


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

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ABSTRACT

Cinnamomum pauciflorum is a valuable aromatic tree of the genus *Cinnamomum* Trew in the family Lauraceae. To better determine its phylogenetic location with other *Cinnamomum* species, the complete chloroplast (cp) genome of *C. pauciflorum* was sequenced. The total cp genome size is 152,766 bp, consisting of a pair of inverted repeats (IRa/b) with a length of 20,074 bp separated by a large single-copy region (LSC) and a small single-copy region (SSC) which are 93,693 and 18,925 bp, respectively. The overall GC content of the cp genome is 39.14%. Maximum-likelihood analysis showed that *C. pauciflorum* has phylogenetic affinities with *Cinnamomum osmophloeum*, *Cinnamomum aromaticum*, *Cinnamomum mollifolium*, and *Cinnamomum tenuipile*, providing new insight into the evolution of Lauraceae.

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Cinnamomum pauciflorum Nees, belonging to the genus *Cinnamomum* Trew in the family Lauraceae, is an aromatic tree species that is mainly distributed in the south of the Yangtze River in China. The principal component distilled from the stem and leaves of *C. pauciflorum* is safrole, which has many applications in the spice industry (Kempriai et al. 2020). To better understand the relationships among *C. pauciflorum* and other *Cinnamomum* species, the whole plastome was sequenced and analyzed within a phylogenetic context.

Fresh young leaves of *C. pauciflorum* were collected from Nanchang (Jiangxi, China; 28.74°N, 115.81°E) for DNA extraction. The experimental material is not an endangered species, and collecting specimens does not require approval. The voucher specimen (ZSS-ZYJ-20200825) was deposited in Jiangxi Forestry Institute (Yongjie Zheng, zyj920581676@gmail.com).

DNA of *C. pauciflorum* was isolated by the modified CTAB method for library construction and sequencing (Jinlu et al. 2013). A 350 bp-insert library was constructed with the NEB Next[®] Ultra[™] DNA Library Prep Kit and sequenced on an Illumina NovaSeq6000, yielding 34,854,648 raw 150 bp paired-end reads. After trimming by fastqc (version:0.11.8), 34,800,926 clean reads were assembled by SPAdes (version: 3.13.0) (Bankevich et al. 2012) using the plastid genome sequence of *Cinnamomum aromaticum* (GenBank: NC_046019) (Xie et al. 2019). The annotated plastid genome sequence has been deposited into GenBank with accession number MW421303.

The chloroplast (cp) genome of *C. pauciflorum*, with a length of 152,766 bp, was 3 bp larger than that of *C. aromaticum* (152,763 bp). The complete cp genome of *C. pauciflorum*

contains a large single-copy (LSC) region of 93,693 bp, a single-copy region (SSC) region of 18,925 bp, and a pair of inverted repeat (IR) regions of 20,074 bp each. The overall GC content is 39.14% (LSC, 37.95%; SSC, 33.82%; IR, 44.43%). The cp genomes were annotated with 120 genes, including 82 protein-coding genes, 34 tRNA genes, and 4 rRNA genes.

A phylogenetic tree was reconstructed to reveal the evolutionary relationship between *C. pauciflorum* and other *Cinnamomum* species, with *Laurus* species as an outgroup (Figure 1). Maximum-likelihood (ML) phylogenetic analyses were performed based on K3Pu + F + I model by iqtree (version:1.6.7) with 1000 bootstrap replicates (Nguyen et al. 2015; Hoang et al. 2018). The phylogenetic reconstruction of the plastome data using ML resulted in a paraphyletic grade of *Cinnamomum* species in which *C. pauciflorum* is nested. While bootstrap support for the backbone topology varied, *C. pauciflorum* formed a moderately supported clade with *Cinnamomum osmophloeum*, *C. aromaticum*, *Cinnamomum mollifolium*, and *Cinnamomum tenuipile*. Data from additional taxa and/or markers are needed to fully resolve these relationships. The complete cp genome of *C. pauciflorum* provides valuable genomic resources for improving our understanding of species phylogeny in Lauraceae, exploring genetic variations, and designing conservation strategies.

