

One dimensional modelling of cyanobacteria dynamics in shallow lakes: application to Missisquoi Bay, Lake Champlain (Canada)

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Introduction

Bloom-forming cyanobacteria remain a persistent nuisance across the world. The development of blue-green algae and their associated toxins disturb lake use and drinking water production (Bartram and Chorus, 1999). Modelling of cyanobacteria is an important tool for understanding their population dynamics. It is also useful for predicting bloom occurrence and to assist with lake management decisions.

Cyanobacteria currently dominate the phytoplankton biomass of Missisquoi Bay in Lake Champlain (Quebec, Canada). The increase in nutrients in the bay, especially phosphorus, is clearly linked to the development of high densities of algae (Fong, 1993; Khan and Ansari, 2005), but do not necessarily mean dominance by cyanobacteria (LCRC, 2005). Extensive investigations have been conducted on nutrient dynamics and contaminant transport modeling, in the bay, however, other factors such as an increase in water temperatures and precipitation events may also affect the development of cyanobacterial blooms.

The objective of this project was to apply the one dimensional hydrodynamic model DYRESM on field data to increase the understanding of the growth and success of toxic cyanobacteria.

Methods

The strength of the model greatly depends on the quality, availability and accuracy of the data used to create input files for the model, thus field measurements have to be regularly performed to validate the model. For that purpose a monitoring system was created.

Field experiments

In 2007, a continuous, real-time monitoring system was developed and implemented in Missisquoi Bay, using an autonomous multi-probe system measuring physicochemical parameters, chlorophyll a and phycocyanin. Extensive field data have been acquired during the summer period, from 2007 to 2010 that include taxonomic counts of cyanobacteria, measurements of nutrient (N and P) and microcystin concentrations. In addition, meteorological data have been obtained from the weather station in nearby Frelighsburg, QC (Canada).

Modelling

The modelling methodology is a single-model approach, using data mining and a determinist model, applied to one species of toxic cyanobacteria: *Microcystis aeruginosa*, a toxic freshwater species which occurs worldwide and is responsible for water quality problems in Missisquoi Bay.

The one dimensional DYRESM model was applied because it is suitable for modelling shallow reservoir and lakes. It assumes that horizontal variations in the water are less important than vertical variations. The model simulates the vertical distribution of temperature, salinity and density in lakes and reservoirs. It requires meteorological data as input, including averages for air temperature, wind speed, rainfall, longwave radiation and vapour pressure. Daily inflow and outflow volumes as well as temperature in the inflows are also required as boundary conditions, and are essential for setting up a representative water balance.

Results and Discussion

Field measurements

Data mining is essential to understand which variables affect the development of cyanobacteria. Water temperature, inflows from tributaries and wind speed have been found to be the main factors that control the growth and spatial distribution of cyanobacteria in Missisquoi Bay. Thermal stratification of the water enhanced the stratification of cyanobacteria. Indeed, optimal growth temperature of *M. aeruginosa* and *M. flos-aquae*, the dominant species on June 28th, varies from 24°C to 34°C (Robarts and Zohary, 1987), which drives them to develop near the surface where water is warmer.

Simulations

The Dyresm model was calibrated over a three-month period from July 18th to October 14th 2008 and validated for the summer period of 2010. The winter period was excluded from the data set as field measurements have not been performed in winter – only meteorological and inflows data are available for that period – and the model used does not include ice formation. The dominant phytoplankton community was modelled and combinations of various environmental conditions were simulated to predict potential cyanobacterial bloom formation. Results will be presented on the correlation between predicted and measured values.

Conclusion

The good correlation between field measurements and simulation results showed that the model developed with DYRESM appears to be an appropriate model to simulate cyanobacteria dynamics in Missisquoi Bay. Further investigation on this model will be conducted to include the CAEDYM model, an aquatic ecosystem model, which simulates a range of biological and chemical processes, expressing variables such as nutrients, phytoplankton biomass and zooplankton biomass which are commonly associated with ecological water quality.

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