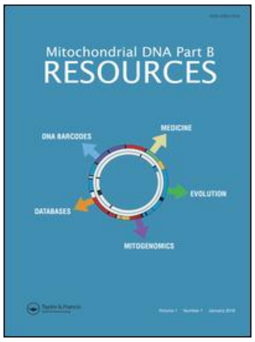

Mitochondrial DNA Part B
Resources

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MITOGENOME ANNOUNCEMENT

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The complete mitochondrial genome of an Antarctic moss *Chorisodontium aciphyllum* (Hook. f. & Wilson) Broth

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ABSTRACT

The cold-adapted species *Chorisodontium aciphyllum* is widespread in the maritime Antarctic. Here, we sequenced complete mitochondrial genome of *C. aciphyllum* (GenBank accession number: MK651511), and this is the first report on the mitogenome of the order Dicranales. Its length is 105,766 bp and it contains three ribosomal RNA (rRNA), 24 transfer RNA, and 40 protein-coding genes. The mitochondrial structure and gene order was similar to other bryophytes. Phylogenetic tree based on combined analysis with amino acids sequences of 36 mitochondrial genes in *C. aciphyllum*, 24 Bryophyta, and three Marchantiophyta showed conserved relationship of the bryophyte in accordance with evolutionary structure.

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Antarctic moss; Dicranales; mitochondrial genome; *Chorisodontium aciphyllum*

The *Chorisodontium* Broth. consists of two distinct morphological groups which have different geographical areas reflecting its ecological preferences. The austral group comprises six species and occurs in the south cool-temperate zone, while the neo-tropical group consists of three species (Ochyra et al. 2008). One of the austral cool-adapted species, *Chorisodontium aciphyllum*, is widespread in the northern maritime Antarctic and its regrowth was observed from a cold-based glacier after about 400 years of ice cover (Roads et al. 2014). Although several mitochondrial genomes from Bryophyta have been studied (Terasawa et al. 2007; Liu et al. 2014; Yoon et al. 2015), there is no report for the order of Dicranales. Here, we report the mitogenome of *C. aciphyllum* as genomic resources for studying Antarctic bryophytes.

Moss samples were collected from a population growing under natural conditions near the King Sejong Antarctic Station (62°13′S; 58°47′W), on the Barton Peninsula of King George Island in January 2014. The dried specimen was deposited into KOPRI Herbarium (https://kvh.kopri.re.kr) in Korea with the number KOPRI-MO00881.

Total genomic DNA was extracted from a $2 \times 2\,\text{cm}^2$ patch of *C. aciphyllum* and used to prepare the library through 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 *Physcomitrella patens* mitogenome (GenBank accession number: NC_007945), and PCR and Sanger sequencing methods were performed to verify the results or any ambiguous regions in the contig. Ribosomal RNA and exon-intron boundaries were further confirmed against orthologs from other species. Transfer RNA genes were verified using the tRNAscanSE program (Lowe and Eddy 1997).

Mitogenome of *C. aciphyllum* (GenBank accession number:MK651511) has a total length of 105,766 bp (86 X average coverage). Its GC ratio is 40.3%, similar to that of *P. patens* (40.6%) and it contains three ribosomal RNA (rRNA), 24 transfer RNA, and 40 protein-coding genes. The mitochondrial structure and gene order was similar to other bryophytes.

To construct a phylogenetic tree representing the position of *C. aciphyllum* within bryophytes, we compared amino acids sequences of 36 mitochondrial genes of *C. aciphyllum* with publicly available 24 Bryophyta and three Marchantiophyta. Alignment was conducted using 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 the Maximum likelihood (ML) analysis and evolutionary distances were computed based on the JTT matrix-based method. Supports for internal branches were tested using the bootstrap analyses of 1000 replications (Figure 1). Analysis of *C. aciphyllum* dataset for the moss order Dicranales provides convincing support for many traditionally recognized genera and identifies higher level phylogenetic structure (Liu et al. 2014).

The information of the *C. aciphyllum* mitogenome will be useful for evolutionary studies of the bryophytes, including Antarctic species.