Authors' contributions

Yongjie Zheng analyzed the data and wrote the paper; Yanfang Wu contributed the plant materials; Xinliang Liu performed the experiments; Yicun Chen and Yangdong Wang conceived and designed the

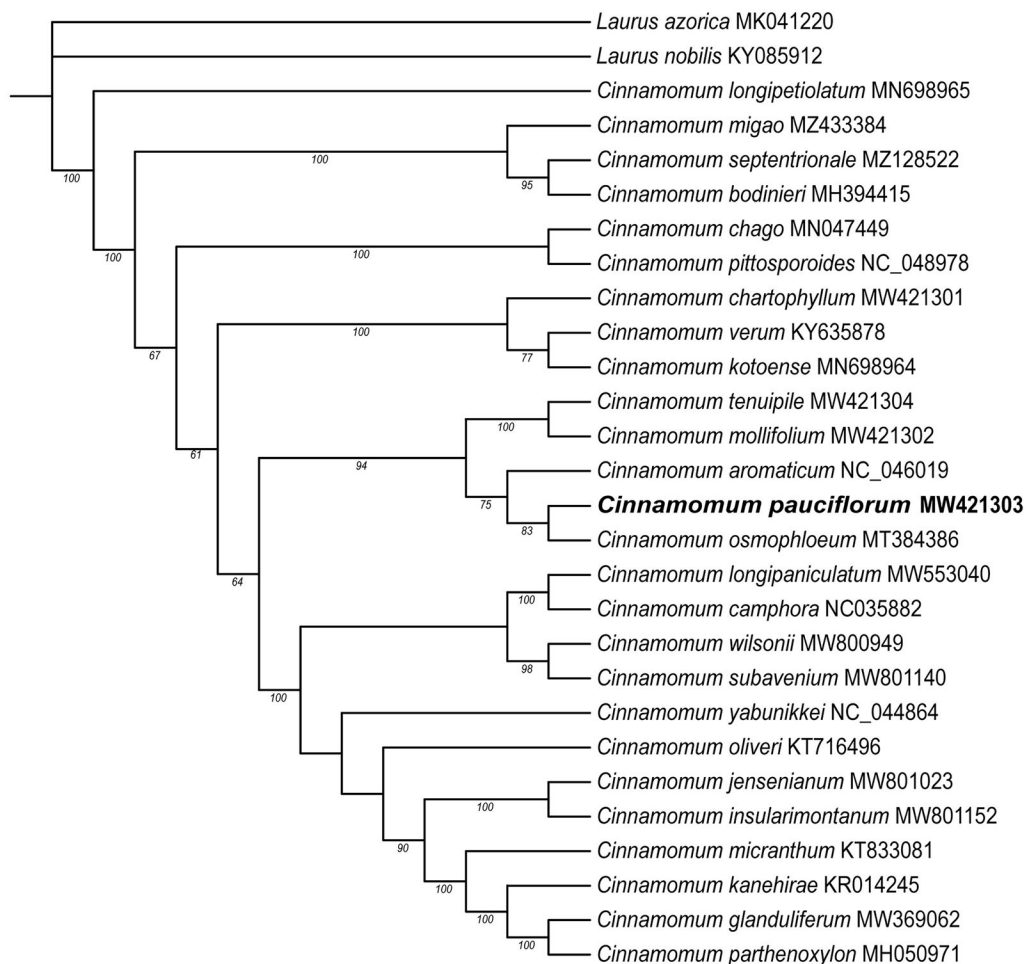


Figure 1. The maximum-likelihood phylogenetic tree for *C. pauciflorum* based on the complete plastid genome sequences. Bootstrap support values ($n = 1000$) are shown at each node.

experiments, reviewed drafts of the paper. All authors agree to be accountable for all aspects of the work.

Disclosure statement

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

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov> (<https://www.ncbi.nlm.nih.gov/>) under the accession no. MW421303. The

associated BioProject, SRA, and Bio-Sample numbers are PRJNA749389, SAMN20368931, and SRR15235414, respectively.

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