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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of *Douinia plicata* (Lindb.) Konstant. et. Vilnet (Scapaniaceae, Jungermanniales)

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ABSTRACT

Douinia plicata (Lindb.) Konstant. & Vilnet is the endemic species in Northeast Asia. Here, we reported complete mitochondrial genome of *D. plicata*. It is 144,206 bp long and includes 72 genes (42 protein-coding genes, three rRNAs, and 27 tRNAs). The overall GC content is 45.1%. Intergeneic variations against *S. amplicata*, which is slightly higher than intraspecific variations of *S. ampliata* and *W. denudata*. Phylogenetic trees show *D. plicatum* is clustered with three *Scapania* mitochondrial genomes with high supportive values, which is congruent with previous studies.

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Douinia plicata; mitochondrial genome; Scapaniaceae; Jungermanniales; Korea

Douinia plicata (Lindb.) Konstant. & Vilnet was described from the Sakhalin in Russian Far East by Lindb. as *Diplophyllum plicatum* (Lindberg 1872). Since then, according to the results of researchers (Evans 1900; Persson 1949; Potemkin 1999), this species was transferred to *Diplophylleia* (Rchb.) Trevis., *Macrodiplophyllum* (H.Buch) Perss., and *Scapania* (Dumort.) Dumort. Recent molecular phylogenetic studies of family Scapaniaceae show that this species is of the genus *Douinia* (Vilnet et al. 2010; Heinrichs et al. 2012; Söderström et al. 2016; Bakalin et al. 2019). Whole organelle genome sequences will provide better resolution for uncovering phylogenetic relationship by providing more informative sequence variations (Kim et al. 2019; Park, Choi, et al. 2019; Choi, Kwon, et al. 2020; Choi, Min, et al. 2020; Park et al. 2020). We completed mitochondrial genome sequence of *D. plicata* for understanding its phylogenetic position.

The plants of *D. plicata* collected in Taebaek city, Korea (Voucher in Jeonbuk National University Herbarium (JNU); Contact: Seung Se Choi, hepaticae@nie.re.kr; 5 October 2019, S.S. Choi, CS-1910996b; 37.101486N, 128.917547E) was used for extracting DNA with DNeasy Plant Mini Kit (QIAGEN, Hilden, Germany). Paired-end sequencing library was constructed using Illumina TruSeq Nano DNA Library Preparation Kit (Illumina, San Diego, CA) following manufacturer's recommendations with around 350-bp DNA fragments. 2.44-Gbp raw sequences obtained using NovaSeq6000 at Macrogen Inc., Korea was filtered by Trimmomatic v0.33 (Bolger et al. 2014) . Mitochondrial genome was completed by Velvet v1.2.10 (Zerbino and Birney 2008), SOAPGapCloser v1.12 (Zhao et al. 2011), BWA v0.7.17 (Li 2013), and SAMtools v1.9 (Li et al. 2009) under the environment of Genome Information System (GelS; http://geis.infoboss.co.kr/; Park et al., in preparation). Geneious R11 version v11.0.5 (Biomatters Ltd, Auckland, New Zealand) was used for annotation based on *Scapania ampliata* mitochondrial genome (MT755612; doi:10.1080/23802359.2021.1882892).

The mitochondrial genome of *D. plicata* (GenBank accession is MW091500) is 144,205 bp long (GC ratio is 45.1%). It contained 72 genes (42 protein-coding genes, three rRNAs, and 27 tRNAs). Gene order of *D. plicata* mitochondrial genome is identical to those of *Scapania ciliata* and *S. ampliata*. 1,129 SNPs (0.783%) and 175 INDELs (coverage is 3257 bp; 2.25%) were found against *S. ampliata* mitochondrial genome: number of intergenic SNPs is significantly larger than those of intraspecific SNPs identified from *Marchantia polymopha* subsp, *ruderalis* (7 SNPs; 0.0038%; Kwon et al. 2019b), *Dumortiera hirsuta* (12 SNPs; 0.0067%; Kwon et al. 2019a; Dong et al. 2019), and *Wiesnerella denudata* (149 SNPs; 0.80%; Choi, Min, et al. 2020); while coverage of 175 intergeneric INDELs (3,257 bp; 2.25%) is also little higher than those of interspecific INDELs of *S. ampliata* (2,242 bp; 1.56%; doi:10.1080/23802359.2021.1882892) and intraspecific INDELs of *Wiesnerella denudata* (3,033 bp; 1.62%; Choi, Min, et al. 2020). Meanwhile, it is higher than those of angiosperm species, *Liriodendron tulipifera* (2,117 bp; 0.38%; Park, Kim, et al. 2019) and *Arabidopsis thaliana* (1,088 bp; 0.30%; Park et al., in preparation). The slightly larger numbers of intergenic variations than those of intraspecific variations reflect the distance between *Douinia* and *Scapania* close enough.

