

## Comparative analysis of microbial community on ferro-manganese crusts from Takuyo-Daigo seamount and Ryusei seamount

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### Purpose

Ferro-manganese crusts (Mn crusts) are the rocks covered with iron and manganese oxides and are widely distributed on the seafloor. Due to rapidly depleting land-based mineral resources, oceanic mineral deposits gain greater significance. Mn crusts are known for enrichment of several transition metals like Cu, Ni, Fe, Co, Pt etc. They are abundant in the seafloor and it is expected that they contribute greatly to the material circulation between hydrosphere and lithosphere. The microbes inhabiting the surface of the crusts may have a major role in the material circulation, especially on carbon and nitrogen. Previous electron microscopic observations demonstrated the existence of microbes on Mn crusts. However, there is a lack of molecular studies on species diversity and abundance. Thus, a comparative study was undertaken to analyze the diversity and abundance of microbes on the Mn crusts from Takuyo-Daigo seamount and Ryusei seamount

### Method

Mn crusts, ambient sediments and seawater were collected from four sampling points at Takuyo-Daigo Seamount NT09-02 cruise in Feb 2009. The water depth of each sampling point was 1200 m, 1419 m, 2209 m and 2991 m, respectively. Mn crusts, ambient sediments and seawater were collected from two sampling points at Ryusei seamount on KY11-02 cruise in Feb 2011. The water depth of each sampling point was 1194 m, 2079 m, respectively. DNA was extracted from each sample, followed by amplification of 16S rRNA gene and *amoA* (ammonia monooxygenase, subunit A) gene using universal primers and bacterial/archaeal *amoA* specific primers respectively. Clone libraries were constructed and nucleotide sequences were determined. The microbial community compositions and diversity were analyzed by phylogenetic and statistical analysis. Copy numbers of the 16S rRNA and *amoA* genes of bacteria and archaea were estimated by quantitative PCR.

### Result and Discussion

Quantitative PCR estimated that both bacterial and archeal abundance in the ferro manganese crust from the Takuyo-Daigo were about  $10^6$  to  $10^7$  cells/g, respectively. Archaea was dominated in the three of four Mn crust samples (50~83 % of total cell numbers) analyzed.

Comparing the microbial community of Mn crusts, sediment and seawater it is evident that Mn crusts consist of a significantly different microbial composition from the others, suggesting the uniqueness of the ecosystem.

Phylotypes closely related to Marine crenarchaeota Group I (MGI) were detected from six Mn crust samples, collected from the two seamounts. MGI includes ammonia oxidizing archaean which is distributed ubiquitously in the ocean. Phylotypes closely related to *Nitrosospira*, an ammonia oxidizing bacteria were present in four Mn crusts sample collected from the Takuyo-Daigo seamount. Abundance of the ammonia oxidizers were confirmed by sequencing and quantitative PCR analysis of bacterial and archaeal *amoA* gene. The copy number of bacterial and archaeal *amoA* gene was estimated as  $10^5$  to  $10^6$  copy/g.

This study demonstrated a high abundance of ammonia oxidizers in ferro-manganese crusts, which signifies the possible role of ammonia oxidizers as the primary producers in ferro-manganese crusts.

Keywords: ferro-manganese crusts, microbial ecosystem, 16S rRNA gene