sole carbon and energy source (Hanson and Hanson, 1996). It has been reported that methanotrophs can oxidize more than 90% of CH_4 produced from sediments and play an important ecological function in mitigating CH_4 emissions from freshwater lake systems (Deng et al., 2017; Michaud et al., 2017). Based on the phylogeny, morphological and physiological characteristics, aerobic methanotrophs can be divided into three clades: γ -Proteobacteria, α -Proteobacteria and Verrucomicrobia (Bowman, 2006; Semrau et al., 2010). The initial step of CH_4 oxidation to CO_2 is catalysed by methane monooxygenase (MMO), which includes particulate MMO (pMMO) and soluble MMO (sMMO) encoded by *pmoA* and *mmoX* genes, respectively (Smith and Murrell, 2009). The *pmoA* gene has been widely used as a biomarker to identify aerobic methanotrophs due to its existence in almost all known methanotrophs except *Methyloferula* and *Methylocella* (Dumont and Murrell, 2005).

The community structure and activities of methanotrophs vary with environmental conditions (i.e., water physiochemical variables) in lakes. Mayr et al. (2020) reported that *Methylosoma*, *Methylobacter* and *Crenothrix* were the main methanotrophs in the hypolimnion of Lake Rotsee in Switzerland, and their community varied with water temperature, nutrients, dissolved oxygen (DO) and CH_4 concentrations. The relative abundance of *Methylobacter* increase with decreasing water temperature and increasing DO concentration, while the relative abundance of *Crenothrix* increase with increasing CH_4 concentration (Mayr

et al., 2020). Yang et al. (2019) found that lake eutrophication could increase the abundance of α -Proteobacteria methanotrophs, while the lower total nitrogen (TN) concentration in the water was suitable for the growth of *Methylobacter*. The CH_4 oxidation potential (MOP) is reported to be positively correlated with the oxidation–reduction potential (ORP) of overlying water and negatively correlated with the $\text{NH}_4^+\text{-N}$ concentration of overlying water in Dianchi Lake, China (Yang et al., 2019). An increase in MOP is also observed to be coupled with the higher abundance of α -Proteobacteria methanotrophs (Lin et al., 2005). Thus, environmental variables are important factors influencing methanotrophic community and MOP, thereby resulting in variations in CH_4 release from lakes.

The growth and decay of algae in eutrophic lakes not only release a large amount of CH_4 , but also produce many odour substances, mainly volatile sulfur compounds (VSCs), which greatly affect the water quality of lakes and the lives of the surrounding residents (Wu et al., 2021a). VSCs such as H_2S , CH_3SH , $(\text{CH}_3)_2\text{S}$ and $(\text{CH}_3)_2\text{S}_2$ can be produced during algae accumulation, bloom and decay (Liu et al., 2019; Liu et al., 2020). The VSCs in eutrophic lakes can cause odour pollution owing to their low olfactory threshold (Chen et al., 2010; Lee et al., 2017). In 2007, high concentrations of VSCs, including CH_3SH , $(\text{CH}_3)_2\text{S}$, $(\text{CH}_3)_2\text{S}_2$ and $(\text{CH}_3)_2\text{S}_3$, were responsible for the drinking water crisis occurred in Wuxi city, China (Zhang et al., 2010). Moreover, VSCs are toxic to microorganisms such as nitrifying bacteria and methanotrophs (Börjesson, 2001; Zhang et al., 2016). Previous studies have reported that H_2S , CS_2 , $(\text{CH}_3)_2\text{S}$ and CH_3SH can inhibit CH_4 oxidation in various environments (Börjesson, 2001; Lee et al., 2011). However, Kim et al. (2013) found that $(\text{CH}_3)_2\text{S}$ had a positive effect on methanotrophic performance in a biofilter. Eutrophic lakes are hot spots of emissions of CH_4 and VSCs, especially during algal blooms and decay. Recently, water eutrophication increased CH_4 emissions from lakes and the estimation of increased

CH₄ emissions have been reported (Zhou et al., 2020; Sun et al., 2021). However, the response of CH₄ and VSC emissions to lake eutrophication and algae growth as well as their correlations with the environmental variants, community structure and activities of methanotrophs remain unclear.

The objective of this study was to explore the impacts of eutrophic levels and algae growth on the emissions of CH₄ and VSCs from eutrophic lakes. Lake Taihu, a typical eutrophic lake in China, was selected for the research object. The physicochemical properties of water were detected in four regions of Lake Taihu and four months (i.e., March, May, August and November) to investigate temporal and spatial eutrophic levels. The emissions of CH₄ and VSCs were determined with an estimation of MOP in water. Additionally, the abundance and community structure of bacteria and methanotrophs in water were analysed as well as effects of environmental variables on microbial community and CH₄ emissions. The obtained results add to our understanding of the impacts of algal growth and decay on microbial metabolism, especially the activities and community structure of methanotrophs, and helps to reduce the emissions of CH₄ and VSCs from eutrophic lakes.

2. Materials and methods

2.1. Study sites and sampling

Lake Taihu is the third largest freshwater lake in China, with an average depth of ~1.9 m (Qin et al., 2007). Lake Taihu is a eutrophic lake with algae blooms from April to October each year (Ji et al., 2021). The trophic level in the northwestern area is much heavier than that in the southeastern area of Lake Taihu due to the higher concentrations of nutrients and prevailing southeast wind (Meng et al., 2021). We chose four regions with different trophic levels, including Meiliang Bay (ML), Gonghu Bay (GH), Xuhu Bay (XH) and the Dapu River mouth (DP), for sampling (30°55'40"-31°32'58" N, 119°52'32"-120°36'10" E, Fig. 1). ML is in the northern area of Lake Taihu with higher cyanobacterial biomass owing to the prevailing southeast wind (Ji et al., 2021). GH is in the northeastern area of Lake Taihu with more aquatic macrophytes, which serves as an important centralized source of drinking water for Suzhou and Wuxi cities in Jiangsu Province (Ding et al., 2020). XH is in the eastern area of Lake Taihu with less algae growth (Liu et al., 2016). DP is in the western area of Lake Taihu with a heavier eutrophic level owing to anthropogenic inputs of nutrients (Shao et al., 2018). Gas and water samples were collected from the four regions in March, May, August and November 2019. Three sampling sites with distances greater than 10 m from each other were conducted in each region. Gas and water samples in triplicate were taken from each sampling site.

Approximately 2 L of surface water at a depth of 0.5 m was collected from each site using a Plexiglass sampler. Approximately 200 mL water sample was taken for measuring AVS with the addition of 220 g L⁻¹ Zn (Ac)₂ to stabilize sulfide (Dong et al., 2012). Approximately 120 mL water sample was fully filled into a serum bottle to determine the dissolved concentrations of CH₄ and VSCs. The temperature, DO, pH, turbidity, Chl-a and phycocyanin concentrations in the surface water at a depth of 0.5 m were detected *in situ* using a multiparameter water quality sonde (YSI 6600, Yellow Springs, USA). The emissions of CH₄ and VSCs were measured using the floating chamber technique as described previously (Gonzalez-Valencia et al., 2014; Wang et al., 2022). The floating chamber consisted of a plexiglass cylinder with an open surface of 0.4 m² and a headspace volume of 6.5 × 10⁻² m³. The floating chamber was equipped with a sampling port and connected with the anchored sampling ship through a rope. Gas samples were withdrawn using a syringe from the floating chamber every 20 min within a 1-h period, and then stored in pre-vacuumed 20 mL vials. Three floating chambers with 1-m interval were used to measure gas emissions in each sampling site.

2.2. MOP determination

A 20-mL water sample was put into a 100-mL sterile serum vial, which was purged with high purity air (99.9%) for ~5 min, and then sealed with a butyl rubber stopper. Purity CH₄ (99.9%) was injected to obtain a concentration of 0.1% (v/v) in the headspace of the vial. Autoclaved water was used as a control. Each water sample was performed in triplicate. The serum vials were placed on a shaker at 130 rpm and 25 °C. A 100-μL gas sample in the headspace of the serum vials was withdrawn to determine the CH₄ concentration in 12-h intervals. The MOP was calculated by a zero-order decrease in the CH₄ concentration in the headspace of the vials (Wang et al., 2011).

2.3. Analytical methods

A part of the water samples was used for analysing physicochemical variables, including concentrations of chemical oxygen demand (COD), total nitrogen (TN), NO₃⁻-N, NH₄⁺-N, total sulfur (TS), SO₄²⁻-S, total iron (TFe) and total phosphorus (TP) to investigate temporal and spatial eutrophic levels. The TP concentration was detected as described by Xiang and Zhou (2011). The concentrations of COD, TN, NH₄⁺-N and NO₃⁻-N were determined as described previously (Eaton et al., 2005). The concentrations of TS, AVS and SO₄²⁻-S were determined using the method described by He et al. (2018). The TFe concentration was detected as described by Yin et al. (2008). The detection limit for COD, TN, NO₃⁻-N, NH₄⁺-N, TS, SO₄²⁻-S, AVS, TFe and TP are 0.2, 0.02, 0.06, 0.1, 0.01, 0.5, 0.003, 0.01 and 0.03 mg L⁻¹, respectively.

The concentrations of CH₄ and VSCs in the gas samples were measured using a gas chromatograph equipped with a thermal conductivity detector (GC-TCD) and a flame ionization detector (FID) (Wang et al., 2011), and HC-3 trace sulfur analyser equipped with a flame photometric detector, respectively (Chen et al., 2017). The GC-TCD was equipped with a GDX-104 column of 2 m with N₂ used as the carrier gas at a flow of 20 mL min⁻¹. The conditions for the GC-FID: DB-624 capillary column; the temperatures of the oven, injector and detector were 120, 250 and 220 °C, respectively. The HC-3 trace sulfur analyser was equipped with a flame photometric detector as described previously (Chen et al., 2017). The emissions of CH₄ and VSCs were calculated as described previously (Gonzalez-Valencia et al., 2014).

The dissolved concentrations of CH₄ and VSCs were determined in triplicate by the headspace equilibration technique (Jacinthé and Groffman, 2001; Xia et al., 2022). In brief, 50 mL purity N₂ was injected into the serum bottle (water sampling bottle) to displace an equal volume of water. The serum bottle was shaken vigorously for 5 min to equilibrate between the headspace and water phases. Then, the gas samples in the headspace were taken to determine the concentrations of CH₄ and VSCs. The dissolved concentrations of CH₄ and VSCs in water were calculated by Henry's law.

