

Amphipod biodiversity and genetic connectivity at Northwest Pacific seamounts with Co-rich ferromanganese crusts

*Eri Ikeuchi¹, Akira Iguchi^{1,2}, Hiroki Kise¹, Hiroyuki Yokooka³, Shogo Kato³, Hideki Sugishima³, Kazumasa Ikeda⁴, Ryuichi Miwa⁵, Miyuki Nishijima¹, Yuichiro Tanaka¹, Junpei Minatoya⁶, Atsushi Suzuki^{1,2}

1. Geological Survey of Japan, AIST, 2. Research Laboratory on Environmentally-conscious Developments and Technologies (E-code), AIST, 3. IDEA Consultants, Inc., 4. Okamoto Glass Co., Ltd., 5. Kaiyo Engineering CO., LTD., 6. Japan Organization for Metals and Energy Security (JOGMEC)

Biodiversity assessment in deep-sea ecosystems is an important issue in elucidating the formation and maintenance of deep-sea ecosystems and in establishing reference areas for future development of deep-sea mineral resources. Even in the vicinity of cobalt-rich ferromanganese crusts, which are present in deep-sea seamounts, there is a need to assess the differences in biodiversity and connectivity among seamounts. Deep-sea amphipods are a taxonomic group that has diversified both ecologically and morphologically, and many individuals are available for ecological study. Thus, deep-sea amphipods have attracted attention in assessing biodiversity in deep-sea environments. However, because the taxonomy is not well developed and is assumed to include many cryptic species, the diversity and connectivity assessment of this taxon has not progressed.

In this study, to assess diversity and connectivity among seamounts with cobalt-rich ferromanganese crusts in the Northwest Pacific, baited traps were installed in each seamount and 693 samples of amphipods were collected. DNA was extracted from these samples and partial nucleotide sequences of the cytochrome c oxidase I (COI) gene region were determined, and molecular operational taxonomic units (MOTUs) were extracted to define putative species and compare community diversity and similarity among seamounts and depths. For MOTUs for which relatively large numbers of individuals were available, single nucleotide polymorphism analysis using MIG-seq was conducted to estimate genetic connectivity among seamounts.

The analysis confirmed that deep-sea amphipod assemblages differed significantly between the flat-topped and basal parts of seamounts, and that there was a pattern of similarity in assemblages among multiple seamounts. We also found that the genetic connectivity of the amphipods is likely to be widely maintained among seamounts separated by geographic distance. The similarity of assemblages among multiple seamounts and the high connectivity maintained among amphipods within the study area, which are considered to have relatively low dispersal ability, indicate that deep-sea amphipods may frequently recruit among seamounts. The findings obtained from the deep-sea amphipods are expected to be used as scientific information for conducting environmental baseline studies and environmental impact assessments in a seamount in future.

Keywords: Co-rich ferromanganese crusts, deep-sea amphipods, biodiversity assessment, connectivity analysis