

MITOGENOME ANNOUNCEMENT



The complete plastome of *Syzygium odoratum* (Lour.) DC. 1928 (Myrtaceae)

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ABSTRACT

Syzygium odoratum (Lour.) DC. 1828 is a deciduous shrub in the family Myrtaceae. This species grows in sparse forests, especially in mountains, valleys, and broad-leaved evergreen forests along streams from 100 to 400 m above sea level. The primary distribution is in southern China (e.g. Guangdong, Guangxi, Hainan, etc.) and other south Asian countries (e.g. Vietnam). Here, we report and characterize the complete plastome from a cultivar of *S. odoratum* (Lour.) DC. 1828. The complete plastome is 159,352 bp in length with a typical structure and gene content found in angiosperms, including two inverted repeat regions (IRs) of 26,472 bp, a large single-copy (LSC) region of 87,993 bp, and a small single-copy (SSC) region of 18,415 bp. The plastome contains 132 genes, consisting of 84 protein-coding genes, 37 tRNA genes, and eight rRNA genes. The overall G/C content in the plastome of *S. odoratum* is 36.9%. By inferring phylogenetic relationships based on the existing data of related taxa, we find that *S. odoratum* is most closely related to *Syzygium acuminatissimum*, (Blume) DC. 1828 given the current sampling. The complete plastome sequence of *S. odoratum* will provide a useful resource for conservation genetics of this species, as well as for phylogenetic studies involving Myrtaceae.

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Syzygium odoratum (Lour.) DC. 1828 is a deciduous shrub in the family Myrtaceae. This species grows in sparse forests, especially in mountains, valleys, and broad-leaved evergreen forests along streams from 100 to 400 m above sea level. The primary distribution is in southern China (e.g. Guangdong, Guangxi, Hainan, etc.) and other south Asian countries (e.g. Vietnam). *Syzygium odoratum* can be used as materials for vehicles, sleepers, bridges, and ship building. Additional important ecological functions include acting as strong windbreaks and sand fixation, therefore, the species can be used for coastal sand greening (Chen 1984). We report the complete plastome of *S. odoratum* in this study (GenBank accession number is MZ929420.1), to improve the quality of collections, medicinal applications, and phylogenetic investigations focused on Myrtaceae.

In this study, fresh leaves of *S. odoratum* were sampled from Ledong county in Hainan, China (109.17°E, 18.75°N). The leaves were dried in silica gel. A voucher specimen (voucher code: Wang et al., A254) and its associated DNA have been deposited in the Herbarium of the Institute of Herbarium of China National GenBank (code of herbarium: HUTB) at Hainan University (<https://ha.hainanu.edu.cn/home2020/>, H.-F. Wang and hfwang@hainanu.edu.cn) under the voucher number Wang et al. A254. Total genomic DNA was extracted from dried leaf tissue with the cetyltrimethyl ammonium bromide (CTAB) protocol of Doyle and Doyle (1987).

This experiment was reported by Zhu et al. (2018) with the sequencing having been done on the BGISEq-500 platform. Cleaned sequencing data of *S. odoratum* were used for plastome assembly using MITObim v1.8 (Hahn et al. 2013). Geneious R8.0.2 (Biomatters Ltd., Auckland, New Zealand) was used to annotate the plastid assembly (MZ929420.1) and the annotation was corrected with DOGMA (Wyman et al. 2004). The results of our study indicate that the complete length of the plastome of *S. odoratum* encompasses 159,352 bp with the typical quadripartite structure of angiosperms, including two inverted repeats (IRs) of 26,472 bp, a large single-copy (LSC) region of 87,993 bp, and a small single-copy (SSC) region of 18,415 bp. The plastome contains 132 genes, consisting of 84 protein-coding genes (seven of which are duplicated in the IR), 37 tRNA genes (eight of which are duplicated in the IR), and four rRNA genes (5S rRNA, 4.5S rRNA, 23S rRNA, and 16S rRNA; all are duplicated in the IR). The overall G/C content of the *S. odoratum* plastome is 36.9%, with the corresponding values of the LSC, SSC, and IR region being 34.7%, 30.6%, and 42.7%, respectively. Comparison of the *S. odoratum* plastome to previously published data shows a high level of gene synteny with one publicly available species, *Syzygium acuminatissimum* (Blume) DC. 1828.

