



Draft genome sequence of a *Globisporangium polare* strain isolated from Antarctic moss

Yuki Shima,¹ Akira Ashida,¹ Nanako Saga,² Yoshiya Akimoto,² Maurizio Camagna,¹ Kevin K. Newsham,³ Masaki Uchida,^{4,5} Motoaki Tojo,² Daigo Takemoto¹

AUTHOR AFFILIATIONS See affiliation list on p. 2.

ABSTRACT *Globisporangium polare* is an oomycete species associated with mosses. Here, we report the draft genome sequence of *G. polare* strain 14-1, isolated from *Sanionia uncinata* (sickle-leaved hook-moss) on Adelaide Island, Antarctica.

KEYWORDS *Globisporangium polare*

Globisporangium is a genus of oomycetes belonging to the phylum Oomycota within the kingdom Straminipila. The genus was formerly classified within *Pythium*, but molecular phylogenetic analyses have demonstrated that it forms an independent monophyletic clade, leading to its reclassification as *Globisporangium* (1, 2). Species of this genus are widely distributed in soils and freshwater environments, and several species are known to infect a broad range of host plants (3, 4). *G. polare* is a psychrophilic oomycete isolated from mosses and freshwater in the Arctic and Antarctic, which has been reported to infect and persist in living plant tissues at low temperatures (5, 6). Here, we report the draft genome sequence of *G. polare* strain 14-1, which was isolated from the moss *Sanionia uncinata* (Hedw.) Loeske—a species adapted to cold and moist environments (7)—collected at Rothera Point, Adelaide Island, Antarctica (67°34'0" S, 68°5'60" W) in November 2007 (Fig. 1A). Shoots of *S. uncinata* were washed with water, placed on NARM medium (8), and incubated in darkness at 4°C. Emerging mycelia were grown on 1.5% water agar at 4°C, and each agar plug containing a single hyphal tip was transferred onto a 10% V8 juice agar plate at 4°C. The cultures were maintained in darkness at 2°C–10°C at Osaka Metropolitan University, Japan. Globose to subglobose sporangia were observed in and around moss tissues (Fig. 1B). For the genomic analyses, the strain was grown on potato dextrose agar at 23°C for 7 days and subcultured in potato dextrose broth at 23°C at 120 rpm for 4 days before fixation in 100% ethanol. DNA was extracted using a NucleoSpin Plant II kit (Takara Bio). Whole-genome sequencing libraries were prepared with a MGIEasy FS DNA Library Prep Set (MGI) and sequenced on a DNBSEQ-G400RS platform (2 × 150 bp). Unless otherwise noted, default parameters were used for all software. Reads were processed with fastp v0.24.0 (9) and assembled *de novo* using SPAdes v3.15.3 (10). Assembly quality was assessed with QUAST v5.0.2 (11). The summary of genome assemblies is shown in Table 1. Protein-coding genes were predicted with BRAKER3 v3.0.8 (12) using the oomycota_odb12 BUSCO data set for protein hints (13). Genome completeness was assessed with BUSCO v6.0.0 using oomycota_odb12 (13), yielding 99.1% complete BUSCOs. The ITS1 and mitochondrial *cox2* sequences were identified in the assembly by BLASTn using reference *Globisporangium* sequences were extracted as single contiguous sequences. The best BLASTn matches supported the assignment of strain 14-1 as *G. polare* (ITS1: 99.9% identity, 89.7% query coverage; *cox2*: 99.6% identity, 100% query coverage; best-hit accessions: ITS1, [KJ716859](#); *cox2*, [KJ595417](#) from *G. polare* CBS118203).

Editor Leighton Pritchard, University of Strathclyde, Glasgow, United Kingdom

Address correspondence to Daigo Takemoto, dtakemo@agr.nagoya-u.ac.jp.

The authors declare no conflict of interest.

See the funding table on p. 3.

Received 3 February 2026

Accepted 20 April 2026

Published 28 May 2026

Copyright © 2026 Shima et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](#).

