


Complete chloroplast genome sequence of *Murraya paniculata* (Rutaceae): a widely used folk medicinal herb

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ABSTRACT

Murraya paniculata, is traditionally used for management of gut, air way and cardiovascular disorders. In this study, we sequenced the complete chloroplast genome of *M. paniculata* based on next-generation sequencing and used the data to assess genomic resources. The chloroplast genome of *M. paniculata* is 160,280 bp in length consisting of large and small single-copy regions of length 87,605 and 18,609 bp, separated by two IR regions of 27,033 bp. The overall GC content was 38.61%. De novo assembly and annotation showed the presence of unique genes with 85 protein-coding genes, 29 tRNA genes, and eight rRNA genes. A maximum-likelihood phylogenomic analysis showed that *M. paniculata* was closely related to *M. caloxylon*.

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Murraya paniculata (Rutaceae), is a folk medicinal plant widely used in Asia as antinociceptive, anti-inflammatory, and antioxidant. (Menezes et al. 2017; Sharma et al. 2017). However, only a few genomic resources have been explored. Chloroplast genome is valuable sources of genetic markers for phylogenetic analyses, genetic diversity evaluation, and plant molecular identification (Dong et al. 2012). Here, we sequenced and analyzed the chloroplast genome of *M. paniculata* based on the next-generation sequencing method (Dong et al. 2013). The main goals of this study were to establish and characterize the organization of the whole chloroplast genome of *M. paniculata* and to retrieve valuable genomic resources for this species.

We collected fresh healthy leaves from *M. paniculata* species growing in the Funing, Yunnan province. Voucher specimen was stored in herbarium of Institute of Chinese Materia Medica (CMMI, accession number 532628LY0238), China Academy of Chinese Medical Sciences. Total genomic DNA was extracted and purified following the method of Chen et al. (2019). Paired-end (2 × 150 bp) sequencing was performed by Novogene Bioinformatics Technology Co. Ltd (Beijing, China), using the Illumina HiSeq X-Ten platform. The paired-end reads were qualitatively assessed and assembled with GetOrganelle (Jin et al. 2019). The annotation was performed with GeSeq (Tillich et al. 2017). The annotated gen-

omic sequence had been submitted to GenBank with the accession number MT747442.

The chloroplast genome of *M. paniculata* is 160,280 bp in length consisting of large and small single-copy regions of length 87,605 and 18,609 bp, separated by two IR regions of 27,033 bp. GC content was 38.61%. The genome consisted of 122 different genes, including 85 protein-coding genes, 29 distinct tRNA genes, and eight rRNA genes.

To confirm the phylogenetic location of *M. paniculata* within the family of Rutaceae, a total of 21 complete cp genomes of Rutaceae were obtained from GenBank, and *Azadirachta indica* in Meliaceae family was used as out-group. The 23 complete chloroplast sequences were aligned by the MAFFT version 7 software (Kato and Standley 2013). Phylogenetic analysis was conducted based on maximum likelihood (ML) analyses implemented in IQ-TREE 2.0.5 (Minh et al. 2020) under the TVM + F + R2 nucleotide substitution model, which was selected by ModelFinder (Kalyaanamoorthy et al. 2017). Support for the inferred ML tree was inferred by bootstrapping with 1000 replicates. Phylogenetic analysis results strongly supported that *M. paniculata* was closely related to *Merrillia caloxylon* (Figure 1). The chloroplast genome of *M. paniculata* will provide useful genetic information for further study on genetic diversity and conservation of Rutaceae species.

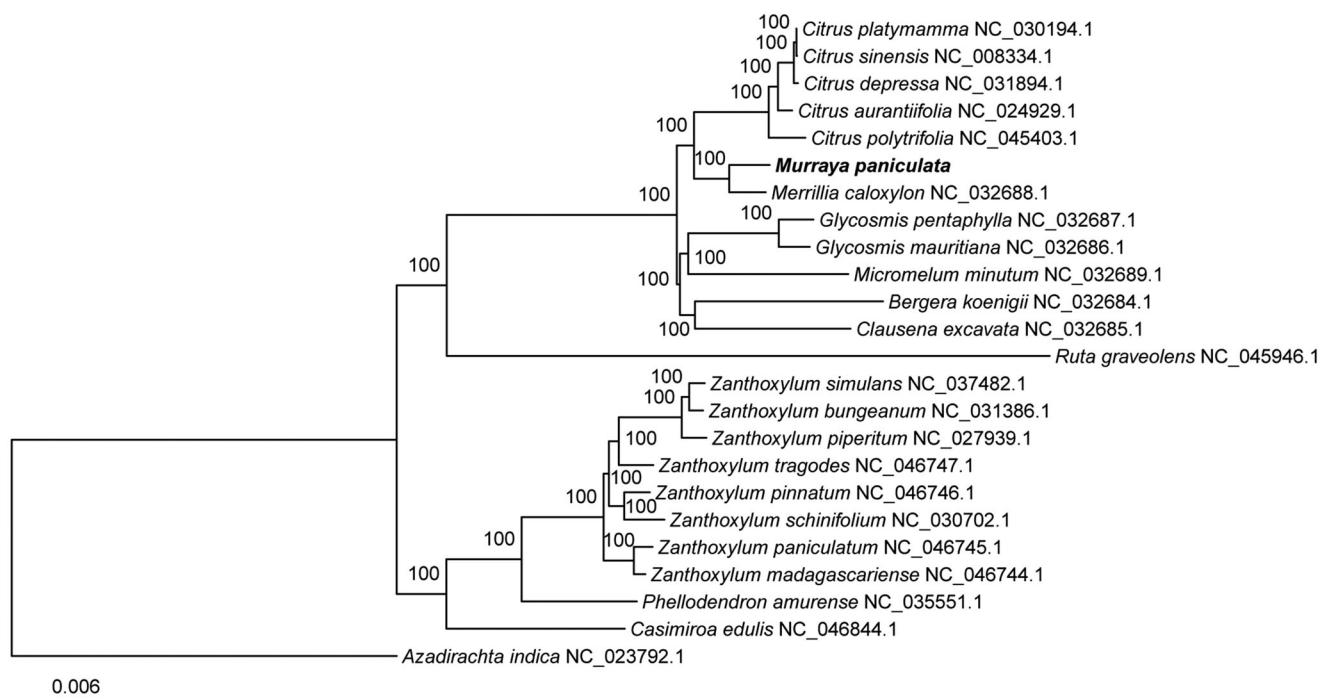


Figure 1. Phylogenetic tree reconstruction of 23 taxa using maximum likelihood (ML) methods based on the chloroplast genome sequences. ML bootstrap support value presented at each node.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov>, reference number MT747442.

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