2.4. DNA extraction, qPCR analyses and MiSeq sequencing

Approximately 1 L of the water sample was filtered through a 0.22-μm microporous membrane to collect microorganisms in water. Then, the microporous membrane was used to extract total DNA using the E. Z. N.A.™ soil DNA extraction kit (Omega Bio-Tek, Inc., Norcross, USA). The DNA concentration was detected using a NanoDrop 2000. The abundances of the bacterial 16S rRNA gene and *pmoA* in the water samples were determined using qPCR as described by Wang et al. (2022) (Supplementary materials). The abundances of the bacterial 16S rRNA gene and *pmoA* were expressed by copies per litre (copies L⁻¹).

The microbial community structure were analysed by applying MiSeq sequencing. The fragment of the V3-V4 region of the bacterial 16S rRNA gene was amplified with the primer set 338F/806R as described previously (Wang et al., 2022; Supplementary materials). The PCR products were sequenced on an Illumina MiSeq platform at Shanghai Majorbio Bio-Pharm Technology Co., Ltd. The sequencing data

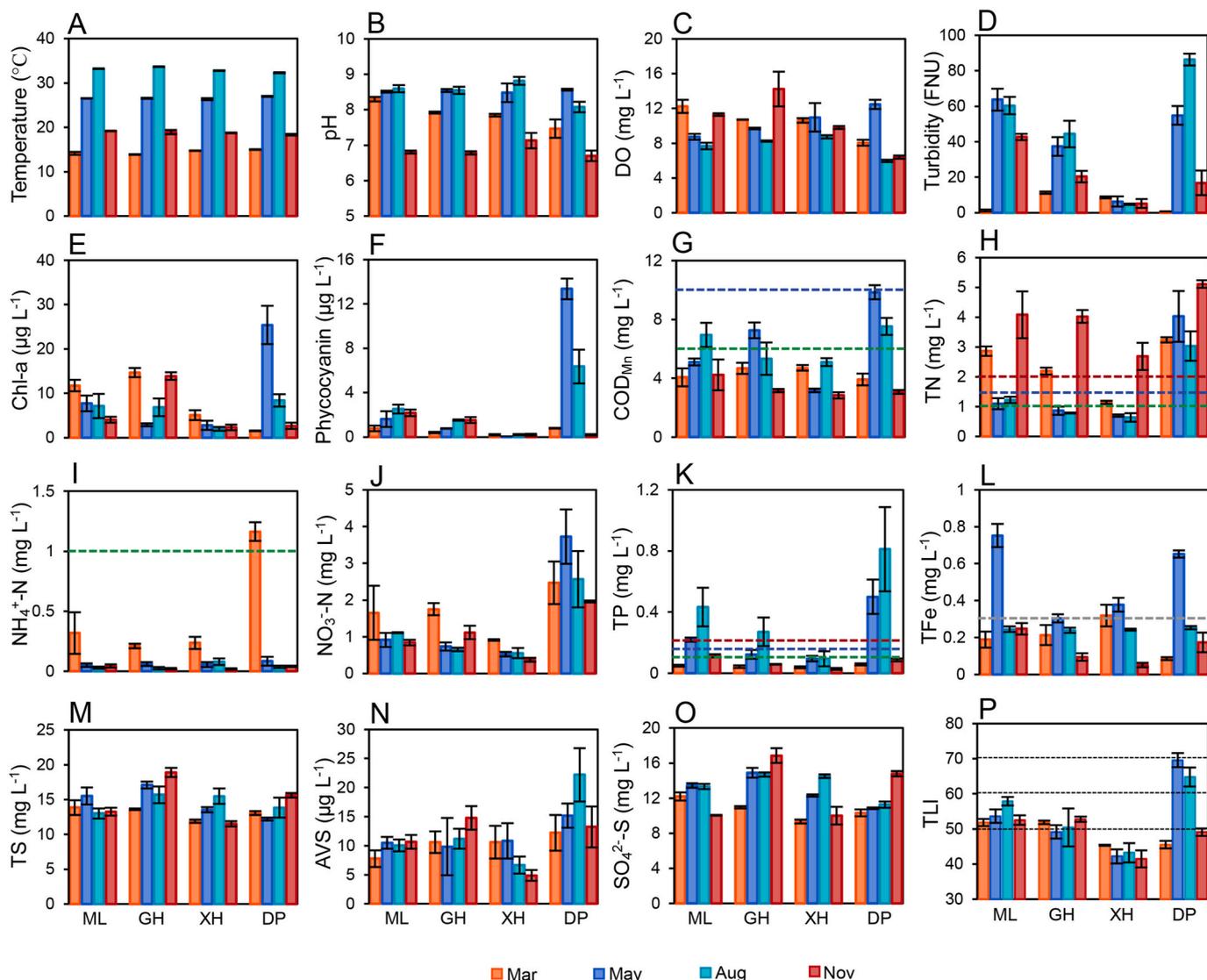


Fig. 2. Temporal and spatial variations of average T (A), pH (B), DO (C), turbidity (D), Chl-a (E), phycocyanin (F), COD_{Mn} (G), TN (H), NH₄⁺-N (I), NO₃⁻-N (J), TP (K), TFe (L), TS (M), AVS (N), SO₄²⁻-S (O) and TLI (P) in water at 0.5-m depth. Error bars indicate standard deviations (n = 9). Green, blue and red dashed lines indicate the limited values of Grade III, IV and V of the environmental quality standards for surface water in China (GB 3838–2002), respectively. Grey dashed line indicates the limited value (≤0.3 mg L⁻¹) of the supplementary standard of the environmental quality standards for surface water in China (GB 3838–2002). Black dashed lines indicate the trophic classification of lake freshwater based on the TLI values.

were analysed on the Majorbio Cloud platform (www.majorbio.com) as described by Wang et al. (2022).

The sequencing data of the bacterial 16S rRNA gene have been deposited in the National Omics Data Encyclopedia (NODE) under the accession number OER241134-241,181.

2.5. Data analysis

The differences among samples were analysed by analysis of variance (ANOVA) using SPSS 23.0. The correlations between the physiochemical variables of water and the microbial community were performed with the packages “corplot” and “psych” in R (4.1.0). Redundancy analysis (RDA) was carried out with the package “vegan” in R (4.1.0) to visualize the community structure dissimilarities and identify the key physiochemical variables.

Trophic lake index (TLI) was used to assess trophic levels of Lake Taihu in different months and regions. TLI was calculated with variables including Chl-a, TP, TN and COD_{Mn} as described by Zhou et al. (2020) and shown in Eqs. (1)–(6).

$$TLI \left(\sum \right) = \sum_{j=1}^m W_j * TLI (j) \tag{1}$$

$$W_j = \frac{r_{ij}^2}{\sum_{j=1}^m r_{ij}^2} \tag{2}$$

$$TLI (Chla) = 10 * [2.5 + 1.086 \ln(Chla)] \tag{3}$$

$$TLI (TP) = 10 * [9.436 + 1.624 \ln(TP)] \tag{4}$$

$$TLI (TN) = 10 * [5.453 + 1.694 \ln(TN)] \tag{5}$$

$$TLI (COD) = 10 * [0.109 + 2.66 \ln(COD)] \tag{6}$$

Where TLI (Σ) is the integrated trophic level index, TLI(j) is the trophic level index of j, W_j is the correlative constant for the TLI of j, r_{ij} is the relative coefficient, which was described by Zhang et al. (2011). j and m represent the parameters (i.e., Chl-a, TP, TN and COD_{Mn}) and the number of parameters, respectively. Based on the TLI (Σ) value, the

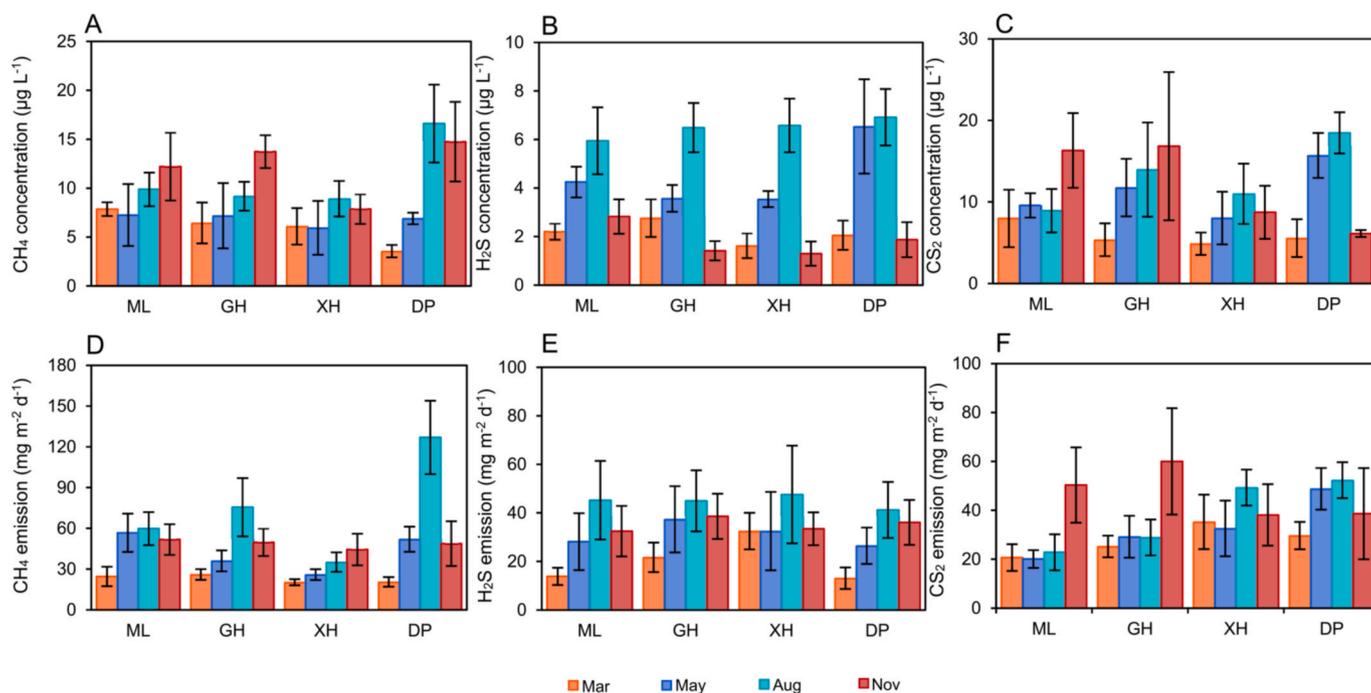


Fig. 3. Average concentrations and emissions of CH₄ (A, D), H₂S (B, E) and CS₂ (C, F) from the four regions in Lake Taihu in four months (i.e., March, May, August and November), respectively. Error bars indicate standard deviations (n = 9).

lake trophic state was classified as oligotrophic (TLI (Σ) < 30), mesotrophic (30 < TLI (Σ) < 50), eutrophic (50 < TLI (Σ) < 60), middle eutrophic (60 < TLI (Σ) < 70), and hypereutrophic (TLI (Σ) > 70).

