

Novel labyrinthulomycete lineages in aquatic moss pillars inhabiting an Antarctic lake

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Labyrinthulomycetes are straminipilan protists that are neglected components of the microbial food chain. However, they occur in detectable amounts mostly in the marine habitats all over the world (Nakai *et al.*, 2013; Nakai & Naganuma, 2015). The labyrinthulomycetes possess the unique ability to produce long-chain polyunsaturated fatty acids such as docosahexaenoic acid and docosapentaenoic acid that are considered essential fatty acids for several organisms (Raghukumar, 2008). While the diversity of labyrinthulomycetes in marine environments has been well documented, information pertaining to their freshwater lineage remains limited. Previously, a molecular ecology study reported a baseline existence of unseen freshwater lineages of aquatic moss pillars inhabiting an Antarctic lake (Nakai *et al.*, 2012; Figure 1). In the present study, we examined moss pillar specimens collected in freshwater lakes (i.e., Lakes Hotoke-Ike and Nogiku-Ike) during the 56th Japanese Antarctic Research Expedition (JARE56). Microscopic observation revealed that cells resembled *Fibrophrys* species (Amphifilidae, Labyrinthulomycetes; Takahashi *et al.*, 2016) and contained orange or amber lipid bodies in the pillar specimens. DNA metabarcoding also detected 18S rRNA gene sequences belonging to Amphifilidae. Remarkably, these sequences were related to the sequences of Amphifilidae reported from various types of environments, including not only freshwater lakes but also a highly acidic river (c.a. pH 2.5) and terrestrial soil. This implies that novel labyrinthulomycete lineages are distributed widely across environments.



Figure 1. Aquatic moss pillars found in Lake Hotoke-Ike, East Antarctica

References

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