Abstract book

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Pro and cons of morphological and genomic approaches for the study of subfossil diatoms in alpine lakes.

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Thanks to the continuous improvement of the High Throughput Sequencing (HTS), the metabarcoding of eukaryotic organisms is being increasingly applied in surveys of freshwater microalgae including diatoms, which are among the most powerful and studied freshwater biological indicators. The HTS-based approach for diatom studies is considered as highly promising since, in comparison to the classical morphological approach, it allows the quick and cheap processing of a large number of samples and does not need highly specialised taxonomical skills for the analyses of the results. The metabarcoding approach has been recently applied also on the study of subfossil diatoms preserved in deep lake sediments aiming at reconstructing past environmental and ecological evolution at secular to millennial scale of temperate lakes. Here we present the results of a comparison between the overall performance of a HTS- and morphological-based study of subfossil diatoms preserved in the sediment of a high-altitude lake (L. Marmotte, 2704 m a.s.l.) located in the Italian Central Alps. Due to the physical and chemical lake settings the HTS approach was viable for samples not older than ca. 150 years. The HTS approach overestimates temporal changes in diatom taxonomic composition and diversity, while the morphological approach shows a higher capacity to provide a realistic picture of the past diatom taxonomic composition and richness, even though it tends to oversee larger taxa.