Partial least squares path modelling (PLS-PM) was performed using R (4.1.0) with the package “plsmpm” to explore the links among latent variables (Petersen et al., 2012). The latent variables in this study included algae growth, environmental variables, VSCs emission, methanotrophic abundance, methanotrophic community structure, MOP and CH₄ emissions. PLS-PM (1000 bootstraps) was used to estimate the path and determine coefficients in this model with the standardization of the variables. The R² of the latent variable of CH₄ emissions was estimated with the goodness of fit (GOF) statistic.

3. Results and discussion

3.1. Temporal and spatial variation of environmental variables and trophic levels

Lake Taihu is located in a subtropical region with the water temperatures of 14–34 °C at the 0.5-m depth from March to November during sampling period (Fig. 2). The water pH value ranged from 7.47 to 8.82 in GH, XH and ML, while it was slightly lower (6.70–7.13) in DP, mainly due to the degradation of organic matter (Wu et al., 2021b). The DO concentrations were lower at 5.97–8.73 mg L⁻¹ in the investigated sites in August than in the others, which could be mainly attributed to two reasons: 1) high temperature decreased oxygen solubility in water (Khangonkar et al., 2012); and 2) algae decomposition consumed DO (Wang et al., 2020). Lower DO concentrations were detected in DP in August and November, mainly due to a large amount of oxygen consumed by the degradation of organic matter, such as decaying algae (Khangonkar et al., 2012; Wang et al., 2015). The turbidity of water in ML, GH and DP was higher in May and August than in March and November, which could be attributed to sediment resuspension in the shallow lake by prevailing southeastern winds in summer (Wu et al., 2013). Among the four regions, the concentrations of Chl-a and phycocyanin were highest in DP, followed by ML and GH, and the lowest was detected in XH. This indicated that the water in the four investigated

regions belonged to different eutrophic levels. Compared to Chl-a, the phycocyanin concentrations were lower in ML and GH in March and November, likely due to the different algae dominance in the four regions (Song et al., 2019). The COD_{Mn} concentration ranged from 2.8 to 4.7 mg L⁻¹ in March and November, and increased 3.2–9.9 mg L⁻¹ in May and August, mainly owing to the high release from the degradation of organic matter in sediments at higher temperatures and the release of algae growth and metabolism (Wu et al., 2021b). The COD_{Mn} concentrations in GH and DP in May and ML and DP in August were above 6 mg L⁻¹ (Grade III of the environmental quality standards for surface water in China (GB 3838–2002)). Among the four investigated sites, DP water had the highest nutrient concentrations including NH₄⁺-N, NO₃⁻-N, TN and TP, followed by ML, GH and XH. Of them, the concentrations of NH₄⁺-N, TN and TP were above Grade III of the environmental quality standards for surface water in China (GB 3838–2002). The peak value of the NH₄⁺-N concentration was observed at 1.2 mg L⁻¹ in DP in March with a low pH value and DO, likely due to high nitrification activities. Similarly, Xiao et al. (2019) also found the high NH₄⁺-N level accompanied with lower DO and pH value in lake water. The TFe concentration was 0.3–0.8 mg L⁻¹ in the four regions in May, which was higher than the supplementary standard (≤ 0.3 mg L⁻¹) of the environmental quality standards for surface water in China (GB 3838–2002). Compared with the concentrations of nutrients and TFe, there was less difference in the concentrations of sulfur compounds including TS, AVS and SO₄²⁻-S among the four regions. The SO₄²⁻-S concentration ranged from 9.3 to 17.0 mg L⁻¹, accounting for 75.9%–94.8% of TS. This indicated that SO₄²⁻-S was the predominant form of sulfur in water.

TLI calculated with the water variables including Chl-a, TP, TN and COD_{Mn} showed that trophic levels of Lake Taihu varied with regions and seasons. The TLI values fluctuated within 49.2–57.9 in ML and GH, indicating the water in ML and GH was eutrophic. Compared with GH, the TLI values in ML were slightly higher in May and August. The TLI values in XH were less than 50, which belonged to mesotrophic level. The TLI values in DP were less than 50 in March and November, while they increased to 64.8 and 69.6 in May and August. These results showed that DP was suffering heavier eutrophication, followed by ML, GH and XH.

3.2. Higher eutrophic levels increase emissions of CH₄ and VSCs from lakes

The dissolved CH₄ concentration in DP was higher (11.1–20.5 μg L⁻¹) in August and November that might be attributed to high temperature and eutrophic levels (Fig. 3). However, the dissolved CH₄ concentration in ML and GH was higher in November than that in August, indicating eutrophic level was the important variable compared to temperature. The highest dissolved H₂S concentration was detected in August ranging from 5.6 to 6.9 μg L⁻¹, followed by May, March and November. H₂S production mainly comes from sulfate reduction and the degradation of organic matter under anaerobic conditions (Hargrave et al., 2008; Rathnayake et al., 2017). Chen et al. (2020) also found that microcystins generated by *Cyanobacteria* could induce desulfhydrase activity for H₂S production. The dissolved CS₂ concentrations were 15.7 and 18.5 μg L⁻¹ in DP in May and August, respectively, which were significantly higher than those in ML and XH ($P < 0.05$), indicating high CS₂ production in DP with a higher eutrophic level.

The CH₄ emissions ranged from 20.4 to 126.9 mg m⁻² d⁻¹ in the investigated sites. A similar result was obtained by Yang et al. (2011) who reported that the CH₄ emissions ranged from 1.6 to 284.9 mg m⁻² d⁻¹ with an average CH₄ emission of 92.3 mg m⁻² d⁻¹ in Lake Taihu. Compared with the global average CH₄ emission of 9.9 ± 27.4 mg m⁻² d⁻¹ from lakes between 24° and 54° latitude (Bastviken et al., 2011), the CH₄ emissions were higher in Lake Taihu, likely due to the higher eutrophic levels (Yang et al., 2011). Among the four seasons, there was no significant difference in the CH₄ emissions in March and November. The CH₄ emission from ML was 56.8 mg m⁻² d⁻¹ in May, which was significantly higher than those from GX and XH ($P < 0.001$). Among the study sites, the highest CH₄ emission was detected in DP (126.9 mg m⁻² d⁻¹) in August, likely owing to the high eutrophic level and temperature. Similar results were also reported in previous studies that eutrophication and high temperature could increase CH₄ emissions from lakes, which were also positively correlated with Chl-a and TP in water (Xiao et al., 2017; Beaulieu et al., 2019). Since the CH₄ production from sediment is the main source of CH₄ emission from freshwater lakes, further studies such as CH₄ oxidation rate and CH₄ consumption models in vertical sediment and water profiles need to be conducted to evaluate CH₄ contribution of eutrophic water to the atmosphere.

VSC emissions including H₂S and CS₂ were also detected in the lake. There was no significant difference in H₂S emissions among the four regions. Among the four months, the H₂S emissions were highest (41.2–47.6 mg m⁻² d⁻¹) in August and lowest (26.5–32.5 mg m⁻² d⁻¹) in March, indicating that temperature was an important factor influencing H₂S emissions. This might be because temperature can affect H₂S solubility in water owing to its weak acidity (Savary et al., 2012). CS₂ is mainly generated from action of H₂S and organic matter, indirect photolysis of organic sulfur precursors, algae growth and biodegradation of organic sulfur compounds (Andreae and Jaeschke, 1992; Gharahveran and Shah, 2018). The highest CS₂ emissions were 50.3 and 60.0 mg m⁻² d⁻¹ from ML and GH in November, respectively, while they were 49.3 and 52.3 mg m⁻² d⁻¹ from XH and DP in August, respectively. This suggested that CS₂ emission could be affected by environmental variables such as sulfur-containing precursors, temperature, organic matter and O₂ concentration (Gharehveran and Shah, 2018). CS₂ emission can be increased with increasing temperature and organic matter content, while O₂ concentration can inhibit CS₂ formation (Gharehveran and Shah, 2018). Statistical analysis showed that CH₄ emissions were positively correlated with the emissions of H₂S and CS₂ (Fig. S1), likely because they were mainly generated from anaerobic degradation of organic matter such as algae decomposition (Liu et al., 2019). Water TLI values were positively correlated with the CH₄ and CS₂ emissions, while they were not related with the H₂S emissions. This might be mainly because H₂S can dissolve easily in water, which can be influenced by environmental variables such as pH and temperature (Cholewinski et al., 2016).

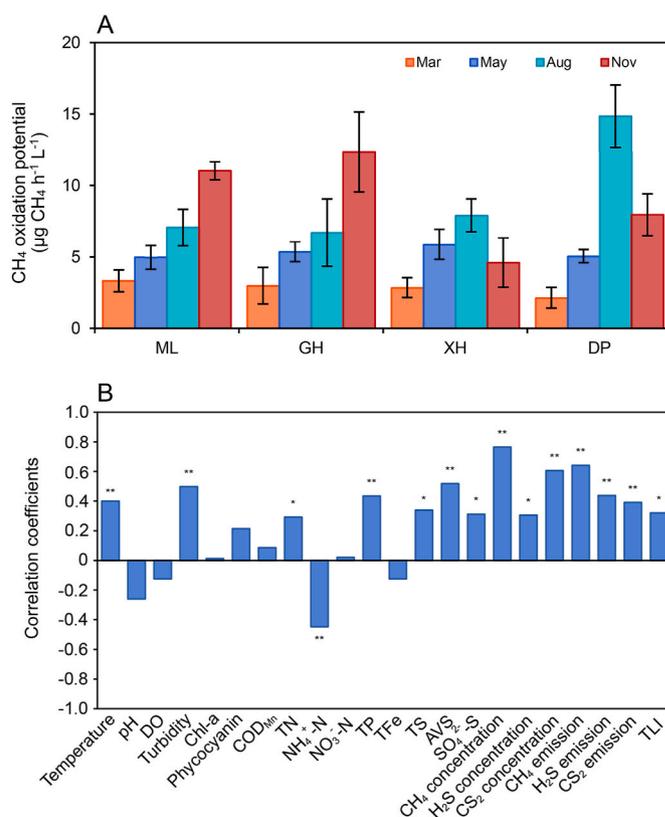


Fig. 4. Average CH₄ oxidation potential (MOP) of water at 0.5-m depth (A) and the correlation coefficients between MOP and environmental variables in Lake Taihu (B). * represents $P < 0.05$. ** represents $P < 0.01$.

