

BBG005-P01

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## Microbial community of oceanic ferro-manganese deposits in the #5 Takuyo Seamount

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Ferro-manganese crusts are observed on the seafloor. Recent studies suggested the presence of microorganisms on the oceanic ferro-manganese crusts (e.g., Xiao-hong et al, 2009). However, little is known about the microbial community on the oceanic ferro-manganese crusts. Because the ferro-manganese oxides and the microbial communities exist in the interface between oceans and crusts, they would play a significant role in the global geochemical cycle.

The aims of this study are (i) to reveal the diversity, abundance and composition of microbial communities on the oceanic ferro-manganese crusts, and (ii) to elucidate the spatial distribution of the microbial communities. Our data will provide insight into generality of the microbial community on oceanic ferro-manganese crusts.

We collected ferro-maganese crusts and nodules, surrounding sediments and ambient seawater from the 5th Takuyo Seamount on NT09-02 cruise in Feb 2009. The water depth of each sampling point was 1200 m, 1419 m, 2209 m and 2991 m, respectively.

DNA was extracted from each sample. We amplified 16S rRNA gene by PCR with prokaryoteuniversal primer set (Uni515F-Uni1407R), constructed and analyzed clone libraries. The microbial community compositions were determined by phylogenetic and statistical analyses. We also estimated the abundance of Bacteria by quantitative PCR.

The abundance of Bacteria was  $1.25 \cdot 2.51 \times 10^{-7}$  cells/g in the ferro-manganese samples. Those of the sediment samples and of seawater samples were  $1.30 \cdot 1.98 \times 10^{-8}$  cells/g or  $5.99 \cdot 8.07 \times 10^{-3}$  cells/ml respectively.

Comparative analysis of the microbial community compositions among the ferro-manganese samples showed that phylotypes (a group of clones having more than 97% sequence similarity) closely related to Nitrosospira, Nitrospira and Marine crenarchaeotic Group I (MGI), of which members include ammonia or nitrite oxidizing chemoautotrophs, were common in these clone libraries. We also detected phylotypes affiliate to Deferribacteres and Deltaproteobacteria, which include some metal reducing bacteria.

Comparing the microbial communities of ferro-manganese, surrounding sediment and ambient seawater samples, no phylotype was common between the ferro-manganese and seawater samples. However, some phylotypes are shared between the ferro-manganese and sediment samples. These phylotypes are closely related to Nitrospira, MGI and Acidobacteria.

These results suggest that microbial communities of the ferro-manganese crust are distinct from those of ambient seawater in the 5th Takuyo Seamount. Our data also suggest that some phylotypes are common between ferro-manganese crusts and surrounding sediments, although there are unique phylotypes in each environment.

Reference

Xiao-hong Wang, Ute Schlosmacher, Filipe Natalio, Heinz C. Schroder, Stephan E. Wolf, Wolfgang Tremel, Werner E.G. Muller, 2009. Evidence for biogenic processes during formation of ferromanganese crusts from the Pacific Ocean: Implications of biologically induced mineralization. Micron 40, 526-535. Keywords: Ferro-manganese crust, microbial community, 16S rRNA gene