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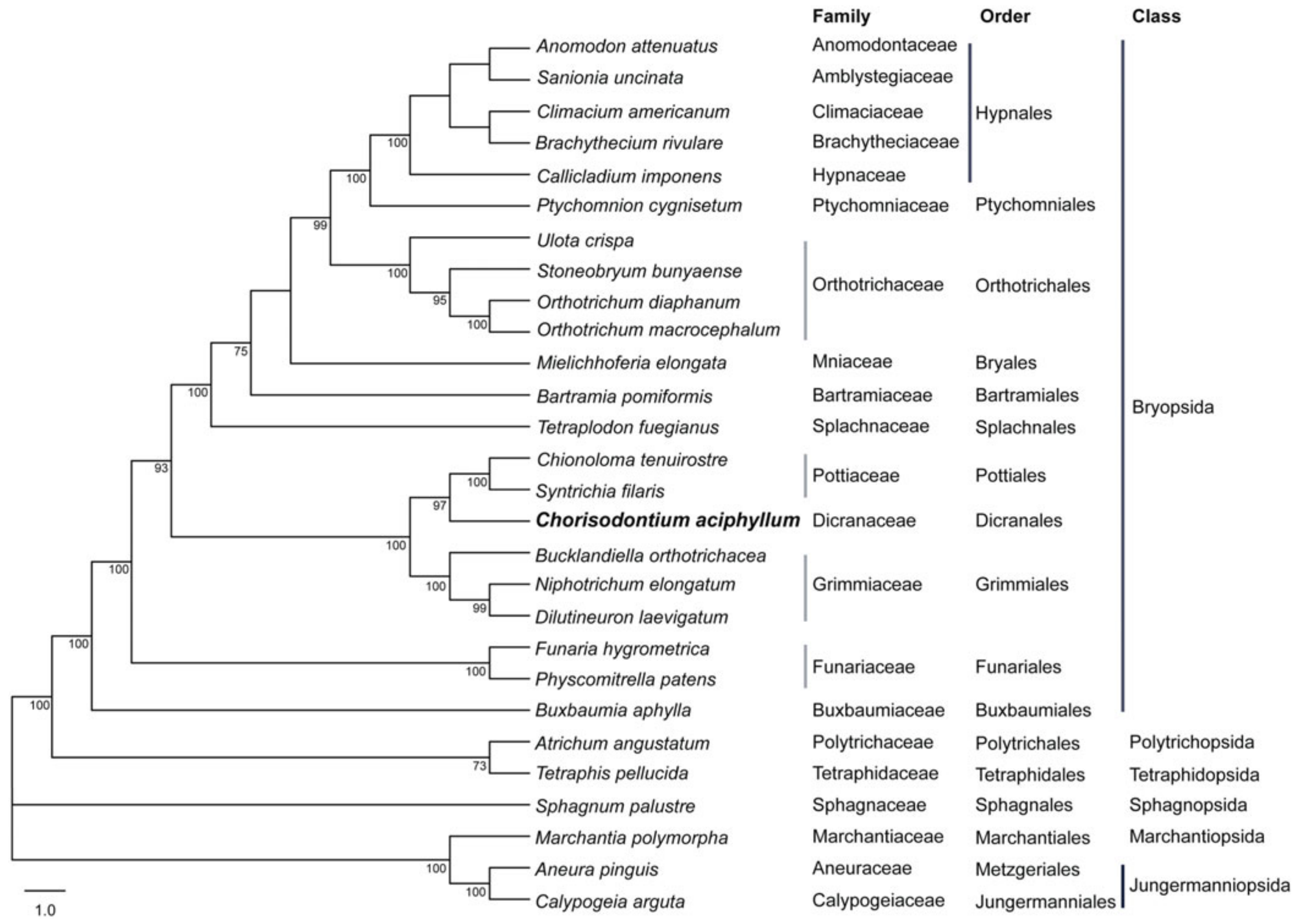

Figure 1. Phylogenetic position of *Chorisodontium aciphyllum* determined using the Maximum-Likelihood method based on combined analysis with amino acids sequences of 36 mitochondrial genes common in all taxa. The bootstrap values (>70) are presented near the corresponding branch. Sequences from liverworts were used as outgroup. GenBank accession number of mitogenomes used are *Aneura pinguis* (NC_026901), *Anomodon attenuatus* (NC_021931), *Atrichum angustatum* (NC_024520), *Bartramia pomiformis* (NC_024519), *Brachythecium rivulare* (NC_031212), *Bucklandiella orthotrichacea* (NC_026974), *Buxbaumia aphylla* (NC_024518), *Callicladium imponens* (NC_024516), *Calypogeia arguta* (NC_035978), *Climacium americanum* (NC_024515), *Codriophorus laevigatus* (NC_025931), *Funaria hygrometrica* (NC_024523), *Lewinskya speciosa* (NC_026121), *Marchantia polymorpha* (NC_037508), *Mielichhoferia elongata* (NC_036945), *Niphotrichum elongatum* (NC_026890), *Orthotrichum diaphanum* (NC_029356), *Orthotrichum macrocephalum* (NC_029355), *Physcomitrella patens* (NC_007945), *Ptychomnion cygnisetum* (NC_024514), *Sanionia uncinata* (NC_027974), *Sphagnum palustre* (NC_024521), *Stoneobryum bunyaense* (NC_031392), *Syntrichia filaris* (NC_027515), *Tetraphis pellucida* (NC_024290), *Tetraplodon fuegianus* (NC_028191), and *Ulota crispa* (NC_031393).

Disclosure statement

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

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