TABLE 1 Summary of *Globisporangium polare* genome assemblies and annotations

Strain	Host plant	No. of read pairs (spots)	N50	GC contents (%)	No. of total bases (bp)	No. of contigs	Sequencing coverage	No. of genes	Results from BUSCO analysis with data set oomycota_odb12			
									Complete BUSCOs (%)	No. of BUSCOs	No. of missing BUSCOs	No. of fragmented BUSCOs
14-1	<i>Sanionia uncinata</i>	11,527,521	44,986	57.9	39,404,733	3,348	174	15,063	99.1	3,431	11	21

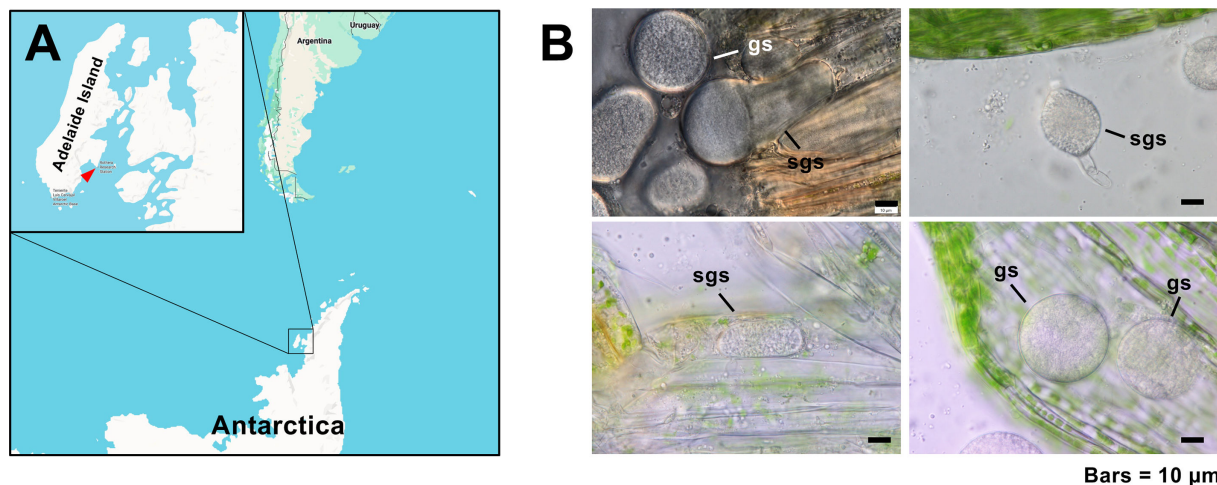


FIG 1 (A) Map of the Antarctic Peninsula showing the location from which *Globisporangium polare* strain 14-1, associated with *Sanionia uncinata*, was sampled (red arrowhead). The map was obtained from Google Maps. (B) Images of globose (gs) to subglobose (sgs) sporangia of *G. polare* developed in and around moss tissues.

ACKNOWLEDGMENTS

This work was supported by a Grant-in-Aid for Challenging Exploratory Research (22K19176) to D.T. and a Grant-in-Aid for Scientific Research (C) (23K11504) to M.T. from the Japan Society for the Promotion of Science, by a research grant (G-2022-2-075) from the Institute for Fermentation, Osaka, to D.T., by the National Institute of Polar Research through Special Collaboration Project no. B24-03 to M.T. and M.U., and by the Arctic Challenge for Sustainability Project (ArCS III, grant no. JPMXD1720251001) for M.T. and M.U. British Antarctic Survey staff assisted with sample collection.

AUTHOR AFFILIATIONS

¹Graduate School of Bioagricultural Sciences, Nagoya University, Nagoya, Japan

²Graduate School of Agriculture, Osaka Metropolitan University, Sakai, Japan

³British Antarctic Survey (BAS), Natural Environment Research Council, Cambridge, United Kingdom

⁴National Institute of Polar Research (NIPR), Tachikawa, Tokyo, Japan

⁵Graduate Institute for Advanced Studies, SOKENDAI, Tachikawa, Tokyo, Japan

AUTHOR ORCIDs

Daigo Takemoto  <http://orcid.org/0000-0002-9816-7882>

FUNDING

Funder	Grant(s)	Author(s)
Japan Society for the Promotion of Science	22K19176	Daigo Takemoto
Japan Society for the Promotion of Science	23K11504	Motoaki Tojo
Institute for Fermentation, Osaka	G-2022-2-075	Daigo Takemoto
National Institute of Polar Research	B24-03	Motoaki Tojo
National Institute of Polar Research	B24-3	Masaki Uchida
Arctic Challenge for Sustainability	JPMXD1720251001	Motoaki Tojo
Arctic Challenge for Sustainability	JPMXD1720251001	Masaki Uchida

