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TITLE: Mitochondrial DNA (COI) analyses reveal that amphipod diversity is associated with environmental heterogeneity in deep-sea habitats

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ABSTRACT:

Abstract The relationship between species diversity and environmental parameters is poorly understood for the mobile macrofauna of deep-sea habitats due to under-sampling and subsequent lack of accurate taxonomic information. To redress this, cytochrome oxidase c subunit I (COI) DNA sequences were used to estimate species diversity and to compare phoxocephalid amphipod assemblages among 20 stations encompassing a range of environmental conditions. Two regions, east (C hatham R ise) and west (C hallenger P lateau) of N ew Z ealand were sampled to depths of 200-1200 m with an epibenthic sled. Using a comparison among identified morphospecies, we found a clear gap in sequence divergences between 6% and 13% and used a 6% threshold to designate molecular operational taxonomic units (MOTU s), as a surrogate to putative species. DNA sequences (n = 297) revealed high total diversity (n = 49 MOTU s), as well as high beta diversity (28 MOTU s found at single location only). Novel phoxocephalid MOTU s were found at most stations, especially on C hallenger P lateau and the flanks of C hatham R ise. Analyses of interstation assemblages revealed a major split between regions, indicating minimal overlap in taxon distributions. A cluster of highly similar stations was identified, broadly distributed over the crest of C hatham R ise, in association with elevated food availability, probably resulting from higher surface productivity and relatively shallow depth. Accordingly, multivariate analysis revealed a strong correlation between phoxocephalid assemblages and food supply. This study highlights the value of molecular approaches, in particular COI sequences, for quantifying and comparing diversity in under-sampled and/or under-studied taxa.

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