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Variation of lipid biomarker composition in *Bathymodiolus sp.* at hydrothermal vents in Okinawa Trough

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<Introduction>

Bathymodiolus sp. host chemoautotrophic bacterial endosymbionts such as sulfur-oxidizing bacteria and/or methane-oxidizing bacteria in their gills. However, no studies have revealed how the mussels incorporate chemoautotrophic bacteria. Tyler (1999) reported that larval of Bathymodiolus sp take planktons and dissolved organic matters in sea water. To investigate the relationship between deep-sea mussels and endosymbionts in Okinawa Trough as the mussels grow, lipid biomarkers and carbon, nitrogen and sulfur isotopic studies of Bathymodiolus sp. are analyzed in this study.

<Samples & analytical methods>

Deep-sea mussels were collected at two different hydrothermal vents: Hatoma Knoll (HTM) during the NT09-11 cruise and Iheya North Knoll (INK) during the NT09-17 cruise. Bathymodiolus sp. were frozen (-20°C) immediately and sent to Kyushu University. After gill tissue segregation, each sample was lyophilized and extracted with organic solvents to analyze lipid biomarkers including hopanoid hydrocarbons and fatty acids by gas chromatography/mass spectrometry (GC/MS) and GC isotope-ratio/mass spectrometry (GC/IRMS).

<Results & discussion>

Gill tissue of all bivalves contained diploptene, which is known as one of specific biomarkers of methanotrophs. The presence of diploptene indicates that all deep-sea mussels of this study host methanotrophic bacteria in the gills. Saturated and unsaturated fatty acids from C_{15} to C_{22} were identified. The most abundant fatty acids was $C_{16:1}$ except the HTM2 sample. However, relative compositions of fatty acids were different each other. The fatty acids from the INK mussels became depleted in 2.5 to 3.7 per mil (relative to PDB) as the mussels grow. These variations in abundance and isotopic compositions could reflect growth stages associated with the activity of bacterial endosymbiont. On the other hand, the carbon isotopic composition of fatty acids from the HTM mussels were very similar each other, probably because they might have already grown up enough.

Keywords: Bathymodiolus sp., Lipid biomarkers, Methanotrouph, Okinawa Trough, Fatty acid composition, Carbon isotopic composition