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Dynamics of dissolved organic carbon after a cyanobacterial bloom in hypereutrophic Lake Taihu (China)

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ABSTRACT

To establish the influence of the cyanobacterial bloom collapse on the characteristics of dissolved organic carbon (DOC) in Lake Taihu, high-molecular-weight dissolved organic matter (HMW-DOM), with sizes between 1 kDa and 0.5 μm, were collected using cross-flow ultrafiltration, from three different eutrophic regions. Isolated HMW-DOM was further characterized by atomic carbon to nitrogen ratio and neutral sugars composition by gas chromatography and mass spectrometry. The results indicated that the cyanobacterial cell lysis induced by nitrate depletion is the likely mechanism for DOC release. The relatively high DOC level was associated with the high chlorophyll *a* concentration in Meiliang Bay, one of the most eutrophic bays in the northern part of the lake. However, no significant correlations were observed between chlorophyll *a* concentration and HMW-DOC concentration during the demise of the cyanobacterial bloom in Lake Taihu. No significant differences were found in the HMW-DOC concentration among the three sampling sites, which were selected to represent different eutrophic status. However, a significant difference in the HMW-DOC concentration was found between October 2009 and January 2010 in all three sampling sites ($p = 0.02$). The HMW-DOC release may be attributed to the cyanobacterial cell lysis after the peak of summer bloom. The similarity in neutral sugar composition between the HMW-DOM and cyanobacterial exopolysaccharides suggests that the cyanobacterial bloom is the source of HMW-DOM. However, the significant correlation between the carbon to nitrogen ratio in HMW-DOM and chlorophyll *a* concentration was only observed in Meiliang Bay, which implies that apart from the cyanobacteria-derived DOC, a fraction of DOC was from riverine input. The decline of the cyanobacterial bloom also changed the overall DOM pool, leading to a shift in the component of HMW-DOM from a C-enriched material to an N-enriched material, as revealed by the variation in the carbon to nitrogen ratios. Overall, these results demonstrate that the quantitative and qualitative DOM is affected by the post-cyanobacterial bloom in Lake Taihu.

Introduction

Bloom-forming cyanobacteria have been observed in Lake Taihu for more than a decade, which is most pronounced from spring to autumn, with maximal chlorophyll *a* (Chl *a*) concentrations in summer (Xu et al., 2010). van Boekel et al. (1992) reported that phytoplankton cell lysis events occur after blooms when large phytoplankton blooms deplete inorganic nutrients. Wetz and Wheeler (2003) also observed a significant accumulation of dissolved organic matter (DOM) after nitrate depletion of the phytoplankton. Consequently, a large amount of DOM is released during phytoplankton cell lysis, which represents an important carbon and nitrogen pool in the microbial food web (Cherrier and Bauer, 2004). Aoki et al. (2008) reported that the algal DOM released from *Microcystis aeruginosa* considerably contributes to the organic matter in Lake Biwa. Understanding the effects of the cyanobacterial bloom on the Lake Taihu ecosystem is important for future predictions and controls of the affected regions. The main objective of this study is to determine if the DOM quality and quantity in Lake Taihu is affected by the cyanobacterial bloom collapse.

DOM can be separated by cross-flow ultrafiltration, resulting in a number of different molecular weight size fractions, such as high and low molecular weight dissolved organic matter (HMW-DOM: >1 kDa; LMW-DOM: <1 kDa) (Benner et al., 1997; Kepkay et al., 1997a). The two most important components of DOM are dissolved organic carbon (DOC) and dissolved organic nitrogen (DON); and phytoplankton blooms have a greater effect on DOC pools relative to DON (Gobler and Sañudo-Wilhelmy, 2003; Wetz et al., 2008). DOC from dead cells mainly consists of high-molecular-weight (HMW) compounds, whereas DOC exported from live cells

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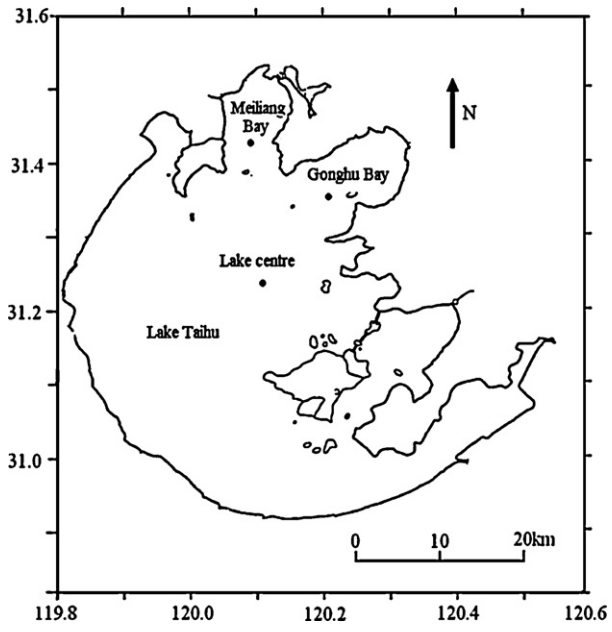

Fig. 1. Location of the sampling sites in Lake Taihu.

are largely made up of low-molecular-weight (LMW) compounds (Lee and Rhee, 1997). Compared to LMW-DOC, HMW-DOC reportedly contains more carbohydrates and is highly bioreactive in the carbon cycle (Amon and Benner, 1994; Pakulski and Benner, 1994; Engelhaupt and Bianchi, 2001). Furthermore, the neutral sugars that are hydrolyzed from more complex carbohydrate structures are known to be major components of fresh DOC from phytoplankton, which is used to fuel heterotrophic bacterial growth (Biersmith and Benner, 1998; Skoog et al., 1999).

