Net overboard: comparing marine eDNA sampling methodologies at sea to unravel marine biodiversity

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Abstract

Environmental DNA (eDNA) analyses are powerful for describing marine biodiversity but must be optimized for their effective use in routine monitoring. To maximize eDNA detection probabilities of sparsely distributed populations, water samples are usually concentrated from larger volumes and filtered using fine-pore membranes, often a significant cost-time bottleneck in the workflow. This study aimed to streamline eDNA sampling by investigating plankton net versus bucket sampling, direct versus sequential filtration including self-preserving filters. Biodiversity was assessed using metabarcoding of the small ribosomal subunit (18S rRNA) and mitochondrial cytochrome c oxidase I (COI) genes. Multi-species detection probabilities were estimated for each workflow using a probabilistic occupancy modelling approach. Significant workflow-related differences in biodiversity metrics were reported. Highest amplicon sequence variant (ASV) richness was attained by the bucket sampling combined with self-preserving filters, comprising a large portion of micro-plankton. Less diversity but more metazoan taxa were captured in the net samples combined with 5 µm pore size filters. Pre-filtered 1.2 µm samples yielded few or no unique ASVs. The highest average (˜32%) metazoan detection probabilities in the 5 µm pore size net samples confirmed the effectiveness of pre-concentrating plankton for biodiversity screening. These results contribute to streamlining eDNA sampling protocols for uptake and implementation in marine biodiversity research and surveillance.

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