

MITOGENOME ANNOUNCEMENT



The complete chloroplast genome of *Syzygium acuminatissimum*

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ABSTRACT

Syzygium acuminatissimum is a valuable hard wood species in southern China. In this study, we sequenced, assembled and annotated the complete chloroplast genome of *S. acuminatissimum*. The complete cp genome of *S. acuminatissimum* was 159,352 bp in length, with a total of 109 unique annotated genes, including 78 protein-coding genes, 27 tRNA genes and 4 rRNA genes. Phylogenetic analysis showed that *S. acuminatissimum* was closely related to its congener *S. aromaticum*.

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Introduction

Syzygium acuminatissimum (Blume) Candolle, belonging to Myrtaceae, is an evergreen tree distributed in the low-latitude subtropical forests of China (Peng and Wang 1995). With perfectly straight trunk and hard wood, it is a valuable material for furniture (Zhou 2001). Previous authors studied leaf photoprotection and cultivation of this species (Liu et al. 2013; Zhu et al. 2018), and phylogenetic position of *Syzygium* in the family Myrtaceae was resolved based on sequences of three chloroplast (cp) fragments (Biffin et al. 2006). In this study, we assembled and annotated the complete cp

genome of *S. acuminatissimum*, and investigated its phylogenetic relationship with related species in this family.

Fresh leaves of an *S. acuminatissimum* individual were collected from the Conghua Baimu Nursery (113°24′06″E, 23°43′04″N), Guangzhou and the voucher specimen (Zhang-20200729) was deposited at the Herbarium of Sun Yat-sen University (SYS), Guangzhou, China. Genomic DNA was extracted using the CTAB method (Doyle and Doyle 1987), and a DNA shotgun library was constructed according to the manufacturer's protocol (reads size: 250 bp) and sequenced on an Illumina HiSeq X TEN platform (Illumina, San Diego,

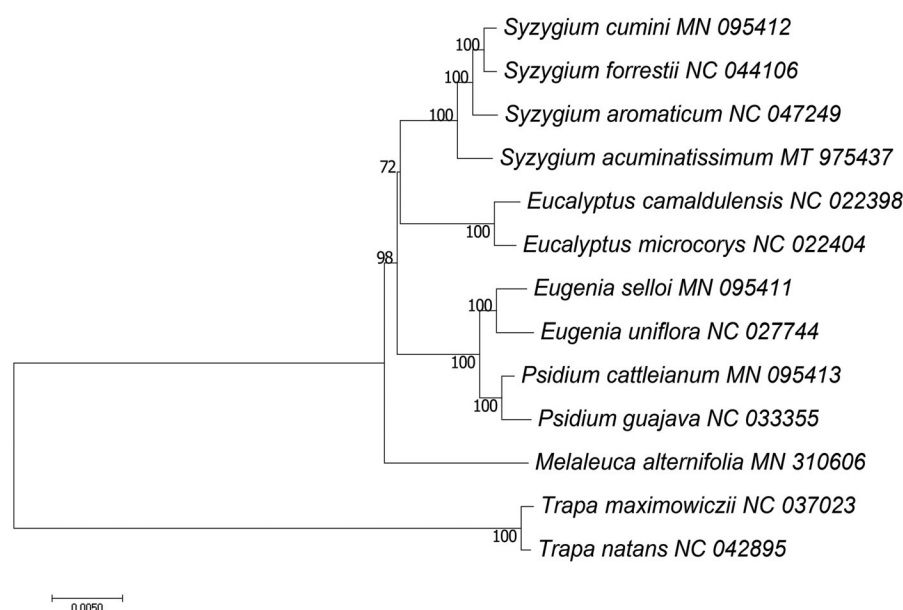


Figure 1. Maximum likelihood tree of 11 Myrtaceae species based on sequences of 78 common chloroplast protein-coding genes. Two Lythraceae species were used as outgroups. Bootstrap support values (%) are shown on branches.

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CA, USA). After quality control with SOAPnuke (Chen et al. 2018), about 2 Gb of clean reads was used to assemble the complete cp genome using SPAdes v3.13.0 (Bankevich et al. 2012), with the cp genome of *Syzygium cumini* (MN095412, template size: 1,58,499 bp) as the reference. Gene annotation was conducted by GeSeq (Tillich et al. 2017). The annotated cp genome sequence was submitted to GenBank (accession number: MT975437).

The complete cp genome of *S. acuminatissimum* was 1,59,352 bp in length with a typical quadrant structure, including a large single-copy (LSC) of 87,993 bp, a small single-copy (SSC) of 18,417 bp, and a pair of inverted repeats (IRs) of 26,471 bp. A total of 109 unique genes, including 78 protein coding genes (PCGs), 27 tRNAs and 4 rRNAs, were annotated. The overall GC content of the cp genome was 34.73%. To resolve the phylogenetic relationships of *S. acuminatissimum* with other species in Myrtaceae, we selected 11 species from Myrtaceae as ingroups and 2 species from Lythraceae as outgroups. Based on 78 common PCGs, we used RAxML (Stamatakis 2014) to construct maximum likelihood (ML) tree with 1000 bootstrap replicates. The phylogenetic tree showed that *S. acuminatissimum* was closely related to *S. aromaticum* (Figure 1). The cp genome of *S. acuminatissimum* in this study provides useful information for future phylogenetic research on this genus.

Disclosure statement

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

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Data availability statement

The data of this study are available on GenBank with the accession number MT975437 (<https://www.ncbi.nlm.nih.gov/nuccore/MT975437>).

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