

The plastid genome of a large hemiepiphytic plants *Ficus altissima* (Moraceae)

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ABSTRACT

Ficus altissima Blume is a hemiepiphytic monoecious 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. altissima* was sequenced. The whole plastome is 160,251 bp in length, consisting of a pair of inverted repeat (IR) regions of 25,886 bp, one large single-copy (LSC) region of 88,470 bp, and one small single-copy (SSC) region of 20,009 bp. The overall GC content of the whole plastome is 35.9%. Further, maximum likelihood phylogenetic analyses was conducted using 29 complete fig plastomes, which support close relationships among *F. altissima*, *F. benjamina*, *F. microcarpa*, and *F. consociata*.

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Ficus altissima Blume, a hemiepiphytic species distributed in tropical and subtropical areas of much of Asia, was assigned to subgenus *Urostigma* section *Conosycea* in the family Moraceae (Berg and Corner 2005). The figs of *F. altissima* are occupied by two *Eupristina* species in southern China: the pollinator *Eupristina altissima* and the cheater *Eupristina* sp. (Zhao et al. 2014; Chen et al. 2018). Adult females of both species share similar biological characteristics but showed different reproductive strategies (Xu et al. 2016). For a better understanding of the relationships of *F. altissima* and other fig species, it is necessary to reconstruct a phylogenetic tree based on high-throughput sequencing approaches.

Fresh young leaves of *F. altissima* 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-10001). 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 with the cp genomes of relatively related species and annotated in Geneious 4.8.

The plastome of *F. altissima* (LAU10101), with a length of 160,251 bp, was 778 bp larger than that of *F. racemosa* (159,473 bp, KT368151). It was also 123 bp, 351 bp and 376 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 25,886 bp, 88,470 bp, and 20,009 bp, respectively. The overall G + C content is 35.9% (LSC, 33.6%; SSC, 28.8%; IR, 42.6%).

Furthermore, based on 29 published plastid genome sequences (Bruun-Lund et al. 2017), we reconstructed a phylogenetic tree (Figure 1) to confirm the evolutionary relationship between *F. altissima* and other species with published plastomes in *Ficus*. Maximum likelihood (ML) phylogenetic analyses were performed based on GTR + F + R3 model in the iqtree version 1.6.7 program with 1000 bootstrap replicates (Nguyen et al. 2015). The ML phylogenetic tree with 54–100% bootstrap values at each node supported that *F. altissima* was closely related to and *F. benjamina*, *F. consociata*, and *F. microcarpa*.

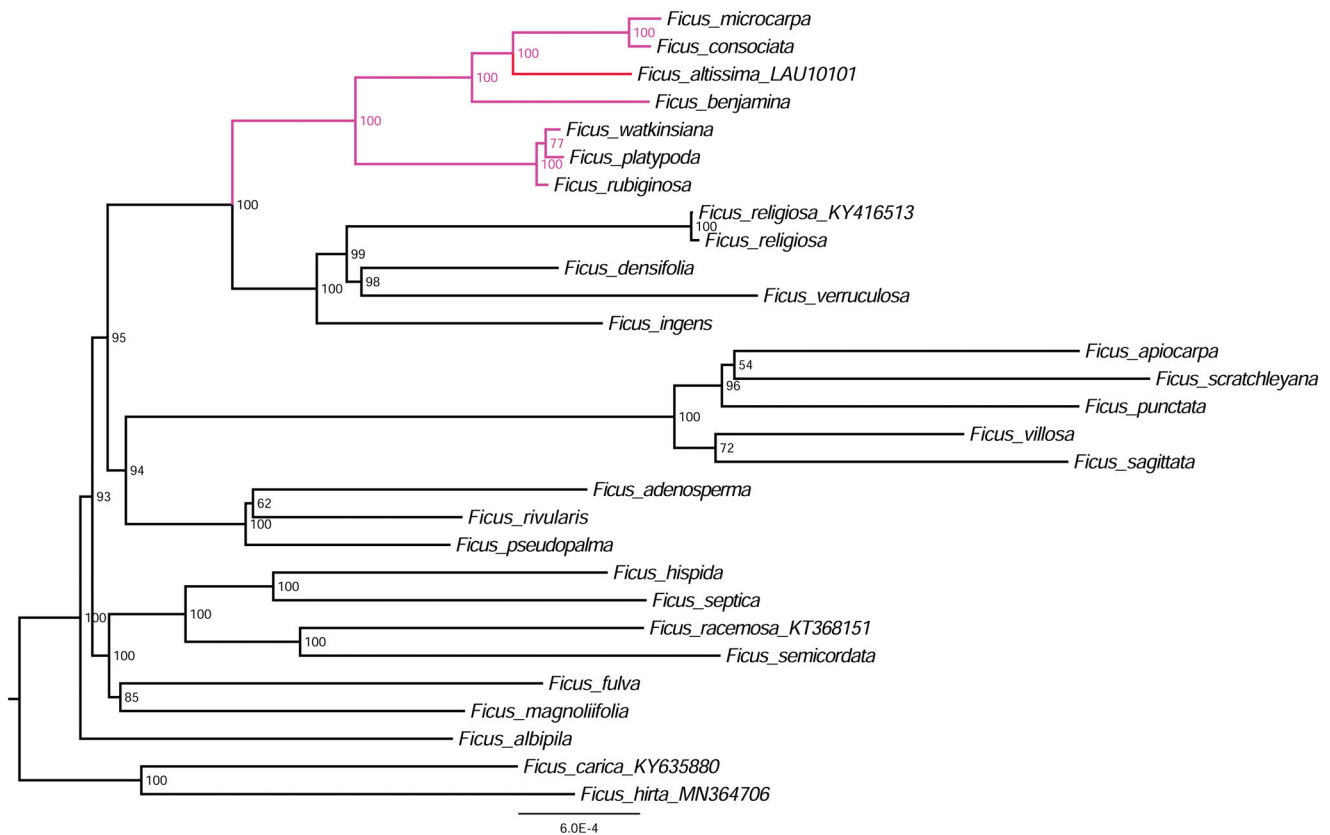


Figure 1. The ML phylogenetic tree for *F. altissima* based on other 27 species plastid genomes.

Disclosure statement

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

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Data availability statement

The data that support the finding of this study are openly available in Moraceae Chloroplast Genome Database (<http://lcgdb.wordpress.com>). Accession numbers are LAU10101.

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