The complete chloroplast genome sequence of the _Manglieta longirostrata_ Sima, a rare and endemic species to China

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**ABSTRACT**

_Manglietia longirostrata_ Sima is a rare and endemic species in China. The complete chloroplast genome (cpDNA) of _M. longirostrata_ was sequenced and assembled in this study. The cpDNA is 160,049 bps in length, contains a large single-copy region (LSC) of 88,098 bp and a small single-copy region (SSC) of 18,861 bp, separated by a pair of identical inverted repeat (IR) regions of 26,571 bp, each. The genome contains 123 genes, including 73 protein-coding genes, 8 ribosomal RNA genes, and 37 transfer RNA genes. Phylogenetic analysis of cp genome of _M. longirostrata_ with 11 chloroplast genomes previously reported in the Magnoliaceae shows that _M. longirostrata_ is close to _Manglietia megaphylla_ with high bootstrap value.

**ARTICLE HISTORY**

Received 28 June 2020
 Accepted 29 June 2020

**KEYWORDS**

Chloroplast genome; endemic species; _Manglietia longirostrata_; Magnoliaceae

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\_Manglietia longirostrata_ (D. X. Li et R. Z. Zhou ex X. M. Hu, Q. W. Zeng et L. Fu) Sima was combined and stated by Sima Yongkang (Sima et al. 2016), Which was described as _Magnolia hookeri_ var. _Longirostrata_ for the long-beaked apex of the follicles and scanning electron micrographs of pollen grains by Hu X. M. & Q. W. Zeng, and they only found one individual in Maocaojing, Malipo County, Yunnan Province, China (Hu et al., 2012). After a careful field study, Sima Yongkang et al. found this species is scattered rarely in southeastern of Yunnan province in China, including Malipo, Yuanyang, and Jingpin county, the altitude range is 900 ~ 1300m, and the species was combined and stated in the genus _Manglietia_ in the Magnoliaceae (Sima et al. 2016). Here, the annotated chloroplast (cp) genome sequence of _M. longirostrata_ has been assembled and submitted to the GenBank with the accession number MT584886 and we performed a phylogenetic analysis which would benefit the genetic and phylogenetic research within this genus species.

The fresh leaves of _M. longirostrata_ were collected from a tree cultivated in Kunming Arboretum, Yunnan Academy of Forestry & Grassland Science, Yunnan Province of China (25°9'5" N, 102°44'45" E). The sheets of the vouchered specimens (Sima and Lu 2012) are stored at the herbaria of YAF and YCP.

Total genomic DNA was extracted from the fresh leaves using Rapid Plant Genomic DNA Isolation Kit. The extracted DNA was sequenced using the Illumina Miseq platform (Illumina, San Diego, CA). In total, 85.1 M of 150-bp raw reads were retrieved. In order to ensure the quality of information analysis, the original reads must be filtered to get lean reads using Trimmomatic (Bolger et al. 2014). Sequencing data were assembled with SPAdes and GapFiller (Boetzer and Pirovano 2012) was used to supplement the GAP of the contig obtained by stitching. The genome was automatically annotated using Prokka (Seemann 2014). OGDRAW v1.3.1 (Greiner et al. 2019) was used to generate a physical map of the cp genome.

The length of the complete cp genome sequence of _M. longirostrata_ is 160,049 bp with four sub-regions: 88,098 bp of large single-copy (LSC) region and 18,864 bp of small single-copy (SSC) region are separated by two inverted repeats (IR) regions, each 26,571 bp, akin to other taxa in the family of Magnoliaceae (Liang et al. 2020). The overall CG content of the _M. longirostrata_ cp genome is 39.30%. The cp genome contained 123 genes, including 73 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. 15 genes (trnA-UGC, trnE-UUC, trnK-UUU, trnS-CA, trnL-UAA, trnC-ACA, trnE-UUC, rps16, rps12, rpl2, atpF, ndhB, ndhA, ycf1, and ycf3) contain intron. The annotated genomic sequence was submitted to GenBank under the Accession Number of MT584886.

The complete cp genome of 9 reported Magnoliaceae species and one _Liriodendron_ species as an outgroup were downloaded from NCBI GenBank and _Lirianttie delavayi_ cp genome sequence from our work before (Liang et al. 2020) for the phylogenetic analysis. The combined datasets of 12 species were aligned by Kalign (Madeira et al. 2019). A maximum-likelihood (ML) tree was constructed in MEGA X with 1000 bootstrap replicates (Kumar et al. 2018). The phylogenetic tree reveals that _M. longirostrata_ is most closely related to _M. megaphylla_ with strong bootstrap support.
(Figure 1) and the genera phylogenetic relationship is almost accord with the phylogenetic tree of *Lirianthe coco* (Sima et al. 2020) and all genera mentioned in this study are monophyletic under the taxonomical system of Magnoliaceae by Sima and Lu (2012). We think that the cp genome resource of *M. longirostrata* will be valuable for future studies in conservation genetics, taxonomy, phylogeny, and breeding in the *Manglietia* species.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Funding**

This study was financially supported by National Natural Science Foundation of China [31760180] and the Yunnan Academy of Forestry & Grassland Innovation Fund Project [ZZCX2017-01].

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**Data availability statement**

1. The cpDNA sequence of *Manglietia longirostrata* of this study are openly available in GenBank at https://www.ncbi.nlm.nih.gov/genbank/, reference number: MT584886.
2. Scientific name of the organism in the paper: *Manglietia longirostrata* Sima.
3. Geographic location of the specimen: Kunming Arboretum, Yunnan Academy of Forestry & Grassland Science, Yunnan Province of China (25° 9′ 5″ N, 102° 44′ 45″ E).

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