

The complete chloroplast genome sequence of the medicinal plant *Paeonia delavayi* Franchet. (Paeoniaceae)

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ABSTRACT

Paeonia delavayi is a medicinal plant commonly used in southwest of China. In this study, we sequenced the complete chloroplast (cp) genome sequence of *P. delavayi* to investigate its phylogenetic relationship in the family Paeoniaceae. The chloroplast genome of *P. delavayi* was 152,872 bp in length with 38.4% overall GC content, including a large single copy (LSC) region of 84,523 bp, a small single copy (SSC) region of 17,053 bp and a pair of inverted repeats (IRs) of 25,646 bp. The cp genome contained 105 genes, including 75 protein coding genes, 27 tRNA genes, and 4 rRNA genes. The phylogenetic analysis indicated *P. delavayi* was closely related to *P. ludlowii*.

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Paeonia is a very complex genus of the Paeoniaceae family, which includes 35 species in the world (Sang et al. 1997). Most of them are widespread in the northern hemisphere: eastern Asia, central Asia, the Himalayas, the Mediterranean region, and Pacific North America (Stern 1946; Tzanoudakis 1983; Hong et al. 2001). There are 15 species in China (Hong et al. 2001). Plants of this genus have been widely used in traditional Chinese medicine for thousands of years (Jiangsu New Medical College 1977). Among these species, *P. delavayi* is the unique species of China and widely distributed in southwest China which have been used in local medicine in the treatment of rheumatoid arthritis, systemic lupus erythematosus, hepatitis, dysmenorrhoea, muscle cramping and spasms, and fever (Jiangsu New Medical College 1977). However, up to now for such medicinal plant, many studies have mainly focussed on describing its interspecific relationship based on DNA fragments in the genus *Paeonia* (ITS and *matK*) (Chou & Tang 2017) and quantitative analysis of high performance liquid chromatography methods (Hua et al. 2017), the genome information of *P. delavayi* is too little published in GenBank, so that insufficient comprehensive genomic resource is conducted for it. At present, we report the chloroplast genome sequence of *P. delavayi* and find its internal relationships

within the family Paeoniaceae, which can provide basic data for further research of genus *Paeonia* species useful genome resource in China.

Fresh and clean leave materials of *P. delavayi* were collected from Yulong county, Yunnan, China (N27°02'36.14", E100°11'30.33"), and the plant materials and a voucher specimen (No. TAE01) were deposited at Tourism and Culture College of Yunnan University (Lijiang). Total genomic DNA was extracted using the improved CTAB method (Doyle 1987; Yang et al. 2014), and sequenced with Illumina Hiseq 2500 (Novogene, Tianjin, China) platform with pair-end (2 × 300 bp) library. About 8.39 Gb of raw reads with 10,500,370 paired-end reads were obtained from high-throughput sequencing. The raw data was filtered using Trimmomatic v.0.32 with default settings (Bolger et al. 2014). Then paired-end reads of clean data were assembled into circular contigs using GetOrganelle.py (Jin et al. 2018) with *Paeonia rockii* (No. MF488719) as reference. Finally, the cpDNA was annotated by the Dual Organellar Genome Annotator (DOGMA; <http://dogma.ccbb.utexas.edu/>) (Wyman et al. 2004) and tRNAscan-SE (Lowe and Chan 2016) with manual adjustment using Geneious v. 7.1.3 (Kearse et al. 2012).

The circular genome map was generated with OGDRAW v.1.3.1 (Greiner et al. 2019). Then the annotated chloroplast

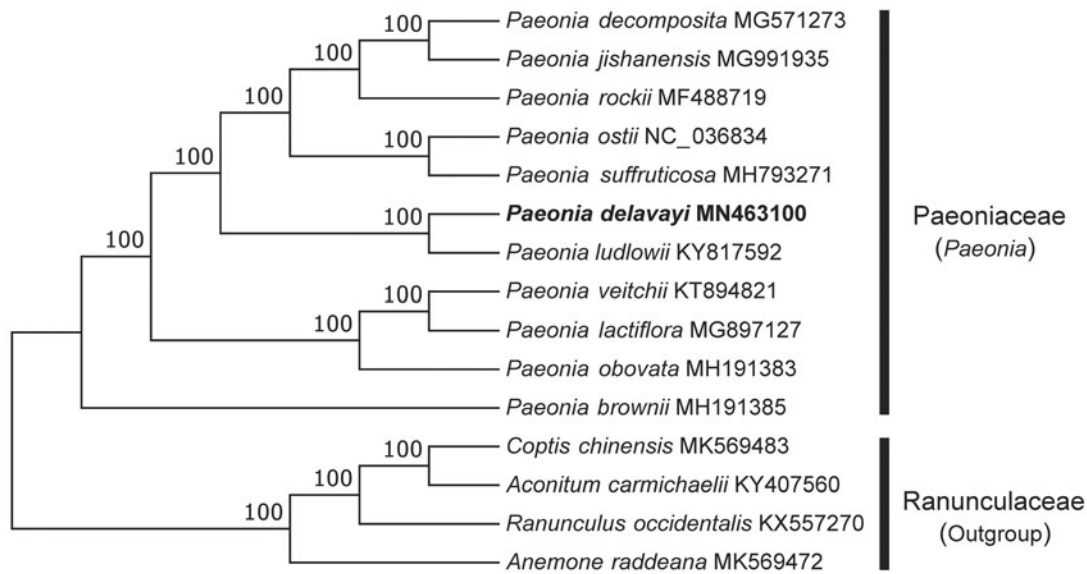


Figure 1. Neighbor-joining (NJ) tree of 11 species within the family Paeoniaceae based on the plastomes using four Ranunculaceae species as outgroups.

genome was submitted to the GenBank under the accession number MH463100. The total length of the chloroplast genome was 152,872 bp, with 38.4% overall GC content. With typical quadripartite structure, a pair of inverted repeats (IRs) of 25,646 bp was separated by a small single copy (SSC) region of 17,053 bp and a large single copy (LSC) region of 84,523 bp. The cp genome contained 105 genes, including 75 protein coding genes, 27 tRNA genes, and 4 rRNA genes. Of these, 18 genes were duplicated in the inverted repeat regions, 9 protein-coding genes, and 5 tRNA genes contain one intron, while three genes (*ycf3*, *rps12* and *clpP*) have two introns.

To investigate its taxonomic status, a total of 11 cp genome sequences of Paeoniaceae species were downloaded from the NCBI database used for phylogenetic analysis. After using MAFFT V.7.149 for aligning (Katoh and Standley 2013), a neighbor-joining (NJ) tree was constructed in MEGA v.7.0.26 (Kumar et al. 2016) with 1000 bootstrap replicates and four Ranunculaceae species (*Coptis chinensis*: MK569483, *Aconitum carmichaelii*: KY407560, *Ranunculus occidentalis*: KX557270, and *Anemone raddeana*: MK569472) were used as outgroups. The results showed that *P. delavayi* was closely related to *P. ludlowii*. (Figure 1). Meanwhile, the phylogenetic relationship in Paeoniaceae was consistent with previous studies and this will be useful data for developing markers for further studies.

Disclosure statement

The authors are highly grateful to the published genome data in the public database. The authors declare no conflicts of interest and are responsible for the content.

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