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An eDNA protocol for monitoring and preserving biodiversity from genes to species: a case study of Alpine amphibians from Trentino

<u>Lucia Zanovello</u>^{1,2}, Alexis Marchesini³, Matteo Girardi², Sonia Endrizzi⁴, Chiara Fedrigotti⁴, Paolo Pedrini⁴, Heidi C. Hauffe²

¹Dept. of Biology, University of Padova, Padova, Italy ²Dept. of Biodiversity and Molecular Ecology, Research and Innovation Centre, Fondazione Edmund Mach, S. Michele all'Adige (TN), Italy

³Dept. of Sustainable Ecosystems & Bioresources, Research and Innovation Centre, Fondazione Edmund Mach, S. Michele all'Adige (TN), Italy

⁴Section of Vertebrate Zoology, Museum of Science (MUSE), Trento, Italy

In the last decade, environmental DNA (eDNA) and metabarcoding have provided new opportunities for the study of biodiversity in space and time. The eDNA metabarcoding approach is increasingly used as a cost effective tool for species detection and community characterization, particularly for elusive species. However, technical challenges and case-specific limitations exist and need to be explored. In this study, we tested if eDNA metabarcoding of water samples can be used for developing an effective protocol for the characterization and monitoring of Alpine amphibian communities. By PCR amplification of a 151 bp COI barcode region using primers specific for amphibians, we aimed at assessing the species composition of several selected wetlands and ponds in an Alpine area, part of the MAB UNESCO 'Alpi Ledrensi and Judicaria' Biosphere Reserve (Trentino, south-eastern Alps). Choosing a widespread and abundant anuran, the common frog (Rana temporaria) as a model species, we tested for differences in detection success among three developmental stages and various freshwater environments. Lastly, by selecting a more specific COI fragment, we also aimed at assessing mtDNA genetic diversity in the focal species, which previous studies have found to be high in the study region and correlated with nuclear diversity. Preliminary findings will be presented here, together with the discussion of technical challenges and potential applications. Amphibians are threatened worldwide by climate change and habitat alterations: the development of a standardized, cost-effective protocol for monitoring amphibian biodiversity at species and genetic levels may represent an important resource for conservation managers.