

Spatial and temporal variation in microbial community and chemistry in a deep-sea hydrothermal field on Southern Mariana

Katsunori Yanagawa[1]; Junichiro Ishibashi[2]; Tetsuro Urabe[3]; Michinari Sunamura[4]

[1] Tokyo Univ. of Science; [2] Earth and Planetary Sci., Kyushu Univ; [3] Earth and Planetary Science, Univ. of Tokyo.; [4] Univ. Tokyo

Primary production of chemolithoautotrophic microorganisms that utilizes reduced materials from subvent feeds rich deep-sea hydrothermal ecosystem. Recent studies based on cultured microorganisms and molecular phylogenetic analysis revealed that a deep-sea hydrothermal field harbored various and peculiar microbial groups including novel ones. Quantitative analysis of the microbial community by cultivation and molecular techniques revealed the existence of these microorganisms, i.e. MG1 crenarchaeota, gamma proteobacteria, and epsilon proteobacteria in the mixing zone of the hydrothermal fluids and ambient seawater. In this study, we focused on a spatial and temporal variation of microbial communities in the mixing zone in southern Mariana hydrothermal field. The microbial community structures were quantified by using a FISH technique and compared with the chemical composition.

Hydrothermal fluid samples for microbial analysis were collected from hydrothermal vents at southern Mariana trough in three expedition cruises by ROV ROPOS and manned submersible Shinkai 6500 during Oct. 2003 to July, 2005. Total 25 hydrothermal fluid samples with various locations and temperatures were collected. Each sample was fixed and cells in the samples were filtered on filters. Total cell density was estimated by direct counting method by staining with DAPI. Density of specific microbial cells were estimated by FISH method using oligonucleotide probes for bacterial cells, archaeal cells, gamma-proteobacterial cells, and epsilon-proteobacterial cells. Chemical composition of the samples, e.g. silicate, pH, and ammonium, were determined on board.

Total cell densities in the hydrothermal samples were $4.4\text{--}30 \times 10^4$ cells/ml, besides $2\text{--}5 \times 10^4$ cells/ml in the ambient seawater. This clearly indicated the existence of hydrothermal-energy dependent microbial communities compared to the ambient seawater. 30 to 80% of DAPI-stained cells were determined as domain bacteria and archaea by FISH. Bacterial population dominated up to 66% of total cells as well as in a general marine and oceanic environment. Archaeal population accounted for 2 to 25% of the total cells and they were especially low in the high-temperature fluids. Epsilon proteobacteria was one of the most important groups to characterize hydrothermal microbial communities. In this study, their population were detected up to 21% of the total cells, however, they accounted for less than 10% of the total cells in 8 samples of the total 12 hydrothermal samples. Note that their population in the high-temperature fluids were lower than 5% of the total cells. These indicated that they mainly inhabit oxidized and medium to low temperature environment. Gamma proteobacteria were predominant in most of the samples and they usually occupied more than half of bacterial cells (3-40% of the total cells). More detailed analysis, e.g. phylogenetic position, physiological characteristics, and the productivity should be needed, however, their large population suggested their ecological importance in the hydrothermal field.

The spatial distribution of the total cells showed that the the microbial population is largest within several meters around the hydrothermal vents. Relationship between the total cell densities and the chemical compositions showed that the population increased in intermediate zone of the hydrothermal vents and ambient seawater. These suggested that major habitats for the population were mixing zone of hydrothermal fluid and the ambient seawater. The hydrothermal fluids were cooled and/or mixed with ambient seawater after venting into seawater or before venting beneath the seafloor. In the hydrothermal area, several types of chemo-environment, e.g. oxic/anoxic, high/low temperature, and rich/poor in reduced chemicals, were developed. These environments are generally believed to be sequential, but the microbial population seemed to be noncontiguous distribution.