

The complete chloroplast genome of *Epimedium elachyphyllum* Stearn (Berberidaceae), an endangered species endemic to China

Fengmei Suo^{a*}, Xiang Liu^{a,b*}, Cheng Zhang^a, Chaoqun Xu^a, Guoan Sheng^a and Baolin Guo^a

^aInstitute of Medicinal Plant Development, Chinese Academy of Medical Science, Peking Union Medical College, Beijing, People's Republic of China; ^bChongqing Academy of Chinese Materia Medica, Chongqing, People's Republic of China

ABSTRACT

Epimedium elachyphyllum, which belongs to Berberidaceae, is only distributed in Guizhou province of China. In this study, the complete chloroplast (cp) genome of *E. elachyphyllum* was sequenced and assembled. The circular genome is 157,201 bp in length, which comprises of a large single-copy region (LSC, 88,519 bp), a small single-copy region (SSC, 17,042 bp), and a pair of inverted repeat regions (IRa and IRb, 25,820 bp). The genome of *E. elachyphyllum* contains 112 unique genes, of which 78 protein-coding genes, 30 tRNA genes, and four rRNA genes. Phylogenetic analysis based on 18 complete cp genome sequences indicated that *E. elachyphyllum* was closely related to *E. dolichostemon*.

ARTICLE HISTORY

Received 14 January 2020
Accepted 19 January 2020

KEYWORDS

Chloroplast genome;
Epimedium elachyphyllum
Stearn; Berberidaceae

Epimedium elachyphyllum, an endangered species endemic to China, is only distributed in a small area in the Guizhou province of China. Due to habitat loss, *E. elachyphyllum* has been classified as endangered in "China Species Red List" (Ministry of Environment Protection of the People's Republic of China 2013). *Epimedium* L. family contains about 60 species intermittently distributed in the Eurasia between Europe and eastern Asia. (Xu et al. 2019). The major bioactive components are flavonoid glycosides in *Epimedium Folium* (Wang et al. 2007; Ma et al. 2011). The therapeutic effects of *E. elachyphyllum* was the same as *E. sagittatum* (sieb. Et zucc.) Maxim (He and Zhang 1994). Previous studies showed that the classification and phylogeny were not completely clear in the *Epimedium* family (Guo et al. 2018). It was reported that the chloroplast genome has a highly conserved sequence ranging approximately 150k bp, which proves more variation information to discriminate closely related plants (Li et al. 2015). Up to now, the complete chloroplast (cp) genome of five *Epimedium* species have been reported (Zhang et al. 2016; Liu et al. 2019). So far, no data are available regarding the chloroplast genome of *E. elachyphyllum*. In this study, we assembled and characterized the complete chloroplast (cp) genome of *E. elachyphyllum* for the first time. The complete chloroplast (cp) genome sequence of *E. elachyphyllum* is a valuable resource for further studies, including species identification and genetic evolution in the family Berberidaceae.

In this study, *E. elachyphyllum* sample was collected from the Songtao County of Guizhou province in China (28°26'N, 108°42'E). A voucher specimen (Zhang218) was deposited at the Herbarium of the Institute of Medicinal Plant (IMPLAD), Beijing, China. Total genomic DNA was extracted from the

fresh leaves of *E. elachyphyllum* using the modified CTAB method (Doyle and Doyle 1987). The high-quality DNA was sheared to the size of 300 bp for the shotgun library construction. The sequencing was performed on an Illumina Novaseq PE150 platform (Illumina Inc, San Diego, CA), and 150 bp paired-end reads were generated. The filtered reads were assembled into the complete chloroplast (cp) genome using the program GetOrganelle v1.5 (Jin et al. 2018) with *E. acuminatum* chloroplast genome (GenBank accession number: NC_029941) as a reference. The annotation of 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 (MN873562).

The complete chloroplast (cp) genome of *E. elachyphyllum* is 157,201 bp in length and shows a typical quadripartite structure, which consists of a large single-copy region (LSC, 88,519 bp), a small single-copy region (SSC, 17,042 bp), and a pair of inverted repeat regions (IRa and IRb, 25,820 bp). The genome of *E. elachyphyllum* contains 112 unique genes, of which 78 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. The total GC content of *E. elachyphyllum* chloroplast genome is 38.77%, while the corresponding GC content of LSC, SSC, IR regions are 37.36%, 32.78%, and 43.16%, respectively. The intron-exon structure analysis indicated that eleven protein-coding genes and seven tRNA genes contained one intron, while four genes (*ycf3*, *clpP* and *rps12*) had two introns.

To identify the phylogenetic relationship of *E. elachyphyllum*, 15 complete chloroplast (cp) genomes of Berberidaceae species were used to reconstruct a maximum-likelihood (ML) phylogenetic tree using RAxML v8.2.10 (Stamatakis 2014), with *Aconitum*

CONTACT Baolin Guo  blguo@implad.ac.cn; Guoan Shen  gashen@implad.ac.cn  Institute of Medicinal Plant Development, Chinese Academy of Medical Sciences, Peking Union Medical College, No.151 MaLianWa North Road, Haidian District, Beijing, 100193, China

*These authors contributed equally to the work.

