

## Diversity, abundance and spatial distribution of microbes on hydrogenetic ferro-manganese crusts of northwest Pacific

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### Introduction

Fe and Mn oxide deposits are often found on the deep seafloor. Basement rock covered with these oxide deposits is called as Ferro-manganese crusts or nodules (here after Mn crusts or Mn nodules). Mn crusts contain so many metal species (ex. Co, Ni, Pt and rare earth element). Mn crust is widely distributed on outcrop of seamount and sea plateau with slow sedimentation rate and Mn nodule is widely distributed on deep ocean basin. Mn crust and nodule covers a large part of seafloor (Usui, 2010). It is possibility that microorganisms on the surface of Mn crust contribute to material circulation on deep seafloor (ex. carbon, nitrogen and metal).

Our group analyzed the microbial community of Mn crust on Takuyo-Daigo seamount at the depth of 2991 m (Nitahara et al., 2011). This result shows that highly diversified microbes present abundantly on the surface of Mn crust. Comparison of the microbial community of Mn crust with that of sediment and seawater shows uniqueness of the microbial community of Mn crust. However, it is not clear that these characteristics are general between Mn crust on different area or different depth. The purpose in this study is to clarify the microbial distribution with the depth profile or geographic location.

### Material and method

We collected Mn crust, sediment and ambient seawater from Takuyo-Daigo seamount (depth 1200 m ~2991 m) and Ryusei seamount (depth 1194 m ~2209 m) with ROV Hyper-Dolphin. Genomic DNA was extracted from the samples. 16S rRNA gene was amplified with the primer set targeting whole prokaryote (Uni516F-Uni1407R). PCR products were cloned and nucleotide sequences were determined. The number of species shared with sample were estimated and principal component analysis (PCoA) were performed based on obtained sequences. The numbers of bacteria and archaea were estimated based on quantitative PCR.

### Results and discussion

The number of microbes is estimated about 107 cells/g on Mn crusts, 108 -109 cells/g in sediments and about 104 cells/ml in seawater based on qPCR results. There is no difference with depth profile.

The results of 16S rRNA gene clone library show that proteobacteria and archaea were dominant in all analyzed clone libraries of Mn crust. Almost all phylotypes of archaea were affiliated with Marine Group I (MGI), including group of ammonia oxidizing archaea. MGI were also detected from seawater, but MGI in Mn crust and seawater were clustered into different clusters. This fact shows the possibility that MGI in Mn crust and seawater were different species and show different adaptation to environment. The phylotypes belong to Nitrosospira (ammonia oxidizing bacteria) and to Nitrospira (nitrite oxidizing bacteria) were also detected from Mn crust. These facts show the possibility that nitrification occurs in the microbial community of Mn crust ubiquitously.

The estimation of numbers of species shared with Mn crusts show that 11-24 % of total species was shared between Mn crust of Takuyo-Daigo seamount and 16-28 % of total species was shared between Takuyo-Daigo seamount and Ryusei seamount collected at the same depth. However, PCoA comparing Mn crust, sediment and seawater of Takuyo-Daigo seamount shows that the microbial communities of Mn crust, sediment and seawater were grouped into different group respectively. Addition of Mn crust of Ryusei seamount to previous PCoA, the result shows that the microbial communities of Mn crust of Takuyo-Daigo seamount and Ryusei seamount were grouped into different group respectively.

Keywords: Ferro-manganese crust, 16S rRNA gene, Archaea, Ammonia oxidizing bacteria and archaea