The complete chloroplast genome of *Epimedium platypetalum* K. Mey. (Berberidaceae), a rare plant species from China

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**ABSTRACT**

*Epimedium* L. is an important medicinal herbaceous genus in the family Berberidaceae. *Epimedium platypetalum* K. Mey. is a plant species only narrowly distributed in the western part of China. Here, the complete chloroplast genome of *Epimedium platypetalum* was assembled. The chloroplast genome of *E. platypetalum* was 159,088 bp in length, with a total GC content of 38.79%. A total of 112 unique genes were identified, among which 78 are protein-coding genes, 30 tRNA genes, and four rRNA genes. Phylogenetic results revealed that *E. platypetalum* formed a sister relationship with *E. membranaceum* K. Mey. Our findings provided valuable data for future research on phylogenetic relationship and germplasm exploration within the genus *Epimedium*.

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Since the classification of *E. platypetalum* from these two regions has remained debatable all along, it is necessary to report the chloroplast genome of *E. platypetalum* collected from the type locality (Wenchuan County, Sichuan province, China) to clarify the phylogenetic position of these two eco-types of *E. platypetalum*.

In this study, *E. platypetalum* was sampled from Wenchuan County of Sichuan province, China (latitude 31.3614 and longitude 103.4971). The specimen and extracted DNA were deposited at Medicinal Plants Authentication Center, Institute of Medicinal Plant Development, Chinese Academy of Medical Science (http://www.implad.ac.cn/, collected by Xiang Liu, zysliux@163.com) under the voucher number Liu18038. The genomic DNA was extracted from the fresh leaves of *E. platypetalum* with the modified CTAB method (Doyle and Doyle 1987), and was then used to generate libraries with an average insert size of 300 bp using the VAHTSTM Universal DNA Library Pren Kit (ExCell Bio. Biological Technology Co., Ltd., Shanghai, China). Genome sequencing was performed with the Illumina Novaseq 6000 platform (Illumina Inc., San Diego, CA), and 150 bp paired-end reads were generated. The assembly of chloroplast genome was conducted using the GetOrganelle v1.5 program (Jin et al. 2018) with *E. acuminatum* (GenBank accession number: NC_029941) as reference. The annotation of chloroplast genome was conducted through the online program CPGAVAS2 (Shi et al. 2019) and assisted with manual correction and the annotated genomic sequence was deposited into GenBank with an accession number (MW483078).

The complete chloroplast genome of *E. platypetalum* (MW483078) was 159,088 bp in length, which was 136 bp shorter than the *E. platypetalum* from Shanxi (MT560421), including two inverted repeat regions (IR\_A and IR\_B, 27,718 bp) separated by a large single copy region (LSC, 86,581 bp) and a small single copy region (SSC, 17,071 bp). The total GC content was 38.79%, with IR regions (43.02%) higher than that in LSC (37.29%) and SSC regions (32.76%). A total of 112 unique genes were identified from the chloroplast genome of *E. platypetalum*, including 78 protein-coding genes, 30 tRNA genes, and four rRNA genes. The intron–exon structure analysis indicated that a total of 18 genes have introns, among which *petB*, *petD*, *rpl16*, *rpl2*, *rpoC1*, *rps16*, *trnA-UGC*, *trnG-UCC*, *trnI-GAU*, *trnK-UUU*, *trnL-UAA*, *trnV-UAC*, *atpF*, *ndhA*, and *ndhB* had one intron, whereas *ycf3*, *rps12*, and *clpP* contained two introns.

