Benchmarking DNA metabarcoding for measuring biodiversity and assessing environmental status

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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 environmental monitoring, this method needs to be benchmarked and calibrated. I will present two studies: one based on eleven marine benthic macroinvertebrate samples of known taxonomic composition and another one based on 21 microzooplankton and 133 mesozooplankton samples collected during the Malaspina circumnavigation. In the first case, the taxonomic compositions have been inferred using alternative laboratory procedures (sample source, DNA extraction method, primer, PCR conditions) and compared to those inferred with morphological identification in order to determine the best conditions for applying metabarcoding to macroinvertebrate diversity based environmental status assessment. In the second case, the zooplankton diversity of real samples has been estimated using different barcodes, primer pairs and combinations of barcodes and/or primer pairs. Additionally, taxonomic information has been extracted from whole metagenomes in order to detect potential biases in amplicon based inferences. I will conclude highlighting the major advantages and limitations of this promising technique.

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