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Abstract Book



Metabarcoding vs. morphological identification for aquatic ecosystem biomonitoring: a case study

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Phytoplankton and benthic diatoms are frequently used as biological quality indicators. However, conventional methods for species identification (light microscopy) are time-consuming and require a high level of taxonomic expertise. The Interreg Alpine Space Eco-AlpsWater project (EAW) has the aim of overcoming these limits, exploring the application of high throughput sequencing (HTS)-based DNA metabarcoding for water quality assessment in the Alpine region. Here, preliminary results obtained from Lake Lugano (CH-IT) are used to evaluate the potential of DNA based approaches. For this purpose, in 2019, 10 littoral sites were sampled for the study of benthic diatoms and one pelagic site was sampled monthly for the study of eukaryotic phytoplankton and cyanobacteria. The HTS sequences of 16S rRNA (V3-V4), 18S rRNA (V4), and rbcL marker genes obtained from eDNA extracted from water and biofilm samples was compared with conventional identification by light microscopy. The genetic approach showed a good consistency with conventional methods, in particular for dominant taxa, although the correspondence between approaches was lower at the genus and, especially, the species level. Moreover, the HTS led to the identification of a higher number of indicator taxa and was found to be a sensitive tool for the detection of rare or invasive species. Therefore, the approach proposed within the EAW project, and HTS methods in general, can be effective in the study of the biodiversity and in the improvement of the ecological quality assessment of waterbodies.