

## Microbial diversity in the unique hydrothermal deposits around the deep-sea hydrothermal system at the Southern Mariana Trough

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Recently, many research groups have reported the microbial habitats supported by the chemical energy around the deep-sea hydrothermal areas. These microbial ecosystems are independent from the continental phototrophic ecosystem.

We found the yellow soft deposits around the hydrothermal vent at the Southern Mariana Trough during the YK05-09 cruise of R/V YOKOSUKA with SHINKAI 6500. These deposits were collected at two hydrothermal points (Marker#16,18). DNA was extracted from these deposits. Small sub-unit (SSU) rDNA sequences were amplified by PCR with universal, archaea-specific, bacteria-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 SSU rDNA sequences derived from each sample.

Some taxonomic groups of the all three domains were detected from both deposit samples collected from Mrk#16 and 18. Some groups, however, were detected only from one of the two samples. Unidentified SSU rDNA sequences with low similarity to the known sequences in the databases were detected from both samples. These unidentified clones suggest the presence of the novel microbes in the hydrothermal deposits. We determine the phylogenetic relationship of these unidentified clones by the phylogenetic analysis.

Microbial cell numbers of both deposit samples estimated by quantitative real time PCR with universal primer sets were more than  $10^8$  cells per gram, which is equal to the continental sediments. quantitative real time PCR with eukaryotic primer sets also showed that eukaryotic cell numbers were less than 1% of total cell numbers. The diversity of microbes in the deposits was observed by florescence and scanning electron microscopy.

The characteristics of microbial community in the unique hydrothermal deposits are followings. First, number of prokaryotes is higher than that of eukaryotes. Second, prokaryotes are more diverse than eukaryotes. Third, the presence of novel prokaryotes and eukaryotes is suggested in the hydrothermal deposit samples. Forth, both common and unique microbes were detected from two different deposit samples. It is suggested that the hydrothermal deposits provide the habitats for diverse microbes, both prokaryotes and eukaryotes, and can be the unique genetic resource. The microbial communities in the two different deposits may reflect the difference in background environments. The elucidation of the physical and geochemical settings will lead us to cultivate novel microbes including extremophiles.