


## The complete plastome of *Spondias dulcis* (Anacardiaceae): an edible deciduous tree species from South America

Xu-Long Yang, Xin-Xin Xu and Hua-Feng Wang 

Sanya Nanfan Research Institute, Hainan University, Sanya, China

### ABSTRACT

*Spondias dulcis* is a deciduous tree in the family Anacardiaceae. The species originates in South America and now is widely cultivated in tropical areas due to its edible fruits. In this study, we find that the length of the complete plastome of *S. dulcis* is 162,256 bp. It includes 35 tRNA genes and eight rRNA genes, 86 protein-coding genes and totally 130 genes. The complete plastome of *S. dulcis* includes a small single-copy (SSC) region of 18,459 bp, a large single-copy (LSC) region of 89,353 bp, and two inverted repeats (IRs) regions of 27,222 bp. The total G/C content of *S. dulcis* is 37.7%. It shows that *S. dulcis* is closely related to *S. mombin* within Anacardiaceae. It will contribute to the conservation genetics of *S. dulcis* and the phylogenetic studies in Anacardiaceae.

### ARTICLE HISTORY

Received 9 June 2022  
Accepted 14 September 2022

### KEYWORDS

Tropical fruits; genetics;  
Hainan; breeding;  
systematics; plastome

### Introduction

*Spondias dulcis* Parkinson (1773) is a deciduous tree in the family Anacardiaceae (Buerki et al. 2010). The species originates in South America and is now widely cultivated in tropical areas (Buerki et al. 2010), partly because its fruits can be eaten. The species is called alien olive due to the fruits looking like olive. Here, we report the complete plastome of *Spondias dulcis*, which is expected to improve the quality of relevant collections and phylogenetic investigation of Anacardiaceae.

In this study, *S. dulcis* Parkinson was sampled from the city of Qionghai in Hainan, China (110.46°E, 19.35°N). The tree of *Spondias dulcis* is 14 meters high and 16 cm in diameter at breast height. A voucher specimen (voucher code: D.-J. Chen, X.-R. Ke, A20, HUTB) and associated DNA were deposited in the Herbarium of Hainan University, Hainan province, China (code of herbarium: HUTB). The experiment was carried out as reported by Zhu et al. (2018). Cleaned sequencing data was assembled with GetOrganelle v1.7.5.0 (Santos and Almeida 2019). The plastome was annotated using the plastome of *Spondias bahiensis* P. Carvalho, Van den Berg and M. Machado (NC\_030526.1) as a reference using Geneious v2021.1.1 (Biomatters Ltd, Auckland, New Zealand).



In this study, we find that the length of the complete plastome of *S. dulcis* is 162,256 bp. It includes 35 tRNA genes and eight rRNA genes, 86 protein-coding genes, and totally 130 genes. The complete plastome of *Spondias dulcis* includes a small single-copy (SSC) region of 18,459 bp, a large single-copy (LSC) region of 89,353 bp and two inverted repeats (IRs) regions of 27,222 bp. Eighteen protein-coding genes are duplicated in the IR. Seven tRNA are duplicated in the IR.

5S rRNA, 16S rRNA, 4.5S rRNA, and 23S rRNA are duplicated in the IR. The overall G/C content in the plastome is 37.7%, of which the corresponding value for the LSC, SSC, and IR regions are 35.7%, 32.2%, and 42.7%, respectively.

Based on existing data of related taxa from NCBI, we reconstructed a phylogenetic tree with RAxML with 1000 bootstraps with CIPRES (<http://www.phylo.org/portal2/logininput.action>). We found that *Spondias dulcis* is more closely related to *Spondias mombin* than other species in this genus in this study (Figure 1). Most nodes in the plastome maximum-likelihood (ML) tree of Anacardiaceae were highly supported. Furthermore, the plastid sequence of *S. dulcis* will promote relevant conservation and phylogenetic investigation of Anacardiaceae. Notably, Spondiadoideae was not supported as monophyletic as reported in previous studies (e.g. Pell et al. 2011; Weeks et al. 2014; Sun et al. 2016). Chen et al. (2016) found that *Spondias*, *Dracontomelon*, and *Buchanania* are in the same clade and sister to the rest of the family with moderate support, however, Muellner-Riehl et al. (2016) found that *Spondias* is closer to *Dracontomelon* than other genera within Anacardiaceae. Therefore, our study would bring great benefits to deepen the understanding complex relationships of plants such as those in Anacardiaceae.

