

# Biomarker analysis of BMS drilling cores from hydrothermal region at South Mariana Trough

# Tomoko Uehara[1]; Hiroshi Naraoka[2]; Yoshinori Takano[3]; Katsumi Marumo[4]

[1] Earth Sci., Okayama Univ; [2] Dept. of Earth Sci. Okayama Univ.; [3] AIST Central 7, MRE; [4] AIST, GSJ

Reduced gases such as hydrogen, methane and hydrogen sulfide are provided from deep-sea hydrothermal vents, which support chemotrophic bacterial activity around the vents as a primary producer. Although sulfur-oxidizing (thiotrophy) and methane-oxidizing bacteria (methanotrophy) are common around surface of modern hydrothermal vents, bacterial community is also interested at the subsurface area. The Archean Park Project has conducted to drill out rock core samples at deep-sea hydrothermal areas of Suiyo Seamount and South Mariana Trough since 2000 by benthic multi-coring system (BMS) drilling. An organic study including molecular and isotopic signatures is one of approaches to deconvolute bacterial community to elucidate the bacterial metabolism and their ecology. In particular, carbon and hydrogen isotopic composition of individual biomarker is a useful means to infer a specific source of bacteria.

In this study, we examined molecular occurrence in the BMS drilling samples from South Mariana Trough in February 2004 (APM01 and APM03). In order to evaluate bacterial niches in the rock and contamination during coring, the drilling sample was analyzed from outer to inner part using organic solvent extraction. At first, the allocated sample of several cm in size was directly rinsed by sonication with dichloromethane/methanol (outer). The rinsed sample was crushed along veins and cracks to a few cm in size followed by extraction with dichloromethane/methanol (semi-inner). Subsequently, the extracted sample was further crushed to fine powder using agate closed-type ball mill. The fine sample powder was also extracted with dichloromethane/methanol (inner). The extracted residue was further extracted by alkaline hydrolysis with KOH/methanol (bound-form). The procedural blank was performed using pre-heated sea sand at 450C for 3h.

In the outer part of all samples, aliphatic acids and alcohols were detected in which C16 and C18 saturated straight-chain fatty acids were the most abundant. Generally APM03 samples are more enriched in these aliphatic compounds than APM01 sample. Carbon isotopic composition of these fatty acids ranged from -29.6 to -26.4 per mil (vs. PDB). Hydrocarbon fraction of outer samples of two APM03 samples contained unresolved complex mixture as a hump on the gas chromatogram with some hopanoids. These molecular signatures suggest that the APM03 samples may be affected by pyrolysis of organic matter or oil contamination during the drilling. However, all samples contained these compounds much more in inner part rather than in semi-inner part. If the detected organic compounds are indigenous from bacterial activity, this molecular distribution may suggest a fine part for bacterial niches rather than large cracks or veins.