

## Catalogue of the microbial diversity in the seep environments of the West Pacific, and an estimate of the seep-activity.

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Microbial diversity studies in the West Pacific deep-sea have performed from the deepest ocean bottom Mariana Trench Challenger Deep at a depth of 11,000 m to Sagami Bay at a depth of 1,000 m. Deep-sea seep environments have been found in worldwide subduction zones at the continental margins. The nutrient and energy flux from sub-seafloor environments harbors cell-abundant and diverse microbial community in deep-sea. We have studied microbial community structures in the seep sediments offshore around Japan, such as Japan Trench (Arakawa et al., 2005), Nankai Trough (Arakawa et al., 2006b), Sagami Bay (Fang et al., 2006) and northeastern Japan Sea (Arakawa et al., 2006a) indicating that communities are in most cases composed of anoxic methane oxidizing archaea (ANME) and sulfate reducing bacteria (SRB) within Euryarchaeota and delta-Proteobacteria, respectively, which are known to be responsible for anaerobic oxidation of methane (AOM) (e.g., Li and Kato, 1999; Boetius et al., 2000; Orphan et al., 2001a, 2001b; Inagaki et al., 2004; Kato and Arakawa, 2004; Kato et al., 2005). Yet the distribution of AOM community associated with the fault activity and its effect of diffused methane remain largely elusive at the West Pacific Margin. The features of microbial diversity in those four deep-sea cold-seep environments (Japan Trench, Nankai Trough, Sagami Bay and northeastern Japan Sea, respectively) were shown in the t-RFLP catalogue.

We have recently performed the microbial analysis at newly discovered area, Kuril Trench at a depth of 3550m and Japan Trench at a depth of 7000m, and the AOM communities have been found at those areas. The results suggested that newly discovered areas could be active the seep-activity, and add those data to the t-RFLP catalogue.

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