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# Complete chloroplast genome sequence of *Mahonia duclouxiana* (Berberidaceae), a medicinal plant in China

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## ABSTRACT

*Mahonia duclouxiana* is a member of the genus *Mahonia* of Berberidaceae and is distributed in South Asia. Here, the complete chloroplast genome sequence of *M. duclouxiana* was reported. The complete chloroplast genome is 165,384 bp in length, which has a large single-copy (LSC) region of 73,477 bp, a small single-copy (SSC) region of 18,563 bp, and two inverted repeat (IR) regions of 36,672 bp. The G/C content in the chloroplast genome is 38.1%. The whole chloroplast genome contains 151 genes, including 38 unique tRNA genes, 105 unique protein-coding genes, and 8 unique rRNA genes. The phylogenetic analysis supported that this species should be included in *Maddenia*. The complete chloroplast genome sequence of *M. duclouxiana* will provide extremely important information in tracing the evolutionary history of the genus *Mahonia* and the development of the medicinal value.

ARTICLE HISTORY

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# KEYWORDS

*Mahonia fortune*; chloroplast genome; genome structure; Berberidaceae

Mahonia duclouxiana Gagnep. 1908, a member of the famous medicinal genus *Mahonia* of Berberidaceae, is distributed in the forest, shrub, roadside, or hillside of Yunnan, Sichuan, and Guangxi provinces of China. It also spread over Myanmar, India, and Thailand (Ying et al. 2011). Its leaves were used as traditional Chinese medicine with the effects of clearing heat, relieving cough, and resolving phlegm, and are often used to treat jaundice, colds, diarrhea, dysentery, hypertension, and bruises (Liu and He 2010). In this study, the complete plastid genome sequence of *M. duclouxiana* (GenBank accession number: MZ086770) was assembled by using the genome skimming approach (Zimmer and Wen 2015). The phylogenetic relationship within this genus was reconstructed.

The sample of *M. duclouxiana* was collected from Guivang Medicinal Botanical Garden, Guizhou Province of China  $(112^{\circ}43' \text{ E}, 25^{\circ}46' \text{ N}, \text{ alt. } 1107 \text{ m})$ . The voucher specimen (TRCGZ005) was deposited in the Herbarium of Northwest A&F University (WUK), China. Total genomic DNA was extracted from fresh leaves by the modified cetyltrimethyl ammonium bromide (CTAB) method (Doyle and Doyle 1987). The libraries were prepared in the Molecular Biology Experiment Center in Southwest China using NEBNext<sup>®</sup> Ultra<sup>TM</sup> II DNA Library Prep Kit and sequenced by Illumina Miseg platform (Illumina, San Diego, CA, USA). 25,347,900 Raw Illumina data were filtered for sequence quality using Trimmomatic v. 0.40. The clean reads of the chloroplast (cp) genome were assembled by using GetOrganelle (Jin et al. 2020). The complete cp genome was annotated with PGA (https://github.com/guxiaojian/PGA) and corrected with DOGMA (Wyman et al. 2004).

The complete chloroplast genome of M. duclouxiana is 165,384 bp in length, which has the typical guadripartite structure. The length of each inverted repeat (IR) is 36,672 bp, those between them are the large single-copy (LSC) and the short single-copy (SSC) with the length of 73,477 and 18,563 bp, respectively. One hundred and fiftyone genes were found in this chloroplast genome, and 105 of them are unique protein-coding genes, 38 are unique tRNA genes and 8 are unique rRNA genes. Most of them occur a single copy, while ten tRNA genes (trnG-UCC, trnT-GGU, trnM-CAU, trnI-CAU, trnI-GAU, trnL-CAA, trnV-GAC, trnA-UGC, trnR-ACG, and trnN-GUU), 23 protein-coding genes (clpP1, psbB, psbT, pbf1, psbH, petB, petD, rps11, rpl36, infA, rps8, rpl14, rpl16, rps3, rpl22, rps19, rpl2, rpl23, ycf2, ycf15, ndhB, rps7, and ycf1) and all of the rRNA genes are duplicated owing to they are located in the IR regions. The protein-coding gene rps12 is repeated three times. The G/C content of the whole chloroplast genome length, LSC, SSC, and IR regions is 38.1%, 36.4%, 32.4%, and 41.2%, respectively.

Total of 18 species (including 17 of Berberidaceae, and *Aconitum brachypodum* of Ranunculaceae as outgroup) were used to obtain the phylogenetic position of *M. duclouxiana* by RAxML with 10,000 bootstraps (Figure 1). The result clearly illustrates that *Mahonia duclouxiana* and other species of *Mahonia* form a clade, which is a sister of *Berberis*. The complete sequence of *M. duclouxiana* will provide useful evidence for further phylogenetic, biogeographical, and barcoding studies.

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Figure 1. The best ML tree was constructed from 18 complete chloroplast genome sequences by RAxML with 10,000 bootstraps.

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## **Disclosure statement**

No potential conflict of interest was reported by the author.

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## Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/

Genbank/update.html under the accession number MZ086770. The associated BioProject, SRA, and BioSample numbers are PRJNA727409, SRR14429474, and SAMN19020770, respectively.

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