For determination of phylogenetic position of *E. platypetalum* from Sichuan (MW483078), phylogenetic analysis was conducted using the complete chloroplast genome sequences of *E. platypetalum* from Shanxi (MT560421) and other 10 species from the NCBI GenBank database. MAFFT v7 (Katoh et al. 2019) was applied to generate sequence alignment. Especially, sequence alignment of the two *E. platypetalum* chloroplast genomes revealed 239 variable sites, among which 66 were detected in CDS regions. The maximum-likelihood (ML) tree was constructed using the RaxmlGUI v1.5b2 program (Silvestro and Michalak 2012) with 1000 bootstrap replicates. The Bayesian inference (BI) tree was constructed with MrBayes 3.2.7 (Ronquist and Huelsenbeck 2003). The Markov chain Monte Carlo (MCMC) algorithm was run for 1,000,000 generations, with one tree sampled every 1000 generation still convergence (the average standard deviation of split frequencies <0.01). The first 20% of trees were discarded as burn-in, and the remaining trees were used to build a 50% majority-rule consensus tree. *Vancouveria hexandra* (Hook.) C. Morren & Decne was selected as the outgroup (Figure 1). As a result, the ML and BI phylogenetic tree
displayed identical topologies. In particular, after the node defining a clade of *Epimedium membranaceum* K. Mey., *Epimedium stellulatum* Stearn and *E. platypetalum* from Sichuan (MW483078) was sister to *E. membranaceum* K. Mey., and the *E. platypetalum* from Shanxi (MT560421) formed a sister relationship with *E. stellulatum*, indicating the difference between the *E. platypetalum* plants from the two distribution regions. Therefore, our study provided valuable information for the understanding of *E. platypetalum* and future phylogenetic and evolutionary studies of *Epimedium* genus.

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**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/ under the accession no. MW483078. The associated numbers are PRJNA749730, SRR15254402, and SAMN20398933, respectively.

**References**

De Smet Y, Goetghebeur P, Wanke S, Asselman P, Samain MS. 2012. Additional evidence for recent divergence of Chinese *Epimedium* (Berberidaceae) derived from AFLP, chloroplast and nuclear data supplemented with characterisation of leaflet pubescence. Plant Ecol Evol. 145(1):73–87.

Doye JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochem Bull. 19(1):11–15.

Fan C, Quan Q. 2012. Research advances in the pharmacological effects of Herba Epimedi. J Anhui Agric Sci. 40(17):9264–9266.

Guo M, Pang X, Xu Y, Jiang W, Liao B, Yu J, Chen, S. 2021. Plastid genome data provide new insights into the phylogenoy and evolution of the genus Epimedium. J Adv Res.

He S. 2014. The genus *Epimedium* of China in color. Guiyang: Guizhou Science and Technology Press; p. 61–63.

Jin J, Yu W, Yang J, Song Y, Yi T, Li D. 2018. GetOrganelle: a simple and fast pipeline for de novo assembly of a complete circular chloroplast genome using genome skimming data. BioRxiv. 4:256479.

Katoh K, Rozewicki J, Yamada KD. 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinform. 20(4):1160–1166.

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

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.

Meyer K. 1922. Berberidaceae. Repertorium Specierum Novarum Regni Vegetabilis. Centralblatt für Sammlung und Veröffentlichung von Einzeldiagnosen neuer Pflanzen. Beih. 12:379–380.

Nock CJ, Waters DL, Edwards MA, Bowen SG, Rice N, Cordeiro GM, Henry RJ. 2011. Chloroplast genome sequences from total DNA for plant identification. Plant Biotechnol J. 9(3):328–333.

Ogisu M. 1996. *Epimedium campanulatum* (Berberidaceae) a new Chinese spursless species from Sichuan. Kew Bull. 51(2):401–404.

Ronquist F, Huelsenbeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics. 19(12):1572–1574.

Shi L, Chen H, Jiang M, Wang L, Wu X, Huang L, Liu C. 2019. CPGAVAS2, an integrated plastome sequence annotator and analyzer. Nucleic Acids Res. 47(W1):W65–W73.

Silvestro D, Michalak I. 2012. raxmlGUI: a graphical front-end for RAxML. Org Divers Evol. 12(4):335–337.

Stearn WT. 2002. The genus *Epimedium* and other herbaceous Berberidaceae. Portland (OR): Timber Press; p. 51–52.

Stearn WT. 1938. *Epimedium* and *Vancouveria* (Berberidaceae), a monograph. J Linn Soc Lond Bot. 51(340):409–535.

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. 197:111550.

Ying T. 2002. Petal evolution and distribution patterns of *Epimedium* L. (Berberidaceae). Acta Phytotaxon Sin. 40(6):481–489.

Zhang Y, Li D. 2011. Advances in phylogenomics based on complete chloroplast genomes. Plant Divers Resour. 33(4):365–375.