The complete chloroplast genome sequence of *Michelia macclurei* (Dandy, 1928) (Magnoliaceae), an important fire-resistant tree species

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**ABSTRACT**

*M. macclurei* (Dandy, 1928) is an evergreen broad-leaved tree species native to South China. This species has great ecological and economic importance. However, the genomic study of *M. macclurei* has lagged far behind. Here, we reported the complete chloroplast genome sequence of *M. macclurei*. The chloroplast genome size of *M. macclurei* was 160,139 bp, consisting of a pair of inverted repeat (IR) regions (26,575 bp), which was separated by a large single copy (LSC) region (88,167 bp) and a small single copy (SSC) region (18,822 bp). A total of 113 unique genes were annotated, including 79 protein-coding genes, 30 tRNA genes, and four rRNA genes. The overall GC content was 39.2%. Phylogenetic analysis based on 16 whole chloroplast genome sequences of *Michelia* species suggested that *M. macclurei* and *M. maudiae* are sister to each other, and jointly sister to *M. chapensis*.

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showed the chloroplast genomes within this genus are conserved in terms of genome size, genome structure, and gene content.

The phylogenetic relationship of *Michelia* was reconstructed using the maximum-likelihood (ML) method based on the multiple alignments of *M. macclurei* and other 15 previously reported chloroplast genomes of *Michelia*, with *Yulania denudata* (JN227740) as an outgroup. ML analysis was conducted based on two data sets: (1) the complete chloroplast genome sequences; and (2) a set of 79 common protein-coding genes, using RAxML-HPC v.8.2.8 (Stamatakis 2014) with 1000 bootstrap replicates on the CIPRES Science Gateway website (https://www.phylo.org/). The phylogenetic topologies based on these two data sets were completely consistent, with 100% bootstrap values at almost all nodes, and identically supported that *M. macclurei* and *M. maudiae* are sisters to each other, and jointly sister to *M. chapensis* (Figure 1).

**Authors’ contributions**

WSJ conceived the project. ZYF and SZ collected samples and performed research. LSS and ZYX analyzed data. WSJ wrote the manuscript. LSS, ZYX, ZYF and SZ revised the manuscript. All authors read and approved the manuscript.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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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 under the accession no. OK046128. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA776621, SRS10788103, and SAMN22811516, respectively.

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**Figure 1.** Phylogenetic tree inferred by maximum likelihood (ML) method based on complete chloroplast genomes of 16 *Michelia* species with *Yulania denudata* as an outgroup. Numbers near the nodes represent ML bootstrap values. The phylogenetic tree based on 79 protein-coding genes is completely consistent with this topology.
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