Genetic resources and Deep sea coral biodiversity of seamounts in the Western Pacific

Seonock Woo*, Sookjin Jang

Korea Institute of Ocean Science and Technology, Busan, 49111 Republic of Korea

Abstract

Patterns of genetic connectivity are increasingly considered in the design of marine protected areas (MPAs) in both shallow and deep water. Currently, patterns of genetic connectivity among deep-sea populations throughout West Pacific seamounts are not well understood. Using the mitochondrial *Cytochrome Oxidase I* and *16S rRNA* genes as genetic markers, this study aimed to elucidate patterns of genetic connectivity among populations of two benthic invertebrates with contrasting life history strategies. In West Pacific region, KC-2 (17°02′~17°17'N, 149°47′~150°03'E) and KC-8 (19°32′~19°53'N, 151°29′~151° 51'E) among the seamounts around Northeastern area from Guam were targeted for the deep sea biodiversity research. In order to get the life resources in the high seas, a total 6 times, 32 hourse of ROV dive, 9 times epibenthic sledge were performed for sample acquisition and most of biological samples were obtained through ROV. We collected coral and sea lily samples and classified using morphology and DNA sequences. Populations of the cnidaria, *Bathypathes* sp. and the crinoidea, *Thalassometra glacilis* were sampled from continental slope, seamount, and offshore rise habitats on the KC-7, KC-8, KC-9 and OSM-x. For the coral, significant population structure was detected among distinct populations on the KC-7, KC-8. Significant genetic differences existed between KC-7 and OSM-X. In contrast, no significant population structure was detected across the study area for the crinoid. Patterns of genetic connectivity in *Thalassometra glacilis* are likely influenced by a number of factors including current regimes that operate on varying spatial and temporal scales to produce potential barriers to dispersal. The results of this study are discussed in the context of existing conservation areas that are intended to manage deep-sea benthic communities in the West Pacific region.

Materials and Methods

The coral and sea lily colony were collected at water depths of approximately 1340 - 1420 m using ROV dive. After collection, only coral polyps were collected then directly frozen in the liquid nitrogen and conserved under the -80˚C until the RNA & DNA extraction and the remaining whole body were preserved in Ethanol. Total RNA was extracted by following the method optimized for the soft coral (Woo et al., 2005). We used HiSeq 3000 sequencing system (Illumina) and briefly we prepared the RNA for transcriptome, then pair-end sequencing and analysed with de novo assembly.

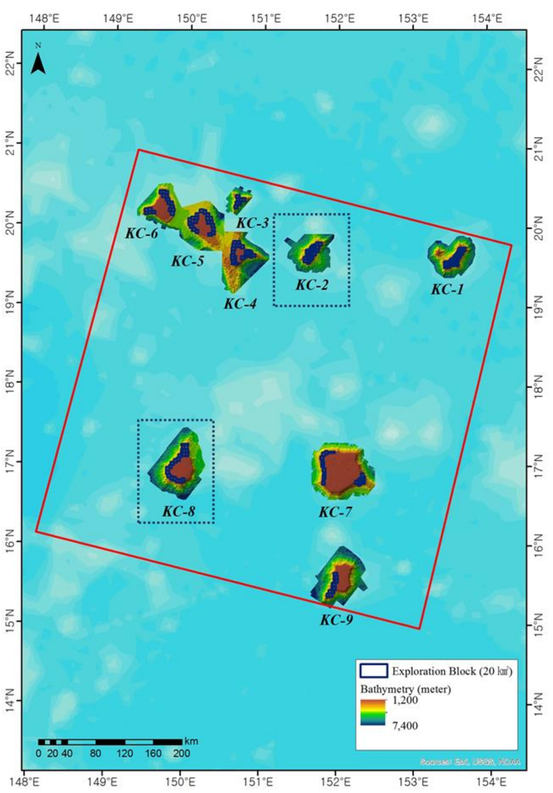


Fig 1. Targeted region for the study

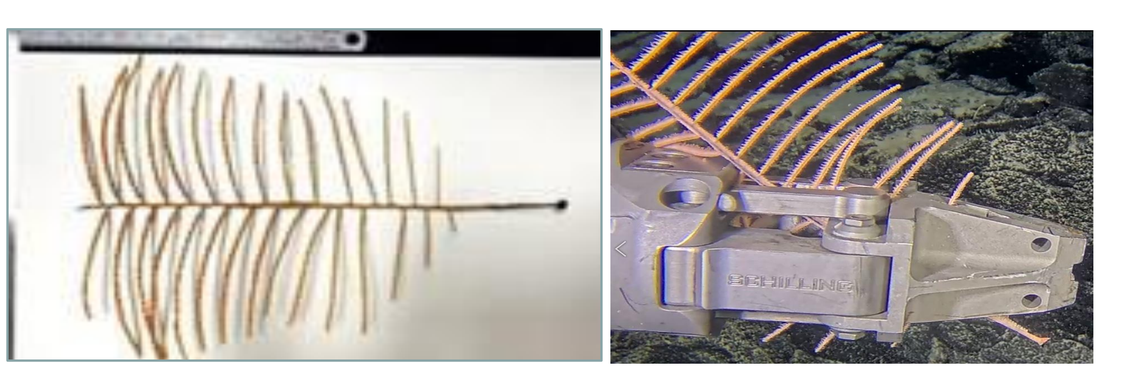


Fig 2. *Bathypathes* sp.



Fig 3. *Thalassometra glacilis*

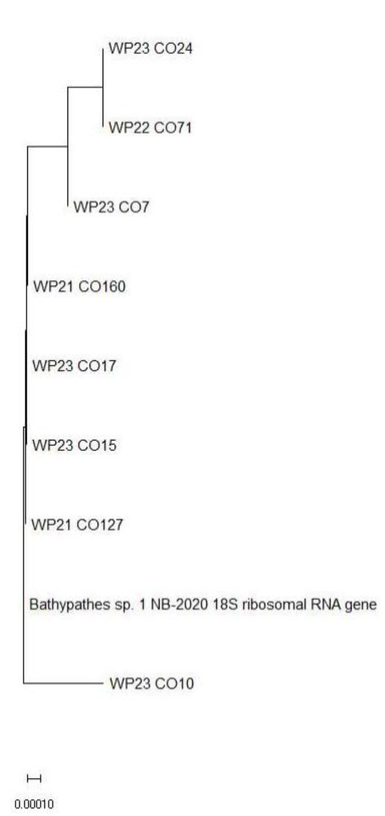


Fig 4. Genetic distance in coral samples

Results

Patterns of genetic connectivity in *Thalassometra glacilis* and *Bathypathes* sp. are likely influenced by a number of factors including current regimes that operate on varying spatial and temporal scales to produce potential barriers to dispersal. The results of this study are discussed in the context of existing conservation areas that are intended to manage deep-sea benthic communities in the West Pacific region and the further study using enough number of samples (sea lily and coral) collected from the related seamounts can show the detailed connectivity among the seamounts and habitat conservation.

Acknowledgement

This research was supported by Korea Institute of Marine Science & Technology Promotion(KIMST) funded by the Ministry of Oceans and Fisheries(20210646) and KIOST project High Sea Biodiversity conservation (PM65590).