

What did we get from the Suiyo Seamount surveys: overview of AP-BIO group activities

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Deep-sea hydrothermal ecosystems are driven with various geo-thermally modified, mainly reduced, compounds delivered from extremely hot subsurface through hydrothermal circulation. To date, some thermophilic microbes isolated from vent chimneys have accelerated studies on not only microbial genome analysis and application, but also origin and evolution of living materials on the earth. However, we have very limited information about the diversity, population, function and spatiotemporal variation of microbes in hydrothermal plume, fluid or sediment, and almost nothing about sub-vent microbes. So, we AP-BIO group started to elucidate fundamental aspects on microbiology and ecology in the hydrothermal ecosystem of Suiyo Seamount as a target, with special concern to the sub-vent biosphere, in this Archaean Park project. To date, we have accomplished new methodological development and bio/ecological findings as follows:

1) Methods and instruments: Development of new sampling systems for environmental microbes and genes, especially a catheter-type growth chamber for collecting and cultivating sub-vent microbes (Higashi et al. FEMS-ME 2004) and a large-scale step-wise filtration system for preventing microbial contamination in drilling with a portable submarine driller (BMS).

2) Microbial diversity and hunting: Findings of new phylotypes in epsilon-Proteobacteria, photosynthetic bacteria, thermophilic Euryarchaeota (Higashi et al. FEMS-ME 2004), as well as new gene information concerning to the sulfur reduction (Nakagawa et al. AEM 2004). Actually, some novel microbial species have been obtained (Mori et al. this meeting).

3) Microbial ecology: Findings that the water column inside the caldera have functioned as a natural growth chamber for a few microbial species (Sunamura et al. AEM 2004) and that many Bacteria cells are present in extremely hot hydrothermal fluids (Sunamura et al. this meeting). Speculation of Archaea habitats through molecular and cellular analyses of fluid samples (Yamagishi et al. this meeting), as well as in situ growth chamber samples (Higashi et al. this meeting).

4) Other topics: Detection of virus-like particles (Chiura et al. this meeting), direct sequencing analysis of environmental genes (Kawarabayashi, this meeting), specification of gene sites enable to regulate growth temperature (Nakamura et al. submitted), wide distribution of halo-tolerant microbes (Okamoto et al. SAM in press), unique cell fusion in thermophiles (Kuwahara et al. this meeting).

Most of these results have been accepted for the publication in high quality international journals, but we cannot get much information about how microbes act and change the surroundings. To overcome this problem, we need to elucidate movements of water and hydrothermal plume, measure in situ microbial/metabolic activities, correlate with stable isotope and mineralogical studies, develop a clean core sampling technique, and stimulate interdisciplinary utilization of microbes isolated. From methodological points of view, however, it is invaluable that we succeeded to drill around active vent fields and collect real sub-vent microbial samples. Using core and borehole water samples from Mariana Trough in 2004, further new findings will come into sight near future.