

Microbial diversity of the bacterial mat sediments in the eastern margin of Japan Sea

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The eastern margin of the Japan Sea is believed to be a convergent plate boundary between the Amurian and Okhotsk plates. The bacterial mats were found at the eastern wall of the Shiribeshi Trough in the Japan Sea at a depth of 3,145 m in 1999. The existence of these bacterial mats might be by cold-seepage oozes out in a wide area through the high gravel of preciousness. In this study, we investigated the microbial diversity of the bacterial mat sediments obtained from the Japan Sea.

We re-visited those bacterial mats site in 2003. Using the manned submersible SHINKAI 6500, bacterial mat sediments and push-core sediments were collected at a depth of about 3,000 m in the Japan Sea. The push-core sediment was collected each 1 cm length. Using the sediment DNA isolation kit, the DNAs were extracted directly from the each sediment sample. Bacterial or Archaeal 16S rDNAs for terminal restriction fragment length polymorphisms (t-RFLP) analysis were amplified by the polymerase chain reaction (PCR). The sequences of the amplified 16S rDNAs were also determined and compared with sequences in the DNA databases. The PCR amplifications of sulfite reductase genes from push-core sediment samples were also performed.

From the t-RFLP analysis, the differences of the 16S digested patterns between the bacterial mat sediments were not observed. In the push-core sediment samples, gamma-Proteobacteria were decreased and unoxic methane oxidizing arcaea and Methanogens were increased in a vertical direction.

From the sequencing and phylogenetic results, the mat sediment samples were included abundant delta-Proteobacteria, which are related to sulfate-reducing bacteria, epsilon-Proteobacteria and Methanogens including the unoxic methane oxidizing archaea. Moreover, some relatives of sulfur-oxidizing bacteria were also observed in the mat samples.

Sulfite reductase genes were identified from push-core sediment samples from 2 to 8 cm depth. Bacterial mat sediment samples and push-core sediment samples of from 0 to 2 cm and from 8 to 23 cm were not identified the sulfite reductase genes.

It was indicated that gamma-Proteobacteria inhabit in surface, sulfate-reducing bacteria inhabit from 2 to 8 cm (probably together with the unoxic methane oxidizing archaea) and Methanogens inhabit deeper than 8 cm.