

## Changes in composition of phytoplankton assemblages due to organic contaminants depending on the sensitivity of dominant species

István Bácsi<sup>1</sup>, Viktória B. Béres<sup>1,2</sup>, Gábor Vasas<sup>3</sup>, Zoltán Novák<sup>1</sup>, Sándor Alex Nagy<sup>1</sup>

<sup>1</sup>University of Debrecen, Department of Hydrobiology, P.O. Box 57, 4010 Debrecen, Hungary, E-mail: istvan.bacsi@gmail.com

<sup>2</sup>Environmental Protection, Nature Conservation and Water Authority, Trans-Tiszanian Region, Hatvan str. 16, 4025 Debrecen, Hungary, E-mail: beres.viktoria@gmail.com

<sup>3</sup>University of Debrecen, Department of Botany, Pharmacognosy Divison, P.O. Box 14, 4010 Debrecen, Hungary, E-mail: vasas.gabor@science.unideb.hu

The problem of chlorinated hydrocarbons accumulation in soil and in groundwater as a consequence of earlier industrial activity is again in the focus of attention nowadays, since the latest results of monitoring showed that the risk of appearance of these compounds in surface waters increased. Effects of chlorinated hydrocarbon contaminants on natural phytoplankton assemblages in shallow lake ecosystems are relatively rarely studied. Although the impact of biodiversity on ecosystem functioning has become one of the most studied area of ecology, the importance of diversity in a changing environment is still poorly understood. Changes in composition of phytoplankton assemblages due to short-chained chlorinated hydrocarbons (tetrachloroethane, tetrachloroethylene and trichloroethylene) were studied in microcosm experiments in summer of 2011 and 2012. Diversity further decreased during treatments in the less diverse 2011 summer community, dominated by the euglenid *Trachelomonas volvocinopsis* Svirenko (its relative abundance was nearly 70%). Diversity did not change significantly during treatments in the more diverse 2012 summer community, dominated by cryptomonads (their relative abundance were 40%). Cryptomonads were extremely sensitive to treatments, they almost completely disappeared from the treated communities. In contrast, the dominant *Trachelomonas volvocinopsis* in 2011, presumably also due to its high competition skills, filled "space" occurring after disappearance of sensitive species. Chlorinated hydrocarbons affect negatively the composition of phytoplankton communities, but there were more resistant species in the more diverse system (2012 summer assemblages in our case), which enabled it to offset the functional impairment resulting from the disappearance of other species.

## Possible anticyanobacterial effects of *Cryptomonas ovata* (Cryptophyta) on *Microcystis aeruginosa* (Cyanobacteria)

Viktória B. Béres<sup>1,2</sup>, Gábor Vasas<sup>3</sup>, István Bácsi<sup>2</sup>

<sup>1</sup>Environmental Protection, Nature Conservation and Water Authority, Trans-Tiszanian Region, Hatvan str. 16, 4025 Debrecen, Hungary, E-mail: beres.viktoria@gmail.com

<sup>2</sup>University of Debrecen, Department of Hydrobiology, P.O. Box 57, 4010 Debrecen, Hungary, E-mail: istvan.bacsi@gmail.com

<sup>3</sup>University of Debrecen, Department of Botany, Pharmacognosy Divison, P.O. Box 14, 4010 Debrecen, Hungary, E-mail: vasas.gabor@science.unideb.hu

Algal taxa could influence the survival and/or growth of other populations in phytoplankton communities by their presence, metabolism, nutrient uptake, and allelochemicals. According to earlier theories, cyanotoxins play an important allelopathic role in planktonic communities. However, there are only few studies in which direct algal-cyanobacterial allelopathy, effects of extracellular toxin content to other algae, or influences of other algal population on active toxin release was discussed. In our study we focused on the effects of non-toxic *Cryptomonas ovata* Ehrenberg to growth, nutrient uptake and extracellular toxin content of toxic *Microcystis aeruginosa* Kützing in mixed cultures (containing both *C. ovata* and *M. aeruginosa* cells) and in *C. ovata* crude extract treated *M. aeruginosa* cultures. The survival and growth of the eukaryotic alga or the cyanobacterium in mixed cultures were closely related on the initial cell numbers of populations. Extracellular toxin contents were

found in the Danube (up to 96.6%) and Channel Hulovo (up to 82.9%), while in the other sites (Lake Kopačko, Channel Čonakut and Lake Sakadaš) their contribution was up to 51.8%. Besides different diatom species, other groups such as cryptophytes and colonial phytomonads which were well represented during the flood period appeared to indicate altered conditions in the floodplain driven by flooding. During the isolation period, different species of Cyanobacteria were dominant followed by chlorococcal green algae. In that time, high values of total phytoplankton biomass in the floodplain sites were found (up to 185.5 mg/L), with high contribution of Cyanobacterial species (up to 92.9%). In the Danube, diatoms remained dominant species exhibiting a different pattern of species succession. According to the redundancy analysis, the development of phytoplankton during the hydrological isolation was associated with a higher water temperature, lower water depth and transparency. Altogether, the location of the floodplain sites in relation to the river and hydrological connectivity between the river and its floodplain significantly influenced the phytoplankton community structure and the overall ecological condition of floodplain microlocalities.

### **Variability of *microcystins* and its synthetase gene cluster in *Microcystis* Lemmermann 1907 and *Planktothrix Anagnostidis et Komárek* water-blooms in shallow lakes of Hungary**

Gábor Vasas, Oszkár Farkas, Gréta Hajdu, Sándor Gonda, Péter Parizsa

Department of Botany, University of Debrecen, Egyetem tér 1., 4032 Debrecen, Hungary, E-mail: [vasas.gabor@science.unideb.hu](mailto:vasas.gabor@science.unideb.hu)

Water-bloom samples of *Microcystis aeruginosa* and *Planktothrix agardhii* were collected from a variety of ponds, lakes and reservoirs in Hungary. Samples were tested with matrix-assisted laser desorption/ionization-time-of-flight mass spectrometry (MALDI-TOF MS) to identify the microcystin forms. The concentration of the microcystins was measured with capillary electrophoresis and the toxicity was tested by sinapis test. DNA was extracted from the samples and tested using a range of primers linked to the biosynthesis of microcystin. The results showed that a wide range of microcystin (MC) forms were detected in the *Microcystis* containing samples, among which MC-LR, -RR, - and -YR were the most common. The highest MC concentration was 15,701 mg g<sup>-1</sup>, which was detected in an angling pond. The samples containing *Planktothrix agardhii* were less toxic, and the most common form was the Asp3-MC-LR.