

**19th WORKSHOP OF THE
INTERNATIONAL
ASSOCIATION
OF PHYTOPLANKTON
TAXONOMY AND ECOLOGY**

TISZAFÜRED, HUNGARY

23–30 September 2022



ABSTRACTS

BIOGEOGRAPHY OF CYANOBACTERIA IN LAKES AND RIVERS BASED ON TAXONOMIC AND FUNCTIONAL TRAIT APPROACHES: RESULTS OF A WIDE HIGH THROUGHPUT SEQUENCING SURVEY IN THE ALPINE REGION

Nico Salmaso¹, Serena Bernabei², Adriano Boscaini¹, Camilla Capelli³, Isabelle Domaizon⁴, Tina Elersek⁵, Claudia Greco², Aleksandra Krivograd Klemenčič⁶, Rainer Kurmayer⁷, Paolo Tomassetti², Maša Zupancic⁵, Leonardo Cerasino¹

¹Research and Innovation Centre, Fondazione Edmund Mach, San Michele all'Adige, Italy

²Italian Institute for Environmental Protection and Research (ISPRA), Roma, Italy

³Institute of Earth Sciences, University of Applied Sciences and Arts of Southern Switzerland (SUPSI), Mendrisio, Switzerland

⁴INRAE, UMR Carrtel, Université Savoie Mont Blanc, Pole R&D ECLA, Thonon les Bains, France

⁵National Institute of Biology, Ljubljana, Slovenia

⁶Slovenian Environment Agency, Ljubljana, Slovenia

⁷Research Institute for Limnology, University of Innsbruck, Mondsee, Austria nico.salmaso@fmach.it

The completeness of biogeographical surveys of cyanobacteria is strongly constrained by several factors that include the comparability of datasets determined by different laboratories and the sensitivity of traditional microscopy methods, which are focused on the larger taxa. Additional factors limiting conventional large-scale biogeographic surveys may include time constraints and the requirement for high taxonomic expertise. Here, we report the results of a wide survey carried out in the framework of the project Eco-AlpsWater in 37 lakes and 23 river sites located throughout the Alps. Focus was on the determination of cyanobacteria in lake plankton, and lake and river biofilms, analysed using a common approach based on high throughput sequencing of 16S rRNA marker genes using MiSeq technologies. The three habitats, namely lake plankton, and lake and river biofilm, had a typical cyanobacterial composition, showing an extremely small number of shared amplicon sequence variants (ASVs) and classified genera. Furthermore, the analyses made it possible to deduce for the first time the distribution of toxigenic species in the Alps, such as *Tychonema*

bourrellyi, a typical anatoxin-a (ATX) producer. The reliability of results was demonstrated by the high significant relationships between ATX and microcystins, and the DNA read abundances of their main producers. The taxonomic differences among habitats were also paralleled by differences observed for the main morpho-functional groups. The ecological significance of these differences was related to the main physiographic and environmental differences of the three aquatic habitats. Finally, the significance and limits implicit in the use of metabarcoding in ecological studies will be critically evaluated.