The complete chloroplast genome of *Epimedium davidii* Franch. (Berberidaceae)

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**ABSTRACT**

*Epimedium davidii*, which belongs to Berberidaceae, is mainly distributed in the southwest of China. In this study, the complete chloroplast genome of *E. davidii* was sequenced and assembled. The circular genome is 159,715 bp in length, which comprises a large single-copy region (LSC, 85,862 bp), a small single-copy region (SSC, 17,081 bp), and a pair of inverted repeat regions (IRa and IRb, 28,386 bp). The chloroplast genome of *E. davidii* contains 112 unique genes, of which 78 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. Phylogenetic analysis indicated that *E. davidii* was closely related to *Epimedium acuminatum*.

The sequencing was performed on an Illumina Novaseq PE150 platform (Illumina Inc., San Diego), and 150 bp paired-end reads were generated. The filtered reads were assembled into the complete chloroplast genome using the program GetOrganelle version1.5 (Jin et al. 2018) with *E. acuminatum* chloroplast genome (GenBank accession number: NC_029941) as a reference. The annotation of the chloroplast genome was conducted through the online program CPGAVAS 2 (Shi et al. 2019), followed by manual correction if required. The annotated genomic sequence has been registered in GenBank with an accession number (MN621353).

The chloroplast genome of *E. davidii* is 159,715 bp in length, which consists of a large single-copy region (LSC, 85,862 bp), a small single-copy region (SSC, 17,081 bp), and a pair of inverted repeat regions (IRa and IRb, 28,386 bp). The total GC content of *E. davidii* chloroplast genome is 38.81%, while the corresponding GC content of LSC, SSC, and IR regions is 37.34%, 32.79%, and 42.85%, respectively. The chloroplast genome of *E. davidii* contains 112 unique genes, including 78 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. Intron-exon structure analysis indicated that nine protein-coding genes and five tRNA genes contained one intron, while three genes (ycf3, clpP, and rps12) had two introns. Eight protein-coding genes (i.e. rpl2, rpl22, rpl23, rps7, rps12, rps19, ndhB, and ycf2), seven tRNA genes (i.e. trnL-CAU, trnL-CAA, trnV-GAC, trnL-GAU, trnA-UGC, trnR-ACG, and trnN-GGU), and four rRNA genes (i.e. rrn4.5S, rrn5S, rrn16S, and rrn23S) are duplicated in the IR regions. Besides, one tRNA gene (trnQ-UUG) is duplicated in the LSC regions.

To identify the phylogenetic relationship of *E. davidii*, 17 complete chloroplast genomes of Berberidaceae species were used to reconstruct a maximum-likelihood (ML) phylogenetic tree.
tree using RAxML version 8.2.10 (Stamatakis 2014), with *Aconitum contortum* as the outgroup (Figure 1). Phylogenetic analysis indicated that *E. davidii* is closely related to *E. acuminatum*. The complete chloroplast genome of *E. davidii* provides useful perspectives into the evolutionary patterns in Berberidaceae family.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**References**

Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochem Bull. 19:11–15.

Guo M, Xu Y, Ren L, He S, Pang X. 2018. A systematic study on DNA barcoding of medicinally important genus *Epimedium* L. (Berberidaceae). Genes. 9(12):637.

Jin JJ, Yu WB, Yang JB, Song Y, Yi TS, Li DZ. 2018. GetOrganelle: a simple and fast pipeline for de novo assembly of a complete circular chloroplast genome using genome skimming data. bioRxiv. 256479.

Li X, Yang Y, Henry RJ, Rossetto M, Wang Y, Chen S. 2015. Plant DNA barcoding: from gene to genome. Biol Rev. 90(1):157–166.

Liu X, Yang Q, Zhang C, Shen G, Guo B. 2019. The complete chloroplast genome of *Epimedium sagittatum* (Sieb. Et Zucc.) Maxim. (Berberidaceae), a traditional Chinese herb. Mitochondrial DNA Part B. 4(2):2572–2573.

Ma H, He X, Yang Y, Li M, Hao D, Jia Z. 2011. The genus *Epimedium*: an ethnopharmacological and phytochemical review. J Ethnopharmacol. 134(3):519–541.

Nguyen PAT, Kim JS, Kim JH. 2015. The complete chloroplast genome of colchicine plants (*Colchicum autumnale* L. and *Gloriosa superba* L.) and its application for identifying the genus. Planta. 242(1):223–237.

Shi L, Chen H, Jiang M, Wang L, Wu X, Huang L, Liu C. 2019. CPGAVAS2, an integrated plastome sequence annotator and analyser. Nucleic Acids Res. 47:65–73.

Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 30(9):1312–1313.

Yang Q, Pan J, Shen G, Guo B. 2019. Yellow light promotes the growth and accumulation of bioactive flavonoids in *Epimedium pseudowushanense*. J Photochem Photobiol B. 97:111550.

Zhang Y, Du L, Liu A, Chen J, Wu L, Hu W, Zhang W, Kim K, Lee SC, Yang TJ, et al. 2016. The complete chloroplast genome sequences of five *Epimedium* species: lights into phylogenetic and taxonomic analyses. Front Plant Sci. 7:306.