

Complete chloroplast genome sequence of *Magnolia sinica* (Y.W.Law) Noot. (magnoliaceae), A critically endangered species with extremely small populations in Magnoliaceae

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ABSTRACT

Magnolia sinica, distributed in Yunnan province of China, is a critically endangered (CR) species based on the IUCN Red List. Here we provide the complete chloroplast (cp) genome sequence of *M. sinica*. Its length is 159,443 bp with four sub-regions: 88,156 bp of LSC region and 18,748 bp of SSC region are separated by two IR regions (each 26,570 bp). The genome contains 79 CDSs, four rRNAs, and 30 tRNAs. Phylogenetic analysis of cp genome of *M. sinica* with previously reported chloroplast genomes shows that *M. yunnanensis* is a sister to *M. sinica* with high bootstrap value.

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As a species belonging to Magnoliaceae, *Magnolia sinica* (Y. W. Law) Noot. is one of flagship species for conservation in China (Wang et al. 2016). It is categorized as Critically Endangered (CR) species in the IUCN Red List based on its restricted distributions: only 52 individuals in eight localities of Yunnan province in China have been reported (Wang et al. 2016). And also, the species has been targeted as one of the 120 PSESP (Plant Species with Extremely Small Populations) priorities for urgently rescuing in China (Chen et al. 2016). Diagnostic characters of this taxon in Magnoliaceae include opened prefoliations and ventrally dehiscent carpels (Figlar and Nootboom 2004). Taxonomic position of this taxon in Magnoliaceae has long been controversial. It has been considered as an independent genus, *Manglietiastrum* Y. W. Law, in Magnoliaceae. However, its taxonomic position has been changed to a section included in subgenus *Talauma* (Nootboom 1985) in *Magnolia*, a section included in *Manglietia* (Liang and Nootboom 1993), or a section included in subgenus *Gynopodium* in *Magnolia* (Figlar and Nootboom 2004). A recent molecular phylogenetic study on Magnoliaceae using 10 chloroplast (cp) DNA regions has recognized 11 major clades in subgenus Magnolioideae (Kim et al. 2001; Kim and Suh 2013).

In this study, we report a complete sequence of cp genome of *M. sinica* (GenBank accession no. NC023241). We extracted DNA from a leaf sample of a tree cultivated in Kunming Institute of Botany, which is propagated from a seed of the wild tree (voucher: *S. Kim 1098* deposited in the

herbarium of the Natural Products Research Institute in the Seoul National University, Korea).

To complete the cp genome of *M. sinica*, we amplified and sequenced 134 PCR fragments covering the entire cp genome region using 268 primers reported previously (Song et al. 2018b). PCR conditions of our experiment followed those of Kim et al. (2011). PCR products were purified with commercial PCR product purification kit (PCR SV; GeneAll, Seoul, Korea), and sequenced with an ABI 3700 sequencer (ABI, Carlsbad, CA) in both directions. We aligned all sequences from PCR products using Sequencher (ver. 4.9; Gene Code Co., Ann Arbor, MI). The completed cp genome was annotated using DOGMA (Wyman et al. 2004).

The cp genome of *M. sinica* is 160,044 bp, containing four subregions: 88,156 bp of large single copy region and 18,748 bp of small single copy region are separated by two inverted repeat regions (each 26,570 bp). The number of identified genes is 113, including 79 CDSs, four rRNAs, and 30 tRNAs. Inverted repeat regions contain 17 genes (six protein-coding genes, four rRNAs, and seven tRNAs). Phylogenetic analysis was performed for 14 previously reported cp genomes in Magnoliaceae and cp genome of *M. sinica* using raxmlGUI (version 1.3; Silvestro and Michalak 2012) with GTR + G + I model and 500 bootstrap replications (Figure 1). Results of analysis demonstrate that *M. sinica* is a sister to *M. yunnanensis* with 100% of bootstrap value. This study will play an important role in conservation and restoration studies on *M. sinica*, a critically endangered species in Magnoliaceae.

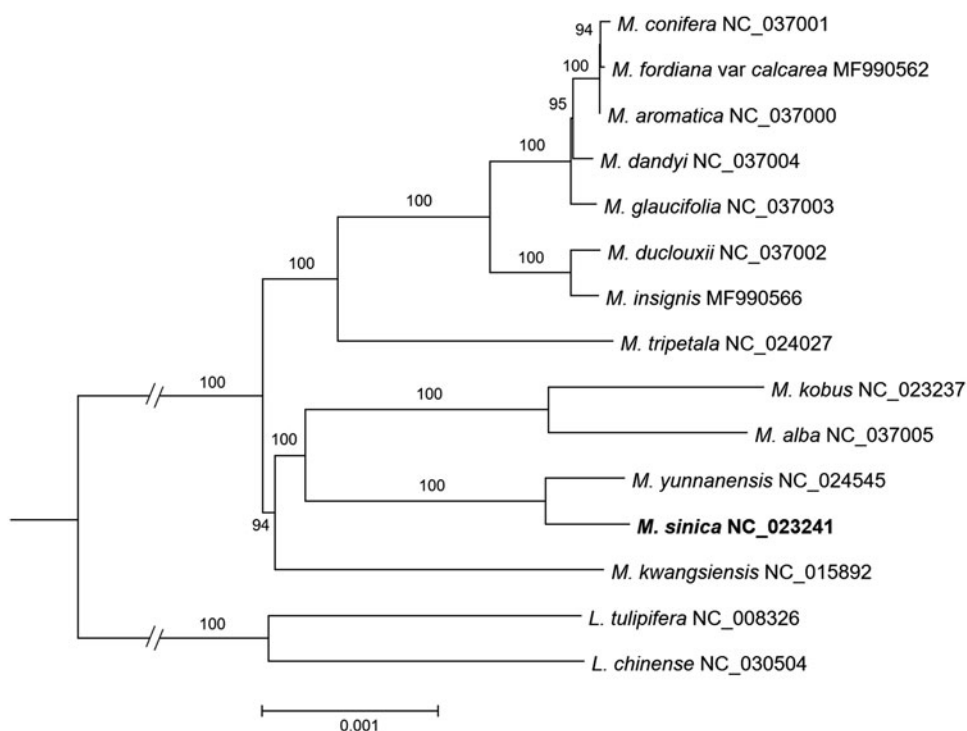


Figure 1. A maximum-likelihood tree constructed for 14 cp genomes from previously reported cp genomes in Magnoliaceae (Cai et al. 2006; Kuang et al. 2011; Yang et al. 2014; Li et al. 2016; Zhu et al. 2016; Wang et al. 2017; Song et al. 2018a; Zheng and Xu 2018) and the cp genome of *Magnolia sinica*. The tree is rooted by two species of subfamily Liriiodendroideae. Numbers above the node indicate bootstrap value (values over 50% are indicated).

Disclosure statement

No potential conflict of interest was reported by the authors.

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