The complete chloroplast genome of Corydalis conspersa

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ABSTRACT

The complete chloroplast genome of Corydalis conspersa was sequenced and assembled. It is a circular form of 187,810 bp in length, which was separated into four distinct regions, a large single-copy (LSC) of 92,280 bp, a small single-copy region (SSC) of 780 bp, two inverted repeats (IR) of 47,375 bp. After annotation, a total of 144 genes were predicted, of which, 98 encode proteins, 8 rRNA, 38 tRNA. The evolutionary history, inferred using neighbour-joining method, indicates Corydalis conspersa was grouped within Papaveraceae, and comprised a clade with Lamprocapnos spectabilis with 100% BS value.

Corydalis conspersa Maxim, belonging to Papaveraceae, is an alpine herb plant, possessing yellow tepals with brown spots. It is distributed mainly in southwest Gansu, southwest Qinghai, northwest and west Sichuan, east and middle Tibet in China, at an elevation from 3500–5300 m (Que et al. 2017). For containing various alkaloids, plants of Corydalis are generally used as febrifuge and detoxicant in traditional Chinese medicine (Zeng et al. 1987; Dae-Keun et al. 2000). Corydalis conspersa, like other species in Corydalis, is used extensively in traditional Tibet medicine in curing of ache, inflammation, anxiety, etc. (Fang et al. 1984; Wang et al. 2019). In previous studies, although chemical composition of this plant has been well documented, the knowledge of the genetics or molecular biology about this important medical plant is still less known. In this study, we report the complete chloroplast genome of C. conspersa.

A sample from Qilian mountains (36°24′30″N, 101°22′6″E) in Qinghai province was used for sequencing. Voucher speci-

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men (HNWP-336861) was deposited in the Herbarium, Northwest Institute of Plateau Biology (HNWP). Total genomic DNA was extracted from 100 mg fresh leaves using a modified CTAB method (Murray and Thompson 1980). Paired-end Libraries with an average length of 350 bp were constructed. Sequencing was performed on the Illumina Novaseq platform (Shenzhen Huitong biotechnology Co. Ltd., Shenzhen, China). The complete cp genome was assembled with the de novo assembler SPAdes (Bankevich et al. 2012). Gene annotation was performed via plan. (Huang and Cronk 2015).

The complete cp genome of *C. conspersa* (GenBank accession no. MN843953) has a typical quadripartite form of 187,810 bp in length and composed of a large single-copy region (LSC, 92,280 bp), a small single-copy region (SSC, 780 bp), two inverted repeats (IR, 47,375 bp). GC content of the genome is 37.9%. A total of 144 genes were predicted on this cp genome, of which, 98 encode proteins, 8 rRNA, 38 tRNA.

Phylogenetic analysis was performed based on complete cp genomes of *C. conspersa* and other eight related species reported in Papaveraceae, three species in Ranunculaceae as out-groups. The sequences were aligned using MAFFT (Katoh et al. 2002) and trimAl was employed to remove ambiguously aligned sites (Capella-Gutierrez et al. 2009). The evolutionary history was inferred using neighbour-joining method in MEGA7.0 (Kumar et al. 2016). Bootstrap (BS) values were calculated from 1000 replicate analysis (Figure 1). As expected, *C. conspersa* was grouped within Papaveraceae and comprised a clade with *Lamprocapnos spectabilis* with 100% BS value. The complete cp genome of *C. conspersa* will be helpful for further studies on population genetics, taxonomy or resources protection.

**Disclosure statement**

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

**Data availability**

The data that support the findings of this study are available from the corresponding author, [J.W], upon reasonable request.

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