



How physiological and physical processes contribute to the phenology of cyanobacterial blooms in large shallow lakes: A new Euler-Lagrangian coupled model



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ABSTRACT

Cyanobacterial blooms have emerged as one of the most severe ecological problems affecting large and shallow freshwater lakes. To improve our understanding of the factors that influence, and could be used to predict, surface blooms, this study developed a novel Euler-Lagrangian coupled approach combining the Eulerian model with agent-based modelling (ABM). The approach was subsequently verified based on monitoring datasets and MODIS data in a large shallow lake (Lake Taihu, China). The Eulerian model solves the Eulerian variables and physiological parameters, whereas ABM generates the complete life cycle and transport processes of cyanobacterial colonies. This model ensemble performed well in fitting historical data and predicting the dynamics of cyanobacterial biomass, bloom distribution, and area. Based on the calculated physical and physiological characteristics of surface blooms, principal component analysis (PCA) captured the major processes influencing surface bloom formation at different stages (two bloom clusters). Early bloom outbreaks were influenced by physical processes (horizontal transport and vertical turbulence-induced mixing), whereas buoyancy-controlling strategies were essential for mature bloom outbreaks. Canonical correlation analysis (CCA) revealed the combined actions of multiple environment variables on different bloom clusters. The effects of buoyancy-controlling strategies (ISP), vertical turbulence-induced mixing velocity of colony (VMT) and horizontal drift velocity of colony (HDT) were quantitatively compared using scenario simulations in the coupled model. VMT accounted for 52.9% of bloom formations and maintained blooms over long periods, thus demonstrating the importance of wind-induced turbulence in shallow lakes. In comparison, HDT and buoyancy controlling strategies influenced blooms at different stages. In conclusion, the approach developed here presents a promising tool for understanding the processes of onshore/offshore algal blooms formation and subsequent predicting.

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1. Introduction

As the third largest freshwater eutrophic lake in China, Lake Taihu has been subject to harmful cyanobacterial blooms (Cyanobacterial Harmful Algal Blooms, CHABs), dominated by *Microcystis* spp. (Paerl and Huisman, 2008). Because of excessive nutrient inputs to the lake, these blooms present a serious threat to drinking water supplies, aquatic life, human health, and the ecological sustainability of the freshwater ecosystem of this region. A central question facing water researchers and managers is how to predict the spatial-temporal

pattern of surface blooms in large shallow lakes. This question is of immense importance for estimating the risk of cyanobacterial occurrence in advance. Understanding the growth and transport process of *Microcystis* is essential for resolving this question (Wynne et al., 2013). Previous studies have identified a host of physiological processes underlying the excessive *in situ* proliferation of *Microcystis* colonies, particularly from the perspective of biological responses (such as nutrient-induced over-enrichment (Reynolds, 2006; Paerl et al., 2011b), photosynthesis (Takamura et al., 1985), colony formation avoiding predation (Reynolds et al., 1981), and buoyancy-controlling strategies (ISP) (Reynolds, 1973; Reynolds et al., 1987; Ndong et al., 2017).

In deep lakes, the response to buoyancy changes (would be on

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the order of days) and *stationary behavior* reduce the chance to accumulation on water surface (Chien et al., 2013; Medrano et al., 2013). Therefore, the occurrence of surface bloom in shallow lake is more sensitive to physical transport process (within minute scale) than that in deep lake (Wallace et al., 2000; Duan et al., 2009; Wang et al., 2017). The physical transport processes of colony comprise of vertical turbulence-induced mixing velocity (VMT) and horizontal drift speed (HDT). Wu et al. (2015) and Cao et al. (2006) emphasized the strong relationship between surface bloom formation and wind-induced turbulence in Lake Taihu (China). The impacts of wind-induced surface drift and wave-induced Stokes drift on offshore/onshore bloom migration have been increasingly acknowledged (Ishikawa et al., 2002; Wu et al., 2010; Deng et al., 2016; Hua et al., 2016). In addition, buoyancy control and vertical transport processes have been also observed to interact (Wallace and Hamilton, 1999; Wallace et al., 2000). Recently, differences in morphology, as a result of different growth environments, which influence colony size, have been shown to contribute to diverse transport patterns (Deng et al., 2016). Therefore, both physiological process (especially ISP) and physical processes (VMT and HDT) should be evaluated to understand the timing and intensity of specific surface blooms (Glibert et al., 2010; Otten et al., 2012). However, few studies and technologies have integrated these nonlinear complex and interactive processes, or compared their respective contributions in shallow lakes.

Using field data to demonstrate the spatial-temporal distribution of surface cyanobacterial blooms presents a considerable challenge. Furthermore, linking this information to bio-physical changes is even more problematic. Recently, satellite imagery (such as MODIS data) has been used to detect the spatiotemporal patterns of surface bloom areas over large domains, relating these patterns to changing environmental conditions (Wynne et al., 2011; Qin et al., 2015). However, the information acquired from satellite imagery might obscure *Microcystis* adaptive migratory movement patterns (buoyancy-controlling strategy), as such patterns are three dimensional, induced by water current and/or wind, especially in shallow lakes. Different responses of growth to variation in light, temperature, and nutrient levels across seasons must also be considered. Thus, numerical techniques might be required to complement satellite data.

