南極コケ坊主生態系における窒素固定菌と脱窒菌の多様性

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Microfloral association for nitrogen cycling in an Antarctic moss pillar inferred from phylogenetic analyses

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Aquatic mosses form unique tower-like structures called “moss pillars (Koke Bouzu in Japanese)” in ultraoligotrophic Antarctic lakes. The pillars consist of distinct redox-affected sections, that is, oxidative exteriors and reductive interiors. On the basis of analyses of fatty acid compositions, 16S/18S rRNA phylotypes, and RuBisCO genotypes (Nakai et al. Polar Biology 2012a, 2012b, 2012c), we had proposed that a “pillar” is a community and habitat of functionally interdependent organisms. Here, we report the diversity of the genes encoding nitrogenase (*nifH*), nitrite reductase (*nirK* and *nirS*), and nitric oxide reductase (*qnorB*) in a pillar. In total, 56 PCR clone libraries were constructed from an entire pillar, and 96 clones from each library (a total of 5,376 clones) were sequenced. Phylogenetic analyses showed that the *nifH* gene sequences of purple photosynthetic γ-proteobacteria, the *nirK* sequences of α-proteobacteria, the *nirS* sequences of β-proteobacteria, and the putative *qnorB* sequences of acidobacteria were dominant in the pillar. Furthermore, cyanobacterial *nifH* sequences were detected only in the exterior of the pillar, whereas sulfate-reducing δ-proteobacterial *nifH* sequences were subdominant in the interior. Such layer-specific distributions were also found during *nirK*, *nirS*, and *qnorB* sequence analyses. These results suggest that different phylogenetic groups participate in the nitrogen fixation and denitrification processes within a pillar. We would like to discuss about the microbial synergy that plays a vital role in the existence and maintenance of the moss pillar ecosystem.

References

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