

The chloroplast genome of aromatic plants *Cinnamomum burmanni* (Lauraceae)

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ABSTRACT

Cinnamomum burmanni (Nees et T. Nees) Blume is a valuable aromatic timber tree of the genus *Cinnamomum* Tree in the family Lauraceae. To better determine its phylogenetic location with respect to the other *Cinnamomum* species, the complete chloroplast genome of *C. burmanni* was sequenced. The total chloroplast genome size is 152,775 bp, consisting of a pair of inverted repeats (IRa/b) with a length of 20,092 bp separated by a large single-copy region (LSC) and a small single-copy region (SSC) which are 93,687 and 18,903 bp, respectively. The overall GC content of the cp genome is 39.1%. Further, maximum-likelihood phylogenetic analysis with K3Pu + F+I model was performed using eleven complete plastomes of the Lauraceae, which revealed that *C. burmanni* is closely related to *C. verum*.

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Cinnamomum burmanni (Nees et T. Nees) Blume is an economically important evergreen tree that mainly distributed in the south of the Yangtze River in China, India, Indonesia, Myanmar, Philippines, and Vietnam (<http://foc.iplant.cn/>). The volatile aromatic oil isolated from the stems and leaves of

C. burmanni are rich in eucalyptol (Liu et al. 2007; Li et al. 2016) and thus represent important woody aromatic plants in the genus *Cinnamomum* (Kumar and Kumari 2019). But currently, there is no clear phylogeny for the *Cinnamomum*. To determine the phylogenetic location of *C. burmanni* with

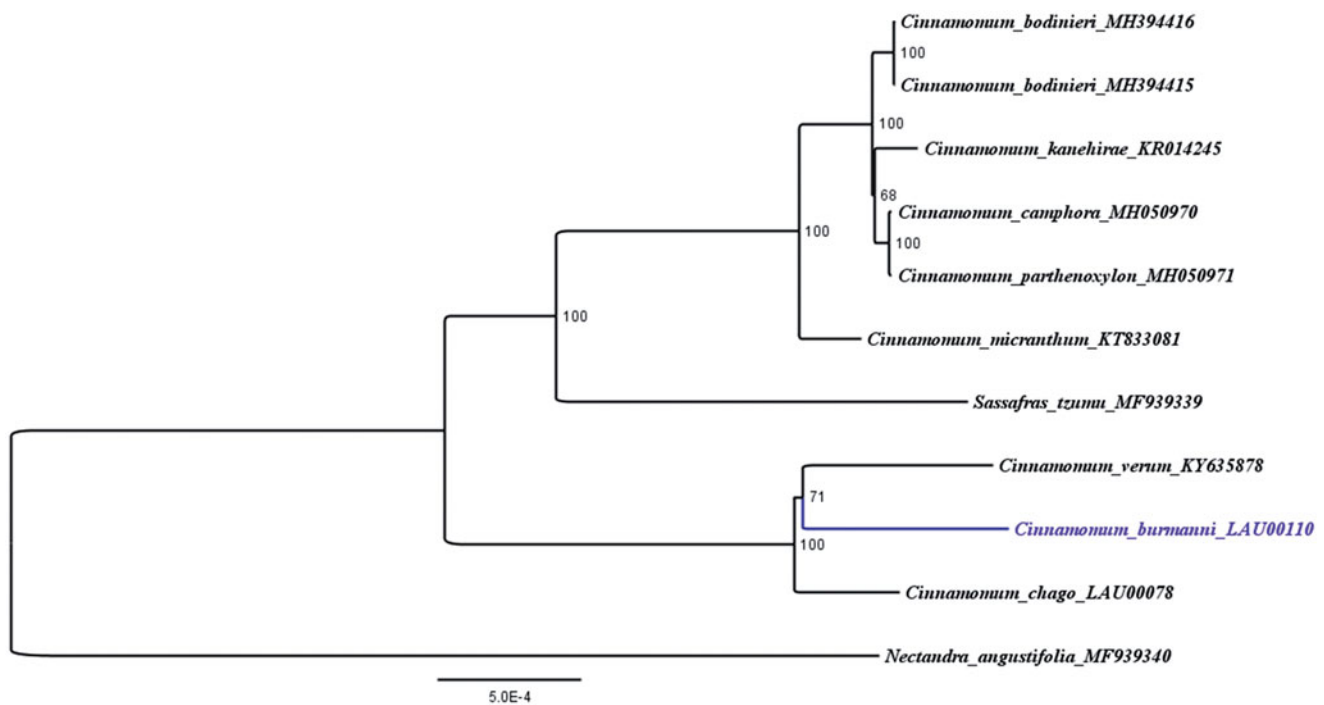


Figure 1. The ML phylogenetic tree for *C. burmanni* based on other 10 species (8 in *Cinnamomum*, 1 in *Nectandra* and 1 in *Sassafras*) plastid genomes.

respect to the other *Cinnamomum* species (Song et al. 2019), the complete chloroplast genome of *C. burmanni* was used to reconstruct a phylogenetic tree based on high throughput sequencing approaches.

Intact, fresh and young leaves of *C. burmanni* were obtained from the Xishuangbanna Tropical Botanical Garden (21.9°N, 101.3°E; 549 m above sea level) for genomic DNA extraction (Doyle and Dickson 1987). The specimens were deposited at the Biodiversity Research Group of XTBG (Accession Number: XTBG-BGR-SY34687). The whole plastid genome was sequenced following Yang et al. (2014), and their 11 universal primer pairs were used to perform long-range PCR for next-generation sequencing. The contigs were aligned using the publicly available plastid genome of *Cinnamomum chago* (Accession Number: LAU00078) (Chen et al. 2019) and annotated in Geneious 4.8.

The chloroplast genome of *C. burmanni* (LAU00110) with a length of 152,775 bp, was the largest of the 11 reported cp genome of *Cinnamomum*, was 10 bp larger than that of *C. verum* (152,765 bp, KY635878) and was 101 bp smaller than that of *C. micranthum* (152,674 bp, KT833081). The complete cp genome of *C. burmanni* composed of a large single-copy (LSC) region of 93,687 bp, a small single-copy (SSC) region of 18,903 bp, and a pair of inverted repeats (IRa/b) of 20,092 bp. The overall GC content is 39.1% (LSC, 38%; SSC, 33.8%; IR, 44.4%).

In order to confirm the evolutionary relationship between *C. burmanni* and other species with published plastomes in *Cinnamomum*, we reconstructed a phylogenetic tree (Figure 1) based on 10 published plastid genome sequences of the Lauraceae. *Nectandra angustifolia* (Accession Number: MF939340) was treated as an out-group (Song et al. 2017). A maximum-likelihood (ML) analysis based on the K3Pu + F + I model was performed with iqtree version 1.6.7 programme using 1000 bootstrap replicates (Figure 1) (Nguyen et al. 2015). The phylogenetic tree reveals that 68–100% bootstrap values at each node supported that *Cinnamomum* species can be divided into two clades, and sisterhood of *C. burmanni* and *C. verum*, followed by *C. chago* in the same clade.

Disclosure statement

No conflict of interest was reported by the authors.

Data archiving statement

The plastome data of the *C. burmanni* will be submitted to Lauraceae Chloroplast Genome Database (<https://lcgdb.wordpress.com>). Accession numbers are LAU00110.

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