



The complete chloroplast genome sequence annotation for *Malania oleifera*, a critically endangered and important bioresource tree

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Abstract

In this study, we characterize the chloroplast genome of *Malania oleifera* Chun et S. Lee, the only species of this genus and member of the Olacaceae family. *M. oleifera* is an interesting seed oil plant for medicinal purposes. It is also a critically endangered species, which is currently recorded on the International Union for Conservation of Nature (IUCN) Red List and in the “Red Data Book of Chinese Plants: the Rare and Endangered Plants”. Its total chloroplast genome length is 125,050 bp, including a large single copy region of 76,387 bp, a short single copy gene region of 15 bp, and a pair of inverted repeats (IRs) of 24,324 bp. We annotated 80 genes in this chloroplast genome, including 51 protein-coding genes, 4 ribosomal RNAs, 4 pseudogenes and 21 tRNA genes. We found 15 genes duplicated in the IR regions, and the overall GC content was found to be 38.17%. Phylogenetic analysis showed that *M. oleifera* is closely related to *Erythralium scandens* comparing nine chloroplast genomes from Santalales.

Keywords Chloroplast genome · *Malania oleifera* · Phylogenetic analysis

Background

Malania oleifera Chun et S. Lee, is the only species of the genus *Malania* within the Olacaceae family, and whose natural distribution is restricted to China within the southeast of Yunnan and the west of Guangxi (Qiu and Lin 1988). It is an excellent tree for the restoration and reconstruction of vegetation in karst region (Lv et al. 2016). The seeds of *M. oleifera* are rich in edible oils and seed oil contains

rich nervonic acid (Lee 1980; Yuan et al. 2009; Tang et al. 2013). Currently, *M. oleifera* is recorded on the IUCN Red List as being vulnerable (Sun 1998). It is also listed as under “second level” of protection in the “Red Data Book of Chinese Plants: the Rare and Endangered Plants” (Fu 1992). Therefore, research is imminent to conserve the valuable genetic resources of *M. oleifera*. So far, few studies on genetic diversity have been reported. We sequenced the chloroplast genome of *M. oleifera* with high-throughput Illumina

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