© 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

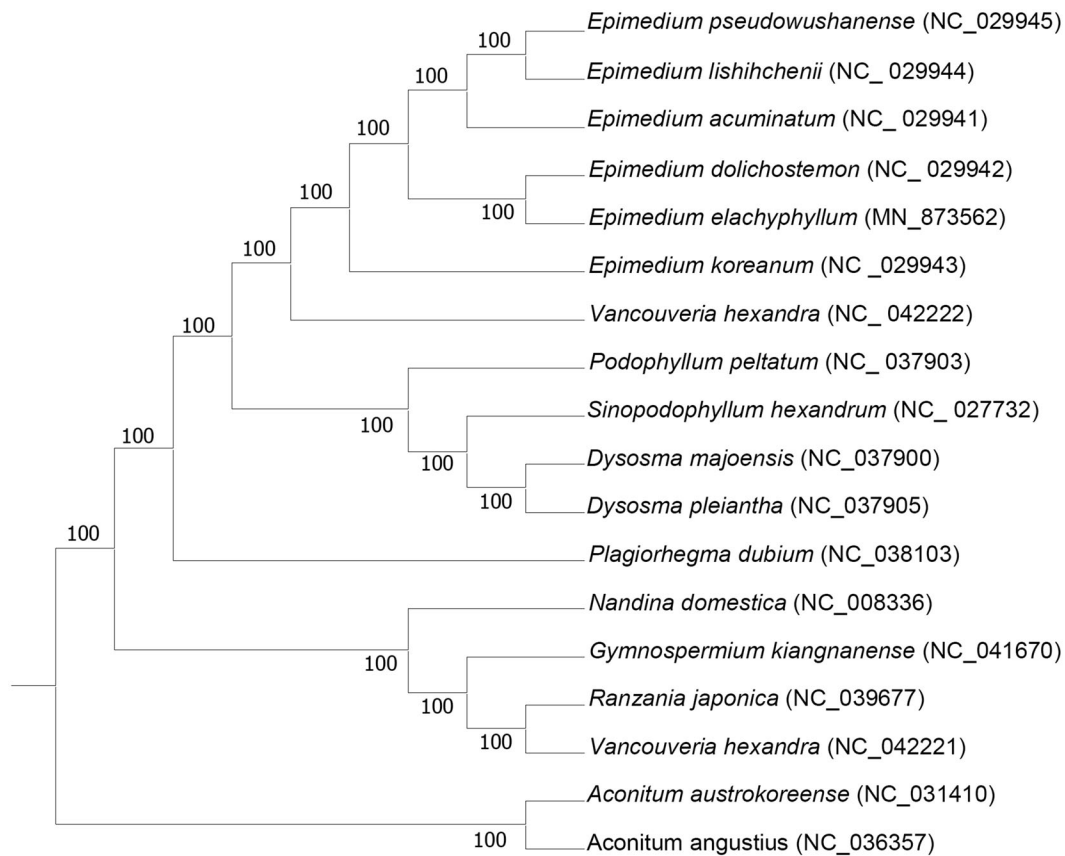


Figure 1. ML phylogenetic tree inferred from 18 complete cp genomes.

angustius and *Aconitum austrokoreense* as the outgroup. Phylogenetic analysis indicated that *E. elachyphyllum* is closely related to *E. dolichostemon* (Figure 1). The published *E. elachyphyllum* chloroplast genome will provide useful information for phylogenetic and evolutionary studies in Berberidaceae.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the CAMS Innovation Fund for Medical Sciences (CIFMS) [2017-12-M-3-013], the National Natural Science Foundation of China [81473302], the Chongqing Science and Technology Bureau [cstc2018jcyjAX0316, cc-cstc-CA-19-2], and the Traditional Chinese Medicine Science and the Technology Projects of Chongqing Health and Family Planning Commission [ZY201802117].

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):637–640.
- He SZ, Zhang TL. 1994. A new species of medicinal plants of *Epimedium* L. from GUIZHOU. *Guihaia.* 14:25–26.
- Jin JJ, Yu WB, Yang JB. 2018. GetOrganelle: a simple and fast pipeline for de novo assembly of a complete circular chloroplast genome using genome skimming data. *bioRxiv.* 4:256479.
- 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 (cp) 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.
- Ministry of Environment Protection of the People's Republic of China. 2013. China species red list: higher plants. http://www.zhb.gov.cn/gkml/hbb/bgg/201309/t20130912_260061.htm.
- 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.
- Wang GJ, Tsai TH, Lin LC. 2007. Prenylflavonol, acylated flavonol glycosides and related compounds from *Epimedium sagittatum*. *Phytochemistry.* 68(19):2455–2464.
- Xu Y, Liu L, Liu S, He Y, Li R, Ge F. 2019. The taxonomic relevance of flower colour for *Epimedium* (Berberidaceae), with morphological and nomenclatural notes for five species from China. *PK.* 118:33–64.
- 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.* 7:306–308.