3.3. Correlation between MOP and environmental variables

The MOP of water ranged from 2.1 to 3.3 μg h⁻¹ L⁻¹ in March, with no significant difference among the four regions (Fig. 4A). The MOP of water gradually increased to 11.0–12.3 μg h⁻¹ L⁻¹ in ML and GH in November. However, the highest MOP was detected at 7.9 and 14.9 μg h⁻¹ L⁻¹ in XH and DP in August, respectively. This was mainly because MOP was influenced by many factors, such as water quality, availability of trace metals, temperature, dissolved CH₄ and O₂ concentration (Schmale et al., 2015; Steinle et al., 2015; Crespo-Molina et al., 2014).

Statistical analysis showed that the MOP was significantly positively correlated with the environmental variables, including temperature, turbidity, TN, TS, AVS, SO₄²⁻-S, TP, dissolved CH₄, H₂S and CS₂ concentrations, while it was negatively correlated with NH₄⁺-N concentration (Fig. 4B). Among the environmental variables, the MOP had the highest correlation coefficient with the dissolved CH₄ concentration. This was mainly because MOP followed Michaelis-Menten kinetics and increased with increasing CH₄ concentration before reaching substrate saturation (Wang et al., 2011). The MOP was positively correlated with the dissolved concentrations of H₂S and CS₂. Previous studies have reported that VSCs such as H₂S, (CH₃)₂S, and CH₃SH can inhibit CH₄ oxidation. The opposite result in this study might be attributed to 1) the relatively low VSC concentrations in water (Kim et al., 2013) and 2) the significantly positive correlation between the dissolved CH₄ and CS₂ concentrations, which indirectly induced the positive relation between CS₂ concentration and MOP. The concentrations of TN and TP can aggravate lake eutrophication and thus induce more CH₄ generation. Therefore, positive correlations were observed between MOP and the concentrations of TN and TP. Yang et al. (2020) indicated that the addition of NH₄⁺-N could inhibit CH₄ oxidation in water and sediment. In this study, a high NH₄⁺-N concentration was detected in the four water regions in March, mainly due to the low nitrification activity at low

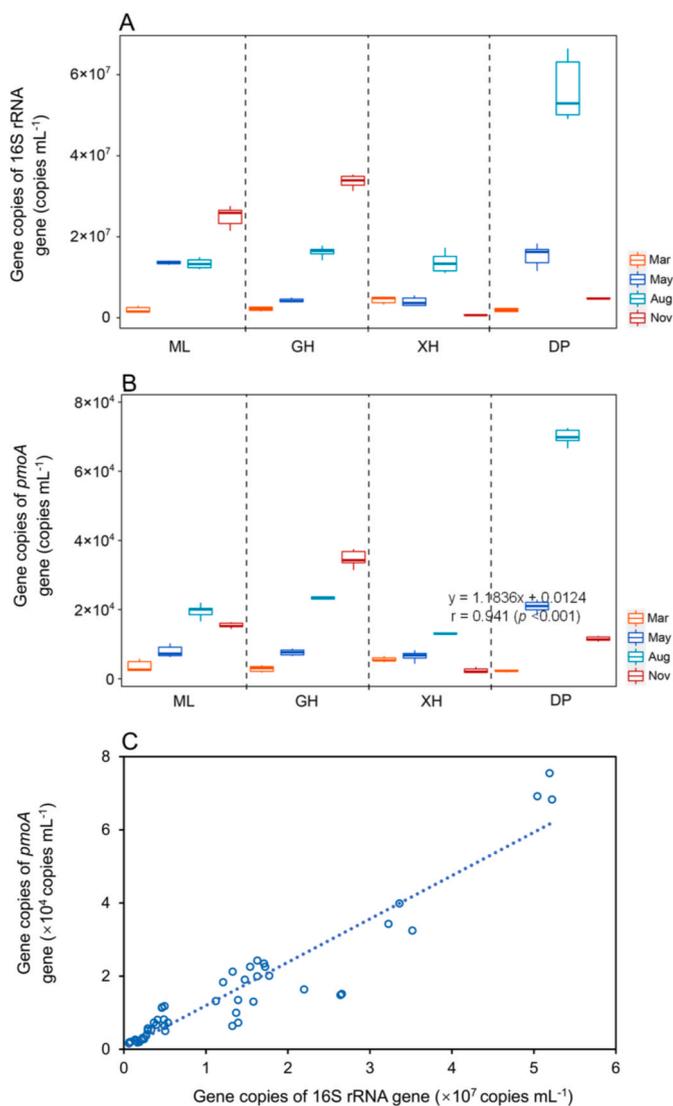


Fig. 5. Abundance of 16S rRNA gene (A) and *pmoA* (B) in water at 0.5-m depth and their relationship (C). Error bars indicate standard deviations ($n = 27$).

temperatures (Bruesewitz et al., 2009). Positive relationships were observed between the MOP and the emissions of CH_4 and VSCs, mainly because the dissolved CH_4 concentration was positively related to the emissions of CH_4 and VSCs in this study. Additionally, we also found the MOP was positively correlated with TLI. This indicated that lake eutrophication could promote CH_4 oxidation, likely owing to the high dissolved CH_4 concentration in eutrophic water.

3.4. Eutrophic levels increase abundance of bacteria and methanotrophs in water

The bacterial abundance varied with season in the investigated lake water (Fig. 5A). The bacterial abundance in ML and GH gradually increased from 1.95×10^6 – 2.22×10^6 copies mL^{-1} in March to 2.5×10^7 – 3.4×10^7 copies mL^{-1} in November. However, the highest bacterial abundance was observed in XH and DP in August. In November, the bacterial abundance decreased slightly in DP, likely due to the lowest DO concentration, which inhibited microbial growth (Yi et al., 2020). In XH, the bacterial abundance was relatively low with a slight increase in August, likely due to the high temperature simulating microbial growth. The difference in bacterial abundance was mainly attributed to temperature and/or eutrophic levels in the four study sites. Domaizon et al. (2013) reported that the abundance of *Cyanobacteria* increased with

increasing temperature. Moreover, the abundance of algae increased with the eutrophic level of lakes, which might induce the higher bacterial abundance of ML and GH in November.

Compared with bacteria, the methanotrophic abundance was low in the lake water. Among the four investigated regions, the highest methanotrophic abundance was detected at 2.0×10^4 copies mL^{-1} in DP in August, likely due to the high dissolved CH_4 concentrations in water (Fig. 5B). The methanotrophic abundance reached a peak value of 3.6×10^4 copies mL^{-1} in GH in November. The methanotrophic abundance was lowest in XH due to the low CH_4 concentration and low eutrophic level. These results suggested that the methanotrophic abundance could be influenced by seasons (i.e., temperature) and dissolved CH_4 concentrations. Sundh et al. (2005) indicated that the methanotrophic abundance was higher in winter than in summer in Sweden, which was attributed to the lower temperature and the minimal inputs of phytoplankton-derived organic substrates that provided a conducive environment for methanotrophs while other bacteria were less competitive (Samad and Bertilsson, 2017). The highest methanotrophic abundance was observed in ML, XH and DP in August, which was consistent with the higher dissolved CH_4 concentration in water. A strong linear relationship was observed between the abundances of bacteria and methanotrophs (Fig. 5C), suggesting that the methanotrophic abundance varied with bacteria in the lake.

3.5. Microbial community succession in water

Proteobacteria, *Actinobacteriota*, *Cyanobacteria* and *Bacteroidota* were the predominant phyla in the lake water, accounting for 50.7%–96.7% of the total reads (Fig. 6). A similar result was found in East Lake in Wuhan, China, where the bacterial community was mainly composed of *Proteobacteria*, *Actinobacteriota*, *Bacteroidetes* and *Cyanobacteria* with a relative abundance of 93.6% (Ji et al., 2019). The relative abundance of *Proteobacteria* varied considerably from 18.9% to 59.5% with a decrease to 12.9%–36.2% in GH and DP in August. In November, the relative abundance of *Proteobacteria* decreased to 9.3%–22.2% in ML and GH, while it increased slightly in DP. *Actinobacteriota* was also dominant in the freshwater system, probably due to their strong adaptability to the various environments (Neuenschwander et al., 2017). The relative abundance of *Actinobacteriota* in GH was 7.5%–20.0% in March and then increased to 24.8%–37.6% in August. The highest relative abundance of *Actinobacteriota* was 22.8%–40.5% in XH and DP in November. The relative abundance of *Cyanobacteria* in lakes reflects eutrophic levels (Ji et al., 2019). The relative abundance of *Cyanobacteria* in ML and GH was low in March and May and then increased to 38.9%–72.7% in November. The highest relative abundance of *Cyanobacteria* was 26.0%–51.3% in DP in August. Compared with the other three study sites, the relative abundance of *Cyanobacteria* was lower in XH. The seasonal variations in the relative abundance of *Cyanobacteria* were affected by temperature and available nutrients (Shan et al., 2019). The abundance of *Cyanobacteria* increased with increasing temperature and N and P concentrations (Xu et al., 2017; Tanvir et al., 2021), which was consistent with the results obtained in this study (Fig. 3H; Fig. 3K).

