

MITOGENOME ANNOUNCEMENT



## The complete chloroplast genome of *Dunnia sinensis* (Rubiaceae): a monotypic species endemic to Guangdong, China

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### ABSTRACT

*Dunnia sinensis*, a monotypic genus of the Rubiaceae, is an Endangered species endemic to China. Its complete chloroplast genome was determined to be 154,909 bp in length and the GC content was 37.80%. The sequence includes a large single-copy region of 84,894 bp, a small single-copy region of 16,973 bp, and the inverted region of 26,521 bp in length. It contains 130 genes, including 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The ML and BI analyses revealed *D. sinensis* was closely related to *Galium mollugo* and *Leptodermis scabrida* with strong bootstrap values belonging to the subfamily Rubioideae.

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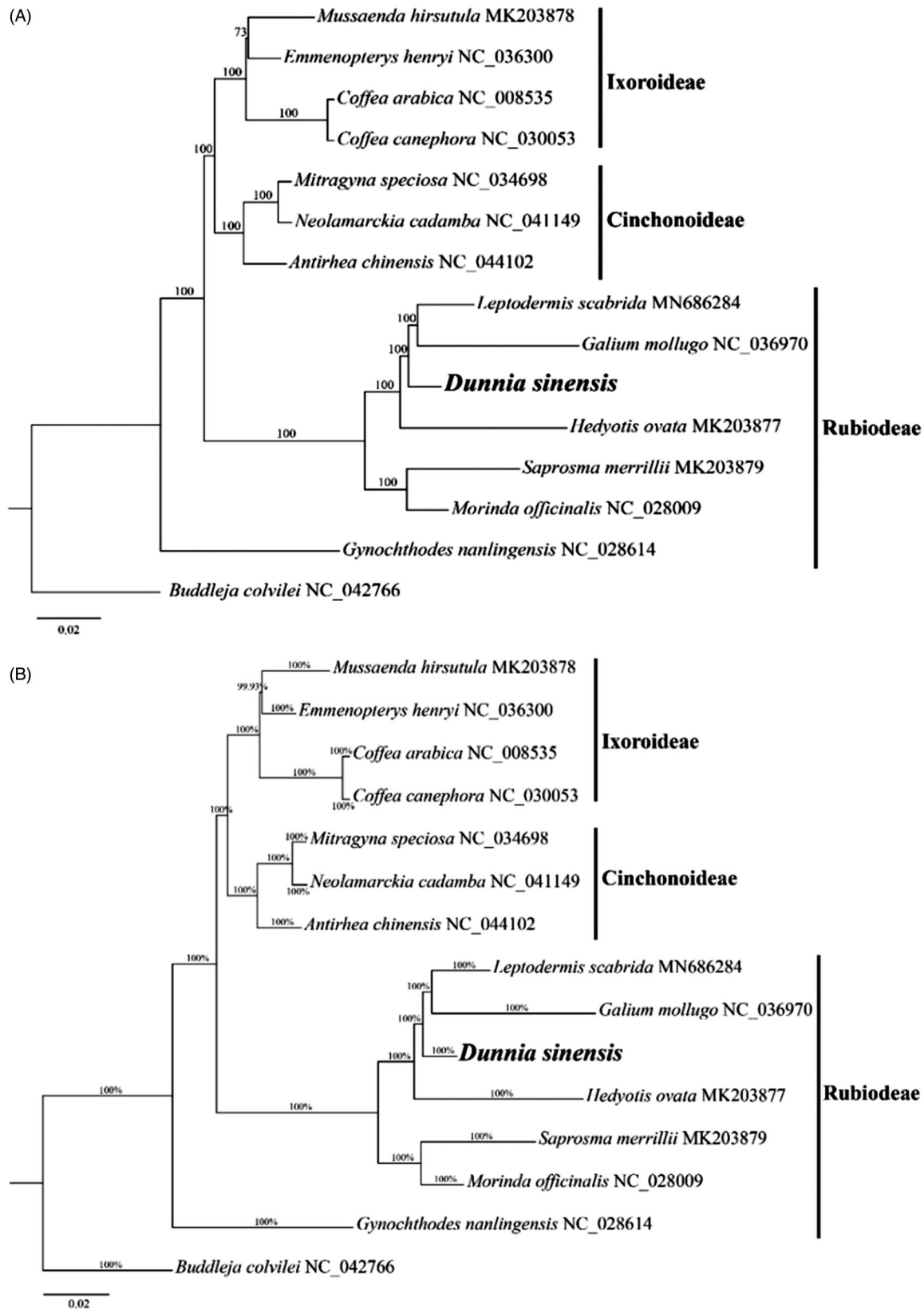
*Dunnia sinensis* Tutch., a monotypic genus of Rubiaceae, is endemic species distributed in the south of Guangdong Province in China (Tutcher 1905; Ridsdale 1978). It is a woody shrub with a height of up to 3 m, flowering from late April to May and fruiting in October and November. Besides great ornamental value, *Dunnia sinensis* was used as an anti-inflammatory drug in folk medicine (Wei et al. 2000). Over the past decades, its habitats, usually along streams or hillside at 100–600 m of altitude, have been seriously destructed for economic development, and therefore it was listed as the national key protected wild species (Chiang et al. 2002; Ge et al. 2002; Wang and Xie 2004). Although its phylogeographic pattern and phylogenetic studies were conducted previously (Chiang et al. 2002; Ge et al. 2002; Rydin et al. 2008), no genome has been reported until now. Therefore, we reported the complete chloroplast (cp) genome of this endangered endemic species (GenBank Accession Number: MN883829) to provide useful genomic information for evolutionary dynamics and conservation evaluation.

