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Integrating metabarcoding with biotic indices to detect point-source contamination in rivers: insights from aquaculture effluents in Trentino in the frame of the project ASTRO

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The application of biological indices (e.g., IBE, STAR_ICMi) to monitor anthropogenic impacts on aquatic ecosystems traditionally relies on the morphological identification of organisms, with inherent trade-offs between effort and taxonomic resolution. As a result, subtle impacts - such as those caused by aquaculture - may sometimes go undetected. Recent advances in molecular techniques to analyze environmental DNA (eDNA) and the increasing availability of annotated sequence datasets can increase the accuracy of identification through the analysis of specific genetic markers. While the analysis eDNA from water samples provides an integrated snapshot of upstream communities, bulk sample eDNA metabarcoding has the capacity to identify point source contaminations, such as those potentially caused by aquaculture. In this study we apply a rapid bulk DNA extraction method to benthic invertebrate samples collected with standard techniques. The aim is to compare morphological and metabarcoding data (COI, 18s rRNA markers) to understand how these methodologies can be integrated to assess the impact of aquaculture, and the effectiveness of mitigation measures, such as filter installations. The project aims to contribute to the development of integrated monitoring techniques that combine traditional and molecular approaches. The ultimate goal is to improve the accuracy, efficiency, and ecological relevance of bioassessment frameworks for freshwater ecosystems facing increasing anthropogenic pressures. This research is part of the ASTRO project financed by the MASAF, *Contratti di filiera* (CUP J38H23001450007).