

南極コケ坊主生態系における真核微生物の驚くべき多様性

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Unsuspected eukaryotic diversity of aquatic moss pillars inhabiting a freshwater lake in East Antarctica, based on 18S rRNA gene analysis

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Aquatic mosses of *Bryum* and *Leptobryum* species in association with green algae, diatoms, and cyanobacteria, form unique tower-like pillars of vegetation (“moss pillars”) in Antarctic lakes (Imura et al., 1999). Moss pillars have distinct redox-affected sections, namely aerobic exterior and anaerobic interior. We previously proposed that a “pillar” is structured based on community and habitat of functionally interdependent organisms; hence, a pillar represents a mini-biosphere or bryosphere. Batteries of 16S rRNA genotypes or phylotypes of eubacteria and cyanobacteria, but not archaeobacteria, have been identified in moss pillars (Nakai et al., 2011). Some phylotypes showed pillar-wide distributions, while others were section-specific. This study analyzed near full-length 18S rRNA gene sequences obtained from two whole moss pillars in Lake Hotoke Ike (formerly known as “B-4”), Skarvsnes, in the vicinity of Syowa Station, East Antarctica. Total 28 PCR clone libraries from two whole moss pillars were constructed, and 96 clones from each library (total 2,688 clones) were randomly selected and sequenced. Homology search suggested that most of the sequences were previously unknown but could be assigned to important phyla including Alveolata, Amoebozoa, Chlorophyta, Fungi, Metazoa, Rhizaria, Rhodophyta, and Stramenopiles. We also found unclassified Alveolata, Amoebozoa, Metazoa, and Stramenopiles. In addition, 18S rRNA sequences related to *Leptobryum pyriforme* and unclassified fungi dominated whole moss pillar libraries, with outer aerobic sections further dominated by Ciliophora (genera *Obertrumia*, *Onychodromopsis*, and *Oxytricha*) and Tardigrada (genus *Diphascion*) and inner anaerobic sections sub-dominated by unclassified Amoebozoa. The 18S rRNA gene-based profiles demonstrated that redox-related factors may control distribution of physiologically functioning microbial species in a whole moss pillar.

References

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[2] Nakai et al. (in press) Microflorae of aquatic moss pillars in a freshwater lake, East Antarctica, based on fatty acid and 16S rRNA gene analyses. *Polar Biology*, Online First, DOI: 10.1007/s00300-011-1090-2