

Nanobacteria in hydrothermal vent areas of the Suiyo Seamount and the Mariana back-arc basin

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Microorganisms that pass through the filters having a pore size of 0.2 micron have been known since 1970s. The 0.2 micron-filterable fraction may contain microorganisms greater than 0.2 micron due to pore connection cell flexibility, and the entity of real 0.2 micron-filterable microorganisms have attracted less microbiological interests. A recent report suggested that 0.2 micron-filterable, as well as 0.2 micron-captured, microorganisms are more involved in microbial loops than previously estimated. In addition, unique phylogenetic lineages of 0.2 micron-filterable bacteria are known in deep groundwater, and the new phylum Nanoarchaeota has been established for Nanoarchaeum equitans. This accumulating set of information indicates that 0.2 micron-filterable microorganisms are not negligible but important ecological players and resources of biological diversity.

Diverse 0.2 micron-filterable strains belonging to Actinobacteria, Alpha-/Beta-/Gammaproteobacteria, Bacteroidetes and Spirochaeta have been isolated and characterized. Considering the practical limitation that only 0.1% of natural populations are cultivable, non-culture-dependent technique such as 16S rRNA gene clone analysis facilitates estimation of phylogenetic diversity of 0.2 micron-filterable microorganisms. However, only a few studies have been done on environmental 16S rRNA gene clones from the 0.2 micron-filterable fractions, e.g., the deep groundwater clones containing novel phylotypes related to the candidate divisions OD1 and OP11 that are specific for 0.2 micron-filterable fractions. Candidate divisions having no cultured counterparts were first proposed for the 16S rRNA gene clones from a hot spring in Yellowstone National Park, and more candidate divisions have been reported from reducing environments such as petroleum-polluted soils and deep-sea sediments. Nevertheless 0.2 micron-filterable clones from a typical reducing habitat, i.e., hydrothermal vents, have not been studied so far. We have thus analyzed 0.2 micron-filterable 16S rRNA gene clones from the hot vents in the western Pacific back-arc hydrothermal systems.

Our target vent sites were the submarine volcano Suiyo Seamount (SSM) and the back-arc vents in Southern Mariana Trough (SMT). While the 0.2 micron-captured SMT samples are being analyzed, extensive studies have been done on the the 0.2 micron-captured SSM samples. The SSM vent plumes yielded the 16S rRNA gene clones Alpha-/Beta-/Gamma-/Epsilonproteobacteria, while the 0.2 micron-captured clones from the vent fluids showed the occurrence of Aquificae, Chlorobia, Alpha-/Gamma-/Delta-/Epsilonproteobacteria, Crenarchaeota, and a novel phylotype related to Nanoarchaeota. In situ cultivation of the 0.2 micron-captured microorganisms in near-vent boreholes demonstrated the occurrence of Alpha-/Epsilonproteobacteria and Euryarchaeota in the emerging warm to hot fluids. This study complements the previous 0.2 micron-capture-based analyses, and reports the occurrence of novel deep-branching phylotypes in the 0.2 micron-filterable fractions.