

Microbial community in seafloor manganese deposit

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Microbial activity has been suggested to be important in forming deep-sea ferromanganese deposit. Gram positive bacteria and fungi was isolated as manganese oxidizing microbes. Meanwhile, SSU rRNA gene sequences of isolated manganese oxidizing microbes were rarely identified in ferromanganese deposits. In the previous studies, diverse SSU rRNA sequences have been identified in ferromanganese deposits, and *Nitrosopumilus* in Thaumarchaeota, which would have manganese oxidizing enzyme *mnxG* gene, is one of the important candidates for the formation of ferromanganese deposits in deep sea. In this study, I analyzed SSU rRNA sequences in total 34 samples of seawater, sediment, and ferromanganese deposits from Takuyo-Daigo Seamount by deep sequencing and statistical methods to determine the potential microbial groups related to ferromanganese deposits. Based on the sample type and microbial community structures, the 34 samples were classified into 4 groups, i.e. Seawater cluster 1, Seawater cluster 2, sediment cluster, and ferromanganese deposit cluster. Detrended Correspondence Analysis showed that the representatives in samples of the ferromanganese deposit cluster is *Acidobacteria*, *Gemmatimonadetes*, *NC10*, *Nitrospirae*, *Rhizobiales* in *Alphaproteobacteria*, *Nitrosomonadaceae* in *Betaproteobacteria*, *NB1* and *Entotheonellales* in *DeltaProteobacteria*, *SBR1093*, *WS3*, *Caldithrix*. As was shown in previous studies, this result indicate that microbes associated with nitrogen cycle are important in the ferromanganese deposits.

Keywords: manganese deposit, microbial community analysis, nitrogen cycle