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The complete mitogenome of the Arctic moss *Aulacomnium turgidum* (Wahlenb.) Schwaegr

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ABSTRACT

The Arctic moss *Aulacomnium turgidum* (Wahlenb.) Schwaegr. is distributed widely above the Arctic Circle and can regenerate successfully after 400 years of ice entombment. Here, we report the complete mitogenome sequence of *A. turgidum* (103,937 bp). The genome contains 3 ribosomal RNAs, 24 transfer RNAs, and 40 protein-encoding genes. In a phylogenetic tree generated using the combined amino acid sequences of 32 mitochondrial genes from *A. turgidum*, 25 Bryophyta, and three Marchantiophyta, the phylogenetic position of *A. turgidum* (Rhizogoniales) is close to that of the Hypnales and Ptychomniales, forming a monophyletic clade with perfect supporting values.

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Svalbard, a Norwegian archipelago, has a typical Arctic environment. Meteorological records for the period 1993–2011 indicate that the annual mean surface air temperatures in this region vary between 2.5 and 5.8°C in summer and –11.4 and –9.4°C in winter (Maturilli et al. 2013). Despite the harsh temperatures, plants with a high tolerance of abiotic stresses, including bryophytes, are widely distributed in this region (Crawford et al. 1994; Liu et al. 2010). Of these, the moss *Aulacomnium turgidum* (Wahlenb.) Schwaegr. is widely distributed above the Arctic Circle, including Svalbard, Greenland, and Alaska (GBIF Secretariat 2017). Because *A. turgidum* can regenerate following 400 years of ice entombment, we postulated that it has very high freezing stress tolerance (La Farge et al. 2013). In this study, we analyzed the mitogenome of *A. turgidum* and conducted a molecular phylogenetic analysis of bryophytes.

Specimens of *A. turgidum* growing under natural conditions were collected near the Korean Dasan Arctic Station (78°55'27" N; 11°56'34" E) in Ny-Ålesund, Svalbard in August 2006. They were placed in plastic containers and transported to Korea, where they were cultivated on BCD solid medium (Ashton and Cove 1977) in a growth room at 25°C with continuous light. A dried specimen was deposited in the Korea Polar Research Institute (KOPRI) Herbarium (<https://kvh.kopri.re.kr>) under the number KOPRI-MO00899.

Total genomic DNA was extracted from 100 µg of a fresh sample of *A. turgidum* and used to prepare the library through TruSeq DNA Sample Prep Kit (Illumina, San Diego, CA). Paired-ends reads were sequenced using Illumina HiSeq2500 at 2 × 101 bp (Illumina, San Diego, CA) and

de novo assembled using CLC Genomics Workbench V7.5 (CLC Bio, Aarhus, Denmark) as described previously (Cho et al. 2019). All contigs were blasted to the *Physcomitrella patens* mitogenome (NC_007945), and contigs with highest identities were selected, joined via serial raw reads mapping processes. The assembled mitogenome sequences were annotated using GeSeq (Tillich et al. 2017) and manually curated with BLAST searches.

Mitogenome of *A. turgidum* (GenBank accession number: MN233806) has a total length of 103,937 bp (48× average coverage). Its GC ratio is 41.1%, similar to that of *P. patens* (40.6%) and it contains 3 ribosomal RNA, 24 transfer RNA, and 40 protein-coding genes. The mitochondrial structure and gene order are similar to those of other bryophytes.

Phylogenetic analyses of *A. turgidum* were performed using the amino acid sequences of 32 genes (8094 amino acids in length) from 28 mitogenomes of 25 Bryophyta and three Marchantiophyta, and were aligned using MAFFT ver. 7 (Katoh and Standley 2013). Maximum-likelihood (ML) and neighbor-joining (NJ) trees with 1000 bootstrap replicates were constructed in MEGA7 (Kumar et al. 2016). The phylogenetic position of *A. turgidum* (Rhizogoniales) was found to be close to those of Hypnales and Ptychomniales, and these species formed a monophyletic clade with perfect bootstrap support (Figure 1). To date, over 60 mitogenomes from Bryophyta have been reported, but this is the first report from the order Rhizogoniales. The *A. turgidum* mitogenome sequence will be useful for evolutionary studies of bryophytes, including Arctic species.

