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Oral Presentation

**Morphological vs genomic approaches for
studying subfossil diatoms in a high-altitude
Alpine lake: *pros* and *cons***

Thanks to the continuous improvement of the High-Throughput Sequencing (HTS) techniques, 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 metabarcoding approach for diatom studies is considered as highly promising since, in comparison to the classical morphological approach, it allows the simultaneous and cheap processing of large numbers of samples and does not need highly specialised taxonomical skills for the analyses of the results. Consequently, the metabarcoding approach has been recently applied also to 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 compare the overall performance of a study, based on both metabarcoding and morphological approaches, of subfossil diatoms preserved in the deep sediments of a high-altitude lake: L. Marmotte, located at 2704 m a.s.l. within the Stelvio National Park in the Italian Central Alps. Short cores were collected from the deepest point of the lakes in August 2017, radiometrically dated and analysed for a set of lithological, geochemical and biological proxies, including diatoms.

A rapid degradation after sedimentation of total eDNA was observed, likely in relation to the aggressive physical lake settings, e.g. strong UV radiation and scorching effect along the lake banks related to the long winter ice cover. Therefore, the metagenomic approach was viable for samples not older than ca. 150 years. The classical morphological approach, although underestimating the abundance of the largest diatom taxa, provided more conservative results compared to metabarcoding, thanks to good valve preservation in the sediments under low water temperatures and acidic pH. In addition, the metabarcoding failed in assigning many small or recently defined/revised genera (e.g., *Psammothidium*, *Adlafia*, *Genkalia*, *Sellaphora*), as well as sporadic taxa (e.g., *Eunotia*, *Cymboplectra*), while it was more reliable than light microscopy in revealing the largest taxa belonging to *Surirella*, *Neidium*, *Pinnularia*. The metabarcoding appeared to over-



estimate the temporal changes in diatom taxonomic composition and diversity, while the morphological approach provided a more realistic picture of diatom temporal changes.

The metabarcoding approach applied to less studied, remote high mountain lakes characterised by aggressive environmental settings appears reliable for general surveys of diatom diversity and changes at medium temporal scale (decades), while detailed ecological studies at secular to millennial scale largely benefit from the classical morphological approach. The improvement of the capacity for genus and species assignment of the diatom metabarcoding appears to be crucial for obtaining a synergic complementarity with the classical morphological approach.