The fresh and healthy leaves of *D. sinensis* were collected from Taishan County, Jiangmen City, Guangdong Province of China (22°14'13.57"N, 112°56'50"E, 66 m). The voucher specimen (Ruijiang Wang, Gangtao Wang, Ying Zhang 4395) was deposited in the South China Botanical Garden Herbarium, Chinese Academy of Sciences (IBSC). The total genomic DNA was extracted from the silica-gel dried leaves following the modified CTAB method (Doyle and Doyle 1987). Then, the genomic library (paired-end, PE = 150 bp) was sequenced on an Illumina Hiseq X Ten platform at Beijing Genomics

Institute (Shenzhen, China). Totally, 2 Gb sequence reads were obtained and used to assemble the cp genome after filtering and trimming the low-quality reads and adaptor sequences. The complete cp genome assembly was executed on NOVOPlasty 2.6.3 (Dierckxsens et al. 2017) with the default k-mer of 39–59, while Geneious version 11.0.3 (Kearse et al. 2012) was used to annotate the genome. *Galium mollugo* (GenBank accession number: NC\_036970) was used as the reference plastid genome for assembling and annotation. The tRNA genes were annotated on ARAGORN (Laslett and Canbäck 2004).

The complete cp genome of *D. sinensis* was 154,909 bp with the typical quadripartite structure of angiosperms, including a small single-copy region (SSC) of 16,973 bp, a large single-copy region (LSC) of 84,894 bp, and the inverted repeat region (IR) of 26,521 bp. The genome harbored 130 genes, including 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The overall GC content in the cp genome of *D. sinensis* was 37.80%, in which the corresponding value of the SSC, LSC, and IR region was 32.10, 35.70, and 42.90%, respectively.

The cp genome sequences of 13 species (Zhang et al. 2020) within Rubiaceae were used to infer the phylogenetic position of *D. sinensis*, using *Buddleja colvilei* Hook. f. & Thoms (Loganiaceae) (NC\_042766) as outgroup. A Maximum Likelihood (ML) tree was constructed by using IQ-TREE (Nguyen et al. 2015) with 1000 bootstrap replicates under the GTR + F + R4 substitution model. Bayesian inference (BI) was also performed with MrBayes v.3.2.6 (Ronquist et al.



**Figure 1.** Maximum likelihood tree (A) and Bayesian inference (B) based on 14 (including *Dunnia sinensis*) whole cp genome sequences in Rubiaceae. Bootstrap support values were shown at the branches. *Buddleja colvilei* served as outgroup.

2012). The ML and BI trees were consistent and robust, showing *D. sinensis* had a close relationship with *Galium mollugo* and *Leptodermis scabrida*, which formed an independent clade of the subfamily Rubioideae (Figure 1). The

phylogenetic relationship of *D. sinensis* with genomic data was uncovered for the first time, largely enriching genetic resources for resolving the complex phylogeny relationship of Rubiaceae.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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## References

- Chiang YC, Ge XJ, Chou CH, Wu WL, Chiang TY. 2002. Nucleotide sequence diversity at the methionine synthase locus in Endangered *Dunnia sinensis* (Rubiaceae): an evaluation of the positive selection hypothesis. *Mol Biol Evol.* 19(8):1367–1375.
- Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. *Nucleic Acids Res.* 45(4):e18.
- Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochem Bull.* 19:11–15.
- Ge XJ, Chiang YC, Chou CH, Chiang TY. 2002. Nested clade analysis of *Dunnia sinensis* (Rubiaceae), a monotypic genus from China based on organelle DNA sequences. *Conserv Genet.* 3(4):351–362.
- Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics.* 28(12):1647–1649.
- Laslett D, Canbäck B. 2004. ARAGORN, a program to detect tRNA genes and tmRNA genes in nucleotide sequences. *Nucleic Acids Res.* 32(1):11–16.
- Nguyen LT, Schmidt HA, Haeseler von A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol Biol Evol.* 32(1):268–274.
- Ridsdale CE. 1978. The taxonomic position of *Dunnia* (Rubiaceae). *Blum J Plant Tax Plant Geog.* 24:367–368.
- Ronquist F, Teslenko M, van der Mark P, Ayres D L, Darling A, Höhna S, Larget B, Liu L, Suchard M A, Huelsenbeck J P, et al. 2012. MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst Biol.* 61(3):539–542.
- Rydin C, Razafimandimbison SG, Bremer B. 2008. Rare and enigmatic genera (*Dunnia*, *Schizocolea*, *Colletocema*), sisters to species-rich clades: phylogeny and aspects of conservation biology in the coffee family. *Mol Phylogenet Evol.* 48(1):74–83.
- Tutcher WJ. 1905. Description of some new species, and notes on other Chinese plants. *J Linn Soc Bot.* 37(258):69–70.
- Wang S, Xie Y. 2004. China species red list. Vol 1. Red List. Beijing: Higher Education Press; p. 407. (in Chinese)
- Wei XY, Xie HH, Ge XJ, Zhang FX. 2000. Iridoids from *Dunnia sinensis*. *Phytochemistry.* 53(8):837–840.
- Zhang Y, Chen S, Wang RJ. 2020. The complete chloroplast genome of *Leptodermis scabrida* (Rubiaceae): an endemic shrub in Himalaya-Hengduan Mountains. *Mitochondrial DNA B.* 5(1):169–170.