Hgcl clade, *Microcystis* PCC-7914 and *Aulacoseira granulata* var. *angustissima* were the most abundant genera in the lake water. Liu et al. (2015) also found that *hgcl* clade predominated in Pearl Estuary, China, likely due to its strong ability to utilize carbohydrates and compete for substrates. The relative abundance of *hgcl* clade was 1.1%–9.8% in March and lower than in the other months owing to the low temperature (Wang et al., 2021). The relative abundance of *hgcl* clade in ML, GH and XH increased to 12.1%–45.8% in May, while it decreased to 5.5%–22.0% in November. However, the relative abundance of *hgcl* clade increased to 19.5%–27.3% in DP in November owing to the high nutrients in the water (Xue et al., 2018) and their strong competition for organic matter (Liu et al., 2018). *Microcystis* is the predominant genus that induces water eutrophication (Cai et al., 2012). *Microcystis* PCC-7914 was not detected in March in the four investigated areas, but

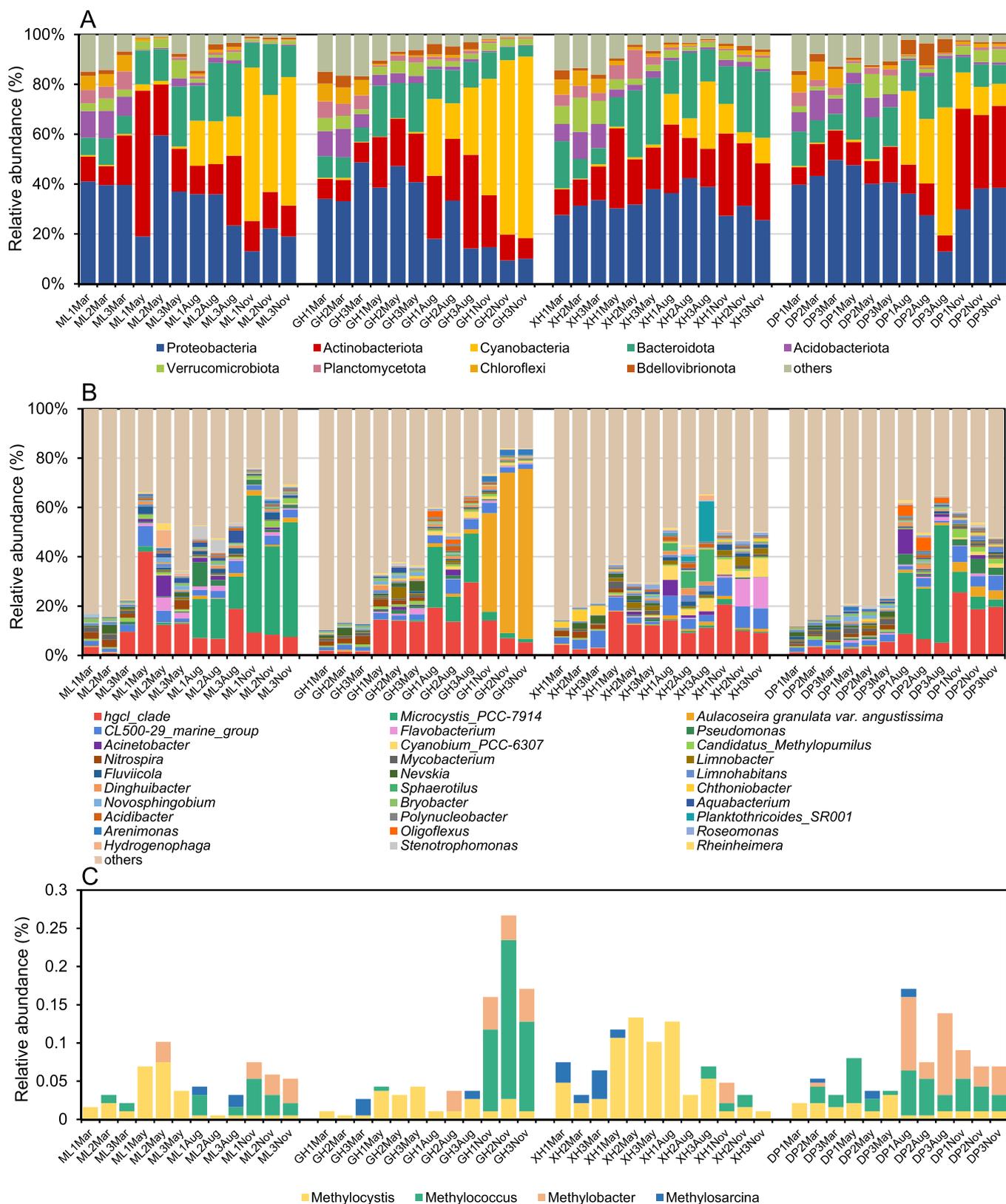


Fig. 6. The taxonomic classification of bacterial 16S rRNA gene reads at phylum (A) and genus (B) levels, and the relative abundance of methanotrophs in water at 0.5-m depth (C).

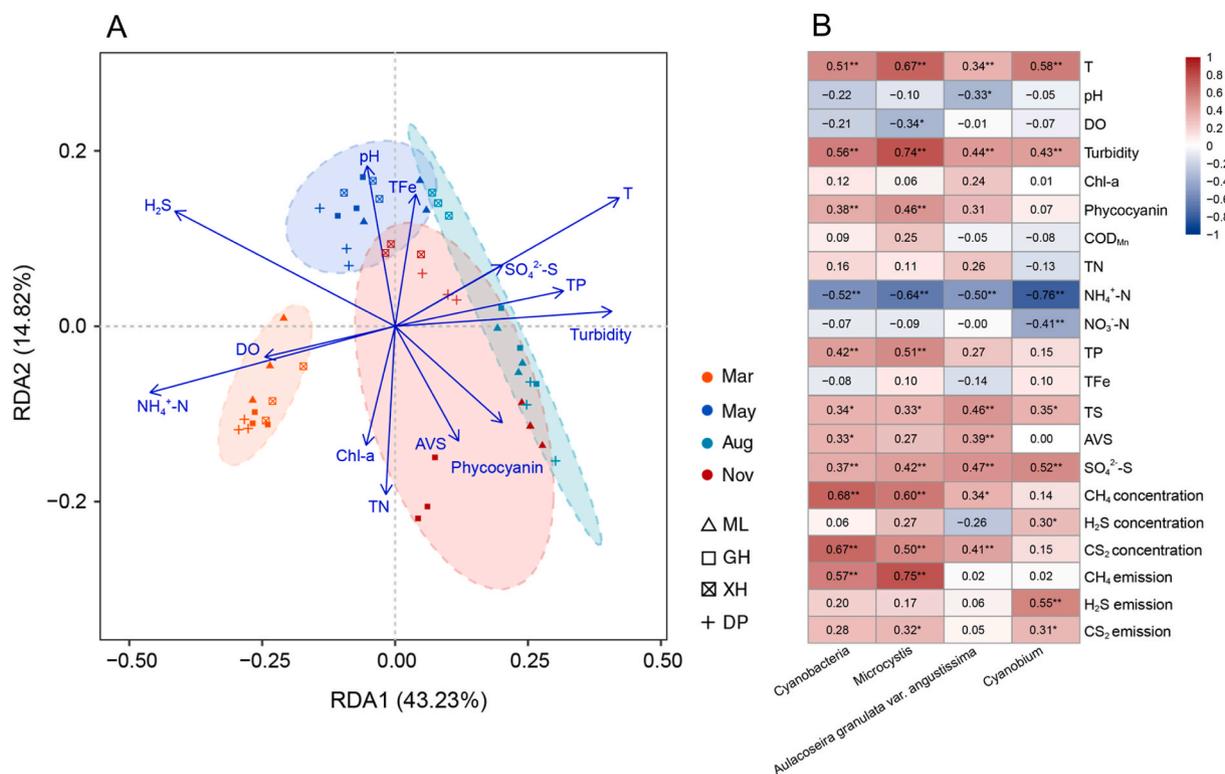


Fig. 7. Redundancy analysis (RDA) showing the relationships between microbial communities and environmental variables ($p < 0.05$) (A) and the correlations between the relative abundance of *Cyanobacteria*, *Microcystis*, *A. granulata* var. *angustissima* and *Cyanobium* and environmental variables (B). The numbers indicate the correlation coefficient. * represents $P < 0.05$. ** represents $P < 0.01$.

the relative abundance of *Microcystis* PCC-7914 increased to 0.1%–2.3% in May. Conroy et al. (2014) found that *Microcystis* could grow in March in Lake Erie and bloomed in May. Compared to Lake Erie, the growth and blooms of *Microcystis* were slightly late in Lake Taihu. The relative abundance of *Microcystis* PCC-7914 significantly increased to 10.7%–48.0% in August, indicating that the serious algae pollution appeared likely due to the high nutrients and suitable temperature (Song et al., 2017). *Aulacoseira granulata* var. *angustissima* is a diatom that can cause eutrophication in freshwater (Hynynen et al., 2004). The relative abundance of *A. granulata* var. *angustissima* was detected at 0.7%–70.1% in November, especially in GH, with the relative abundance of 41.6%–70.1%. Previous studies have also reported that the relative abundance of *A. granulata* var. *angustissima* increased in winter and was higher than that in the other seasons (Loudiki et al., 1994). Hynynen et al. (2004) found that the growth of *A. granulata* var. *angustissima* induced eutrophication in Lake Lievestuoreenjärvi with a relationship with the ratio of P/Si.

α -Proteobacteria methanotroph *Methylocystis* and γ -Proteobacteria methanotrophs *Methylococcus*, *Methylobacter*, *Methylosarcina* were detected in the water samples with low relative abundances of 0.01%–0.27%. Savvichev et al. (2021) also found that the relative abundance of methanotrophs was lower than 0.2% in lakes, and their community changed with seasons. In ML, GH and DP, α -Proteobacteria methanotroph *Methylocystis* was more abundant in March and May than γ -Proteobacteria methanotrophs, while it was less abundant in August and November. This might be because higher nutrients and organic matter are favourable for the growth of γ -Proteobacteria methanotrophs (Yang et al., 2011; Yang et al., 2016).

3.6. Influence of environmental variables on microbial community and CH₄ emissions

The influence of the environmental variables on the microbial

community was estimated by RDA (Fig. 7A). The microbial community in the water samples grouped together in March, which separated from the other seasons, indicating an obvious difference in microbial communities in March. There was a positive relationship between the microbial communities and the concentrations of DO and NH₄⁺-N in March. The microbial communities in May clustered together and were positively related to pH and the concentrations of TFe and H₂S. In August, the microbial communities in ML, GH, and DP grouped together, while those in XH were clustered nearly to May, probably due to the relatively low abundance of *Cyanobacteria* such as *Microcystis* PCC-7914. The microbial communities in November were relatively dispersed, which could be mainly attributed to the different eutrophic levels in the four sites.

The predominant *Cyanobacteria* were *Microcystis*, *A. granulata* var. *angustissima* and *Cyanobium* (Fig. 7B). Positive correlations were observed between the relative abundance of *Cyanobacteria* and temperature, turbidity, TS and SO₄²⁻-S, indicating that these variables could promote algae growth. Yang et al. (2018) also found that an increase in temperature could prompt algae growth. In contrast, the NH₄⁺-N concentration was negatively correlated with the algae abundance, which was in accordance with the result obtained by McCarthy et al. (2009). *Microcystis* is the main microorganism that induces algal blooms and red tides. There were negative correlations between DO and the relative abundance of *Microcystis*. In the initial stage of *Microcystis* growth, a large amount of O₂ could be produced due to the higher photosynthesis than respiration. However, excessive algae growth could prevent O₂ from entering water, and a large amount of O₂ was consumed during algae decay, which could decrease DO concentrations (Wang et al., 2021). There was a positive correlation between TP and the relative abundance of *Microcystis*, indicating that TP might be a key factor inducing algal blooms (Schindler et al., 2008; Song et al., 2017). The positive relationships between the dissolved CH₄ concentration and the relative abundances of *Cyanobacteria*, *Microcystis*, *A. granulata* var.