Twenty-four complete mitochondrial genomes belonging to order Jungermanniales including *D. plicata* were used for constructing neighbor-joining (bootstrap repeat is 10,000),

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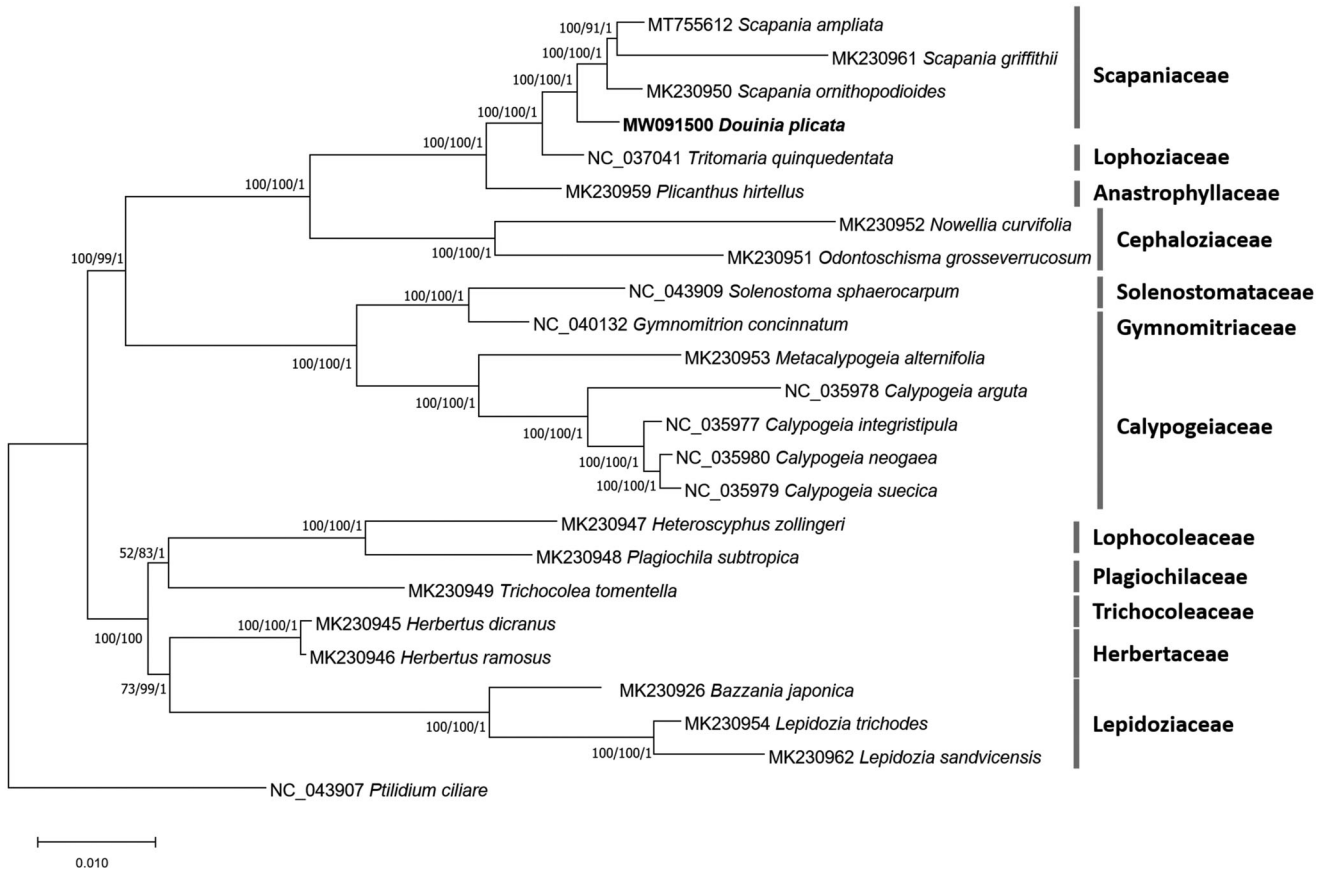

Figure 1. Neighbor-joining (bootstrap repeat is 10,000), maximum-likelihood (bootstrap repeat is 1,000), and Bayesian inference phylogenetic trees of 24 complete mitochondrial genomes. Grey-filled start indicates the clade displaying low supportive values. Phylogenetic tree was drawn based on the maximum-likelihood phylogenetic tree. The numbers above branches indicate support values of maximum-likelihood, neighbor-joining, and Bayesian inference phylogenetic trees, respectively.

maximum-likelihood (bootstrap repeat is 1,000), and Bayesian inference phylogenic trees using MEGA X (Kumar et al. 2018) and MrBayes v3.2.7a (Ronquist et al. 2012) after aligning whole mitochondrial genome sequences using MAFFT v7.450 (Katoh and Standley 2013). Phylogenetic trees show that *D. plicata* is clustered with three *Scapania* mitogenomes belonging to the same family, Scapaniaceae, with high supportive values (Figure 1). It is congruent with previous phylogenetic study (Heinrichs et al. 2012). In the phylogenetic trees, most of the nodes display high supportive values of three trees, indicating that these complete mitochondrial genomes can be used for understanding their phylogenetic relationship well, not like the previous studies which presented incongruent or low supportive values in phylogenetic trees (Kwon, Min, et al. 2019; Choi, Kwon, et al. 2020; Min et al. 2020).

Disclosure statement

The authors declare that they have no competing interests.

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Data availability statement

Mitochondrial genome sequence can be accessed *via* accession number MW091500 in GenBank of NCBI at https://www.ncbi.nlm.nih.gov. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA668541, SAMN16414907, and SRR12807217, respectively.

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