

A DNA metabarcoding approach to profile macrobenthos and zooplankton biodiversity

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Zooplankton and macrobenthos are recognized as good indicators to measure alterations in marine ecosystems. However, biodiversity assessments require accurate species identifications, which are commonly based on morphological features. DNA barcoding (species) and metabarcoding (communities) may provide a fast alternative. Still, the lack of a standardized DNA barcode reference library is currently limiting accurate species identification in both ecosystem components. We developed a flexible DNA metabarcoding pipeline, using Illumina MiSeq (NGS) technology. Different barcoding primers were checked against publicly available sequences to select the most optimal barcode region and primer sequences for the macrobenthos species present in our study area. Next, amplicon sequencing was executed using the COI and 18S target regions and DNA extracts both on individual species, and on pooled samples in which tissues or DNA extracts of different species were mixed. This setup allowed us 1) to check the effectiveness of the primers to detect species in both single and pooled samples; 2) to evaluate which DNA barcode provides the best taxonomic resolution; and 3) to investigate the relationship between read counts per species and the relative proportion of species in mixed samples. We applied the same standardized DNA metabarcoding pipeline to zooplankton, more specifically for a number of ctenophore species, which are quite difficult (especially the young stages) to assess by means of common morphological identifications.

Keywords: DNA (meta)barcoding, macrobenthos, zooplankton, next generation sequencing

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