

# 南極淡水氷河湖雪鳥池におけるバクテリアおよびアーキアの群集構造

茶屋 葵<sup>1</sup>、川又明德<sup>2</sup>、伊村 智<sup>3</sup>、黒沢則夫<sup>1</sup>

<sup>1</sup>創価大学

<sup>2</sup>愛媛県総合科学博物館

<sup>3</sup>国立極地研究所

## Bacterial and Archaeal community structures in glacial freshwater lake Yukidori-Ike, Antarctica

A. Chaya<sup>1</sup>, A. Kawamata<sup>2</sup>, S. Imura<sup>3</sup>, and N. Kurosawa<sup>1</sup>

<sup>1</sup>*Soka University*

<sup>2</sup>*Ehime Prefectural Science Museum*

<sup>3</sup>*National Institute of Polar Research*

A number of researchers reported that Antarctic continent was numerically dominated by microbial communities (Ellis-Evans, 1996; Miteva, 2008), and the microorganisms would play essential roles in biogeochemical cycles in the ice free areas of Antarctic continent. Many studies investigating prokaryotic community structures in Antarctic lakes revealed significantly high bacterial diversity and limited archaeal diversity (e.g. Bowman *et al.*, 2000a, 2000b; Sjöling and Cowan, 2003; Karr, 2003; Kurosawa *et al.*, 2010; Bielewicz, 2011). However, most of these studies focused on saline lakes, and limited information is available regarding the prokaryotic community structures in freshwater lakes. In the present study, the bacterial and archaeal community structures in Antarctic glacial freshwater lake Yukidori-Ike were revealed by 16S rRNA gene clone analysis, and the communities were compared with those of other lakes in polar and temperate regions.

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Lake Yukidori-Ike is located in the mid-Langhovde area, Antarctica. Water sample of the lake was collected 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. Bacterial and Archaeal 16S rRNA gene clone libraries were constructed using metagenomic DNA extracted from the sample. The clones were randomly chosen, sequenced, and identified using EzTaxon and BLASTN.

Bacterial 198 clones were taxonomically identified and grouped into 129 phylotypes in species level and were further classified into 12 phyla. Proteobacteria was the most dominant phylum (50.0%) in Lake Yukidori-Ike and was composed of  $\alpha$ -,  $\beta$ -,  $\delta$ -, and  $\gamma$ -Proteobacteria.  $\beta$ -Proteobacteria was the most dominant class, accounted for 58.6% of Proteobacteria. The second dominant phylum was Cyanobacteria (14.7%) consisting of two orders Nostocales and Oscillatoriales. Other clones consisted of phyla Bacteroidetes (9.6%), Firmicutes (7.6%), Acidobacteria (4.5%), Planctomycetes (4.5%), Verrucomicrobia (4.0%), Ignavibacteria (1.5%), Gemmatimonadetes (1.0%), Choloroflexi (0.5%), and Armatimonadetes (0.5%). The clones affiliated with  $\beta$ -Proteobacteria were related to cultured and uncultured  $\beta$ -Proteobacterial clones isolated from polar, temperate, and subtropical regions. In contrast, most of Cyanobacterial clones were related to the clones detected from polar and alpine environments. Shannon-Weaver index of bacterial species diversity in Yukidori-Ike was remarkably high and the value of 4.8. In contrast to the bacterial diversity, archaeal community was much less diverse. A total of 72 clones were classified into only two phylotypes (YK1A-009 and YK1A-058). Approximately 97.2% of archaeal clones was grouped into the phylotype YK1A-009 which showed 98.5% sequence similarity with *Methanosarcina spelaei* originally isolated from the biofilm of subsurface lake in Romania. Shannon-Weaver index of archaeal species diversity was 0.12. The results of this study help to understand prokaryotic community structure in Antarctic glacial freshwater lakes.