

Cyanobacterial Water Blooms Seriously Change the Structure and Biodiversity of Phytoplankton Assemblages

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Abstract

Pollution of surface waters by nutrients cause serious problems connected with mass development of planctonic cyanobacteria forming water blooms. Cyanobacteria produce a broad spectrum of toxic substances. In our study we tested the influence of cyanobacteria on species composition and abundance of phytoplankton. We used data from two reservoir near the city of Brno, Czech Republic. We found, that during the dominance of cyanobacterial species forming water blooms there is serious reduction on species diversity. Especially diatoms seem to be the most sensitive group of phytoplankton. Diatoms practically disappeared in samples, where cyanobacteria have formed blooms. Several statistical methods like principal component analysis and cluster analysis were applied to analyse biotic interaction and separate samples, where cyanobacteria could be responsible for reduction of phytoplankton diversity. Possible mechanisms of this phenomena should be connected with cyanotoxins produced by water blooms.

1. Introduction

Pollution of surface waters by nutrients cause serious problems connected with mass development of autotrophic organisms. Generally, freshwater ecosystems can be dominated by macrophytes, benthic diatoms, filamentous algae or phytoplankton. In the case of dominance of planctonic cyanobacteria forming water blooms we can see surface scums. Cyanobacterial water blooms are formed by autotrophic gram negative eubacteria, which are extremely adaptable organisms living from polar Arctic regions up to hot springs, from deep oceans up to high mountains with strong UV radiation. Cyanobacteria are K-strateges – they grow slowly and need long time to become dominant. However, if they become dominant in the certain ecosystem, they position is stable and keep a dominant position for a long period.

Cyanobacteria produce a broad spectrum of toxic substances, called cyanotoxins. The most studied cyanotoxins are embryotoxins (effect on humans exposed by drinking water, natural fish reproduction, zooplankton reproduction etc.), hepatotoxins (influence on hepatoma cells integrity and liver function up to liver carcinoma), neurotoxins (affecting central nerve system and behaviour of aquatic and injured animals), immunotoxins and immunomodulants (including allergic reactions, ability to response to external stress signals, number of these compounds have a pharmacological potential and their use is patented), mutagens and genotoxins, nephrotoxins, tumour promoting factors etc. Practically all cyanobacteria are able to produce some toxins affecting other species in aquatic ecosystem. However it is difficult to identify and quantify above mentioned broad spectrum of cyanotoxins. The hypothesis, that all cyanobacteria possess toxic hazard, because all cyanobacteria produce some toxins, is generally accepted by all experts

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working in the field of cyanotoxins. Practical method for estimation of effect of cyanotoxins is quantification of cyanobacterial biomass by microscopic analyses. This method was used also in our study to determine the structure of phytoplankton assemblages in natural ecosystem.

2. Material and methods

We used long-term data from vegetation seasons in stratified Brno reservoir and from shallow reservoir Nové Mlýny to test the hypothesis that cyanobacteria change the species composition and abundance of phytoplankton. Altogether, 266 samples were taken during the time period 2001 – 2004. The number of cells of different taxa was estimated per one ml using standardized methods. The data used in next analysis represented the total number of cells and number of species in following groups: cyanobacteria (Cyanoprokaryota), golden algae (Chrysophyceae), Xantophyceae, diatoms (Bacillariophyceae), brownish-green algae (Cryptophyceae), dinoflagellates (Dinophyceae), euglenoids (Euglenophyceae), green algae - monadoid, coccal, trichal (Chlorophyceae) and conjugating green algae (Conjugatophyceae). The statistical analyses used in the study included correlations, principal component analysis and cluster analysis. The PCA was based on the correlation matrix of log-transformed numbers of cells of 12 taxonomic groups on 266 samples. The PCA coordinates of 266 samples on the first two PCA factors were included to the cluster analysis with Euclidean distances and complete linkage hierarchical algorithm with the aim to found out the groups of samples associated with cyanobacteria and other groups of phytoplankton

3. Results

We found, that during the dominance of cyanobacterial species forming water blooms there is serious reduction on species diversity. Especially diatoms seem to be the most sensitive group of phytoplankton (the correlation between the number of cells of diatoms and number of cells of cyanobacteria: $r_s = -0.608$, $P < 0.001$). Moreover, not only the number of cells of diatoms but also the species richness of diatoms were reduced by cyanobacteria ($r_s = -0.140$, $P < 0.001$). Diatoms practically disappeared in samples, where cyanobacteria have formed blooms. Similar situation holds true for golden algae (the correlation between the number of cells of golden algae and number of cells of cyanobacteria: $r_s = -0.395$, $P < 0.001$), green algae s. l. monadoid (-0.359 , $P < 0.001$) and green algae s. l. coccal ($r_s = -0.547$, $P < 0.001$).

The principal component analysis (PCA) and cluster analysis were applied to analyse biotic interaction and separate samples, where cyanobacteria could be responsible for the reduction of phytoplankton diversity. The first two factors of PCA accounted for 41.6 % of the variability in the data matrix. The negative correlation between cyanobacteria and diatoms as well as between cyanobacteria and green algae was confirmed by PCA (Fig. 1). By the mean of cluster analysis three main groups of samples were distinguished (Fig. 2). Altogether, 72.7 % samples of the first cluster represented samples from April, May and June and were characterised by low dominance of cyanobacteria and high abundance of diatoms, green algae, golden algae, brownish-green algae and dinoflagellates. The second cluster were made mainly of samples from July, August and September (84.3 %) where cyanobacteria dominated and the species richness of phytoplankton was reduced. The third cluster consisted just from 13 samples, from which 61.3 % came from shallow reservoir Nové Mlýny (61.3%) in April and May, respectively. The assemblages of these samples were formed by cyanobacteria, euglenoids and Xantophyceae.

