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PLASTOME ANNOUNCEMENT

The complete plastid genome of a medicinal tree *Lindera chienii* Cheng 1934 (Lauraceae: Laureae)

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ABSTRACT

Lindera chienii Cheng 1934 is an important medicine plant. The first complete plastid genome sequence of *L. chienii* was assembled and analyzed in this study. The plastid genome is 152,744 bp in length with a GC content of 39.15%, contains a large single-copy region of 93,767 bp and a small single-copy region of 18,843 bp, which were separated by a pair of inverted repeat regions of 20,067 bp. A total of 128 genes were detected in the plastid genome, including eight ribosomal RNA genes, 36 transfer RNA genes, and 81 protein-coding genes. The phylogenomic analysis based on plastid genomes supports the close relationships among *Lindera chienii*, *L. megaphylla* and *Litsea acutivena*.

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Lindera chienii Cheng 1934 (Lauraceae), a dominant evergreen shrub, is an important medicinal plant distributed in the Provinces of Zhejiang and Anhui in China (http://www.iplant.cn/foc). The essential oil from leaves of *Lindera* shows a stronger inhibition than amoxicillin against *Staphylococcus aureus* and *Candida albicans* (Wei et al. 2016). *Lindera* belonging to the core Lauraceae, is often confused with genus *Litsea* and *Laurus* (Liao et al. 2018; Tian et al. 2019; Song et al. 2020; Liu et al. 2020; Liu et al. 2022). For a better understanding of the relationships of *L. chienii* and other Laureae species, we assembled and analyzed the complete plastid genome of *L. chienii* for the first time.

Fresh leaf samples of *L. chienii* were collected from Nanjing Zhongshan Botanical Garden (Jiangsu, China; Long. 118°50′3.19″ E, Lat. 32°03′9.67″ N, 45 m). The voucher was deposited at the Biodiversity Research Group of Xishuangbanna Tropical Botanical Garden (Accession Number: XTBG-BRG-SY36085, Song Yu, songyu@xtbg.ac.cn). Total genomic DNA were extracted with a modified CTAB method (Doyle and Dickson 1987). Genome was sequenced on the Illumina HiSeq 2000 platform at BGI-Shenzhen. About 1.7 Gb pair-end (150 bp) raw reads were obtained. The plastid genome of *L. chienii* was assembled and annotated using GetOrganelle pipe-line (Jin et al. 2020) and GeSeq (https://chlorobox.mpimp-golm.mpg.de/geseq.html) with *Lindera glauca* (MG581443) served as the reference.

The complete plastid genome of *L. chienii* was 152,744 bp in length. The plastid genome possessed a typical quadripartite structure, consisting of a large single-copy (LSC) region (93,767 bp), a small single-copy (SSC) region (18,843 bp), and two inverted repeat (IRa and IRb) regions (20,067 bp). A total of 128 genes were found in the plastid, including 36 transfer RNA (tRNA) genes, eight ribosomal RNA (rRNA) genes and 81 protein-coding genes. The GC content of the complete plastid genome was 39.1%, and those of LSC, SSC, and IR regions were 37.94, 33.90 and 44.43%, respectively.

In order to investigate the phylogenetic relationship between *L. chienii* and related species in Laureae, the complete plastid genome sequences of *L. chienii* and other 49 taxa in Laureae were aligned by MAFFT v7.450 (Katoh et al. 2019). Maximum likelihood (ML) phylogenetic analyses were performed by the IQ-TREE v2.1.1 (Minh et al. 2020) with 1000 bootstrap replicates, and the best model TIM + F+R2 was selected based on IQ-TREE (Figure 1). The result showed that *Lindera* species grouped into four clades. *L. chienii* was located in the same clade with two *Laurus*, five *Litsea*, and seven other *Lindera* species. *L. chienii* is closed related to *L. megaphylla* and *Litsea acutivena* with 100% bootstrap value.

