

MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of an Antarctic moss *Syntrichia filaris* (Müll.Hal.) R.H. Zander

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Abstract

The mitogenome of the *Syntrichia filaris* (GenBank accession number KP984758) has a total length of 106,343 bp and consists of 40 protein-coding genes, 3 ribosomal RNA (rRNA) and 24 transfer RNA. The mitochondrial structure and gene order was similar to other Bryophytes. Phylogenetic tree based on the combined analysis of amino acid sequences of 31 mitochondrial genes common in *S. filaris*, 17 Bryophyta and 3 Marchantiophyta, was well congruent with traditional species relationship of the moss order Pottiales.

Keywords

Antarctic moss, mitochondrial genome, *Syntrichia filaris*

History

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The *Syntrichia* Brid. is a cosmopolitan genus, containing about 80 species. It is well established in all continents, including Antarctic. *Syntrichia filaris* is an amphiatlantic subantarctic species and one of the largest species of the Pottiaceae in the Antarctic. The species is widely distributed in the South Orkney, South Georgia and South Shetland Islands in the Northern maritime Antarctic (Ochyra et al., 2008). Until now, 18 mitochondrial genomes from Bryophyta are reported (Liu et al., 2011, 2014; Sawicki et al., 2014), and here we report the mitogenome of *S. filaris* as genomic resource for studying Antarctic Bryophytes.

Moss samples were collected from a 3 × 3 cm patch of *S. filaris* from a population growing under natural conditions in vicinity of the Korean King Sejong Antarctic Station (62°14'29"S; 58°44'18"W), on the Barton Peninsula of King George Island in January 2014. The dry specimen was deposited into KOPRI Herbarium (<https://kvh.kopri.re.kr>) in Korea with the accession number KOPRI-MO00049.

Total genomic DNA was extracted from a 3 × 3 cm² patch of *S. filaris*. TruSeq DNA sample preparation kits were used and sequenced in one lane of Illumina MiSeq 2 × 300 bp (Illumina, San Diego, CA). The resulting reads were *de novo* assembled using CLC Genomics Workbench V7.5 (CLC bio, Aarhus, Denmark). All contigs were blasted to the *Physcomitrella patens* mitogenome (GenBank accession number: NC_007945), and PCR and Sanger sequencing methods were performed to verify contig ends or any ambiguous regions in the contig. The mitogenome annotation was performed with the CLC Genomics

Workbench program using extracted annotations from *P. patens* and then manually confirmed. Ribosomal RNA and exon-intron boundaries were further confirmed against orthologs from other species. Transfer RNA genes were verified using the tRNAscan-SE program (Lowe & Eddy, 1997).

Mitogenome of *S. filaris* (GenBank accession number: KP984758) has a total length of 106,343 bp (57 × average coverage). The mitogenome consists of 40 protein-coding genes, 3 ribosomal RNA (rRNA) and 24 transfer RNA. The mitochondrial structure and gene order were similar to other Bryophytes.

To construct a phylogenetic tree to show the position of *S. filaris* within Bryophytes, we aligned amino acids sequences of 31 mitochondrial genes of *S. filaris*, 17 Bryophyta and 3 Marchantiophyta species, which are publicly available. All downstream analyses were performed using the program MEGA6 (Tamura et al., 2013). Phylogenetic trees were constructed from the data sets using the Maximum Parsimony (MP) analysis based on the SPR algorithm, and the Maximum likelihood (ML) analysis based on the JTT matrix-based model. Supports for internal branches were tested using the bootstrap analyses of 1000 replications in both MP and ML analyses. Analysis of *S. filaris* dataset for the moss order Pottiales provides convincing support for many traditionally recognized genera and identifies higher level phylogenetic structure (Figure 1) (Cox et al., 2000; Liu et al., 2014; Magombo, 2003).

The information of the *S. filaris* mitogenome will be useful for evolutionary studies of the Bryophytes, including Antarctic species.

