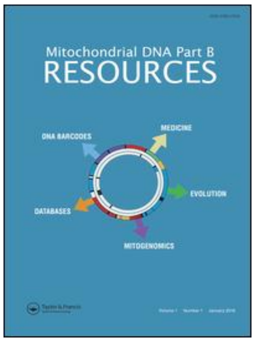

Mitochondrial DNA Part B
Resources

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MITOGENOME ANNOUNCEMENT

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

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ABSTRACT
Syntrichia filaris is one of the common mosses in the northern maritime Antarctic. In this study, we determined the complete chloroplast genome of *S. filaris* (GenBank accession number MK852705) to provide a genetic resource for phylogenetic study on Bryophytes. It is of 136,227 bp length, containing 8 ribosomal RNA (rRNA), 37 transfer RNA, and 85 protein-coding genes. The chloroplast genome structure and gene order were similar to other bryophytes. Phylogenetic tree based on combined amino acids sequences of 72 chloroplast genes common in *S. filaris*, 7 Bryophyta, 1 Anthocerotophyta, and 2 Marchantiophyta, was congruent with the traditional position of Pottiales in Bryophytes.

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Antarctic; Pottiales; chloroplast genome; *Syntrichia filaris*

The genus *Syntrichia* Bird. is cosmopolitan and its diversity is conspicuously high in the cool temperate and polar regions in the Southern Hemisphere. *Syntrichia filaris* is mostly common in the northern maritime Antarctic and one of the principal components of the moss hummock subformation predominantly developed in places with running water (Ochyra 1998; Ochyra et al. 2008). *Syntrichia filaris* is reddish or yellowish brown and frequently misidentified as *Hennediella* species in the wet habitats. Recently, the genomic resources of mitogenome and chloroplast genome from the Antarctic bryophyte specimens have been provided (Liu et al. 2014; Yoon et al. 2016; Byun et al. 2019). However, the genomic data of the Antarctic moss are still limited. In this study, we determined the complete chloroplast genome sequence of *S. filaris* to provide the genetic resources for better understanding of phylogenetic relationship between closely related genera within Pottiaceae which has been known to be one of the most taxonomically difficult families.

Moss samples were collected from a population growing under natural conditions near the King Sejong Antarctic Station (62°13′11.3″S; 58°45′88.4″W), on the Barton Peninsula of King George Island in January 2013. The dried specimen was deposited into KOPRI Herbarium (https://kvh.kopri.re.kr) in Korea (KOPRI-MO00565).

Total genomic DNA was extracted from a 1 cm^2 patch of *S. filaris* and used to prepare the library with TruSeq DNA Sample Prep Kit (Illumina, San Diego, CA). Paired-ends reads were sequenced using Illumina MiSeq 2 × 300 bp (Illumina) and *de novo* assembled using CLC Genomics Workbench V7.5 (CLC bio, Aarhus, Denmark). All contigs were blasted to the *Syntrichia ruralis* chloroplast genome (GenBank accession number NC_012052), and Sanger sequencing methods were performed to verify the results or any ambiguous regions in the contig. BLAST, GeSeq (Tillich et al. 2017), were used to align and annotate the chloroplast genome.

The complete chloroplast genome of *S. filaris* (GenBank accession number MK852705) has a total length of 136,227 bp (145× average coverage). Its GC ratio is 28.25%, similar to those of *S. ruralis* (28.34%) and *Physcomitrella patens* (28.51%), and it contains 8 ribosomal RNA (rRNA), 37 transfer RNA, and 85 protein-coding genes. The chloroplast genome structure and gene order were similar to other bryophytes.

To construct a phylogenetic tree to represent the position within Bryophytes, we compared amino acids sequences from 72 chloroplast genes of *S. filaris* with publicly available 7 Bryophyta, 1 Anthocerotophyta, and 2 Marchantiophyta. Alignment was conducted by MAFFT (Katoh and Standley 2013) and downstream analyses were performed using the program MEGA7 (Kumar et al. 2016). Phylogenetic tree was constructed from the datasets using the Maximum Likelihood method based on the JTT matrix-based model (Figure 1). The result provides convincing support for many traditionally recognized families and identifies higher level phylogenetic structure as in the previous reports with mitogenome analysis of *S. filaris* (Liu et al. 2014; Yoon et al. 2016).

The information of the *S. filaris* chloroplast genome will be useful for evolutionary studies with organelle genomes of the bryophytes, including Antarctic species.

