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Abstract Book

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Microalgae-based biodiversity and biomonitoring: Strengths and gaps of high-throughput sequencing applications

Dr Nico Salmaso[1], Dr Rainer Kurmayer[2], Dr Ute Mischke[3], Dr Camilla Capelli[4], Dr Tina Elersek[5], Dr Fabio Lepori[4], Giulia Riccioni[1], Dr Frédéric Rimet[6], Dr Marine Vautier[6], Dr Isabelle Domaizon[6]

[1]*Research and Innovation Centre, Fondazione Edmund Mach,* [2]*University of Innsbruck, Research Department for Limnology,* [3]*Bavarian Environment Agency,* [4]*University of Applied Sciences and Arts of Southern Switzerland (SUPSI),* [5]*Department of Genetic Toxicology and Cancer Biology, National Institute of Biology,* [6]*INRAE, Université Savoie Mont Blanc, CARRTEL*

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The development of culture-independent high throughput sequencing (HTS) has opened new horizons in the study of aquatic biodiversity for fundamental and applied research. The limitations in the use of traditional approaches to the identification of organisms, which are based on the identification of morphological traits, have promoted several studies that aimed to integrate new HTS technologies in regulatory biomonitoring, such as WFD (CE) and WPO (CH). In the Alpine region, one of the main objectives of the Interreg Alpine Space Eco-AlpsWater project is to develop and apply HTS methods for monitoring cyanobacteria and bacteria, microalgae, and fish, integrating and harmonizing conventional approaches. Here, we will focus on the results obtained for "algal" assemblages, i.e. cyanobacteria and microalgae in plankton and biofilms, analysed using 16S and 18S rRNA marker genes. The survey was conducted in 37 lakes and 23 river sites. The specific points discussed in this investigation include the overall diversity recovered by HTS and light microscopy (LM); the taxonomic coverage of 16S and 18S rDNA sequences in NCBI taxonomic databases; the fraction of species identified by LM that are represented with at least one corresponding molecular marker (16S-18S) in the NCBI databases; the definition of methods to evaluate the reliability of LM classifications based on their correspondence with HTS sequences; the definition of phylogenetic approaches to fine-tune the taxonomic classifications obtained from the bioinformatic pipelines. The results are building a solid knowledge base for evaluating the range of applications and complementarities of HTS in the next generation biomonitoring systems.