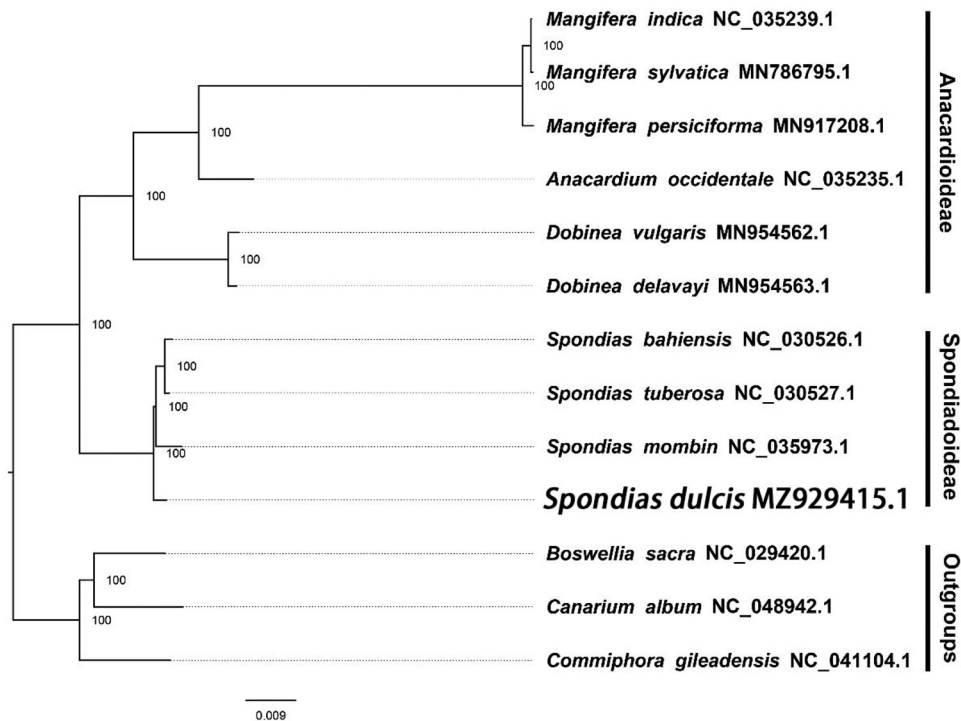
### Ethics statement

The study was approved by the institutional review board of Hainan University, Haikou, China. The collection of plant materials was conducted in accordance with guidelines provided by the Hainan University and Hainan province regulations. Field studies complied with Hainan province legislation.

**CONTACT** Hua-Feng Wang  279745044@qq.com  Sanya Nanfan Research Institute, Hainan University, Sanya, China

© 2022 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.



**Figure 1.** The maximum likelihood phylogeny obtained from 13 complete plastid sequences by RAxML. Support values are shown with bootstrap values at the nodes.

## Author contributions

Hua-Feng Wang designed the project. Xu-Long Yang and Xin-Xin Xu analyzed and interpreted the data; Xu-Long Yang and Xin-Xin Xu drafted the manuscript. Hua-Feng Wang revised it critically for intellectual content. All authors approved the final version of the manuscript.

## Disclosure statement

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

## Funding

This study is funded by the Hainan Province Science and Technology Special Fund [ZDYF2022XDNY190] and Hainan Provincial Natural Science Foundation of China [421RC486]. The funding information are inner funding of Hainan province.

## ORCID

Hua-Feng Wang  <http://orcid.org/0000-0003-3331-2898>

## Data availability statement

The results of the genome sequence data are publicly available in NCBI GenBank (<https://www.ncbi.nlm.nih.gov/>) with registration number MZ929415.1. The associated BioProject, SRA and Bio-Sample numbers are PRJNA748537, SRR15651129 and SAMN20858429 respectively. A specimen was deposited at Hainan University (<https://ha.hainanu.edu.cn/home2020/>) under the voucher number D.-J. Chen, X.-R. Ke, A20.

## References

- Buerki S, Lowry PP, Alvarez N, Razafimandimbison SG, Küpfer P, Callmander MW. 2010. Phylogeny and circumscription of Sapindaceae revisited: molecular sequence data, morphology, and biogeography support recognition of a new family. *Plecevo*. 143(2):148–159.
- Chen Z-D, Yang T, Lin L, Lu L-M, Li H-L, Sun M, Liu B, Chen M, Niu Y-T, Ye J-F, et al. 2016. Tree of life for the genera of Chinese vascular plants. *J Syst Evol*. 54(4):277–306.
- Muellner-Riehl AN, Weeks A, Clayton JW, Buerki S, Nauheimer L, Chiang YC, Cody S, Pell SK. 2016. Molecular phylogenetics and molecular clock dating of Sapindales based on plastid *rbcL*, *atpB* and *trnL-trnF* DNA sequences. *Taxon*. 65(5):1019–1036.
- Pell SK, Mitchell JD, Miller AJ, Lobova TA. 2011. Anacardiaceae. In: Kubitzki K, editor. *The families and genera of flowering plants. X. Flowering plants: Eudicots. Sapindales, Cucurbitales, Myrtaceae*. Berlin: Springer; p. 7–50.
- Santos V, Almeida C. 2019. The complete chloroplast genome sequences of three *Spondias* species reveal close relationship among the species. *Genet Mol Biol*. 42(1):132–138.
- Sun M, Naeem R, Su J-X, Cao Z-Y, Burleigh JG, Soltis PS, Soltis DE, Chen Z-D. 2016. Phylogeny of the Rosidae: a dense taxon sampling analysis. *J Syst Evol*. 54(4):363–391.
- Weeks A, Zapata F, Pell SK, Daly DC, Mitchell J, Fine PVA. 2014. To move or evolve: contrasting patterns of intercontinental connectivity and climatic niche evolution in “Terebinthaceae” (Anacardiaceae and Burseraceae). *Front Genet*. 5:409.
- Zhu ZX, Mu WX, Wang JH, Zhang JR, Zhao KK, Friedman CR, Wang HF. 2018. Complete plastome sequence of *Dracaena cambodiana* (Asparagaceae): a species considered “vulnerable” in Southeast Asia. *Mitochondrial DNA B Resour*. 3(2):620–621.