Quantification of microbial community structure in a deep-sea hydrothermal field on Southern Mariana

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Hydrothermal fluids emitted from deep sea hydrothermal vents contains microbes of sub-vent biosphere. Microbes in high-temperature fluids indicated hot and anoxic environment under hydrothermal fields, while microbes in low and intermediate temperature fluids indicated oxic environment, which contained oxygen, nitrate, and sulfate entrained from seawater. Microbial community of sub-vent was proposed to be hierarchical structure with depth from the seafloor, which related with the mixing ratio of hydrothermal fluids and seawater. The mixing ratio affected the predominant microbial community above the seafloor in hydrothermal fields. For microbial metabolism, both electron acceptor and electron donor are important. Hydrothermal fluids contain lot of reduced chemicals, which possibly utilized by microbes as electron donor, but contain little electron acceptor. Therefore entraining of seawater into sub-vent were important to supply electron acceptors for chemolithoautotrophs in basically anoxic sub-vent biosphere. In this study, we investigated microbial community structures in various hydrothermal fluids under various mixing ratio of seawater by using CARD-FISH, and aimed to clarify the microbial community structure in each niches of sub-vent biospheres formed by different mixing ratio of hydrothermal fluids and seawater.

Total 14 hydrothermal fluid samples with various temperatures were collected at the hydrothermal field in the spreading axis of Southern Mariana back-arc basin from 2003 to 2005. We applied 10 oligonucleotide probes to detect various microbial groups and counted the stained microbial cells under fluorescent microscope. The microbial community structures of the samples were compared similarities by cluster analysis. Bacterial communities were classified into 4 groups, e.g. ambient seawater group, intermediate hydrothermal fluid group, 2005 group, and high-temperature hydrothermal fluid group, which corresponded to the difference of the mixing ratio between hydrothermal fluids and seawater. The ambient seawater samples were characterized by delta proteobacteria, which accounted for approximately 20% of total Bacterial cells. The cluster of intermediate temperature samples were characterized by diverse shape and large size (more than 100 ?m in length) of microbial cells, and high abundance (up to 35% of total Bacteria cells) of epsilon proteobacteria. The samples in this cluster were collected in different sampling year and sampling site, suggesting that the microbial community in this cluster was regulated by the physiochemical condition rather than the temporal variations. In the cluster of high-temperature samples, occurence and abundance of alpha proteobacteria were characteristic and they account for up to 18% of total Bacteria cells. Samples collected in 2005 constructed one cluster, which was characterized by the dominance of beta proteobacteria. These samples were collected from various temperature of hydrothermal vents. This indicated that temporal changes of microbial community occured in 2005. The chemical composition and the temperature of the samples indicated that the beta-proteobacteria population was derived from subvent biosphere. Our results demonstrated that entraining of seawater fluctuate microbial community in sub-vent biosphere, while hydrothermal environment without contribution of seawater implied ecosystmes characterized by alpha or beta proteobacteria.