Agent-based models (ABM) have been widely applied to capture 2-D and 3-D transport trajectories of cyanobacteria over periods of several days (Dippner et al., 2011; Wynne et al. 2011, 2013; Henrichs et al., 2015). Most ABM models are forced with the physical environment from an Eulerian model, allowing the agents (each representing certain cyanobacteria) to “drift around”, thus experiencing different biological processes with water quality variables. In ABM models, the system properties are said to “emerge” from the properties of the individual particles (Grimm and Railsback, 2005). Both individual physiological properties and physical drivers could be easily integrated into agent-based equations to describe complex ecological processes, as described in Hellweger et al. (2008) and Glibert et al. (2010). However, the calibration of phytoplankton parameters in ABM is difficult because of the enormous computation requirements. Therefore, the preliminary calibrated Euler-based physical-biological model (which describes the concentration of the distribution of cumulative individuals) should be integrated into ABM to obtain associated physiological parameters of cyanobacteria and water quality variables. The increasingly complex Euler-based ecological models help us to capture the response of ecological systems to the external environment (Butenschön et al., 2016; Rolighed et al., 2016). The Fortran-based Framework for Aquatic Biogeochemical Models (FABM) was developed by Bruggeman and Bolding (2014), in which the biochemical model was arbitrarily connected to a physical

model. Here, we combined a self-contained complex biological model (called GEM) to a well-known hydrodynamic model (FVCOM) by FABM. This Euler-based model was used to calibrate the physiological parameters for phytoplankton.

In Lake Taihu in China, algae begin to emerge from the sediment and aggregate to form the early blooming stage (April–June) before mass propagation during the mature blooming stage (July–October), when the water temperature is persistently high (Kong and Fao, 2005; Cao and Yang, 2010). Therefore, we assumed that the blooms detected at different stages have specific physiological and physical characteristics. In the present study, we improved the original agent-based model of Wang et al. (2017b), and tested our hypothesis. Furthermore, we evaluated the performance of the coupled Euler-Lagrangian model using field investigated data and MODIS data to demonstrate our ability to reproduce the spatial patterns of algal blooms and characterize the physiological and physical variables of blooms. We also used the coupled model to simulate several scenarios and identify the individual contributions of physiological processes and physical processes of *Microcystis* to surface bloom in the shallow lake system. Our results are expected to provide new insights on the parameters that drive algal blooms, thus providing a basis on which to predict onshore/offshore blooms in such a large domain.

2. Material and methods

2.1. Study area

Lake Taihu (30°55′40″–31°32′58″ N; 119°52′32″–120°36′10″ E) is located in the lower part of the Yangtze River Delta, China. It is a well-known large, shallow, and eutrophic lake (Fig. 1). Lake Taihu covers an area of about 2338 km² with an average depth of 1.9 m and maximum depth of 2.64 m. Severe cyanobacterial blooms occur between April and October (Hu et al., 2006). The cyanobacteria are primarily *Microcystis* spp., which is a colony-forming cyanobacterial species consisting of mucilage, gas vesicles, and cells (Qin et al.,

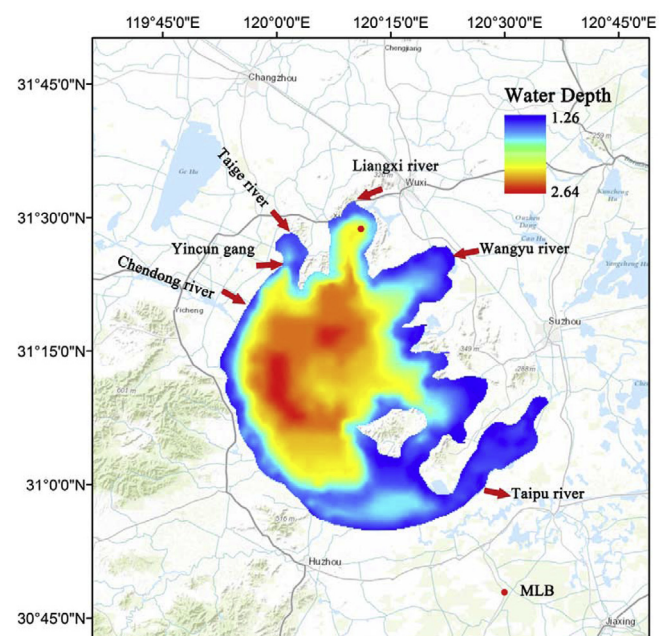


Fig. 1. Maps showing the location of the study area and monitoring stations. The main polluted inflows and outflows have been drawn. The red circle represents the sampling area (MLB) where the biomass of *Microcystis* was monitored. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

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