Bryosphere within an Antarctic moss pillar

Ryosuke Nakai[1, 2], Tomoya Baba[3], Katsuhiko Yanagihara[3], Hiroshi Kagoshima[3],
Takashi Abe[4], Takeshi Naganuma[5], Satoshi Imura[6], Hironori Niki[1]
[1] *National Institute of Genetics*
[2]*Research Fellow of the Japan Society for the Promotion of Science*
[3]*Transdisciplinary Research Integration Center*
[4]*Graduate School of Science and Technology, Niigata University*
[5]*Graduate School of Biosphere Science, Hiroshima University*
[6]*National Institute of Polar Research*

The aquatic moss, *Leptobryum wilsonii*, forms underwater tower-like structures called "moss pillars" (Koke Bouzu, in Japanese) in ultra-oligotrophic Antarctic lakes. These pillars comprise distinct redox-affected sections, that is, oxidative exteriors and reductive interiors. Our objective here was to understand how such a unique ecosystem survives in such extreme environments. Using biochemical and molecular methods, we studied the microbiome of aquatic moss pillars, based on the fatty acid profile, rDNA genotyping, and metagenomic information. Our results indicated that the bacterial communities differed among the exterior, upper-interior, and lower-interior sections, and that more than 60% of the obtained 16S rDNA phylotypes were of a novel taxa at the species, genera, or class levels. Furthermore, a wide range of eukaryotic 18S rDNA phylotypes related to algae, ciliates, fungi, nematodes, rotifers, and tardigrades were present in the pillar. In parallel, we analyzed the diversity of functional genes encoding the CO_2-fixing enzyme RuBisCO, nitrogenase (*nifH*), nitrite reductase (*nirK* and *nirS*), and nitric oxide reductase (*qnorB*), all of which are involved in carbon and nitrogen cycling in a pillar. Phylogenetic analyses revealed that cyanobacterial RuBisCO genotypes were found exclusively in the pillar exterior; however, genotypes related to chemoautotrophic bacteria were detected in the lower-interior of the pillar. Furthermore, γ-proteobacterial *nifH* showed pillar-wide distribution, while cyanobacterial *nifH* sequences were specific to the exterior, and sulfate-reducing δ-proteobacterial *nifH* sequences were subdominant in the interior. Such microbial functional zonation, as reflected by the redox gradient in a pillar, was also identified during analyses of other gene sequences. These findings will shed light on the mechanisms underlying the maintenance of the "bryosphere" within these pillars.

Figure 1. Antarctic moss pillars found in Lake Hotoke-Ike.

References

Imura S, Bando T, Saito S, Seto K, Kanda H (1999) Benthic moss pillars in Antarctic lakes. *Polar Biology*, **22**, 137–140.

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.

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.

Nakai R, Abe T, Baba T, Imura S, Kagoshima H, Kanda H, Kohara Y, Koi A, Niki H, Yanagihara K, Naganuma T (2012) Diversity of RuBisCO gene responsible for CO_2 fixation in an Antarctic moss pillar. *Polar Biology*, **35**, 1641–1650.