

The reconstruction of ecological interactions through eDNA metabarcoding analyses on ice cores extracted from the largest and deepest southern European Alps glacier: Adamello, Italy

Cristiano Vernesi¹, Alexis Marchesini¹, Matteo Montagna², Matteo Girardi¹, Antonella Cristofori¹, Valter Maggi³, Daniela Festi⁴, Camilla Wellstein⁴, Stefan Zerbe⁴, Klaus Oeggl⁵

¹Fondazione Edmund Mach/Research and Innovation Centre (Italy), ²Università degli Studi di Milano (Italy), ³University of Milano Bicocca (Italy), ⁴Freie Universität Bozen-Bolzano (Italy), ⁵University of Innsbruck (Italy)

For inferring environmental changes through time, ice cores offer a twofold advantage: good preservation of eDNA and detailed timescale, possibly at year and season level. In the CALICE project, we aim at estimating biodiversity changes in the Adamello glacier catchment area, experiencing in recent times dramatic land-use and climatic modifications. The retrieved 45 m ice core would in fact encompass the last 70-80 years, according to tritium radioactivity results.

Identifying plant and insect species would reveal how their ecological interaction (e.g. pollination) responded to global changes, thus shedding light on functional biodiversity modifications from macro- to micro-scale landscape level.

Co-amplification of untargeted organisms, taxonomic resolution, preferential amplification of some taxa and contamination represent the major limitations of PCR-based eDNA metabarcoding.

We developed a target enrichment approach on eDNA extracted from the first basal 10 m of the ice core. We targeted, through a synthesised bait, about 10 kb representing the most variable regions of cpDNA across a wide range of plant taxa. Approximately 8 kb of mtDNA were targeted in insects. After baits hybridization with eDNA, libraries assembly and massive sequencing, the resulted reads were compared to specific reference databases: PhyloAlps (cpDNAs of all the plant taxa of the Alps) and a custom-made database for plants and insects, respectively.

This sequence capture metabarcoding proved to be more efficient to infer plant and insects biodiversity, therefore showing the potential of ice cores as very informative climatic and biological archive for addressing the impact of global change on biodiversity.