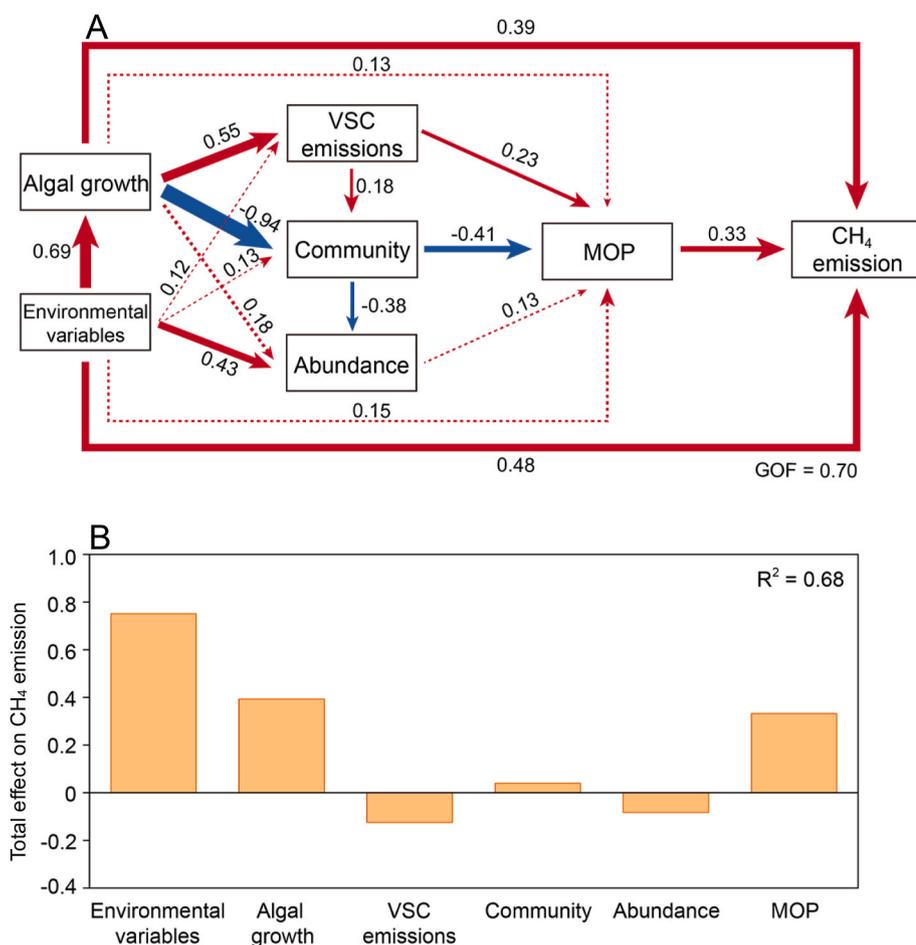


Fig. 8. Partial least squares path modelling (PLS-PM) presenting the direct and indirect effect of environmental variables and algae growth (i.e., the temporal and spatial relative abundance of algae obtained by MiSeq sequencing) (A) and the total effect of significant factors (B) on CH₄ emission from Lake Taihu. Red and blue arrows indicate positive and negative relationships, respectively. Continuous and dashed arrows indicate significant and nonsignificant relationships, respectively. The thickness of the lines indicates the strength of path coefficients. The values near the lines indicate the absolute values of path coefficients. The values near the lines indicate the absolute values of path coefficients. R^2 indicates the values explained by the independent latent variables. Goodness of fit (GOF) indicates assessment of the model.

angustissima were observed. The dissolved H₂S concentration was positively correlated with the relative abundance of *Cyanobium*, and the dissolved CS₂ concentration was positively correlated with the relative abundance of *Cyanobacteria*, *Microcystis* and *A. granulata* var. *angustissima*, indicating that different types of algae could affect VSC production. Similarly, we found there was significantly positive correlations between the relative abundance of *Cyanobacteria* and *Microcystis* and the CH₄ and VSC emissions. Of them, the relative abundance of *Cyanobium* were positively correlated with the H₂S and CS₂ emissions, and the relative abundance of *Microcystis* was positively correlated with the CS₂ emission. These results indicated that algae growth could stimulate the CH₄ and VSC emissions. *Microcystis* and *Cyanobium* might be the predominant contributors to VSC emissions during algal blooms in freshwater lakes.

To deeply understand the influence of algae on CH₄ emissions, we conducted PLS-PM to explore the direct and indirect effects (Fig. 8). The model revealed that the environmental variables had positive effects on algal growth (i.e., the temporal and spatial relative abundance of algae obtained by MiSeq sequencing) with a path coefficient of 0.69, especially temperature, turbidity, NH₄⁺-N and TP were significantly correlation with algal growth. The environmental variables and algal growth could both influence CH₄ emissions. Algal growth could promote VSC emissions, which had a correlation with MOP with a positive coefficient of 0.23. This might be because the CH₄ emission was positively related to the emissions of VSCs in this study (Fig. S1), and thus indirectly correlated with the MOP.

4. Conclusions

The CH₄ and VSC emissions from Lake Taihu increased with

eutrophic levels and temperature. The MOP had significantly positive correlations with TLI and the environmental variables, including temperature, turbidity, TN, TS, AVS, SO₄²⁻-S, TP, dissolved concentrations of CH₄, H₂S and CS₂, while it was negatively correlated with the NH₄⁺-N concentration. Eutrophic levels could increase the abundance of bacteria and methanotrophs in lake water. *α-Proteobacteria* methanotroph *Methylocystis* was more abundant in March and May than *γ-Proteobacteria* methanotroph, while it was less abundant in August and November. The relative abundance of *Cyanobacteria*, including *Microcystis*, *A. granulata* var. *angustissima* and *Cyanobium* had significantly positive correlations with temperature, turbidity, SO₄²⁻-S and total sulfur. Algae growth could stimulate the CH₄ and VSC emissions. *Microcystis* and *Cyanobium* might be the predominant contributors to VSC emissions during algal blooms in freshwater lakes. These findings indicated improving water quality and controlling algal growth might be an effective way to reduce emissions of CH₄ and VSCs from lakes.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.envpol.2022.119435>.