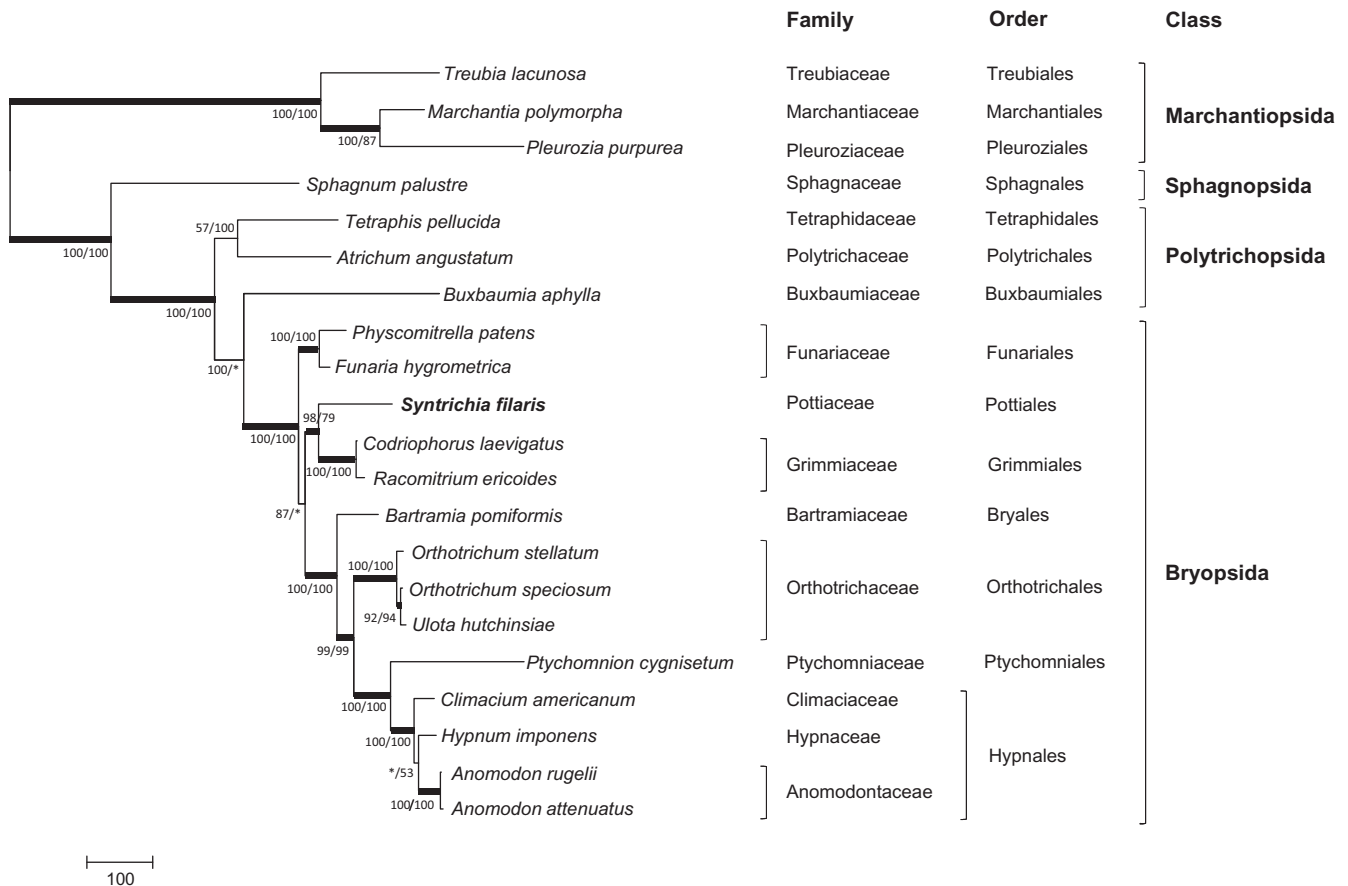


Figure 1. Phylogenetic position of *Syntrichia filaris* determined by Maximum Parsimony analysis based on combined analysis with amino acid sequences of 31 mitochondrial genes common in all taxa. The bootstrap values (>50) are presented near the corresponding branch (ML/MP). Branches that were supported by above 70% bootstrap values are indicated by bold lines. Sequences from Marchantiopsida were used as outgroup. GenBank accession numbers of mitogenomes used are *Anomodon attenuatus* (NC_021931), *Anomodon rugelii* (NC_016121), *Atrichum angustatum* (NC_024520), *Bartramia pomiformis* (NC_024519), *Buxbaumia aphylla* (NC_024518), *Climacium americanum* (NC_024515), *Codriophorus laevigatus* (NC_025931), *Funaria hygrometrica* (NC_024523), *Hypnum imponens* (NC_024516), *Marchantia polymorpha* (NC_001660), *Orthotrichum speciosum* (NC_026121), *Orthotrichum stellatum* (NC_024522), *Physcomitrella patens* (NC_007945), *Pleurozia purpurea* (NC_013444), *Ptychomnion cygnisetum* (NC_024514), *Racomitrium ericoides* (NC_026540), *Sphagnum palustre* (NC_024521), *Syntrichia filaris* (KP984758), *Tetraphis pellucida* (NC_024290), *Treubia lacunosa* (NC_016122), and *Ulota hutchinsiae* (NC_024517).

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This work was supported by Korea Polar Research Institute (PE15020 and PE15070).

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