

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

茶屋葵¹、川又明德²、伊村智³、黒沢則夫¹

¹ 創価大学 工学部

² 愛媛県総合科学博物館

³ 国立極地研究所

Bacterial community structure in Antarctic freshwater lake Yukidori-Ike

A. Chaya¹, A. Kawamata², S. Imura³, and N. Kurosawa¹

¹ Faculty of Engineering, Soka University

² Ehime Prefectural Science Museum

³ National Institute of Polar Research

Previous studies showed that Antarctic prokaryotes were remarkably diverse and represent most major evolutionary groups^[1,2,3]. However, the information of prokaryotic communities inhabiting Antarctic lakes is limited to a few regions. Particularly, there are very little reports about prokaryotic communities in Antarctic freshwater lakes. In the present study, we aimed to investigate the phylogenetic composition of bacterial communities in the freshwater lake Yukidori-Ike (69.14.26S, 39.45.23E) located in the central part of Langhovde, Antarctica.

The water sample including surface sediment was collected on December 26, 2012 during the 54th Japanese Antarctic Research Expedition. The lake water temperature and pH were 5.4°C and 7.5, respectively. The bacterial 16S rRNA gene clone library was constructed using the metagenomic DNA extracted from the sample. The clones were randomly chosen, sequenced, and identified by using EzTaxon^[4].

Thirty-five clones were grouped into 30 phylotypes and were dominantly affiliated with β -proteobacteria (43%). This class consisted of six genera *Rhodoferrax*, *Aquicola*, *Propionivibrio*, *Undibacterium*, *Rubrivivax*, *Polaromonas*, and six uncultured phylotypes that could not be affiliated with any known genera. Other clones consisted of Cyanobacteria (14%), δ -proteobacteria (11%), *Bacterioidetes* (11%), *Acidobacteria* (11%), α -proteobacteria (6%) and *Planctomycetes* (3%). These results showed that the bacterial diversity in Yukidori-Ike is very high. However, biodiversity coverage in this analysis is still very low, and a more number of clones are now investigated to reveal more comprehensive bacterial community structure in this lake.

References

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