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**Metabarcoding based monitoring for improving marine environmental management**

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**Abstract**

DNA metabarcoding, the taxonomic assignment of individuals from an environmental sample based on their DNA sequences, could represent a faster, cheaper and more accurate alternative to morphological identification for assessing the entire taxonomic composition of thousands of samples simultaneously. Yet, before it can be routinely applied for biodiversity studies and assist environmental management, this method needs to be benchmarked, calibrated and standardized. We have applied DNA metabarcoding to i) study the global ocean plankton diversity, by analyzing hundreds of samples collected during the Malaspina circumnavigation, ii) assess sea floor integrity, by analyzing sediment macroinvertebrate samples used for coastal monitoring, iii) understand marine food webs, by analyzing fish stomach contents and iv) detect invasive species introduced through ballast water, by analyzing fouling, plankton and free DNA collected from commercial ports. For each of these applications, we have developed sampling procedures, laboratory protocols and bioinformatic pipelines and have compared metabarcoding derived results with traditional observations. Our studies pinpoint steps of the process that are crucial for obtaining accurate assessments and provide guidelines for the application of metabarcoding in marine monitoring and evaluation programs. Ultimately, our results will assist the implementation of this technique within policies such as the Water and Marine Strategy Framework Directives, the Ballast Water Management Convention, or the Common Fisheries Policy.

**Keywords**: metabarcoding, monitoring, biotic indices, standardization, benchmarking

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