Complete chloroplast genome sequence of *Epimedium shuichengense* S. Z. He (Berberidaceae), an endangered species endemic to China

Fulin Yan a,b, Lilang Li b, Shunzhi He a, Shenghua Wei a and Qingwen Sun a

a College of Pharmacy, Guizhou University of Traditional Chinese Medicine, Guiyang, China; b State Key Laboratory of Medicinal Plant Efficacy and Utilization, Guizhou Medical University, Guiyang, China

**ABSTRACT**

*Epimedium shuichengense* S. Z. He is a rare and endangered species endemic to Guizhou, China. In this study, the complete chloroplast (cp) genome of *E. shuichengense* was sequenced. The total cp genome size was 157,046 bp in length, with 38.8% of GC content, including four distinct regions: the large single-copy region (LSC, 88,394 bp), small single-copy region (SSC, 17,048 bp), and a pair of inverted repeat regions (IRs, each for 20,820 bp). The whole cp genome of *E. shuichengense* encoded 130 unique genes, including 85 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Phylogenetic analysis with the previously reported cp genomes showed that all the samples of *Epimedium* are grouped into one group, which can be easily separated from out groups, and *E. shuichengense* with *E. borealiguizhouense* into a supported branch.

**ARTICLE HISTORY**

Received 18 March 2020
Accepted 27 March 2020

**KEYWORDS**

Berberidaceae; chloroplast genome; Epimedium shuichengense

**CONTACT**

Shenghua Wei weishenghua6512@126.com; Qingwen Sun sqw1978_2006@126.com College of Pharmacy, Guizhou University of Traditional Chinese Medicine, DongQing south road, University town, Huaxi district, Guiyang city, Guizhou province, China

© 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.
The phylogenetic analysis was carried out using the complete cp genome sequences of *E. shuichengense*, 15 reported *Epimedium* species, *Nandina* and *Berberis* of Berberidaceae as outgroup (Figure 1). The results showed that all the 15 species of the *Epimedium*, endemic to China, clustered into a supported branch and were separated from *E. koreanum* distributed in Korea. *Epimedium shuichengense* with *E. borealiguizhouense* into a supported branch. The phylogenetic relationships of 16 species of *Epimedium* based on the cp genome data were not closely related to floral characters. This cp genome is the first report for the *E. shuichengense* and will be useful data for developing markers for further studies on resolving the relationship within the *Epimedium*.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Funding**

This work was supported by China Guizhou Provincial Science & Technology Department [Grant No. [2019]5658]; China Guizhou Provincial Education Department [Grant No. KY[2017]018]; Special subsidy for public health services of traditional Chinese medicine [Grant No. 2018YFC1708101], and Ministry of Science and Technology [2018YFC1708101].

**References**

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol*. 19(5):455–477.

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

He SZ. 2014. *Color map of the genus Epimedium* in China. Guiyang: Guizhou Science and Technology Press.

Jiang J, Zhao BJ, Song J, Jia XB. 2016. Pharmacology and clinical application of plants in *Epimedium* L. *Chin Herbal Med*. 8(1):12–23.

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 cp genome using genome skimming data. *BioRxiv*. 256479. 1101/256479

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. *Geneious Basic*: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*. 28(12):1647–1649.

Lowe TM, Chan PP. 2016. *tRNAscan-SE* On-line: integrating search and context for analysis of transfer RNA genes. *Nucleic Acids Res*. 44(W1):W54–W57.

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.

Qu XJ, Moore MJ, Li DZ, Yi TS. 2019. *PGA*: a software package for rapid, accurate, and flexible batch annotation of plastomes. *Plant Meth*. 15:50.

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

Wang Y-Y, He S-Z, Guo B-L. 2009. A new species of *Epimedium* (Berberidaceae) from Guizhou. *Acta Botanica Yunnanica*. 30(4):423–420.

Wu X, Li DX, Deng WL. 2010. Pharmacological progress of *Epimedium* on reproductive and endocrine system. *Chin J Exp Trad Med Formulae*. 16(8):223–227.

Xu Y, Hua H, Yong J, Li R, Li F, Liu Y, Xiaofang H. 2019. Taxonomic study of *Epimedium* L.: status, issues and prospect. *Guilin*. 26(12):1–17. [http://kns.cnki.net/kcms/detail/45.1134.Q.20191226.1000.002.html](http://kns.cnki.net/kcms/detail/45.1134.Q.20191226.1000.002.html)

Ying J, Boufford DE, Brach AR. 2000. *Epimedium* Linnaeus. *Flora China*. 29:262–298.

**Figure 1.** Phylogenetic tree produced by maximum likelihood (ML) analysis base on chloroplast genome sequences from 18 species of *Epimedium*, *Nandina* and *Berberis*. Shown next to the nodes are bootstrap support values based on 1000 replicates.