# 南極コケボウズから分離した微生物の系統地理学的解析

中井亮佑 [1, 2]、黒沢則夫 [3]、伊村智 [4, 5]、仁木宏典 [1, 5]
[1] *国立遺伝学研究所*
[2] *日本学術振興会特別研究員*
[3] *創価大学*
[4] *国立極地研究所*
[5] *新領域融合研究センター*

# Phylogeographic analysis of microorganisms isolated from Antarctic moss pillars

Ryosuke Nakai[1, 2], Norio Kurosawa[3], Satoshi Imura[4, 5], Hironori Niki[1, 5]
[1]*National Institute of Genetics*
[2]*Superlative Postdoctoral Fellow of the Japan Society for the Promotion of Science*
[3]*Soka University*
[4]*National Institute of Polar Research*
[5]*Transdisciplinary Research Integration Center*

Aquatic mosses of the genera *Bryum* and *Leptobryum* form unique tower-like structures called “moss pillars” in Antarctic lakes. These pillars consist of distinct redox-affected sections that have oxidative exteriors and reductive interiors. Our previous analyses based on fatty acid composition and 16S rRNA gene sequences showed that bacterial communities differed among the exterior, upper-interior, and lower-interior sections of the moss pillars and that more than 60% of the observed 16S rRNA phylotypes were novel taxa at the species, genera, or class levels {1}. In addition, 18S rRNA-based analysis revealed that a wide range of unique eukaryotic phylotypes related to algae, ciliates, fungi, nematodes, rotifers, and tardigrades were present in the pillars {2}. Thus, we proposed that a “moss pillar” is a habitat that supports communities of phylogenetically diverse organisms. Here, we report the phylogeny and biogeography of cultivated bacteria from moss pillar specimens obtained by the 54th Japanese Antarctic Research Expedition (JARE-54). Nearly 20 isolates were selected after culture on several growth media. Phylogenetic analysis based on rRNA gene sequences showed that the isolates belonged to the following four major phylogenetic groups: *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, and *Bacteroidetes*. The sequences of several isolates showed <97% similarity with those of previously cultured strains, implying that the isolated bacteria were potentially novel species. The sequence of the *Polaromonas* isolate (*Betaproteobacteria*) was almost identical to those obtained from acid mine drainage, ground water, natural mineral water after bottling, and soil. Recently, *Polaromonas* species have been isolated from cold environments and their sequences have also been detected in gene libraries from alpine environments worldwide {3}. Our results suggest that their distribution range is wider than expected. Additionally, our *Polaromonas* isolate could pass through 0.2-μm pore-size “sterile” filters, suggesting that they can form ultra-micro-sized cells during their life cycle. If the formation of sub-0.2-μm cells is common among *Polaromonas* species, 0.1-μm filters should be used for their isolation instead of 0.2-μm filters. As this is an ongoing study, we will report more phylogeographic data of other isolates in the presentation.

**References**

1. Nakai R, Abe T, Baba T, Imura S, Kagoshima H, Kanda H, Kanekiyo A, Kohara Y, Koi A, Nakamura K, Narita T, Niki H, Yanagihara K, Naganuma T (2012) Microflorae of aquatic moss pillars in a freshwater lake, East Antarctica, based on fatty acid and 16S rRNA gene analyses. *Polar Biology* **35**: 425–433.
2. Nakai R, Abe T, Baba T, Imura S, Kagoshima H, Kanda H, Kohara Y, Koi A, Niki H, Yanagihara K, Naganuma T (2012) Eukaryotic phylotypes in aquatic moss pillars inhabiting a freshwater lake in East Antarctica, based on 18S rRNA gene analysis. *Polar Biology* **35**: 1495–1504.
3. Darcy JL, Lynch RC, King AJ, Robeson MS, Schmidt SK (2011) Global distribution of *Polaromonas* phylotypes - Evidence for a highly successful dispersal capacity. *PLoS ONE* **6**: e23742. doi:10.1371/journal.pone.0023742