

The re-sequencing and re-assembly of complete chloroplast genome of *Melastoma dodecandrum* (Melastomataceae) from Fujian, China

Yang Hao^{a,b,c}, Zhenying Wen^{a,b}, Bin Chen^{a,b}, Wenchao Han^{a,b}, Zhongjian Liu^{a,b} and Donghui Peng^{a,b}

^aCollege of Landscape Architecture, Fujian Agriculture and Forestry University, Fuzhou, China; ^bKey Laboratory of National Forestry and Grassland Administration for Orchid Conservation and Utilization at College of Landscape Architecture, Fujian Agriculture and Forestry University, Fuzhou, China; ^cNingxia Polytechnic, Yinchuan, China

ABSTRACT

The plant genus *Melastoma* of the family Melastomataceae is comprised of nine species and one variety in China. *Melastoma dodecandrum* is the only creeping species of this genus. Previous study has reported the complete chloroplast genome of *M. dodecandrum* from Guangzhou, China, but there may be some differences between plant populations from different regions. Herein, we reported the complete chloroplast genome of *M. dodecandrum* from Fuzhou, China, which was assembled from Pacbio and whole genome data was sequenced. The sequence has a circular molecular length of 156,598 bp and contained 129 genes. Phylogenetic analysis indicated that *M. dodecandrum* was closely related to *M. candidum* in Melastomataceae. The study aims to provide insights for the future studies on the differences in molecular evolution level between plant populations of *M. dodecandrum* and taxonomy of *Melastoma*.

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The genus *Melastoma* has undergone species radiation. It might have happened during the last one million years (Renner and Meyer 2001), it has approximately 100 species in total with nine species and one variety in China (Chen 2007). *Melastoma dodecandrum*, the only creeping species within *Melastoma* genus, is widely distributed in tropical and subtropical regions of China except Hainan (Editors Commitment 1984). Recent study (Zheng et al. 2019) has finished the complete chloroplast genome sequencing of *M. dodecandrum* (GenBank accession MH748092, the sequence was not released on NCBI, accessed on 11 May 2019), which is a circular molecule of 156,611 bp in length from Guangzhou, China. Herein, we report a different result of 156,598 bp length in *M. dodecandrum* from Fuzhou, Fujian, to integrate the future studies on the differences in molecular evolution level between plant populations from different regions of *M. dodecandrum* and taxonomy of *Melastoma*.

For the re-assembly of this chloroplast genome, the sequence data were extracted from the total sequencing data from whole-genome of a *M. dodecandrum* individual sampled from Fuzhou, Fujian, China (N 26°13'19", E 119°17'27") using Pacbio sequencing effort. The voucher specimen is kept at the Fujian Agricultural and Forestry University Herbarium (Med-01). Approximately 10 Gb of Pacbio sequence data were extracted from the total sequencing output and input into Organelle PBA (Soorni et al. 2017)

to assemble the chloroplast genome. Annotation of the chloroplast genome was performed using the Dual Organellar GenoMe Annotator (DOGMA) online tool (Wyman et al. 2004) and Geneious ver. 2019.1.1 (Li et al. 2019), then manually verified and corrected by comparison with *Opisthocentra clidemioides* (GenBank accession KX826828).

The complete chloroplast genome sequence of *M. dodecandrum* (GenBank accession MK836406) was 156,598 bp in length, with a large single-copy (LSC) region of 85,992 bp, a small single-copy (SSC) region of 18,286 bp, separated by two inverted repeat (IR) regions of 26,160 bp each. It was predicted to contain 129 genes, including 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The overall GC content was 37.2%. While the chloroplast genome sequence of *M. dodecandrum* from Guangzhou (Zheng et al. 2019) was 156,611 bp in length, and the corresponding values in LSC, SSC, and IR regions were 86,015 bp, 17,096 bp, and 26,750 bp, respectively. There may be two reasons for the difference in the length of *M. dodecandrum*, the different species of reference annotation and the differences between plant populations.

The phylogenetic tree was constructed to demonstrate the relationships between *Melastoma* and other genera. The chloroplast genome of *M. dodecandrum* was aligned with other 19 chloroplast genome sequences of Melastomataceae and 3 Myrtaceae species as outgroup, using RAXML

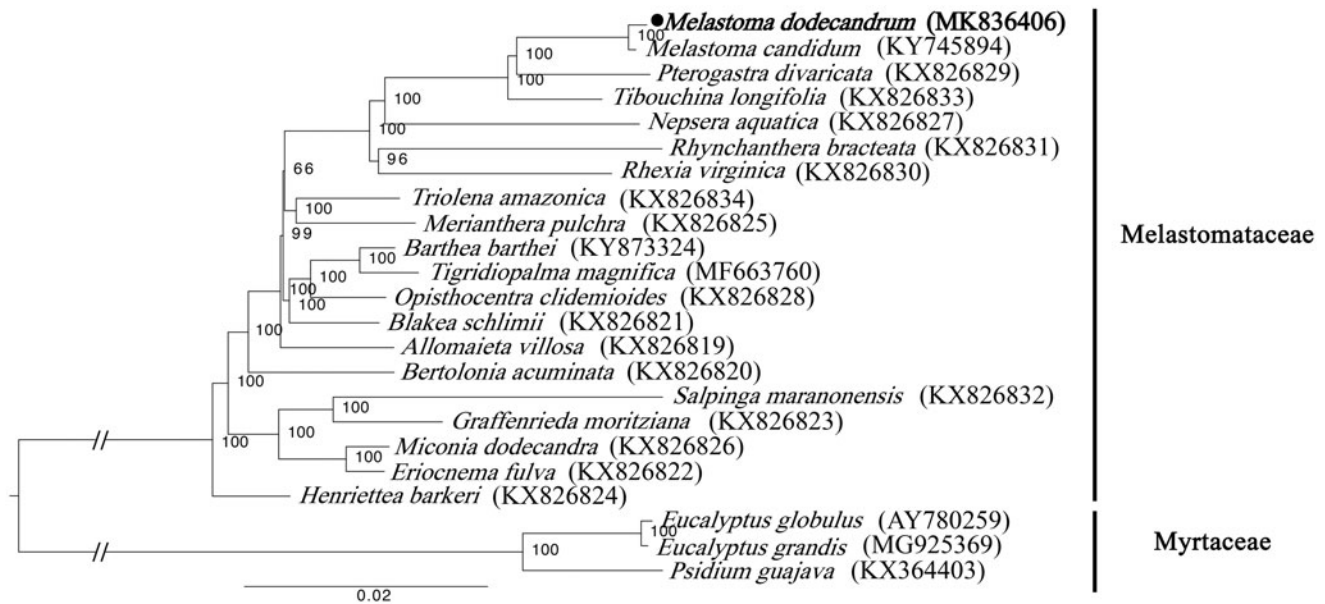


Figure 1 Maximum likelihood tree of Melastomataceae based on complete chloroplast genomes, with Myrtaceae species as outgroup. Bootstrap support values (based on 1000 replicates) are shown next to the nodes. Scale in substitutions per site.

(Stamatakis 2014) to construct the maximum likelihood tree (Figure 1). The maximum likelihood tree indicates that *M. dodecandrum* is phylogenetically close to *M. candidum*.

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Disclosure statement

No potential conflict of interest was reported by the authors.

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