Abstract

[Project Information]

Project Title :	Investigation of Zooplankton Diversity in the Global Oceans to Understand Future Impacts of Climate Change on Marine Ecosystems
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[Abstract]

Marine zooplankton are key organisms that connect lower and higher trophic levels and serve as indicator species, as they rapidly respond to changes in the marine environment. However, their high diversity (with >7,000 species) and classification through morphology requires taxonomic expertise and experience. There are also identification challenges associated with cryptic species and immature stages that cannot be identified morphologically. Molecular methods address this by enabling accurate species identification. In particular, metabarcoding analysis is a promising technique that can reveal community structures rapidly and accurately based on massive amounts of sequences produced by next-generation sequencing. The international working group MetaZooGene aims to enhance global data on zooplankton metabarcoding. However, reference sequence data from the western North Pacific Ocean off Japan remains insufficient, highlighting an urgent need to enrich both metabarcoding and reference sequence datasets for this area. Thus, the aim of this study was to increase the reference sequence and large-scale metabarcoding data of marine zooplankton in the western North Pacific, thus contributing to the activity of MetaZooGene. An additional aim was to integrate the metabarcoding method into marine monitoring systems to track changes in marine ecosystems under climate change. For the reference sequence, a genome-skimming technique was established for marine zooplankton. This method allows for the efficient acquisition of valuable sequences, such as mitochondrial genomes and rDNA sequences, and is superior to the conventional DNA barcoding method. This study focused on key species in Japan and yielded more than 600 datasets. Moreover, a multi-region approach was used to improve the zooplankton metabarcoding analysis, and large-scale diversity and community structures of zooplankton across the Indian and Pacific Oceans were investigated. Metabarcoding was also applied to zooplankton communities around Japan to reveal their diversity and species distributions. Because the metabarcoding method was adapted for ocean monitoring around Japan, in this study a system to capture future changes

in marine ecosystems was established. In total, almost 400 new data were obtained for the metabarcoding analysis, successfully contributing to the work of MetaZooGene. In this study, a large amount of genome-skimming and metabarcoding data were collected, and these datasets can be used to further understand zooplankton diversity, ecology, and evolution.

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