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Title: Assessment of an abyssal near-bottom zooplankton community via metabarcoding

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The growing likelihood of deep-sea polymetallic nodule mining has increased the need to improve understanding of the structure, diversity, and spatial distribution of abyssal benthic-pelagic zooplankton communities. Unfortunately, high morphological diversity, small size, and restricted diagnostic features, as well as very limited knowledge of the taxonomy of this faunal assemblage, make it challenging and time consuming to identify deep-sea zooplankton to the genus or species level, which constricts community assessment. Abyssal zooplankton was collected with plankton pumps (63- μ m) in the eastern Clarion Clipperton Fracture Zone (CCZ - 4,100 m depth), and samples were split for molecular and morphological analyses. Amplicons from the 18S rRNA, 12S rRNA, and mtCOI genes were sequenced on the MiSeq platform to determine species richness, diversity, and spatial variability of the benthic-pelagic zooplankton assemblage in the abyssal tropical North Pacific. This community was characterized by high diversity and species richness, as well as high dominance by several copepod taxa. We assess metabarcoding as an approach to characterizing zooplankton community composition through comparisons of paired molecular and morphological taxonomic analyses of quantitative sample splits, and across five markers from three gene loci. We also report results of rarefaction analyses to assess the sequence coverage required to capture the diversity of this community. Characterization of the abyssal ecosystem of the CCZ is needed to provide baseline conditions in advance of anticipated mining of the mineral-rich polymetallic nodules, and metabarcoding could be an effective approach for rapid and comprehensive assessment of the benthic-pelagic zooplankton community in this region.

Keywords: Abyssal, benthic-pelagic, zooplankton, metabarcoding, 18S, 12S, mtCOI

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