



CYANOBACTERIAL BLOOMS : TOXICITY, DIVERSITY, MODELLING AND MANAGEMENT

«B-BLOOMS 2»

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CYANOBACTERIAL BLOOMS : TOXICITY, DIVERSITY, MODELLING AND MANAGEMENT

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Jean-pierre Descy, Samuel Pirlot, Gisèle Verniers, Yannick Lara, Annick Wilmotte, Wim Vyverman, Pieter Vanormelingen, Jeroen Van Wichelen, Ineke Van Gremberghe, Ludwig Triest, Anatoly Peretyatko , Etienne Everbecq, Geoffrey A. Codd. **Cyanobacterial blooms :** *toxicity, diversity, modelling and management "B-Blooms 2"*. Final Report Phase 1. Brussels : Belgian Science Policy 2009 – 4 p. (Research Programme Science for a Sustainable Development)

The B-BLOOMS2 project consists of a study of cyanobacteria blooms in Belgium, involving sampling of a set of reference lakes in Flanders, Brussels and Wallonia, and the use of different approaches to assess environmental conditions, cyanobacterial diversity, potential toxicity through detection of the mcy genes, and toxin measurement using different techniques. The program was run for the years 2007 and 2008. Five reference lakes were selected: two lakes in Flanders (Westveld and Donkmeer), two in Brussels (Ixelles ponds 1 and 2) and one lake in Wallonia (Falemprise). Sampling was done on a regular basis (once a week or every fortnight from March to October). It comprised: water samples with measurements of nutrients and limnological variables, phytoplankton and zooplankton collection, subsampling for molecular analyses, isolation of strains in cultures and toxin analyses, collection of daily weather data. Phytoplankton was assessed at least at the class level, and cyanobacteria were counted and identified at least at genus level. A common protocol (see www.bblooms.be) was defined by the coordinator, and followed by the different teams. Samples were also collected through BLOOMNET, a network involving water users and managers in the different regions. In parallel, simulation models were developed for testing measures for bloom reduction in one of the lakes, and a probabilistic model was developed for predicting cyanobacterial bloom occurrence in ponds of the Brussels region.

Here we report (i) observations of phytoplankton composition with an emphasis on cyanobacteria in the reference lakes, and on environmental conditions associated with blooms development, (ii) genetic diversity assessed by DGGE and 16 S rRNA sequencing, (iii) genotoxicity assessed by detection of *mcy* genes, (iv) actual toxicity by measurement of cyanotoxins in water and in bloom material, (v) the results of Lake Falemprise simulation, and (vi) the results of the predictive modelling applied to the cyanobacterial blooms in the Brussels's ponds.

Phytoplankton and cyanobacteria dynamics were described in detail for the different lakes. Among the main results of the study already available, it can be stressed that most blooms consisted of potentially toxic belonging to the genera *Aphanizomenon*, *Microcystis*, *Planktothrix* and *Anabaena*. Observations and statistical analyses showed that, besides clearly depending on weather conditions and nutrient loading, cyanobacterial blooms were influenced to a varying degree by biotic interactions, such as nature and size of the planktonic grazers (Brussels ponds and Falemprise) or by parasites (amoebae and chytrids, in Donkmeer and Westveld). The assessment of bloom diversity was greatly improved by the molecular approaches, and change in strain dominance was shown in some lakes. The majority of DGGE bands amplified and sequenced showed high similarity with potentially toxic *Microcystis* and *Plankthotrix*.

A database on bloom molecular diversity in Belgian freshwaters (the ARB database) has been developed.

Several genes of the *mcy* cluster were regularly detected in the bloom samples: a total of 102 samples were extracted and tested for presence of mcy genes in the Brussels and Walloon regions in 2007 and 2008. While in 2007, only a part of the samples were positive, in 2008, the *mcyA/B/E* genes were detected in most samples, as in Falemprise and in Ixelles ponds, showing the presence of potentially toxic *Microcystis* in the majority of samples. A RFLP analysis showed succession of different *mcyE* genotypes in the same freshwater body.

Analysis has been carried out at University of Dundee using HPLC analysis of bloom samples and immunoassays, for determining particulate and dissolved toxins in the environment. Microcystins were also measured in single colonies or filaments isolated from environmental samples, using quantitative immunoassays. Toxin analyses showed presence of microcystins in all samples tested, the concentration of which exceeded the WHO guideline value (1 μ g L⁻¹) quite frequently if not all the time. Wide variations versus sample date were found in the compartmentation of microcystins between soluble and particulate phases.120 individual colonies and filaments have been analysed: the quotas measured ranged from 45.4 to 1620 picograms per colony or filament.

A modified simulation model, derived from the PEGASE model as applied to the Eau d'Heure watershed, has shown its ability to simulate cyanobacterial blooms in Lake Falemprise, and it can be used as predictive tool for future sewage treatment scenarios. However, improvements are still needed in order to fully adapt the model to lakes deep enough to develop summer stratification.

The predictive models developed for Brussels ponds allowed to calculate the probability of bloom occurrence in these ponds, with a considerable seasonal and interannual variation in the probability. The highest probability, based on the data from all the ponds studied, was shown by the combination of all the variables measured. This approach permits to identify the ponds prone to cyanobacterial bloom development and thus can help managers to focus their monitoring program on the most problematic ponds.

All these results will help understanding the mechanisms behind cyanobacterial bloom development and toxin production, and, from a management point of view, call for measures for blooms reduction for preventing public exposure to harmful blooms.