Complete chloroplast genome sequences of *Corydalis edulis* and *Corydalis shensiana* (Papaveraceae)

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**ABSTRACT**

*Corydalis* DC., the largest genus of Papaveraceae, was recognized as one of the most taxonomically challenging plant taxa. Due to the lack of genetic information used in previous studies, species discrimination and taxonomic assignment in *Corydalis* have not been fully solved. Here, the complete chloroplast genomes were reported for *Corydalis edulis* Maxim. and *Corydalis shensiana* Liden, with their genome sizes being 154,395 and 155,938 bp, respectively. Both of the chloroplast genomes comprise two inverted repeat (IR) regions, separated by a large single-copy (LSC) region and a small single-copy (SSC) region, and encode 130 genes, including 85 protein-coding genes, 8 ribosomal RNA genes, 37 transfer RNA genes. Our study will provide novel insight into the molecular phylogeny and classification of *Corydalis*.

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rpoC1, and rps16) contained one intron and 3 (clpP, rps12, and ycf3) contained two introns. The overall structure, gene content, and arrangement of the cp genomes of C. edulis and C. shensiana were quite similar to but with higher quality than two previously reported Corydalis species, in which several subunits of NADH-dehydrogenase genes were absent or with partial sequence (such as ndhC, ndhD, ndhF, and ndhI) (Kanwal et al. 2019).

Sixteen cp genomes of Papaveraceae were fully aligned with MAFFT v7.3 (Katoh and Standley 2013), and the maximum-likelihood (ML) tree was constructed using all coding sequences under the GTRGAMMA model with 100 bootstrap replicates by RAxML v.8.2.1 (Stamatakis 2014). Euptelea pleiosperma J. D. Hooker & Thomson was chosen as an outgroup. The result showed that the four Corydalis species (C. edulis, C. shensiana, C. trisecta and C. conspersa) are strongly supported as monophyletic (Figure 1).

Figure 1. ML tree inferred from the coding sequences of 16 chloroplast genomes in Papaveraceae. Numbers above each node indicate bootstrap values. The asterisks show nodes supported by a bootstrap value of 100%.

Data availability statement

The assembled cp genomes of this study are openly available in NCBI at https://www.ncbi.nlm.nih.gov/WebSub/?form=history&tool=genbank, reference number (MW110633 and MW110634). The raw data that support the findings of this study are available on request from the first author LY. The data are not publicly available due to their containing information that could compromise the privacy of research participants.

Disclosure statement

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References

Greiner S, Lehwark P, Bock R. 2019. OrganellarGenomeDRAWE (OGDRAW) version 1.3.1: expanded toolkit for the graphical visualization of organellar genomes. Nucleic Acids Res. 47(W1):W59–W64.

Kanwal N, Zhang X, Afzal N, Yang J, Li ZH, Zhao GF. 2019. Complete chloroplast genome of a Chinese endemic species Corydalis trisecta Franch. (Papaveraceae). Mitochondrial DNA Part B. 4(2):2291–2292.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30(4):772–780.

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.

Ren FM, Wang YW, Xu ZC, Li Y, Xin TY, Zhou JG, Qi YD, Wei XP, Yao H, Song JY. 2019. DNA barcoding of Corydalis, the most taxonomically complicated genus of Papaveraceae. Ecol Evol. 9(4):1934–1945.

Rogers SO, Bendich AJ. 1988. Extraction of DNA from plant tissues. Plant Mol Biol. A6:1–10.

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

Wang YW. 2006. Study on the phylogenetic of Corydalis [Ph.D. Dissertation]. Beijing (China): Institute of Botany, Chinese Academy of Sciences.

Wicke S, Schneeweis GM, dePamphilis CW, Müller KF, Quandt D. 2011. The evolution of the plastid chromosome in land plants: gene content, gene order, gene function. Plant Mol Biol. 76(3–5):273–297.

Zhang ML, Su ZY, Liden M. 2008. Corydalis DC. In: Wu ZY, Raven PH, Hong DY, editors. Flora of China. Vol. 7. Beijing (China): Science Press; St. Louis (MO): Missouri Botanical Garden Press. p. 295–428.