

16S rRNA および *AmoA* 遺伝子を用いた南極淡水湖沼雪鳥池における バクテリアの群集構造解析

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Bacterial diversity and community structure in Antarctic freshwater lake Yukidori-Ike revealed by 16S rRNA and *AmoA* genes

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Previous Antarctic studies have revealed significant prokaryote diversity, particular among bacteria (Franzmann *et al.* 1996; Bowman *et al.* 2000; Kurosawa *et al.* 2010). However, many studies of bacterial community structure in Antarctica have focused on saline lakes, and only limited information is available regarding the bacterial community structure in freshwater lakes. In the preliminary experiment, we detected ammonium oxidizer *Nitrosospira* related 16S rRNA gene clones in Antarctic fresh water lake Yukidori-Ike. In the present study, we aimed to investigate the phylogenetic composition of bacterial communities in Yukidori-Ike by using 16S rRNA gene together with ammonia monooxygenase subunit A gene (*amoA*).

Lake Yukidori-Ike is located in the mid-Langhovde, Antarctica (69° 14' 26" S, 39° 45' 23" E). We collected water sample from the lake on December 26, 2012 during the 54th Japanese Antarctic Research Expedition. During sampling, the water temperature and pH were 5.4°C and 7.5, respectively. A bacterial 16S rRNA gene and *amoA* clone libraries were constructed using metagenomic DNA extracted from the sample. The clones were randomly chosen, sequenced, and identified using EzTaxon and BLASTN.

Concentrations of NO₃, NO₂, SiO₂ and NH₄ of the lake-water were 5.18 μM, 0.13 μM, 25.6 μM and 1.27 μM, respectively. PO₄ concentration was below detection limits. These data indicated that Lake Yukidori-Ike is classified as an oligotrophic lake. Total 76 clones were taxonomically identified and grouped into 56 phylotypes that were further classified into 11 groups. β-Proteobacteria (31.6%) was the dominant class in Lake Yukidori-Ike in contrast to the Antarctic saline lakes where Cyanobacteria, Planctomycetes or α-Proteobacteria were dominant. Other clones consisted of Cyanobacteria (17.1%), Firmicutes (14.5%), α-Proteobacteria (10.5%), Bacterioidetes (7.9%), Acidobacteria (5.3%), Chlorobi (2.6%), δ-Proteobacteria (2.6%), unclassified Proteobacteria (2.6%), Verrucomicrobia (2.6%), γ-Proteobacteria (1.3%) and Planctomycetes (1.3%). These results indicated that the bacterial diversity in Yukidori-Ike was remarkably high, and the dominance of β-Proteobacteria is most distinguishable property of bacterial community of lake Yukidori-Ike. On the other hand, total 84 *amoA* clones were classified into eight phylotypes affiliated with β-Proteobacteria. A 74% of *amoA* clones consisting of three phylotypes were identified as members of genus *Nitrosospira*. Other five phylotypes were also order Nitrosomonadales, but could not be identified in genus level. The results of this study help to understand bacterial community structures in Antarctic freshwater lakes.

References

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