

## The plastid genome of winter cropping plants *Ficus tinctoria* (Moraceae)

Huanhuan Chen<sup>a,b</sup> , Qing Liu<sup>c</sup> and Lizhou Tang<sup>a,b</sup>

<sup>a</sup>College of Biological Resource and Food Engineering, Qujing Normal University, Qujing, PR China; <sup>b</sup>Key Laboratory of Yunnan Province Universities of the Diversity and Ecological Adaptive Evolution for Animals and Plants on YunGui Plateau, Qujing Normal University, Qujing, PR China; <sup>c</sup>School of Resources and Environment, Baoshan University, Baoshan, PR China

### ABSTRACT

*Ficus tinctoria* subsp. *gibbosa* (Blume) Corner is a hemiepiphytic dioecious fig species of the genus *Ficus* in the family Moraceae. To better determine its phylogenetic location with respect to the other *Ficus* species, the complete plastid genome of *F. tinctoria* was sequenced. The whole plastome is 160,342 bp in length, consisting of a pair of inverted repeat (IR) regions of 25,859 bp, one large single-copy (LSC) region of 88,526 bp, and one small single-copy (SSC) region of 20,098 bp. The overall GC content of the whole plastome is 35.9%. Further, maximum likelihood (ML) phylogenetic analyze was conducted using 23 complete fig plastomes, which support close relationships among *F. tinctoria*, *F. heteropleura*, *F. obscura*, and *F. deltoidea*.

### ARTICLE HISTORY

Received 6 June 2020  
Accepted 20 June 2020

### KEYWORDS

*Ficus tinctoria*; chloroplast genome; phylogenetic analysis

*Ficus tinctoria* subsp. *gibbosa* (Blume) Corner, a hemiepiphytic species distributed in tropical and subtropical areas of much of Asia, was assigned to subgenus *Sycidium* in the family Moraceae (Berg and Corner 2005). In contrast to other figs of seasonal climates, which have low production in winter, both sexes of *F. tinctoria* produce major crops at the coldest time of the year (Chen et al. 2015). This unique phenological strategy has evolved to maximize seed dispersal and establishment in seasonal climate (Chen et al. 2015). For a better understanding of the relationships of *F. tinctoria* and other fig species, it is necessary to reconstruct a phylogenetic tree based on high-throughput sequencing approaches.

Fresh young leaves of *F. tinctoria* in Xishuangbanna (Yunnan, China; Long. 101.2611 E, Lat. 21.9275 N, 555 m) were picked for DNA extraction (Doyle and Dickson 1987). The voucher was deposited at the Biodiversity Research Group of Xishuangbanna Tropical Botanical Garden (Accession Number: XTBG-BRG-10002). The whole plastid genome was sequenced following Zhang et al. (2016), and their 15 universal primer pairs were used to perform long-range PCR for next-generation sequencing. The contigs were aligned with the cp genomes of relatively related species and annotated in Geneious version 4.8.

The plastome of *F. tinctoria* (LAU10102), with a length of 160,342 bp, was 869 bp larger than that of *F. racemosa* (159,473 bp, KT368151). It was also 32, 260, and 285 bp smaller than that of *F. hirta* (160,374 bp, MN364706), *F. carica* (160,602 bp, KY635880), and *F. religiosa* (160,627 bp, KY416513). The length of the inverted repeats (IRs), large single-copy (LSC), and small single-copy (SSC) regions of *F.*

*altissima* was 25,859, 88,526, and 20,098 bp, respectively. The overall G + C content is 35.9% (LSC, 33.6%; SSC, 2.9%; IR, 42.6%).

Furthermore, based on 23 published plastid genome sequences (Bruun-Lund et al. 2017), we reconstructed a phylogenetic tree (Figure 1) to confirm the evolutionary relationship between *F. tinctoria* and other species with published plastomes in *Ficus*. Maximum likelihood (ML) phylogenetic analyses were performed base on GTR + F + R2 model in the iqtree version 1.6.7 program with 1000 bootstrap replicates (Nguyen et al. 2015). The ML phylogenetic tree with 42–100% bootstrap values at each node supported that *F. tinctoria* was closely related to and *F. heteropleura*, *F. obscura*, and *F. deltoidea*.

### Disclosure statement

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

### Funding

This work was supported by [Yunnan Agricultural Foundation Projects] under grant [Number: 2017FG001 (-051)]; [The Project of Key Laboratory of Insect Resources Conservation and Utilization in Western Yunnan] under grant [Number: YJF(2019)No.57].

