Metagenetic community analysis of marine planktonic copepods in the Pacific

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Planktonic copepods are among the most important zooplankton in marine food webs and biogeochemical cycles, and their community structures have a pronounced effect on global marine ecosystems. Here, we investigated the community structures of epipelagic and mesopelagic copepods in the Pacific (40°S-68°N) using metagenetic analysis of nuclear large subunit ribosomal DNA. This method is taxonomically comprehensive, avoids time-consuming morphological classification, and provides genetic information on DNA sequences. Latitudinal community and diversity gradients were evident in the epipelagic layer, and these gradients were clearly correlated with environmental changes in water temperature and chlorophyll a concentration in particular. High diversity was observed in the tropical and subtropical areas, with a peak in the North Pacific subtropical gyre. This pattern was also observed in the mesopelagic layer within relatively stable water environments, suggesting the influence of epipelagic ecosystems on mesopelagic communities. Although diversity was higher in the mesopelagic layer than in the epipelagic layer, the epipelagic community was composed of various taxonomic groups with high genetic diversity. Specific taxonomic groups were diverse in the mesopelagic layer, indicating that different mechanisms maintain diversity within each layer. Distribution patterns were clearly different between low-latitude (tropical and subtropical zones) and high-latitude (transition, subarctic, and arctic zones) groups. Phylogenetic analysis revealed recent divergence of the high-latitude group, suggesting that a relatively short evolutional history is a factor underlying the low diversity at high latitudes. These results indicate that both environmental and evolutionary factors have determined the current diversity and biogeography of planktonic copepods.

Keywords: Copepoda; metagenetics; diversity; community structure; Pacific Ocean

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