

## The complete mitochondrial genome of a moss Korea *Climacium dendroides* (Hedw.) F. Weber & D. Mohr

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### ABSTRACT

The complete mitochondrial genome of *Climacium dendroides* (GenBank accession number MN942036) was 104,860 base pairs in length, containing 40 protein-coding genes, 3 ribosomal RNA (rRNA), and 24 transfer RNA (tRNA). The base composition was 29.6% A, 29.4% T, 21.0% G, and 19.8% C and its G + C content was 41.0%. The mitochondrial structure and gene order was similar to other Bryophytes. Phylogenetic tree based on the combined analysis of 33 protein-coding genes was well congruent with traditional species relationship of the moss order Hypnales.

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Moss; *Climacium dendroides*; mitochondrial genome

*Climacium* is one of the small genus in Hypnales, but morphologically distinctive genus ('commonly known as Tree-moss') distributed mainly in the Northern Hemisphere and also in New Zealand (Shaw et al. 2012). This species is widely distributed in swamp areas such as wetlands, peatland edges, the edges of lakes and reservoirs flushes, and humus-rich wood in Korea. Until now, 19 mitochondrial genomes from Bryophyta are reported (Yoon et al. 2015), and here, we report the mitogenome of *C. dendroides* as genomic resource for studying Korea Bryophytes.

In this study, *C. dendroides* specimen for complete mitogenome sequencing was collected from a 5 × 5 cm patch from a population growing under natural conditions of Jilmoen wetland, Odasan (37°45'59.6N; 128°42'17.6E) on 5 July 2019. The specimen was deposited into JNU Herbarium in Korea with the accession number PSJ 20190705-1.

After performing quality control (QC), passed total genomic DNA which was extracted from *C. dendroides* is proceeded with the library construction. The sequencing library is prepared by random fragmentation of the DNA sample, followed by 5' and 3' adapter ligation. Adapter-ligated fragments are then PCR amplified and gel purified. Illumina SBS technology utilizes a proprietary reversible terminator-based method that detects single bases as they are incorporated into DNA template strands. Overall, reads' quality, total bases, total reads, GC (%), and basic statistics are calculated. Using quality filtered reads, de novo assembly is performed. A best k-mer is selected with various stats from assembly results (number of contigs, sum of contigs, N50, etc.) and a best-assembled sequence set is determined. After that, reads



belonging to contigs that match mtDNA using BLAST are assembled again. When the end of the contigs are overlapped, contigs are connected to form a circular contig using in-house script. After whole genome is assembled, the location of protein-coding sequences, tRNA genes, rRNA genes, and tmRNA genes are identified and their functions are annotated. Mitogenome of *C. dendroides* has a total length of 104,860 bp. It consists of 40 protein-coding genes, 3 rRNA, and 24 tRNA. The mitochondrial structure and gene order were similar to other Bryophytes.

To construct a phylogenetic tree to show the position of *C. dendroides* within Bryophytes, we aligned amino acids sequences of 33 mitochondrial genes of *C. dendroides*, 18 Bryophyta, and 3 Marchantiophyta species, which are publicly available. All downstream analyses were performed using the program MEGA 7 based on maximum likelihood analysis with JTT matrix-based model (Figure 1) (Kumar et al. 2016). Supports for internal branches were tested using the bootstrap analyses of 1000 replications in ML analyses. Analysis of *C. dendroides* dataset for the moss order, Hypnales provides convincing support for many traditionally recognized genera and identifies higher-level phylogenetic structure (Figure 1) (Cox et al. 2000; Magombo 2003; Liu et al. 2014).

The information of the *C. dendroides* mitogenome will be valuable for evolutionary studies of the Bryophytes, such as systematic Korean species.

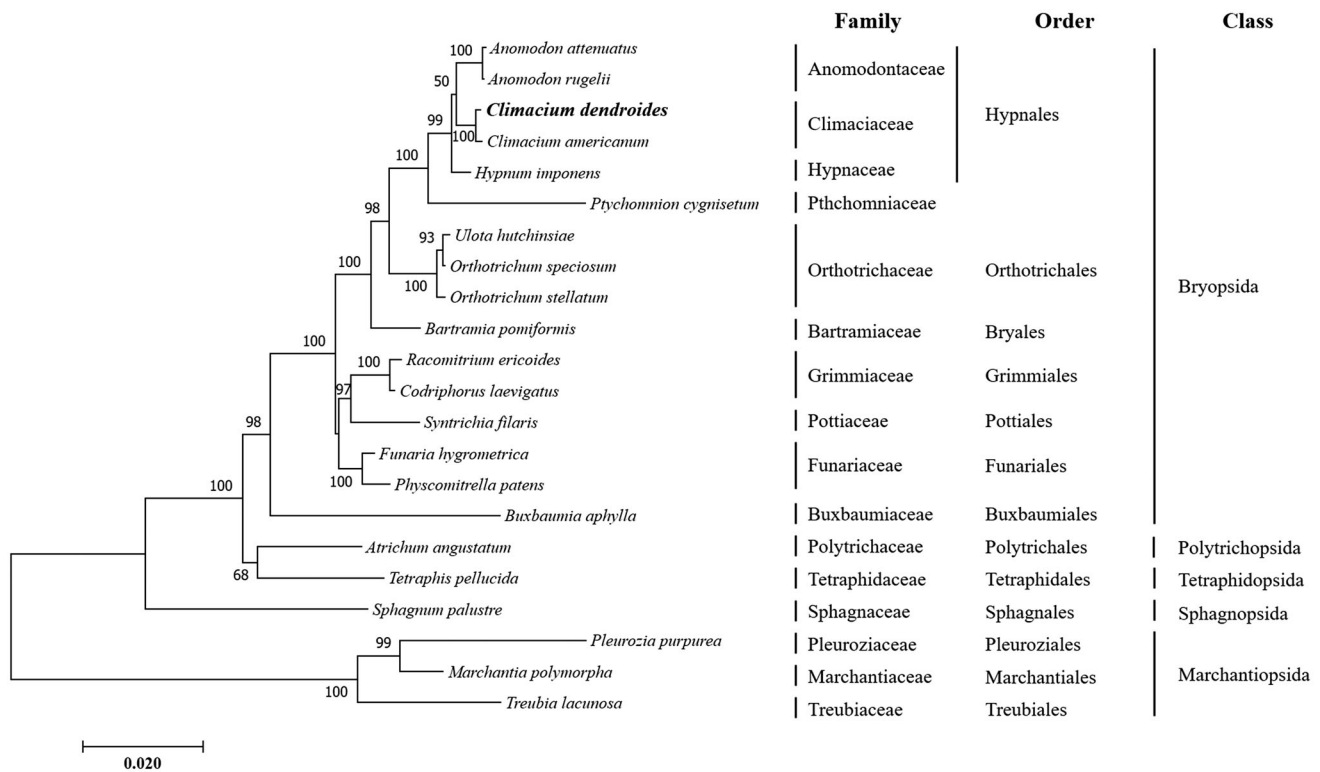
### Disclosure statement

No potential conflict of interest was reported by the authors.

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**Figure 1.** Phylogenetic position of *Climacium dendroides* determined by maximum likelihood analysis based on 33 protein coding genes common in all taxa. A bootstrap values above 50% are indicated at each node. 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).

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