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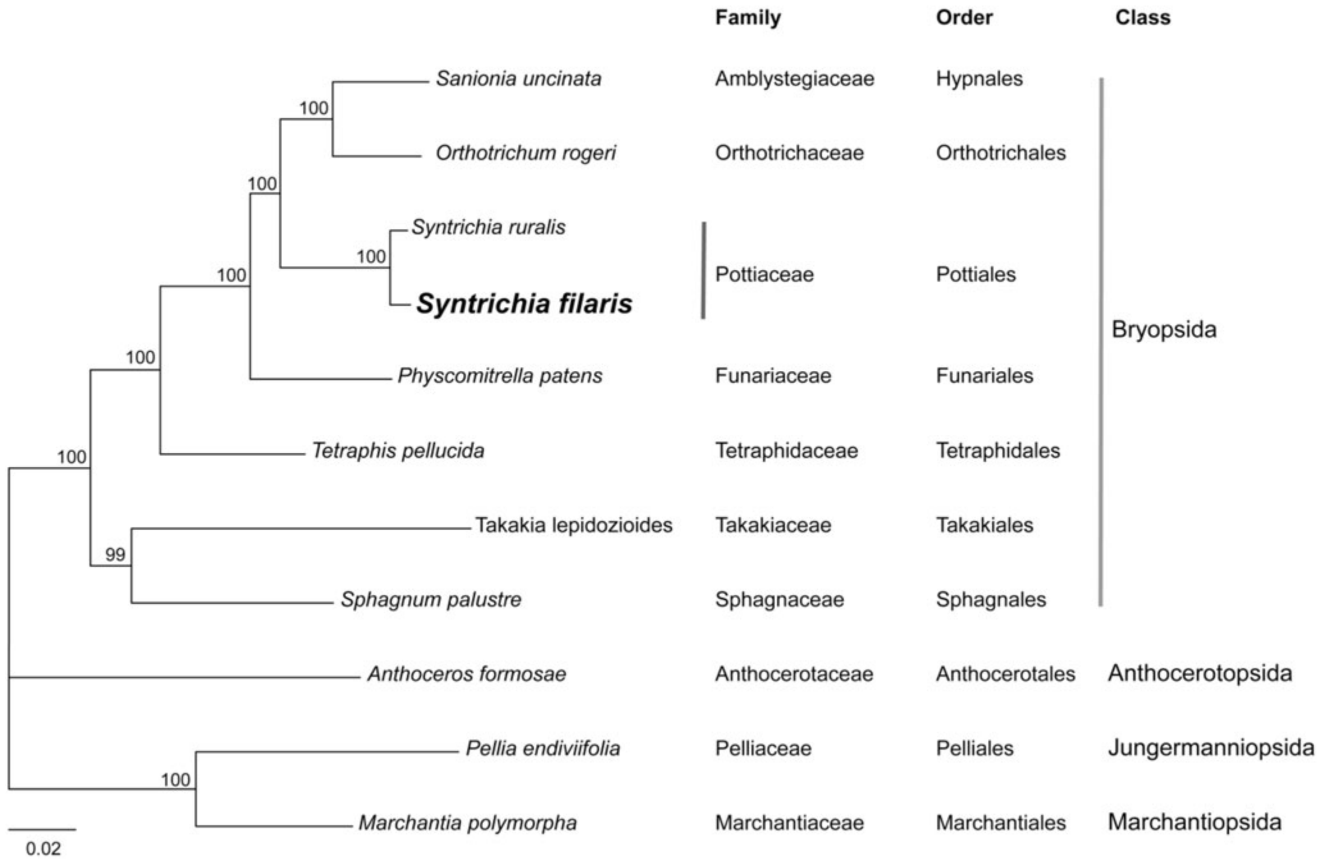

Figure 1. Phylogenetic position of *Syntrichia filaris* determined by using the maximum likelihood method based on combined analysis with amino acids sequences of 72 chloroplast genes common in all taxa. The bootstrap values of 1000 replicates are presented near the corresponding branch. Sequences from hornwort and liverworts were used as outgroup. GenBank accession number of chloroplast genomes used are *Anthoceros formosae* (NC_004543), *Marchantia polymorpha* (NC_037507), *Orthotrichum rogeri* (NC_026212), *Pellia endiviifolia* (NC_019628), *Physcomitrella patens* (NC_037465), *Sanionia uncinata* (NC_025668), *Sphagnum palustre* (NC_030198), *Syntrichia filaris* (MK852705), *Syntrichia ruralis* (NC_012052), *Takakia lepidozioides* (NC_028738), and *Tetraphis pellucida* (NC_024291).

Disclosure statement

No potential conflict of interest was reported by the authors.

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