

Metagenetic Sequencing of Zooplankton Communities in the High-Diversity Central North Pacific

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Abstract

Marine zooplankton are important intermediate trophic level consumers in the ocean, and the subtropical North Pacific holds global maxima in species diversity for these communities. Zooplankton assemblages in this region include several species complexes, with many understudied and morphologically cryptic species. We used metagenetic sequencing to characterize zooplankton community composition across depth (0-1500m) at an open ocean time series site in the central North Pacific (Station ALOHA), using depth-stratified 1m² MOCNESS samples that were size fractionated into 5 size classes (0.2-0.5 mm, 0.5-1 mm, 1-2 mm, 2-5 mm, >5 mm). Our goals were to quantify the fraction of the community that is currently undescribed, identify taxonomic groups that contain large numbers of undescribed species and may be important to biogeochemical cycling in the ocean, and establish a metagenetic method that can be used to effectively characterize the species richness of epipelagic and mesopelagic communities in this region. Amplicons from several DNA loci, including mitochondrial cytochrome *c* oxidase subunit I and 12S rRNA, and nuclear 18S and 28S rRNA genes were sequenced on the MiSeq Illumina platform to characterize community composition. We evaluate species composition across metagenetic marker regions, pelagic depth zones, day and night-time MOCNESS tows, and compare our findings with prior species lists from the region. Our results are an important contribution to establishing standardized metagenetic methods for marine zooplankton communities.

Keywords: metabarcoding, metagenetics, mtCOI, 18S rRNA, species diversity

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