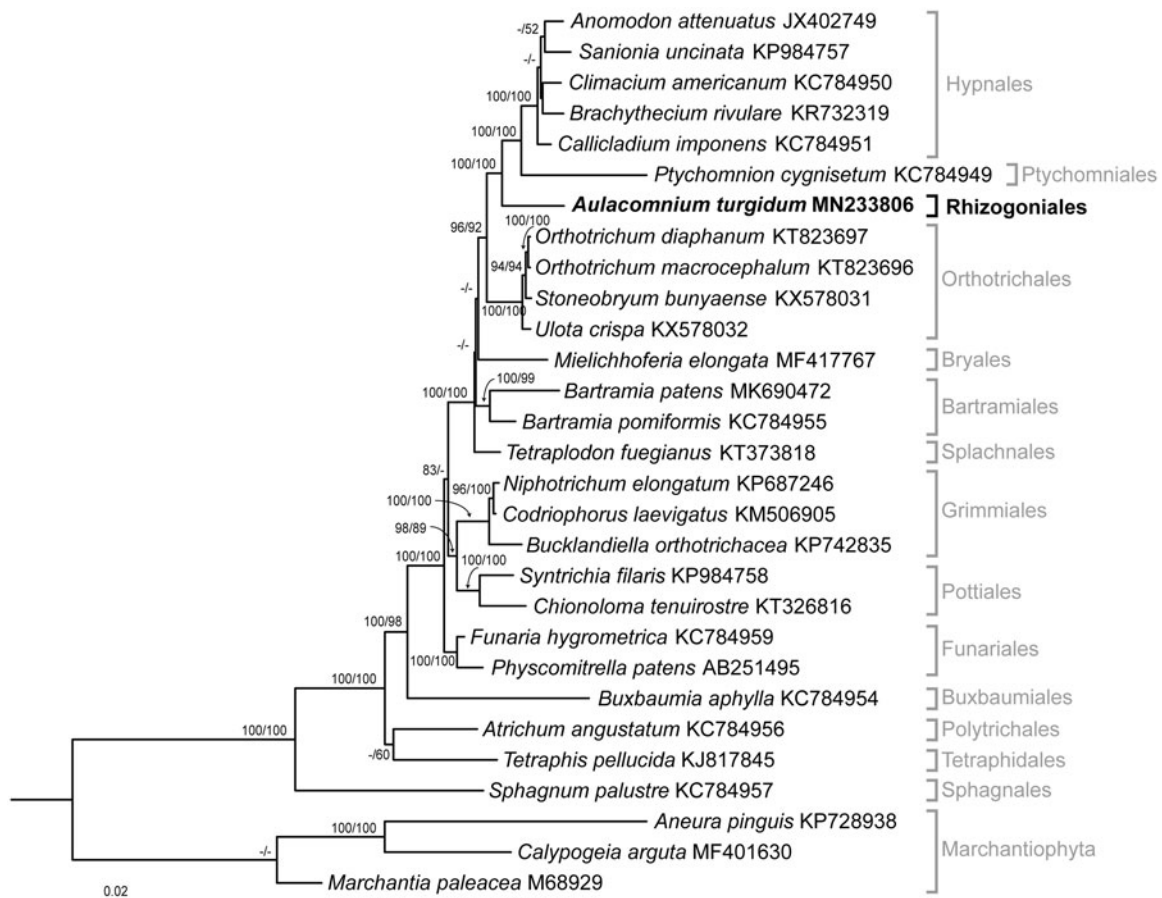


Figure 1. Maximum-likelihood (ML) tree inferred from the amino acid sequences of 32 mitochondrial genes with JTT + G + F parameters in MEGA7. ML and NJ trees were constructed using 1000 bootstrap replicates. Bootstrap values above 80 and 50 are shown on the branches of the ML and NJ trees, respectively.

Disclosure statement

The authors report no conflict of interest. The authors alone are responsible for the content and writing of the paper.

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