AUTHOR CONTRIBUTIONS

Yuki Shima, Data curation, Formal analysis, Investigation, Writing – original draft | Akira Ashida, Investigation, Methodology, Supervision | Nanako Saga, Investigation | Yoshiya Akimoto, Investigation | Maurizio Camagna, Investigation, Methodology, Supervision | Kevin K. Newsham, Investigation, Supervision, Writing – review and editing | Masaki Uchida, Funding acquisition, Investigation, Supervision | Motoaki Tojo, Conceptualization, Funding acquisition, Investigation, Supervision | Daigo Takemoto, Conceptualization, Funding acquisition, Investigation, Supervision, Writing – original draft, Writing – review and editing

DATA AVAILABILITY

The draft genome assembly of *Globisporangium polare* strain 14-1 has been deposited in DDBJ/EMBL/GenBank under the whole-genome shotgun project [BAAJAQ01](#) and is available as a genome assembly under accession number [GCA_054786475.1](#) (assembly name: Gp_assembly_01). The raw sequencing reads are available in the DDBJ Sequence Read Archive under accession number [DRR794741](#) and BioProject accession number [PRJDB38039](#).

REFERENCES

- Thines M. 2018. Oomycetes. *Curr Biol* 28:R812–R813. <https://doi.org/10.1016/j.cub.2018.05.062>
- Uzuhashi S, Kakishima M, Tojo M. 2010. Phylogeny of the genus *Pythium* and description of new genera. *Mycoscience* 51:337–365. <https://doi.org/10.1007/s10267-010-0046-7>
- Liu Y, Vaghefi N, Ades PK, Idnurm A, Ahmed A, Taylor PWJ. 2023. *Globisporangium* and *Pythium* species associated with yield decline of *Pyrethrum* (*Tanacetum cinerariifolium*) in Australia. *Plants (Basel)* 12:1361. <https://doi.org/10.3390/plants12061361>
- Molin C, Ribeiro NR, Matsumoto MN, Fernando Giasson N, Brollo J, Zanardo B, Pelissoni M, Capitanio S, Comin T, Deuner CC, et al. 2021. Damping - off of soybean in southern Brazil can be associated with different species of *Globisporangium* spp. and *Pythium* spp. *Plant Pathol* 70:1686–1694. <https://doi.org/10.1111/ppa.13397>
- Tojo M, van West P, Hoshino T, Kida K, Fujii H, Hakoda A, Kawaguchi Y, Mühlhauser HA, Van Den Berg AH, Küpper FC, et al. 2012. *Pythium polare*, a new heterothallic oomycete causing brown discolouration of *Sanionia uncinata* in the Arctic and Antarctic. *Fungal Biol* 116:756–768. <https://doi.org/10.1016/j.funbio.2012.04.005>
- Tojo M, Fujii N, Yagi H, Yamashita Y, Tokura K, Kida K, Hakoda A, Herrero M-L, Hoshino T, Uchida M. 2021. Identification and isolation pattern of *Globisporangium* spp. from a *Sanionia* moss colony in Ny-Ålesund, Spitsbergen Is., Norway from 2006 to 2018. *Microorganisms* 9:1912. <https://doi.org/10.3390/microorganisms9091912>
- Virtanen RJ, Lundberg PA, Moen J, Oksanen L. 1997. Topographic and altitudinal patterns in plant communities on European arctic islands. *Polar Biol* 17:95–113. <https://doi.org/10.1007/s003000050111>
- Morita Y, Tojo M. 2007. Modifications of PARP medium using fluzaninam, miconazole, and nystatin for detection of *Pythium* spp. in soil. *Plant Dis* 91:1591–1599. <https://doi.org/10.1094/PDIS-91-12-1591>
- Chen S, Zhou Y, Chen Y, Gu J. 2018. Fastp: an ultra-fast all-in-one FASTQ preprocessor. *Bioinformatics* 34:i884–i890. <https://doi.org/10.1093/bioinformatics/bty560>
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>
- Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. *Bioinformatics* 29:1072–1075. <https://doi.org/10.1093/bioinformatics/btt086>
- Gabriel L, Bruna T, Hoff KJ, Ebel M, Lomsadze A, Borodovsky M, Stanke M. 2024. BRAKER3: fully automated genome annotation using RNA-seq and protein evidence with GeneMark-ETP, AUGUSTUS, and TSEBRA. *Genome Res* 34:769–777. <https://doi.org/10.1101/gr.278090.123>
- Manni M, Berkeley MR, Seppely M, Simão FA, Zdobnov EM. 2021. BUSCO update: novel and streamlined workflows along with broader and deeper phylogenetic coverage for scoring of eukaryotic, prokaryotic, and viral genomes. *Mol Biol Evol* 38:4647–4654. <https://doi.org/10.1093/molbev/msab199>