

The complete chloroplast genome of *Plagiorhegma dubia* Maxim., a traditional Chinese medicinal herb

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ABSTRACT

Plagiorhegma dubia Maxim. is a traditional Chinese medicinal herb from *Plagiorhegma*, Berberidaceae, which is distributed in the northeast of China, Korea, Russia. The complete chloroplast genome is 152,468 bp in length, with large single copy (LSC 82,257 bp) and small single copy (SSC 16,599 bp) regions separated by a pair of inverted repeats (IR 26 805 bp). The genome has a total of 113 genes including 79 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. Phylogenetic analysis shows that *P. dubia* is closely related with *Sinopodophyllum hexandrum* and *Epimedium* species. The results are of great implication for the development and utilization of *P. dubia* and the phylogenetic researches on Berberidaceae.

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Plagiorhegma dubia Maxim is a perennial herbaceous plant and the only species of the genus *Plagiorhegma* of Berberidaceae, Ranales, which is distributed in Northeast China, Korea, Russia (Ying et al. 2011). As the traditional Chinese medicinal material, the rhizome of *P. dubia* contains berberine, and has antipyretic, antidotal, stomachic and anti-diarrhoeal clinical effects (Arens et al. 1985; Jeong and Sivanesan 2016). Furthermore, *P. dubia* has potential as a new ornamental garden plant which has attractive heart-shaped leaves and light purple flowers. The species has potential as a new ornamental garden plant (Rhie et al. 2014).





The total genomic DNA of *P. dubia* was extracted from its fresh leaves which were collected in Tonghua of Jinlin Province, China (N 41°43'48" E 125°59'24"). An Illumina paired-end (PE) genomic library was prepared and sequenced. High quality reads were obtained from the total pair-end (PE) raw reads and assembled by the CLC-quality genome assembler (ver 4.06bata) (Kim et al. 2015). All of the contig sequences were aligned and ordered to the reference cp genome of *Nandina domestica* (NC_DQ923117) using MUMmer (Kurtz et al. 2004). Sequence gaps were filled by Gapcloser included in the SOAP package vl.12 (Li et al. 2010). Four junctions between LSC/IRs and SSC/IRs were validated with PCR-based conventional Sanger sequencing.

The genes in the chloroplast genome were predicted by the Dul Organellar GenoMe Annotator (DOGMA; Wyman

et al. 2004). The BLAST tools and ORF finder at NCBI website (<http://www.ncbi.nlm.nih.gov/>) were also used in the gene annotations. The tRNA genes were verified with tRNAscan-SE (Lowe and Eddy 1997). The circular cp genome maps were drawn by the Organellar Genome DRAW tool (OGDRAW; Lohse et al. 2007) with subsequent manual editing.

The complete chloroplast genome of *P. dubia* was submitted to NCBI, and the accession number of nucleotide sequence is MG397139. The nucleotide sequence was 152,468 bp, and was assembled into a single circular which presented a typical quadripartite structure including one large single-copy region (82,257 bp), one small single copy (16,599 bp), and a pair of inverted repeat regions (IRa and IRb) of 26805 bp. The GC content of the chloroplast genomes was 38.15%. The 113 unique genes in the sequence were composed of 79 protein-coding genes, 30 tRNA genes and four rRNA genes.

The phylogenetic analyses sampled *P. dubia* and other nine Berberidaceae species. These nine species had been sequenced on chloroplast genome, including four *Epimedium* species (Lee et al. 2015; Sun et al. 2016; Zhang et al. 2016), *Sinopodophyllum hexandrum* (Meng et al. 2017), two *Berberis* species (NC_KM057374, NC_KM057375), *Nandina domestica* (Moore et al. 2006), *Gymnosepermium microrrhynchum* (NC_KM057373). ML phylogenetic tree was constructed based

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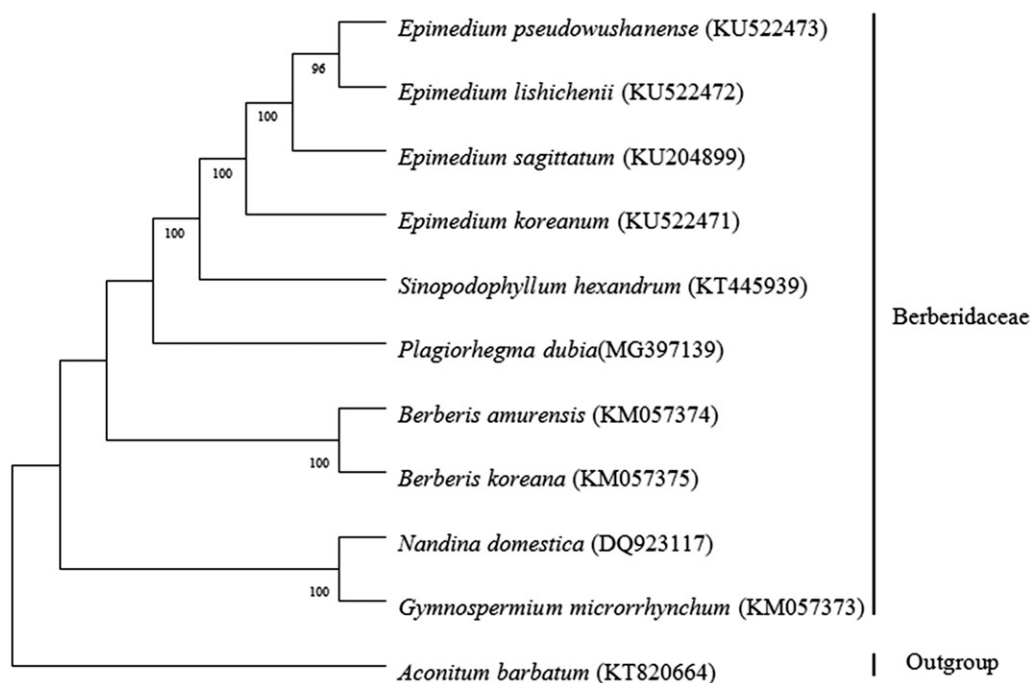


Figure 1. Using MEGA7.0, ML phylogenetic tree was constructed based on the entire chloroplast protein-coding sequences of ten Berberidaceae species including *P. dubia* and *Aconitum barbatum* of Ranunculaceae as an outgroup.

on the entire chloroplast protein-coding sequences of these 11 species using MEGA7.0 (Kumar et al. 2016). The results showed that the ten Berberidaceae species grouped into a monophyletic branch (Figure 1). In accordance with previous phylogenetic studies on Berberidaceae (Kim and Jansen 1994; Wang et al. 2007; Zhang et al. 2012), inter-genera relationships of the family were closely related with chromosome base number. *N. domestica* with $x=10$ and *G. microrrhynchum* with $x=8$ clustered into a clade. *Berberis amurensis* and *B. koreana* are with $x=7$ and formed a branch. *Epimedium koreanum*, *E. sagittatum*, *E. lishichenii*, *E. pseudowushanense*, *S. hexandrum*, *P. dubia* are with $x=6$ and had most closest relationships. The results are of great implication for the Phylogenetic researches on Berberidaceae.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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