

# Microbial Community in the Hydrothermal System at the Southern Mariana Trough

# Shingo Kato[1]; Motoo Utsumi[2]; yutaka kawarabayasi[3]; Hiroshi, X. Chiura[4]; Junichiro Ishibashi[5]; Katsumi Marumo[6]; Tetsuro Urabe[7]; Akihiko Yamagishi[1]

[1] Dep. Mol. Biol., Tokyo Univ. Pharm. Life Sci.; [2] Inst. of Agric. and Forest Eng., Univ. of Tsukuba; [3] IBRF, AIST; [4] ICU, NS, Biol; [5] Earth and Planetary Sci., Kyushu Univ; [6] AIST, GSJ; [7] Earth and Planetary Science,

Univ. of Tokyo,

The ecosystem around hydrothermal system is supported by reducing compounds provided by the hydrothermal system. There is a substantial body of research results on hydrothermal areas. However, such studies have been focused mainly on natural vents, chimneys and bacterial mats. These studies have suggested the presence of a sub-surface microbial community. Our study aimed at expanding the current knowledge by analyzing hydrothermal samples of water collected from drilled holes bored around hydrothermal areas.

Microbial samples were collected at the Southern Mariana Trough during the TN167 cruise (15 to 27 March 2004) of R/V Thomas G. Thompson with the remotely operated vehicle (ROV) ROPOS. The Southern Mariana Trough located where the Mariana Trench turns from north-south to east-west significantly. At this area, back-arc spreading occurs near the island arc volcanic row. The hydrothermal systems were found around the spreading center in May 2003 (Fryer site) and at the top of the sea-mount located far from the south spreading center (Pika site). In January 2004, we carried out sub-seafloor drilling with BMS (Benthic Multi-coring System) at these two hydrothermal areas. Inside a wall of the drilled holes were supported by the titanium pipes.

In this study, the fluid eluted from casing pipes were collected. One liter of collected fluids was filtered through cellulose acetate membrane filters to trap microbial cells. DNA was extracted from each sample, 16S rDNA sequences were amplified by PCR with universal or archaea-specific primers. The rDNA fragments were cloned and the sequences were determined. Phylogenetic analysis of the partial 16S rDNA derived from each sample showed that the PCR clones from hydrothermal fluid were significantly different from those found in the ambient seawater. These results suggest that the contamination of microbes that occurs during the hydrothermal water sampling at the mouth of the pipe is insignificant. Archaeal clones (Hot Spring related clones and Methanogen related clones) and bacterial deep branching clones were obtained, suggesting the presence of a hot area beneath the bored holes, despite the low fluid temperature at the top opening of the casing pipes. Similar clone-patterns were found between the axial site (Fryer site) and the off-axis site (Pika site). This finding is consistent with the similarity between chemical characteristics of the end-members of the hydrothermal fluids at these sites.