Taylor & Francis
Taylor & Francis Group

MITOGENOME ANNOUNCEMENT

🔓 OPEN ACCESS   ✓ Check for updates

Characterization of the complete chloroplast genome of *Corydalis inopinata* Prain ex Fedde (Papaveraceae)

Xiaodong Xu[a] and Dong Wang[a,b]   iD

[a]School of Life Sciences, Central China Normal University; Key Laboratory for6 Geographical Process Analysis and Simulation, Wuhan, Hubei Province, China; [b]Bio-resources key Laboratory of Shaanxi Province, Shaanxi University of Technology, Hanzhong, China

ABSTRACT

The complete chloroplast genome of *Corydalis inopinata* Prain ex Fedde was assembled and characterized in this study. The chloroplast genome was 181,335 bp in length, consisting of a large single-copy (LSC) region of 91,727 bp, a small single-copy (SSC) region of 1502 bp, and a pair of inverted repeat (IR) regions of 44,053 bp. It encoded 110 unique genes, including 68 protein-coding genes, 29 tRNA genes, 4 rRNA genes, and 9 pseudogenes. Phylogenetic analyses by maximum likelihood (ML) and Bayesian inference (BI) revealed that *C. inopinata* was closely related to *C. conspersa* Maxim. with full support in the present sampling. The complete plastid genome provided in this work would be useful for elucidating the taxonomy, phylogeny, and evolution of *C. inopinata* and other related species.

Corydalis DC., one of the largest genus in Chinese flora, stands out for its complex, variable, interconnected and intergrading morphological characters (Wu et al. 1996). To date, relatively few molecular researches have been done on this taxon, leaving us with many unresolved questions about its taxonomy, phylogeny, and evolution. In the present study, we characterized and reported the complete plastid genome of *C. inopinata* Prain ex Fedde, a cushion-like alpine perennial herb, and investigated its phylogeny within Ranunculales.

The fresh leaves and voucher specimens of *C. inopinata* were collected from its wild population (Jiangzi, Xizang, China, 28°54′N, 90°9′E, D. Wang et al. 140599), and deposited in the herbarium of Central China Normal University (CCNU). Total genomic DNA was isolated using CTAB method (Doyle and Doyle 1987). Library with an insert size of about 350 bp was constructed, and sequenced using Illumina NovaSeq 6000 (Illumina, San Diego, CA) at Novogene (Tianjin, China). Approximately 7.63 Gb raw data were generated, and then the raw reads were filtered using fastp v0.20.1 (Chen et al. 2018). The cleaned reads were assembled *de novo* using GetOrganelle v1.6.2 (Jin et al. 2018) with chloroplast genome of *Lamprocapnos spectabilis* (L.) Fukuhara (NC_039756) as reference. The assembled chloroplast genome was annotated using PGA (Qu et al. 2019) with the chloroplast genome of *L. spectabilis* (NC_039756) as reference, checked manually, and submitted to National Center for Biotechnology Information (NCBI, accession number: MT755641). To investigate the phylogeny of *C. inopinata*, 99 shared genes among *C. inopinata*

and another 16 representative Ranunculales species from NCBI (accession numbers were provided in Figure 1) were aligned using MAFFT v.7 (Katoh and Standley 2013). The best-fit nucleotide substitution model was determined by jModeltest v2.1.10 (Darriba et al. 2012) using the Akaike information criterion (AIC). Maximum likelihood (ML) and Bayesian inference (BI) phylogenetic analyses were conducted using RAxML v8.2.12 (Stamatakis 2014, -m GTRGAMMA -N 1000 -f a) and MrBayes v3.2.7 (Ronquist et al. 2012, GTR+I + G model, ngen = 1,000,000, samplefreq = 100, nchains = 4, burnin = 2500), respectively.

