

## Microbial community around hydrothermal fields at the southern Mariana Trough

# Shingo Kato[1]; Katsunori Yanagawa[2]; Michinari Sunamura[2]; Junichiro Ishibashi[3]; Takeshi Kakegawa[4]; Harue Masuda[5]; Tetsuro Urabe[6]; Akihiko Yamagishi[1]

[1] Dep. Mol. Biol., Tokyo Univ. Pharm. Life Sci.; [2] Univ. Tokyo; [3] Earth and Planetary Sci., Kyushu Univ; [4] IMPE., Tohoku Univ.; [5] Dept. Geosci., Osaka City Univ.; [6] Earth and Planetary Science, Univ. of Tokyo,

<http://www.ls.toyaku.ac.jp/%7Elcb-7/>

Substantial research has been done on the microbial community around the deep-sea hydrothermal vent. Hydrothermal fluids contain reduced-compounds, e.g.,  $H_2$ ,  $H_2S$ ,  $CH_4$ ,  $Fe^{2+}$ , which can serve as electron donors in microbial metabolism. Seawater contains oxidized-compounds, e.g.,  $O_2$ ,  $SO_4^{2-}$ ,  $NO_3^-$ , which serves as electron accepters. These redox couples, especially aerobic metabolism using  $O_2$ , can provide a large amount of energy for living cells. The sub-seafloor mixing zone around deep-sea hydrothermal areas, where hydrothermal fluid are mixing with seawater, is proposed to have highest biomass in hydrothermal vent communities. We obtained evidence to support the fact that iron-oxidizers play an important rule in the mixing zone beneath seafloor.

In this study, we focused on the microbial habitat at hydrothermal area on the back-arc spreading center, at the southern Mariana Trough. Some hydrothermal vents were found both on-axis (Snail site, Y site, Kaiko site) and off-axis (Archaeon site, Pika site). The difference in geological settings and the heterogeneity of hydrothermal fluids at back arc are expected to provide generality and specificity in microbial habitat under seafloor around hydrothermal area. We analyzed various hydrothermal samples, i.e., sulfide structures, microbial mats, vent fluids, and discharging fluids from drilled holes, collected from these hydrothermal areas by culture-independent methods based on 16S rRNA gene. We aim to expand our knowledge of microbial ecosystem at deep-sea hydrothermal system.

As in the past studies at other hydrothermal areas, hydrogen/sulfide-oxidizers in epsilon-proteobacteria, sulfate-reducers in delta-proteobacteria, thermophilic hydrogen-oxidizers in Aquificae, hyperthermophilic sulfate-reducers in Archaeoglobales, were detected in the sulfide structures. In contrast to sulfide samples, iron-oxidizers in zeta-proteobacteria and methane-oxidizers in gamma-proteobacteria were detected in the microbial mats. The abundance of zeta-proteobacteria were 7% and 22% in total cells of each mat sample analyzed by quantitative PCR using a zeta-proteobacteria specific primer set. No epsilon-proteobacteria related clone was detected in the mat samples. Iron-oxidizers (zeta-proteobacteria) were also detected in fluids collected from drilled holes. In addition, sulfide-oxidizers in gamma-proteobacteria were recovered from same fluids samples. Notably, zeta-proteobacteria was dominant bacteria (more than 60% in total bacterial cells) in fluids of the drilled holes judging from FISH analysis using a zeta-proteobacteria specific probe.

In conclusion, we estimate the microbial community at the southern Mariana Trough, where iron-oxidizers seem to play an important rule in sub-seafloor mixing zone.