**The complete chloroplast genome sequence of *Manglietia yuyuanensis* (Magnoliaceae)**

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**ABSTRACT**

*Manglietia yuyuanensis* is an important afforestation and excellent broad-leaved tree species in southern China. In this study, we assembled the complete chloroplast genome of *M. yuyuanensis* based on the illumina sequences, sequence analysis showed the genome was 160,078 bp in length presenting a typical quadripartite structure and contains an inverted repeat region (IR, 26,467 b), a small single-copy (SSC) region, and a large single-copy (LSC) region (18,785 and 88,359 bp, respectively). The overall GC content was 39.27%. The sequence contained 128 unique genes, including 81 protein-coding genes, 38 tRNA genes, and 8 rRNA genes. The maximum-likelihood (ML) phylogenetic analysis revealed that *M. maudiae* was closely related to *Manglietia insignis*. A phylogenetic analysis revealed that *M. yuyuanensis* is closely related to *Manglietia glaucifolia*, with the genus *Manglietia*.

Additionally, MITObim version 1.8 ([https://github.com/chrishah/MITObim. . . . . . . . . .](https://github.com/chrishah/MITObim)) was used to assemble the complete circular cp genome sequence (Hahn et al. 2013). The cp genome was annotated and manually adjusted with CpGAVAS (Liu et al. 2012). The circular plastid genome map was completed with the help of the online program OrganellarGenome DRAW (OGDRAW) (Lohse et al. 2013) and the annotated sequence was submitted to NCBI.

The complete cp genome sequence of *M. yuyuanensis* was 160,078 bp in length presenting a typical quadripartite structure and contains an inverted repeat region (IR, 26,467 b), a small single-copy (SSC) region, and a large single-copy (LSC) region (18,785 and 88,359 bp, respectively). The overall GC content was 39.27%. In total, 128 genes were annotated, including 81 (63.28%) protein-coding genes (PCGs), 38 (29.69%) tRNA genes, and 8 (6.25%) rRNA genes, one gene (0.78%) were inferred to be pseudogenes. Ten PCGs (rps12, rpl2, trnV-UAC, trnL-UAA, atpF, trn68, trnG-AUA, ndhA, trnA-UGC, and ndhB) contained one intron, while *clpP* and *ycf3* each contained two introns.

For their phylogenetic placements within the family Magnoliaceae, phylogenetic analysis was conducted based on the maximum-likelihood (ML) analysis of the complete cp genomes of *M. yuyuanensis* with those of obtained from 30 other species of Magnoliaceae reported in Genbank of NCBI database using MEGA version7.0 (Kumar et al. 2016) ([https://www.megasoftware.net. . . . . . . . .](https://www.megasoftware.net)). The phylogenetic analysis showed that *M. yuyuanensis* was closely related to *Manglietia glaucifolia*, forming a clade included in *Manglietia* (Figure 1). The genus *Manglietia* was phylogenetically closer to one another than to the other 23 taxa within the subfamily Magnolioideae. The cp genome of *M. yuyuanensis* will...
provide useful genomic resources for further study on genetic diversity and conservation of this species.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Figure 1. Maximum likelihood phylogenetic tree of 30 selected Magnoliaceae chloroplast genome sequences. Bootstraps (1000 replicates) are shown at the nodes.
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