To ascertain how the composition of DOC is affected by the decline of cyanobacterial bloom, the DOC characteristics after a pelagic bloom in 2009 were studied in three different eutrophic regions in Lake Taihu. The concentrations of Chl *a*, DOC, and HMW-DOC were analyzed and HMW-DOM was characterized in terms of neutral sugar composition and carbon to nitrogen ratio (C:N). The resulting data provides insight into the dynamics, sources, molecular composition, and degradability of the DOC released from cell lysis of the cyanobacterial bloom induced by nitrate depletion.

Materials and methods

Site description

Lake Taihu is one of the largest freshwater lakes in China and it is located in the southeastern part of the Yangtze River Delta (latitude 30°55′40″–31°32′58″N; longitude 119°52′32″–120°36′10″ E), with an area coverage of 2340 km^2. An annual serious cyanobacterial bloom occurs in late May or early June, and the large volume of cyanobacteria colonies is driven to the western and northern areas of the Lake Taihu by the high frequency of southwest winds (Wu and Kong, 2009). In this study, surface water samples from Lake Taihu were taken monthly from August 2009 to March 2010. The sampling sites were categorized into the following regions: (1) Meiliang Bay, one of the most eutrophic bays in the northern part of the lake, with a high density of *Microcystis* scum in summer (Chen et al., 2003); (2) Lake centre, an open lake without serious pelagic blooms during summer; and (3) Gonghu Bay, a bay used to be dominated by submerged macrophytes (Zhang et al., 2006), and is now less eutrophic than Meiliang Bay (Fig. 1).

In the present study, the results of microscopical analysis indicates that cyanobacteria account for more than 95% of the phytoplankton biomass for the three sampling sites during all sampling periods. Chl *a* concentrations were used to represent the biomass of cyanobacteria. Although *Microcystis* is the dominant cyanobacterial species (Chen et al., 2003), *Anabaena* appear from November 2009 to January 2010. Lower biomass (<5%) of Bacillariophyta and Cryptophyta occur in January and Chlorophyta in March 2010, respectively.

Analytical procedures

Three replicate measurements of each sample were performed. Chl *a* collected on a GF/F filter and extracted with 90% acetone, was measured using the method described by Yan et al. (2004). Ultrafiltration was performed with a Millipore Pellicon standard system using a 1 kDa regenerated cellulose PLAC filter cartridge (filter area 0.5 m^2), which is suitable for applications during plankton blooms (Guéguen et al., 2002). Water samples were filtered through a 0.5-μm pore size filter prior to ultrafiltration. The ultrafiltration procedure for the collected samples has been described by Guo and Santschi (1996). HMW-DOM is defined as the fraction between 1 kDa and 0.5 μm. DOC (<0.5 μm) and HMW-DOC (1 kDa to 0.5 μm) were analyzed by high temperature catalytic oxidation method using a total organic carbon analyzer (Shimadzu TOC-V CPN, Japan) (Zhang et al., 2006). After ultrafiltration, aliquots of both retentate and ultrafiltrate were sampled for a DOC mass balance (Guo et al., 1995; Guo and Santschi, 1996). The HMW-DOM concentrate was freeze-dried to yield a powdered sample and stored in a freezer (<−20 °C) until further analysis.

The neutral sugar composition of HMW-DOM was determined according to Handa and Yanagi (1969). For the acid hydrolysis of HMW-DOM, 100–200 mg of dry samples were dissolved in 1 mL of 2 M trifluoroacetic acid. This mixture was heated in a tightly capped glass vial at 121 °C for 2 h (Aluwihare et al., 2002). Neutral sugars were then quantified as alditol acetates by gas chromatography and mass spectrometry (Agilent 7890-5975C). The contribution of individual neutral sugars to the total neutral sugars is expressed in mole percentage (mol%). The isolated HMW-DOM samples were analyzed for C:N ratio using a EuroVector elemental analyzer (Guo et al., 2009).

Statistical analysis

The SPSS 16.0 software package was used for statistical analysis. Mean differences were determined using a two-tailed *t*-test. Differences were considered significant at $p < 0.05$. The Chl *a*, NO_3^-, DOC, HMW-DOC, neutral sugar composition, and C:N ratio data are presented as mean ± standard deviation.

Results

Chl a and nitrate concentration

The average Chl *a* concentration was higher in Meiliang Bay than in Gonghu Bay and Lake centre from June to October. The Chl *a* concentration peaked in July in all the three lake regions, which then decreased and maintained at low levels. In January, the Chl *a* concentration increase, particularly in Meiliang Bay and Gonghu Bay, but then returned to relatively low levels in March (Fig. 2a). The nitrate concentrations increased continuously in all three lake regions, but an obvious drop occurred in October, when the lowest nitrate concentration was observed in Lake centre and Gonghu Bay (Fig. 2b).

DOC and HMW-DOC concentration

The DOC concentration showed a clear increase at the sampling sites, with the maximum DOC concentration being higher in Meiliang Bay than of both other sites. In Meiliang Bay, the maximum