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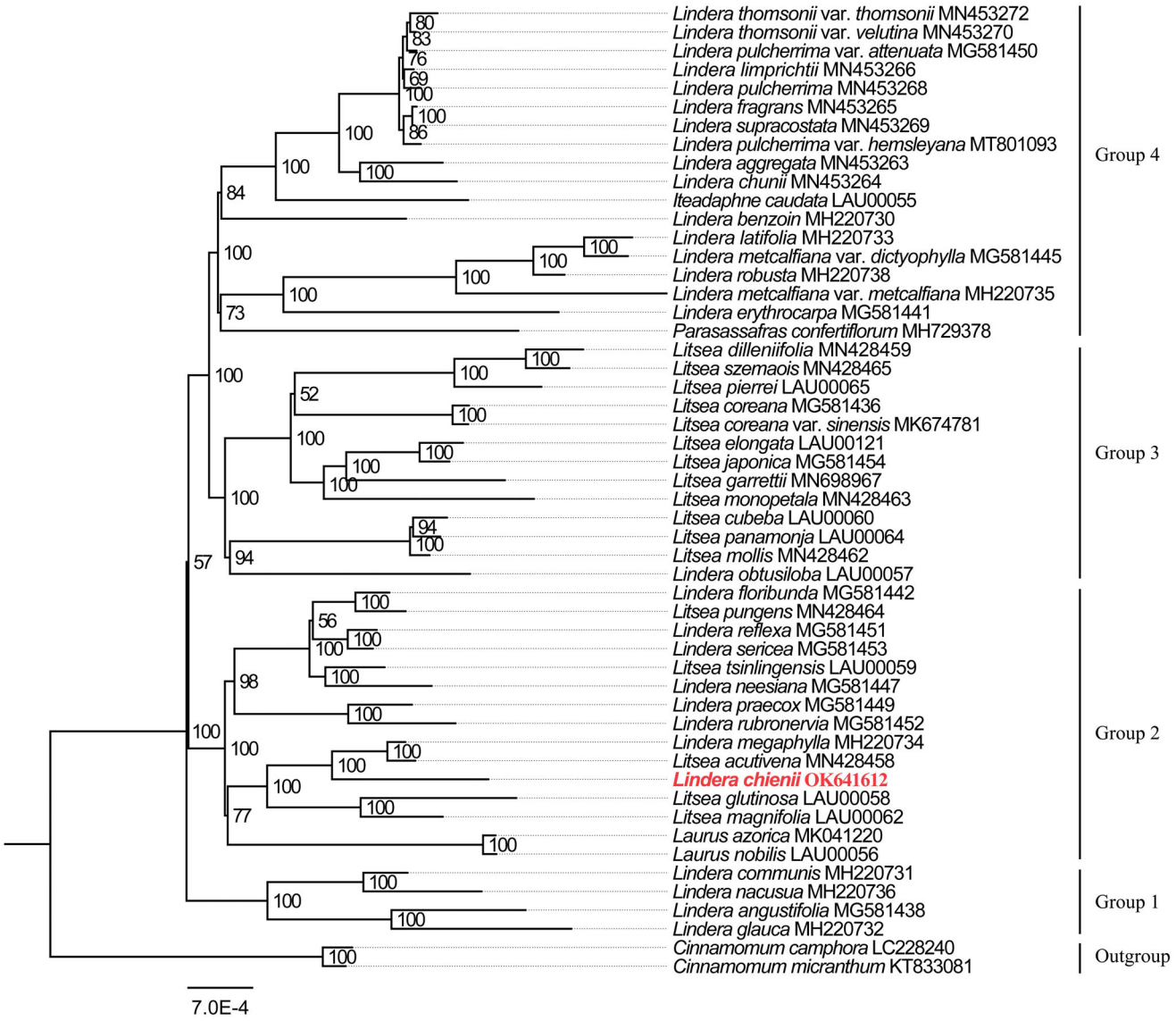

Figure 1. The maximum-likelihood phylogenetic tree constructed with plastid genomes of Laureae.

Author contributions

Chao Liu and Lihong Han were involved in the conception and design, analyses and interpretation of the data and writing of the manuscript; Huanhuan Chen and Jian Cai performed the analysis and interpretation of the data; Lihong Han revised it critically for intellectual content. All authors were involved in the final approval of the version to be published. All authors agree to be accountable for all aspects of the work.

Ethical approval

We confirm that all the research meets ethical guidelines and adheres to the legal requirements of the study country.

Disclosure statement

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

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. OK641612. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA778332, SRR16841626, and SAMN22942607 respectively.

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