References

- Andreae, M.O., Jaeschke, W.A., 1992. Exchange of sulphur between biosphere and atmosphere over temperate and tropical regions. In: Howarth, R.W., Stewart, J.W.B., Ivanov, M.V. (Eds.), *In: Sulphur Cycling on the Continents: Wetlands, Terrestrial Ecosystems, and Associated Water Bodies*. Wiley, New York.
- Bastviken, D., Cole, J., Pace, M., Tranvik, L., 2004. Methane emissions from lakes: dependence of lake characteristics, two regional assessments, and a global estimate. *Global Biogeochem. Cycles* 18, GB4009.
- Bastviken, D., Tranvik, L.J., Downing, J.A., Crill, P.M., Enrich-Prast, A., 2011. Freshwater methane emissions offset the continental carbon sink. *Science* 331, 50–50.
- Beaulieu, J.J., DelSontro, T., Downing, J.A., 2019. Eutrophication will increase methane emissions from lakes and impoundments during the 21st century. *Nat. Commun.* 10, 1375.
- Börjesson, G., 2001. Inhibition of methane oxidation by volatile sulfur compounds (CH₃SH and CS₂) in landfill cover soils. *Waste Manag. Res.* 19, 314–319.
- Borrel, G., Jezequel, D., Biderre-Petit, C., Morel-Desrosiers, N., Morel, J.P., Peyret, P., Fonty, G., Lehours, A.C., 2011. Production and consumption of methane in freshwater lake ecosystems. *Res. Microbiol.* 162, 832–847.
- Bowman, J., 2006. The methanotrophs-The families *Methylococcaceae* and *Methylocystaceae*. In: Dworkin, M., Falkow, S., Rosenberg, E., Schleifer, K.H., Stackebrandt, E. (Eds.), *The Prokaryotes: A Handbook on the Biology of Bacteria*, pp. 266–289. New York.
- Brusewitz, D.A., Tank, J.L., Hamilton, S.K., 2009. Seasonal effects of zebra mussels on littoral nitrogen transformation rates in Gull Lake, Michigan, USA. *Freshw. Biol.* 54, 1427–1443.
- Cai, Y., Kong, F., Shi, L., Yu, Y., 2012. Spatial heterogeneity of cyanobacterial communities and genetic variation of *Microcystis* populations within large, shallow eutrophic lakes (Lake Taihu and Lake Chaohu, China). *J. Environ. Sci.* 24, 1832–1842.
- Chen, J., Xie, P., Ma, Z., Niu, Y., Tao, M., Deng, X., Wang, Q., 2010. A systematic study on spatial and seasonal patterns of eight taste and odor compounds with relation to various biotic and abiotic parameters in Gonghu Bay of Lake Taihu, China. *Sci. Total Environ.* 409, 314–325.
- Chen, M., Yao, X.Z., Ma, R.C., Song, Q.C., Long, Y., He, R., 2017. Methanethiol generation potential from anaerobic degradation of municipal solid waste in landfills. *Environ. Sci. Pollut. Res. Int.* 24, 23992–24001.
- Chen, X., Liu, Y., Yang, L., Hu, X., Jia, A., 2020. Hydrogen sulfide signaling protects *Chlamydomonas reinhardtii* against allelopathic damage from cyanobacterial toxin microcystin-LR. *Front. Plant Sci.* 11, 1105.
- Cholewinski, A., Dengis, J., VictorMalkov, V., Leonenko, Y., 2016. Modeling of CO₂ injection into aquifers containing dissolved H₂S. *J. Nat. Gas Sci. Eng.* 36, 1080–1086.
- Conroy, J.D., Kane, D.D., Briland, R.D., Culver, D.A., 2014. Systemic, early-season *Microcystis* blooms in western Lake Erie and two of its major agricultural tributaries (Maumee and Sandusky rivers). *J. Great Lake Res.* 40, 518–523.
- Crespo-Medina, M., Meile, C.D., Hunter, K.S., Diercks, A.R., Asper, V.L., Orphan, V.J., Tavormina, P.L., Nigro, L.M., Battles, J.J., Chanton, J.P., Shiller, A.M., Joung, D.J., Amon, R.M.W., Bracco, A., Montoya, J.P., Villareal, T.A., Wood, A.M., Joye, S.B., 2014. The rise and fall of methanotrophy following a deepwater oil-well blowout. *Nat. Geosci.* 7, 423–427.
- Deng, Y.C., Liu, Y.Q., Dumont, M., Conrad, R., 2017. Salinity affects the composition of the aerobic methanotroph community in alkaline lake sediments from the Tibetan Plateau. *Environ. Microbiol.* 73, 101–110.
- Ding, J., Jiang, H., Wu, X., Zhang, S., Razanajatovo, R.M., Zou, H., 2020. Investigation and assessment of environmental pollution in Gonghu Bay, Taihu Lake, China: a year-long study. *Hum. Ecol. Risk Assess.* 26, 906–920.
- Domaizon, I., Savichtcheva, O., Debroas, D., Arnaud, F., Villar, C., Pignol, C., Alric, B., Perga, M.E., 2013. DNA from lake sediments reveals the long-term dynamics and diversity of *Synechococcus* assemblages. *Biogeosciences* 10, 3817–3838.
- Dong, J., Li, Y., Feng, R., Zhao, J., Yu, H., 2012. The preservation method of water samples to determine sulfide in groundwater by the methylene blue spectrophotometric method. *Rock Miner. Anal.* 31, 868–871.
- Downing, J.A., Prairie, Y.T., Cole, J.J., Duarte, C.M., Tranvik, L.J., Striegl, R.G., McDowell, W.H., Kortelainen, P., Caraco, N.F., Melack, J.M., Middelburg, J.J., 2006. The global abundance and size distribution of lakes, ponds, and impoundments. *Limnol. Oceanogr.* 51, 2388–2397.
- Dumont, M.G., Murrell, J.C., 2005. Community-level analysis: key genes of aerobic methane oxidation. *Methods Enzymol.* 397, 413–427.
- Eaton, A.D., Clesceri, L.S., Greenberg, A.D., 2005. *Standard Methods for the Examination of Water and Wastewater*, twenty-first ed. American Public Health Association/American Water Works Association/Water Environment Federation, Washington DC.
- Gharehveran, M.M., Shah, A.D., 2018. Indirect photochemical formation of carbonyl sulfide and carbon disulfide in natural waters: role of organic sulfur precursors, water quality constituents, and temperature. *Environ. Sci. Technol.* 52, 9108–9117.
- Gonzalez-Valencia, R., Magana-Rodriguez, F., Gerardo-Nieto, O., Sepulveda-Jauregui, A., Martinez-Cruz, K., Anthony, K.W., Baer, D., Thalasso, F., 2014. *In situ* measurement of dissolved methane and carbon dioxide in freshwater ecosystems by off-axis integrated cavity output spectroscopy. *Environ. Sci. Technol.* 48, 11421–11428.
- Hanson, R.S., Hanson, T.E., 1996. Methanotrophic bacteria. *Microbiol. Rev.* 60, 439–471.
- Hargrave, B.T., Holmer, M., Newcombe, C.P., 2008. Towards a classification of organic enrichment in marine sediments based on biogeochemical indicators. *Mar. Pollut. Bull.* 56, 810–824.
- He, R., Yao, X.Z., Chen, M., Ma, R.C., Li, H.J., Wang, C., Ding, S.H., 2018. Conversion of sulfur compounds and microbial community in anaerobic treatment of fish and pork waste. *Waste Manag.* 76, 383–393.
- Hynynen, J., Palomäki, A., Meriläinen, J.J., Witick, A., Mäntykoski, K., 2004. Pollution history and recovery of a boreal lake exposed to a heavy bleached pulping effluent load. *J. Paleolimnol.* 32, 351–374.
- Jacinte, P.A., Groffman, P.M., 2001. Silicone rubber sampler to measure dissolved gases in saturated soils and waters. *Soil Biol. Biochem.* 33, 907–912.
- Ji, B., Liang, J., Ma, Y., Zhu, L., Liu, Y., 2019. Bacterial community and eutrophic index analysis of the East Lake. *Environ. Pollut.* 252, 682–688.
- Ji, X., Wu, T., Xiao, J., Yang, K., Sun, Z., Yang, Z., Yang, T., Hu, R., 2021. Strong spring winds accelerated the recruitment and reinvasion of cyanobacteria. *Environ. Sci. Pollut. Res.* 28, 16855–16866.
- Khangaonkar, T., Sackmann, B., Long, W., Mohamedali, T., Roberts, M., 2012. Simulation of annual biogeochemical cycles of nutrient balance, phytoplankton bloom(s), and DO in Puget Sound using an unstructured grid model. *Ocean Dynam.* 62, 1353–1379.
- Kim, T.G., Lee, E.H., Cho, K.S., 2013. Effects of nonmethane volatile organic compounds on microbial community of methanotrophic biofilter. *Appl. Microbiol. Biotechnol.* 97, 6549–6559.
- Lee, E.H., Yi, T., Moon, K.E., Park, H., Ryu, H.W., Cho, K.S., 2011. Characterization of methane oxidation by a methanotroph isolated from a landfill cover soil, South Korea. *J. Microbiol. Biotechnol.* 21, 753–756.
- Lee, J., Rai, P.K., Jeon, Y.J., Kim, K.H., Kwon, E.E., 2017. The role of algae and cyanobacteria in the production and release of odorants in water. *Environ. Pollut.* 227, 252–262.
- Lin, J.L., Joye, S.B., Scholten, J.C.M., Schäfer, H., McDonald, I.R., Murrell, J.C., 2005. Analysis of methane monooxygenase genes in Mono Lake suggests that increased methane oxidation activity may correlate with a change in methanotroph community structure. *Appl. Environ. Microbiol.* 71, 6458–6462.
- Liu, C., Shao, S., Zhang, L., Du, Y., Chen, K., Fan, C., Yu, Y., 2019. Sulfur development in the water-sediment system of the algae accumulation embay area in Lake Taihu. *Water* 11, 1817.
- Liu, C., Zhu, Y., Wang, J., Guan, J., Duo, H., 2018. Impact of Tai water discharged on bacterial community structure in river in different seasons. *Res. Env. Sci.* 31, 893–900.
- Liu, C.Y., Xu, G.B., Deng, X., Zhang, H.H., Liu, T., Yang, G.P., 2020. Changes in concentrations of biogenic sulfur compounds in coastal waters off Qingdao, China during an *Ulva prolifera* bloom. *Mar. Pollut. Bull.* 152, 110940.
- Liu, J., Fu, B., Yang, H., 2015. Phylogenetic shifts of bacterioplankton community composition along the Pearl Estuary: the potential impact of Hypoxia and nutrients. *Front. Microbiol.* 6, 64.
- Liu, X., Zhang, Y., Shi, K., Lin, J., Zhou, Y., Qin, B., 2016. Determining critical light and hydrologic conditions for macrophyte presence in a large shallow lake: the ratio of euphotic depth to water depth. *Ecol. Indicat.* 71, 317–326.
- Loudiki, M., Cazaubon, A., Hasnaoui, M., 1994. Multi-year dynamic of a population of *Aulacoseira granulata* Sim. Var. *angustissima* (Mueller) (Bacillariophyceae) in the Hassan I lake-reservoir (Morocco). *Ecol. Mediterr.* 20, 109–120.
- Mayr, J.M., Zimmermann, M., Dey, J., Brand, A., Wehrli, B., Bürgmann, H., 2020. Growth and rapid succession of methanotrophs effectively limit methane release during lake overturn. *Commun. Biol.* 3, 108.
- McCarthy, M.J., James, R.T., Chen, Y., East, T.L., Gardner, W.S., 2009. Nutrient ratios and phytoplankton community structure in the large, shallow, eutrophic, subtropical Lakes Okeechobee (Florida, USA) and Taihu (China). *Limnology* 10, 215–227.
- Meng, L., Zhao, Z., Lu, L., Zhou, J., Luo, D., Fan, R., Li, S., Jiang, Q., Huang, T., Yang, H., Huang, C., 2021. Source identification of particulate organic carbon using stable isotopes and n-alkanes: modelling and application. *Water Res.* 197, 117083.
- Michaud, A.B., Dore, J.E., Achberger, A.M., Christner, B.C., Mitchell, A.C., Skidmore, M.L., Vick-Majors, T.J., Priscu, J.C., 2017. Microbial oxidation as a methane sink beneath the west Anarctic Ice Sheet. *Nat. Geosci.* 10, 582–586.
- Neuenschwander, S.M., Ghai, R., Pernthaler, J., Salcher, M.M., 2017. Microdiversification in genome-streamlined ubiquitous freshwater Actinobacteria. *ISME J.* 12, 185.
- Perga, M.E., Maberly, S.C., Jenny, J.P., Alric, B., Pignol, C., Naffrechoux, E., 2016. A century of human-driven changes in the carbon dioxide concentration of lakes. *Global Biogeochem. Cycles* 30, 93–104.
- Petersen, D.G., Blazewicz, S.J., Firestone, M., Herman, D.J., Turetsky, M., Waldrop, M., 2012. Abundance of microbial genes associated with nitrogen cycling as indices of biogeochemical process rates across a vegetation gradient in Alaska. *Environ. Microbiol.* 14, 993–1008.
- Qin, B.Q., Xu, P.Z., Wu, Q.L., Luo, L.C., Zhang, Y.L., 2007. Environmental issues of lake Taihu, China. *Hydrobiologia* 581, 3–14.
- Rathnayake, R.M.L.D., Sugahara, S., Maki, H., Kanaya, G., Seike, Y., Satoh, H., 2017. High spatial resolution analysis of the distribution of sulfate reduction and sulfide oxidation in hypoxic sediment in a eutrophic estuary. *Water Sci. Technol.* 75, 418–426.
- Samad, M.S., Bertilsson, S., 2017. Seasonal variation in abundance and diversity of bacterial methanotrophs in five temperate lakes. *Front. Microbiol.* 8, 142.
- Savary, V., Berger, G., Dubois, M., Lachapagne, J.C., Pages, A., Thibeau, S., Lescanne, M., 2012. The solubility of CO₂+H₂S mixtures in water and 2 M NaCl at 120 degrees C and pressures up to 35 MPa. *Int. J. Greenh. Gas Control* 10, 123–133.

