

Phylogenetic diversity of labyrinthulomycetes in Antarctic freshwater lakes

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Labyrinthulomycetes are heterotrophic straminipilan protists and occur in detectable amounts mostly in the marine habitats. They possess the unique ability to produce long-chain polyunsaturated fatty acids such as docosahexaenoic acid (DHA) and docosapentaenoic acid (DPA) and to degrade a wide variety of organic substrates by means of extracellular enzymes. While the phylogenetic diversity and distribution of labyrinthulomycetes in marine environments has been well documented, information pertaining to their freshwater lineage remains limited. In addition to the several lineages already documented from the freshwater environments (e.g. species of the genera *Diplophrys* and *Fibrophrys*), our previous clone library surveys reported a baseline existence of unseen freshwater lineages inhabiting aquatic mosses in an Antarctic lake (Nakai *et al.*, *Polar Biol.*, 2012). In the present study, we examined moss specimens and lake water samples collected from the freshwater lakes in the vicinity of Syowa Station during the 56th Japanese Antarctic Research Expedition (JARE56). Using the 18S rRNA gene amplicon sequencing, we detected nine phylotypes belonging to labyrinthulomycete groups. These phylotypes showed very low sequence similarity (<90%) with known cultured labyrinthulomycetes, and they formed an independent cluster on the phylogenetic tree. This implies that uncultured labyrinthulomycetes with high phylogenetic novelty are distributed in the studied lakes. As this is an ongoing study, we will report more sequence data of other lakes in the presentation.

Reference

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.