

Microbial diversity in the unique hydrothermal sediment around hydrothermal systems at the Southern Mariana Trough

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The ecosystem around hydrothermal system is supported by reducing compounds provided by the hydrothermal system. The microbial communities around hydrothermal vents have been analyzed and many novel microbes have been isolated from the hydrothermal samples, such as basaltic rocks, hydrothermal fluids and chimneys. In this study, we report microbial community in unique hydrothermal sediments. We found the yellow soft sediment around the hydrothermal vent at the Southern Mariana Trough during the YK05-09 cruise (21 July to 10 August 2005) of R/V YOKOSUKA with SHINKAI 6500. The Southern Mariana Trough located where the Mariana Trench turns from north-south to east-west significantly. In this area, back-arc spreading occurs near the island arc volcanic row. Our study aimed at elucidating the microbial community in the hydrothermal sediments.

These yellow sediment samples were collected at two hydrothermal points (Marker#16,18) by the special sampling instrument (M-type sampler). DNA was extracted from these sediments. Small sub-unit rDNA sequences were amplified by PCR with universal, archaea-specific and eukarya-specific primer pairs. The rDNA fragments were cloned and the sequences were determined. Microbial diversity was estimated by phylogenetic analysis of the partial 16S or 18S rDNA derived from each sample.

Various microbes belonging to three domains were detected from these sediment samples. Methylotrophic bacteria are predominant in the sediment collected at Marker#18, while no methylotroph was detected at Marker#16. Although deep-branching eukaryotic rDNA clones were detected from the sample at Marker#16, Annelida-related rDNA clones were detected from the sample at Marker#18. These results suggest the difference between environments around Marker#16 and Marker#18. Many unidentified rDNA clones were also detected from these sediments. The bacterial rDNA clones belonging to the sixth subdivision of the phylum Proteobacteria (S. Kato et al, 2005) were obtained from both sediments.