4. Conclusion

According to our results we conclude that cyanobacteria influence phytoplankton abundance. Possible mechanisms of these phenomena should be connected with cyanotoxins produced by water blooms.

5. Acknowledgements

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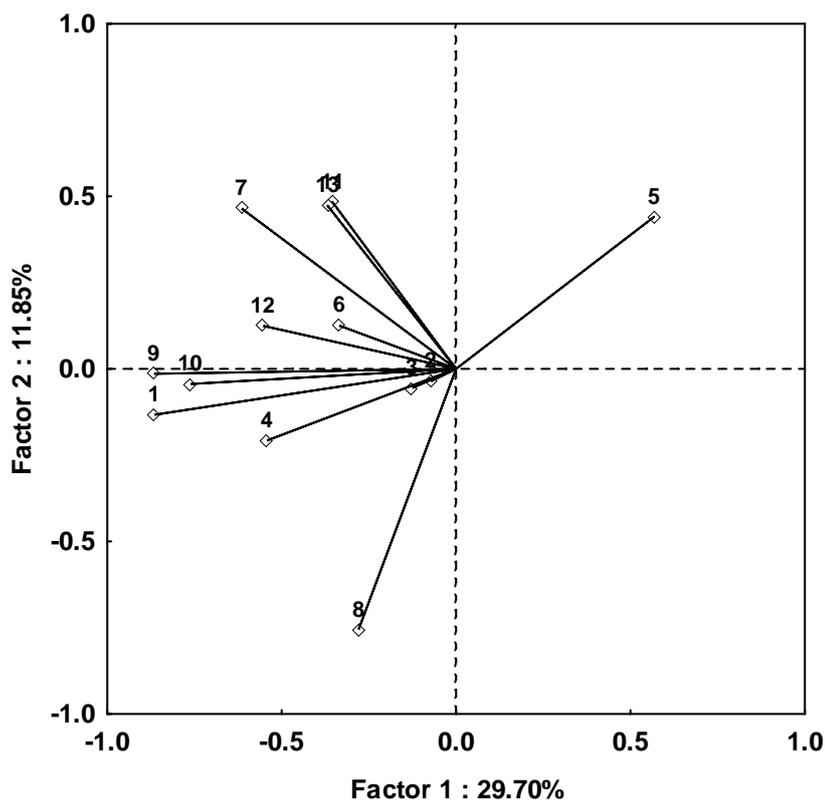


Fig. 1: Position of phytoplankton groups on the first two axis of PCA. 1. Bacillariophyceae, 2. Bacteria, 3. Conjugatophyceae, 4. Cryptophyceae, 5. Cyanoprokaryota, 6. Dinophyceae, 7. Euglenophyceae, 8. Flagellata apochr., 9. Chlorophyceae s. l. coccal, 10. Chlorophyceae s. l. monadoid, 11. Chlorophyceae s. l. trichal, 12. Chrysophyceae, 13. Xanthophyceae.

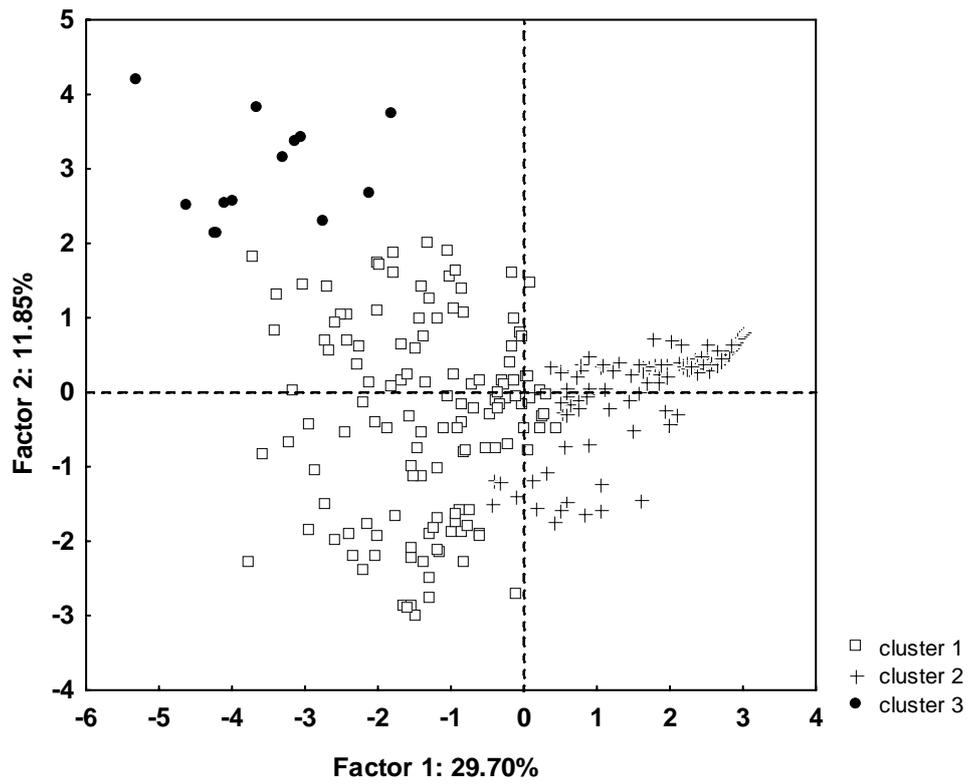


Fig. 2: Position of samples on the first two axis of PCA. 1. Groups of samples were defined by mean of the cluster analysis.