We used RAxML (Stamatakis 2006) with 1000 bootstraps under the GTRGAMMA1 substitution model to reconstruct a maximum-likelihood (ML) phylogeny of eight published

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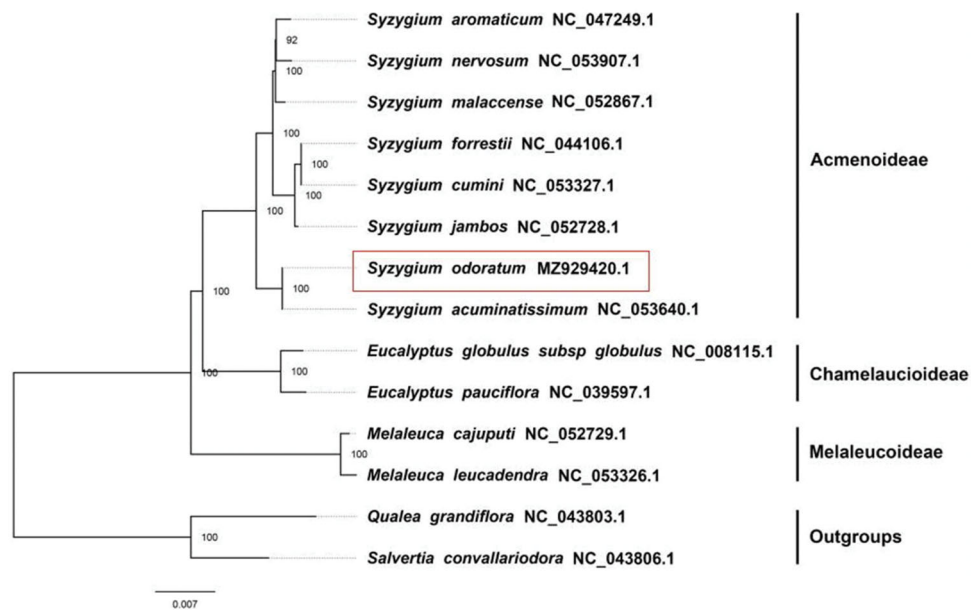


Figure 1. The maximum-likelihood phylogeny recovered from 14 complete plastome sequences using RAxML. The focal species of this study, *S. odoratum* (GenBank accession MZ929420.1). The box means the newly reported complete plastome of *Syzygium odoratum* in this study.

complete plastomes of *Syzygium*, using *Qualea grandiflora* Mart. 1824, (NC043803.1) and *Salvertia convallariodora* A. St.-Hil. 1820 (NC043806.1) as outgroups. By inferring phylogenetic relationships based on the existing data of related taxa, we find that *S. odoratum* is most closely related to *S. acuminatissimum* given the current sampling (Figure 1). Most nodes in the plastome ML tree were highly supported. The plastid sequence of *S. odoratum* has promotes the relevant conservation and phylogenetic investigation of Myrtaceae, bringing great benefits to deepen the understanding of species within the family.

Acknowledgements

Ethics statement: The study was approved by the institutional review board of Hainan University, Haikou, China. The collection of plant materials is carried out in accordance with guidelines provided by the Hainan University and Hainan province regulations. Field studies comply with Hainan province legislation.

Authors contributions

Hua-Feng Wang and De-Jia Hou involved in the conception and design, Li-Da Chen analyzed and interpreted the data; Li-Da Chen and De-Jia Hou drafted the manuscript, Hua-Feng Wang revised it critically for intellectual content; and all authors finally approved the version to be published; and that all authors agree to be accountable for all aspects of the work.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The genome sequence data supporting the results of this study are publicly available in GenBank of NCBI (<https://www.ncbi.nlm.nih.gov/>) with registration number MZ929420.1. The associated BioProject, SRA, and Bio-Sample numbers are SRR15651130, PRJNA748537, and SAMN20858405, respectively.

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