### ORCID

Huanhuan Chen  <http://orcid.org/0000-0001-9477-1014>

**CONTACT** Lizhou Tang  [tangbiology@163.com](mailto:tangbiology@163.com)  College of Biological Resource and Food Engineering, Qujing Normal University, Qujing, PR China

© 2020 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-NonCommercial License (<http://creativecommons.org/licenses/by-nc/4.0/>), which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

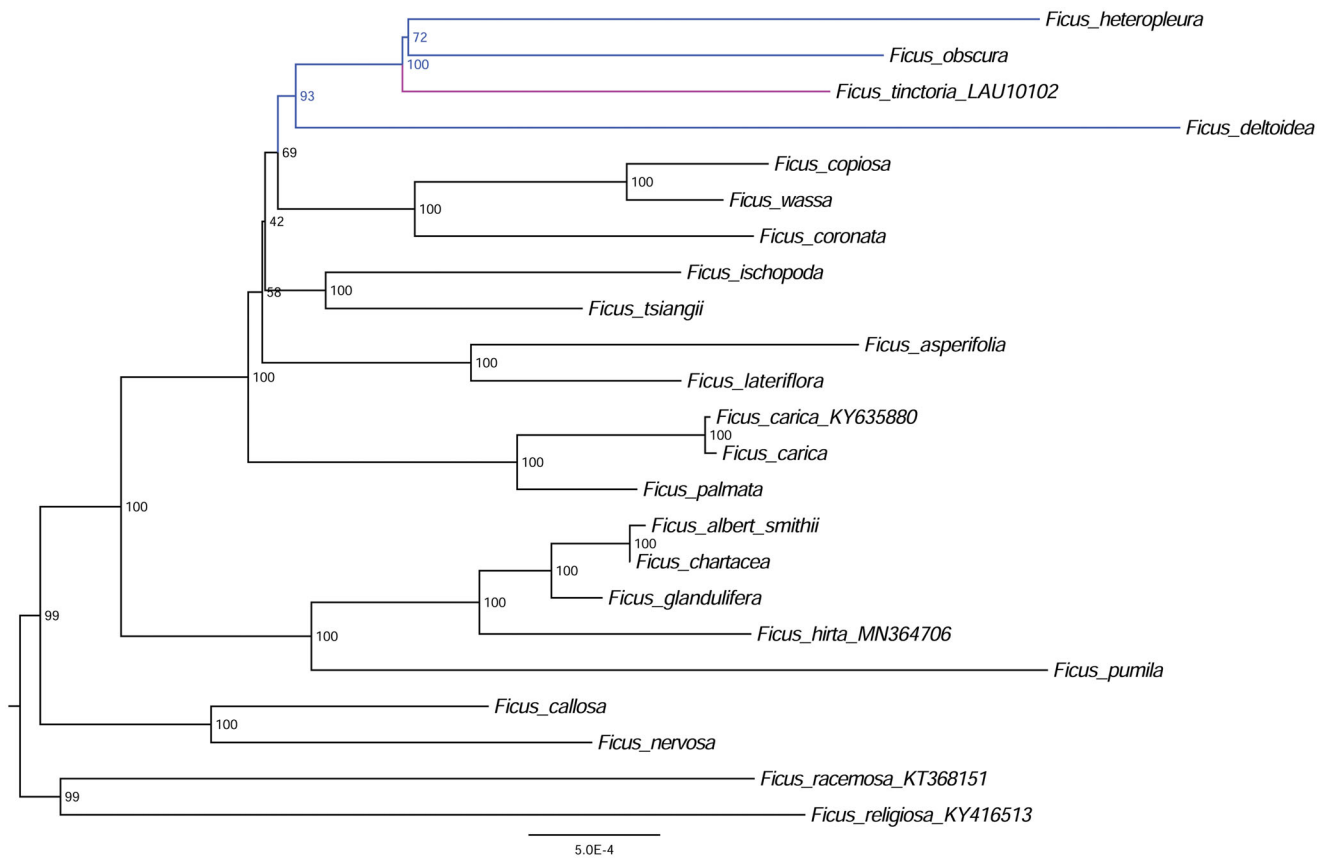


Figure 1. The ML phylogenetic tree for *F. tinctoria* based on other 22 species plastid genomes.

## Data availability statement

The data that support the finding of this study are openly available in Moraceae Chloroplast Genome Database (<http://lsgdb.wordpress.com>). Accession number is LAU10102.

## References

- Berg CC, Corner E. 2005. Moraceae (Ficus) in: Flora Malesiana. Series I, Vol. 17. Leiden, The Netherlands: Nooteboom H. D. National Herbarium of Netherland; p. 1–625.
- Bruun-Lund S, Clement WL, Kjellberg F, Rønsted N. 2017. First plastid phylogenomic study reveals potential cyto-nuclear discordance in the evolutionary history of *Ficus* L. (Moraceae). *Mol Phylogenet Evol.* 109: 93–104.
- Chen HH, Peng YQ, Zhang Y, Corlett RT. 2015. Winter cropping in *Ficus tinctoria*: an alternative strategy. *Sci Rep.* 5:16496.
- Doyle JJ, Dickson EE. 1987. Preservation of plant samples for DNA restriction endonuclease analysis. *Taxon.* 36(4):715–722.
- Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol Biol Evol.* 32(1):268–274.
- Zhang T, Zeng CX, Yang JB, Li HT, Li DZ. 2016. Fifteen novel universal primer pairs for sequencing whole chloroplast genomes and a primer pair for nuclear ribosomal DNAs. *J Syst Evol.* 54(3):219–227.