

# Metabarcoding hyperdiverse marine communities in temperate kelp forests: an experimental approach to inform future studies.

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## Abstract

Classical taxonomic approaches to quantifying biodiversity can be notoriously laborious and restrictive. Instead, molecular metabarcoding is emerging as a rapid, high-throughput and cost-effective tool to catalogue biodiversity. Despite the appeal of metabarcoding however, methodological and procedural biases must be understood before robust biodiversity inferences can be made. Here, we use CO1 metabarcoding to characterize marine eukaryote communities associated with the holdfasts of *Ecklonia radiata*, the dominant eco-engineering kelp of temperate New Zealand and Australia. To establish a standardized and reproducible community metabarcoding protocol, we examined the influence of different sample preparation, laboratory and bioinformatic steps on inferences of species richness and composition for kelp-holdfast communities. Specifically, we examined: the effect of fractioning the community into different size classes, the replicability of results across DNA extractions, PCR reactions, and sequencing. Overall, our approach identified 18 marine eukaryote Phyla in the holdfast communities. We found that size fractioning the sample before DNA extraction enabled detection of a greater diversity of taxa, especially smaller organisms. When compared with traditional morphology-based inventories of kelp-holdfast biodiversity, we found that although the taxonomic precision of our metabarcoding approach at the species and genus level was limited by the availability of reference sequences in public repositories, we recovered a greater number of operational taxonomic units, and a greater taxonomic breadth of organisms than morphological surveys. Based on our findings, we provide methodological guidelines for the use of metabarcoding as a tool for surveying and monitoring the hyperdiverse species assemblages associated with kelp-holdfasts.

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