

## Online database of Antarctic microbial strains catalogue and genome information

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Fungi in Antarctica are concerned about the drastic shrinkage of their habitats due to global warming in recent years. However, only five species and eight strains of fungi isolated from near Syowa Station have been preserved by Japanese microbial culture collections. These fungi are also attracting attention as a new microbial resource because of their specific characteristics at cold temperatures. In this study, we aimed to construct a strain database and a genome database of Antarctic fungi, which have attracted attention as microbial resources but have rarely been preserved in Japanese microbial culture collections.

To construct a strain database, we first attempted to identify 600 strains isolated from samples taken from around Showa Station in Antarctica. The results were as follows. The 584 strains successfully amplified by PCR were sequenced by capillary sequencing.

As a result of DNA sequence analysis, 42 isolates were ascomycetes and could be classified into 15 genera and 15 species. 142 isolates were basidiomycetes and could be classified into 9 genera and 19 species. The remaining 400 isolates were bacterial, so the 16S rRNA, a bacterial marker gene, was amplified by PCR and its gene sequence was determined to confirm that the isolates were bacterial.

The strains identified to fungal species were cultured in yeast peptone dextrose liquid medium (YPD, Difco) and potato dextrose liquid medium at 10°C for 1 week with shaking. Each culture was dispensed into 1 mL of 2 mL cryovials, to which was added 1 mL of 40% glycerol solution containing 10% trehalose, assigned a strain number beginning with NIPR, and stored in a deep freezer at -80°C.

Strain number, species name, sample collection location, and marker gene sequence information are compiled into one database. The database is available on the website of the Bioscience Group of the National Institute of Polar Research (<https://www.nipr.ac.jp/biology/>).

Some strains were selected, and genomic DNA was extracted from these strains and whole genome sequence analysis was performed using a next-generation sequencer. Gene sequence and gene function predictions were then made from the whole genome sequences. These data are being constructed as a genome database of polar fungi. The genome database is currently in beta version with a password (<https://antarcfungi.annotation.jp/>), and is scheduled to be released without password on the website of the Bioscience Group, NIPR (<https://www.nipr.ac.jp/Biology/>) around October 2024.

By releasing the strain and genome databases of these Antarctic fungi, we aim to establish Antarctic fungi as a new microbial resource in the future.

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