The complete chloroplast genome of *C. inopinata* was 1,81,335 bp in length, exhibiting typical angiosperm quadripartite structure. The large single-copy (LSC), inverted repeat (IR), and small single-copy (SSC) were 91,727 bp, 44,053 bp, and 1,502 bp, respectively. Inversion and translocation of about 5 kb (*rbcL*, *atpB*, *atpE*, and *trnM-CAU*) was observed in the LSC. The IRs expanded markedly into the SSC, resulting in the IRs 15 kb longer than the average. In total, 110 genes were predicted, including 68 protein-coding genes, 29 tRNA genes, four rRNA genes, and nine pseudogenes (eight *ndh* gene and *trnV-UAC*). Three genes (*accD*, *ndhJ*, and *ndhI*) were absent in this chloroplast genome. Twenty-four genes were duplicated in the IR, including eight protein-coding genes, four rRNA genes, eight tRNA genes, and four pseudogenized *ndh* genes. The GC content of the complete chloroplast genome, LSC, IR, and SSC regions were 40.93%, 39.85%, 42.17%, and 34.38%, respectively. The ML and BI analyses both
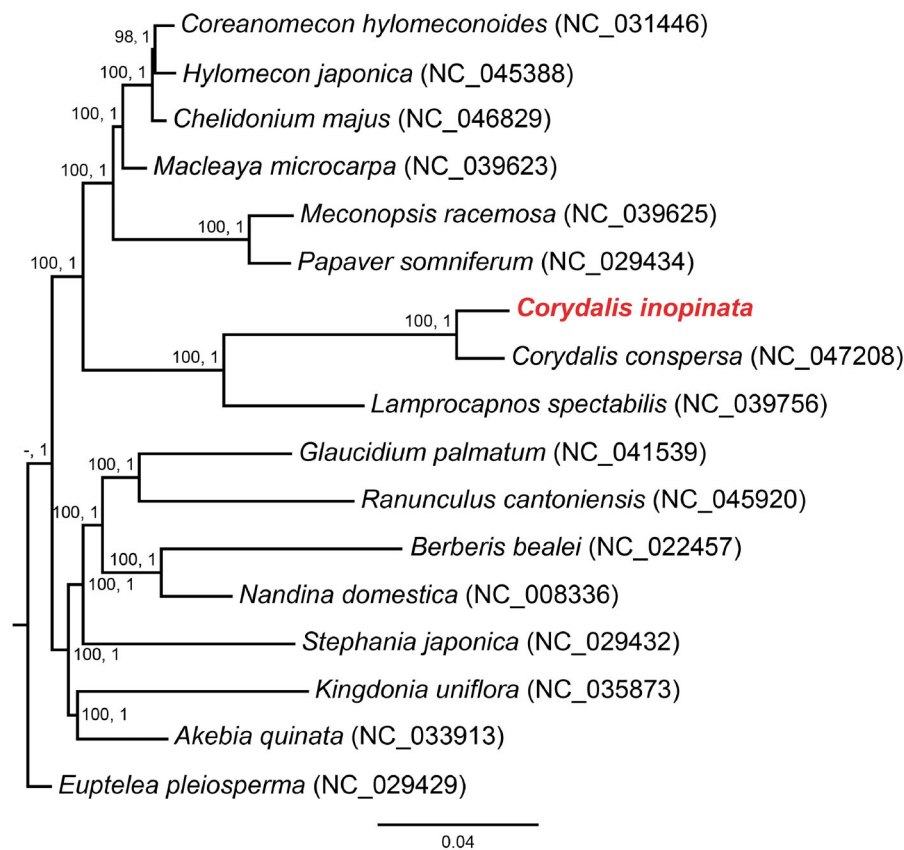
Figure 1. ML and BI phylogenetic tree based on *C. inopinata* and another 16 Ranunculales species, with ML bootstrap values (left) and BI posterior probability (right) indicated near the nodes.

revealed that *C. inopinata* belonged to Fumarioideae (Papaveraceae) clade, and *C. inopinata* was closely related to *C. conspersa* Maxim. with full support in the present sampling (Figure 1).

The complete plastid genome provided in this work would be useful for elucidating the taxonomy, phylogeny, and evolution of *C. inopinata*, and providing molecular data for future research in *Corydalis* as well.

Disclosure statement

Funding

ORCID

Dong Wang (ID) http://orcid.org/0000-0003-1874-7690

Data availability statement

References

Chen SF, Zhou YQ, Chen YR, Gu J. 2018. fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics. 34(17):i884–i890.

Darriba D, Taboada GL, Doallo R, Posada D. 2012. jModelTest 2: more models, new heuristics and parallel computing. Nat Methods. 9(8):772.

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

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

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 Methods. 15(1):50.

Ronquist F, Teslenk M, Van der Mark P, Ayres D, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol. 61(3):539–542.

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

Wu ZY, Zhuang X, Su ZY. 1996. The systematic evolution of *Corydalis* in relation to florogenesis and floristic regionalization in the world. Acta Bot Yunnan. 18:241–267.