- Savvichev, A., Rusanov, I., Dvornikov, Y., Kadnikov, V., Kallistova, A., Veslopolova, E., Chetverova, A., Leibman, M., Sigalevich, P.A., Pimenov, N., Ravin, N., Khomutov, A., 2021. The water column of the Yamal tundra lakes as a microbial filter preventing methane emission. *Biogeosciences* 18, 2791–2807.
- Schmale, O., Leifer, I., Deimling, J.S.V., Stolle, C., Krause, S., Kießlich, K., Frahm, A., Treude, T., 2015. Bubble transport mechanisms: indications for a gas bubble-mediated inoculation of benthic methanotrophs into the water column. *Continental Shelf Res.* 103, 70–78.
- Schindler, D.W., Hecky, R.E., Findlay, D.L., Stainton, M.P., Parker, B.R., Paterson, M.J., Beaty, K.G., Lyng, M., Kasian, E.M., 2008. Eutrophication of lakes cannot be controlled by reducing nitrogen input: results of a 37-year whole ecosystem experiment. *Proc. Nat. Acad. Sci. USA* 105, 11254–11258.
- Semrau, J.D., DiSpirito, A.A., Yoon, S., 2010. Methanotrophs and copper. *FEMS Microbiol. Rev.* 34, 496–531.
- Shan, K., Song, L., Chen, W., Li, L., Liu, L., Wu, Y., Jia, Y., Zhou, Q., Peng, L., 2019. Analysis of environmental drivers influencing interspecific variations and association among bloom-forming cyanobacteria in large, shallow eutrophic lakes. *Harmful Algae* 84, 84–94.
- Shao, K., Bai, C., Hu, Y., Tang, X., Gao, G., 2018. Spatial variations in the predation of nano-protzoa on bacteria in Lake Taihu, China. *J. Freshw. Ecol.* 33, 267–272.
- Smith, T.J., Murrell, J.C., 2009. Methanotrophy/methane oxidation. In: *Encyclopedia of Microbiology*, third ed. Academic Press, Oxford, pp. 293–298.
- Song, H., Xu, J., Lavoie, M., Fan, X., Liu, G., Sun, L., Fu, Z., Qian, H., 2017. Biological and chemical factors driving the temporal distribution of cyanobacteria and heterotrophic bacteria in a eutrophic lake (West Lake, China). *Appl. Microbiol. Biotechnol.* 101, 1685–1696.
- Song, Y., Xue, Y., Gao, Y., Jin, Y., 2019. Distribution of epipelagic algae and related environmental nutrients in Taihu Lake, revealed by HPLC analysis. *Mar. Freshw. Res.* 70, 849–856.
- Steinle, L., Graves, C.A., Treude, T., Ferré, B., Biastoch, A., Bussmann, I., Berndt, C., Krastel, S., James, R.H., Behrens, E., Böning, C.W., Greinert, J., Sapart, C.J., Scheinert, M., Sommer, S., Lehmann, M.F., Niemann, H., 2015. Water column methanotrophy controlled by a rapid oceanographic switch. *Nat. Geosci.* 8, 378–382.
- Sun, H., Lu, X., Yu, R., Yang, J., Liu, X., Cao, Z., Zhang, Z., Li, M., Geng, Y., 2021. Eutrophication decreased CO₂ but increased CH₄ emission from lake: a case study of a shallow Lake Ulansuhai. *Water Res.* 201, 117363.
- Sundh, I., Bastviken, D., Tranvik, L.J., 2005. Abundance, activity, and community structure of pelagic methane-oxidizing bacteria in temperate lakes. *Appl. Environ. Microbiol.* 71, 6746–6752.
- Tanvir, R.U., Hu, Z., Zhang, Y., Lu, J., 2021. Cyanobacterial community succession and associated cyanotoxin production in hypereutrophic and eutrophic freshwaters. *Environ. Pollut.* 290, 118056.
- Wang, J., Chu, Y., Schäfer, H., Tian, G., He, R., 2022. CS₂ increasing CH₄-derived carbon emissions and active microbial diversity in lake sediment. *Environ. Res.* 208, 112678.
- Wang, J., Fan, H., He, X., Zhang, F., Xiao, J., Yan, Z., Feng, J., Li, R., 2021. Response of bacterial communities to variation in water quality and physicochemical conditions in a river-reservoir system. *Glob. Ecol. Conserv.* 27, e01541.
- Wang, J., Jiang, X., Zheng, B., Niu, Y., Wang, K., Wang, W., Kardol, P., 2015. Effects of electron acceptors on soluble reactive phosphorus in the overlying water during algal decomposition. *Environ. Sci. Pollut. Res.* 22, 19507–19517.
- Wang, J., Xia, F.F., Bai, Y., Fang, C.R., Shen, D.S., He, R., 2011. Methane oxidation in landfill waste biocover soil: kinetics and sensitivity to ambient conditions. *Waste Manag.* 31, 864–870.
- Wang, Q., Li, X., Yan, T., Song, J., Yu, R., Zhou, M., 2020. Laboratory simulation of dissolved oxygen reduction and ammonia nitrogen generation in the decay stage of harmful algae bloom. *J. Oceanol. Limnol.* 39, 500–507.
- West, W.E., Creamer, K.P., Jones, S.E., 2016. Productivity and depth regulate lake contributions to atmospheric methane. *Limnol. Oceanogr.* 61, S51–S61.
- Wu, A., Wang, Y., Friese, K., Zhang, L., Han, C., Kang, D., Shen, Q., 2021a. Spatial and seasonal distribution of 2-methylisoborneol in a large eutrophic shallow lake, China. *Water Air Soil Pollut.* 232, 387.
- Wu, X., Ma, T., Du, Y., Jiang, Q., Shen, S., Liu, W., 2021b. Phosphorus cycling in freshwater lake sediments: influence of seasonal water level fluctuations. *Sci. Total Environ.* 792, 148383.
- Wu, T., Qin, B., Zhu, G., Zhu, M., Li, W., Luan, C., 2013. Modeling of turbidity dynamics caused by wind-induced waves and current in the Taihu Lake. *Int. J. Sediment Res.* 28, 139–148.
- Wuebbles, D.J., Hayhoe, K., 2002. Atmospheric methane global change. *Earth Sci. Rev.* 573, 177–210.
- Xia, T., Zhang, W., Li, H., Wang, H., He, P., Wang, X., 2022. Rivers draining contrasting landscapes exhibit distinct potentials to emit diffusive methane (CH₄). *Sci. Total Environ.* 807, 150898.
- Xiao, Q., Xu, X., Duan, H., Qi, T., Qin, B., Lee, X., Hu, Z., Wang, W., Xiao, W., Zhang, M., 2020. Eutrophic lake Taihu as a significant CO₂ source during 2000–2015. *Water Res.* 170, 115331.
- Xiao, Q., Xu, X., Zhang, M., Duan, H., Hu, Z., Wang, W., Xiao, W., Lee, X., 2019. Coregulation of nitrous oxide emissions by nitrogen and temperature in China's third largest freshwater lake (Lake Taihu). *Limnol. Oceanogr.* 64, 1070–1086.
- Xiao, Q., Zhang, M., Hu, Z., Gao, Y., Hu, C., Liu, C., Liu, S., Zhang, Z., Zhao, J., Xiao, W., Lee, X., 2017. Spatial variations of methane emission in a large shallow eutrophic lake in subtropical climate. *J. Geophys. Res.-Bioge.* 122, 1597–1614.
- Xiang, S., Zhou, W., 2011. Phosphorus forms and distribution in the sediments of Poyang Lake, China. *Int. J. Sediment Res.* 26, 230–238.
- Xu, H., Paerl, H.W., Zhu, G., Qin, B., Hall, N.S., Zhu, M., 2017. Long-term nutrient trends and harmful cyanobacterial bloom potential in hypertrophic Lake Taihu, China. *Hydrobiologia* 787, 229–242.
- Xue, Y., Liu, F., Sun, M., Jiang, X., Geng, J., Teng, J., Xie, W., Zhang, H., Chen, X., 2018. Community structure and influencing factors of bacterioplankton in spring in Zhushan Bay, Lake Taihu. *Environ. Sci.* 39, 1151–1158.
- Yang, H., Xie, P., Ni, L.Y., Fower, R.J., 2011. Underestimation of CH₄ emission from freshwater lakes in China. *Environ. Sci. Technol.* 45, 4203–4204.
- Yang, J., Tang, H., Zhang, X., Zhu, X., Huang, Y., Yang, Z., 2018. High temperature and pH favor *Microcystis aeruginosa* to outcompete *Scenedesmus obliquus*. *Environ. Sci. Pollut. Res.* 25, 4794–4802.
- Yang, Y., Chen, J., Tong, T., Li, B., He, T., Liu, Y., Xie, S., 2019. Eutrophication influences methanotrophic activity, abundance and community structure in freshwater lakes. *Sci. Total Environ.* 662, 863–872.
- Yang, Y., Tong, T., Chen, J., Liu, Y., Xie, S., 2020. Ammonium impacts methane oxidation and methanotrophic community in freshwater sediment. *Front. Bioeng. Biotechnol.* 8, 250.
- Yang, Y., Zhao, Q., Cui, Y., Wang, Y., Xie, S., Liu, Y., 2016. Spatio-temporal variation of sediment methanotrophic microorganisms in a large eutrophic lake. *Microb. Ecol.* 71, 9–17.
- Yi, W., Gao, Z., Liu, L., Zhu, Q., Hu, G., Zhou, X., 2020. Acute toxicity assessment of drinking water source with luminescent bacteria: impact of environmental conditions and a case study in Luoma Lake, East China. *Front. Environ. Sci. Eng.* 14, 109.
- Yin, H.B., Fan, C.X., Ding, S.M., Zhang, L., Zhong, J.C., 2008. Geochemistry of iron, sulfur and related heavy metals in metal-polluted Taihu Lake sediments. *Pedosphere* 18, 564–573.
- Zhang, J., Ni, W., Luo, Y., Stevenson, R.J., Qi, J., 2011. Response of freshwater algae to water quality in Qinshan lake within Taihu Watershed, China. *Phys. Chem. Earth* 36, 360–365.
- Zhang, X., Chen, C., Ding, J., Hou, A., Li, Y., Niu, Z., Su, X., Xu, Y., Laws, E.A., 2010. The 2007 water crisis in Wuxi, China: analysis of the origin. *J. Hazard Mater.* 182, 130–135.
- Zhang, W., Ge, X., Li, Y., Yu, Z., Li, Y., 2016. Isolation of a methanotroph from a hydrogen sulfide-rich anaerobic digester for methanol production from biogas. *Process Biochem.* 51, 838–844.
- Zhou, Y., Song, K., Han, R., Riya, S., Xu, X., Yeerken, S., Geng, S., Ma, Y., Terada, A., 2020. Nonlinear response of methane release to increased trophic state levels coupled with microbial processes in shallow lakes. *Environ. Pollut.* 265, 114919.