

## 深海化学合成生物群集に生息する底生性カイアシ類集団の遺伝的連結性

## Population connectivity of benthic copepods in deep-sea chemosynthetic communities

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Meiobenthos are small (<1mm) benthic animals living on seafloor. Although their considerable diversity in marine environment, only less attention is paid for meiobenthos than macro- and mega-benthos. Copepod is the most abundant crustacean in meiobenthos in deep-sea hydrothermal vent environment, and a copepod family Dirivultidae is one of the most successful vent taxa. However, only little is known about ecology and evolution of dirivultids. In the present study, we examined efficiencies of several DNA extraction methods available for copepods, and estimate population connectivity of dirivultid copepods of the genus *Stygiopontius* in the western Pacific hydrothermal vent fields. DNA extraction efficiency was increased when the morphology of copepod was destructed. However, even the DNA extraction with the lowest concentration (~5ng/μL) was sufficient to obtain sequence data by Sanger sequencer. Genetic diversities of *Stygiopontius* copepods were different among oceanographic regions, higher in back-arc basins in the southern Pacific than in volcanic arc. In both regions, local populations were not significantly separated genetically based on partial mtCOI sequence. The present result contributes to our knowledge of ecology of meiobenthos, and establishment of environmental assessment tool using meiobenthos in deep-sea hydrothermal vent fields.

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