

## The re-sequencing of complete chloroplast genome of *Cinnamomum camphora* (Lauraceae) from Quanzhou, China

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### ABSTRACT

*Cinnamomum camphora* is a precious species for its significance of timber. It is also the main component of the subtropical evergreen broad-leaved forest. We report a chloroplast genome of *C. camphora* from Quanzhou, China. The complete chloroplast genome is 152,730 bp in length consisting of a pair of inverted repeat (IR) regions of 19,968 bp, a small single-copy (SSC) region of 18,874 bp, and a large single-copy (LSC) region of 93,706 bp, respectively. The chloroplast genome encoded 116 genes, including 79 protein-coding genes, 36 tRNA genes, and eight rRNA genes. This result will provide useful genomic basis for the phylogenetic research of Lauraceae.

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*Castanopsis camphora* belongs to Lauraceae, it mainly distributed in the tropical and subtropical regions of China, which is an important timber and special economic forest species in Fujian Province (Gao et al. 2018). Modern pharmacological studies have shown that *C. camphora* possesses manifold physiological activities, such as anti-inflammatory (Ye et al. 2018), antioxidant (Gao et al. 2018), antibacterial (Zhou et al. 2017), anti-cancer (Zhang et al. 2019), and anti-fungal (Pragadheesh et al. 2013). So, *C. camphora* is often used to treat inflammation related diseases. However, there are few studies of *C. camphora* on genomic at present. Recent studies (Chen et al. 2017; Wu et al. 2017, 2019) have finished the complete chloroplast genomes sequencing of *C. camphora* (GenBank accession MH050970; GenBank accession MF156716; GenBank accession LC228240) from Xi'an, Nanjing and Taiwan, China. In order to compare the chloroplast differences among different provenances, in this study, we report the complete chloroplast genome of *C. camphora* from Quanzhou, China based on Illumina pair-end sequencing platform, which will establish important basis for the further studies on the phylogenetic analysis of Lauraceae.

Leaf samples of *C. camphora* were collected from Xiangyang (Quanzhou, Fujian, China; 118°29'40.80"E, 25°15'58.39"N), and were dried using silica gel immediately. The voucher specimen is kept at the Herbarium of College of Forestry, Fujian Agriculture and Forestry University (specimen code FAFU08017). Total genomic DNA extraction from fresh leaf tissue, with 500 bp randomly interrupted by the Covaris ultrasonic breaker for library construction. The constructed library was sequenced PE150 using Illumina HiSeq Xten platform, approximately 2GB data generated. Illumina data were filtered by script in the cluster (default parameter:

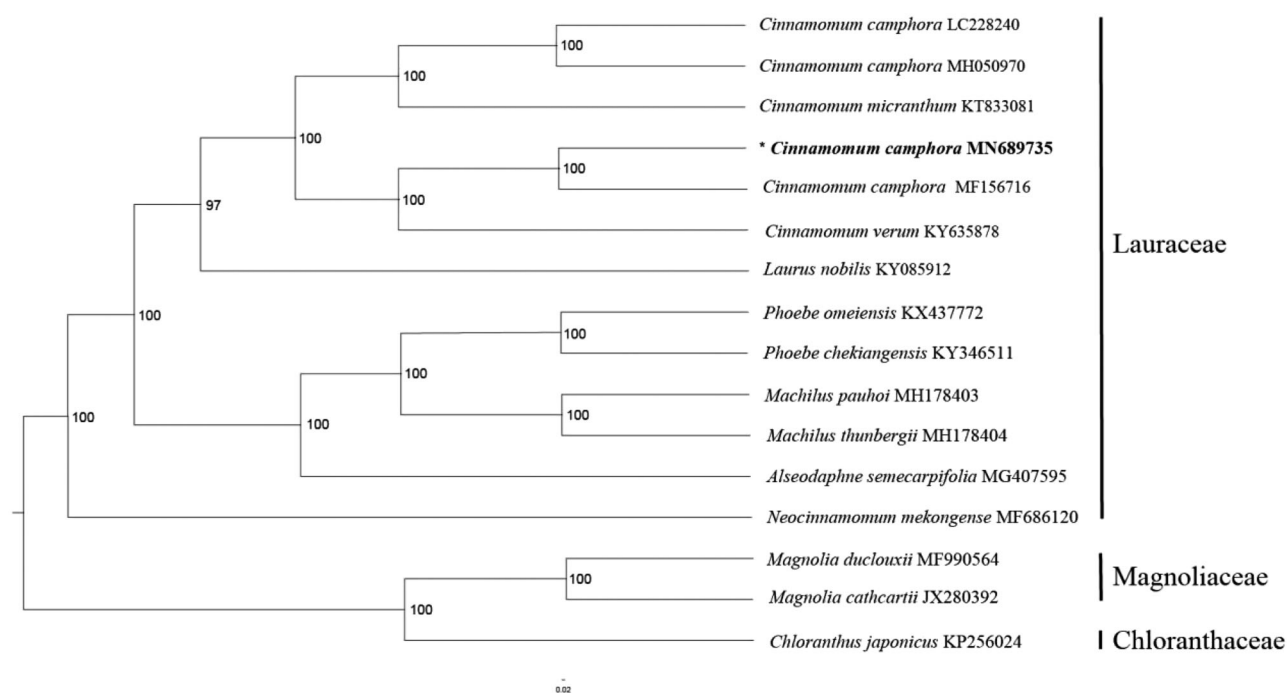
-L 5, -p 0.5, -N 0.1). Chloroplast genome assembled by GetOrganelle pipe-line (<https://github.com/Kinggerm/GetOrganelle>), which can get the plastid-like reads, and the reads were viewed and edited using Bandage (Wick et al. 2015). Assembled chloroplast genome annotation base on comparison with *C. micranthum* (KT833081) using Geneious v 11.1.5 (Biomatters Ltd., Auckland, New Zealand) (Kearse et al. 2012). The annotation result was drawn with the online tool OGDRAW (<http://ogdraw.mpimp-golm.mpg.de/>) (Lohse et al. 2013). The complete chloroplast genome sequence of *C. camphora* was deposited in GenBank (accession number MN689735).

The complete chloroplast genome of *C. camphora* had a total sequence length of 152,730 bp with a biased GC content of 39.2%. It is composed of four parts, a pair of inverted repeats (IR) regions of 19,968 bp, a large single-copy (LSC) region of 93,706 bp, and a small single-copy (SSC) region of 18,874 bp, respectively. A total of 116 unique genes were annotated in *C. camphora* cp genome, including 79 protein-coding genes (PCGs), 36 tRNA genes, and eight rRNA genes. To investigate phylogenetic status of *C. camphora*, a maximum-likelihood (ML) analysis was re-constructed from the complete chloroplast genomes of 16 species using the RAxML software (Stamatakis 2014) performed, including 13 complete chloroplast genomes of Lauraceae, and other three species (*Magnolia duclouxii*, *Magnolia cathcartii*, and *Chloranthus japonicus*) as outgroups (Figure 1). They all downloaded from NCBI GenBank. The sequences were aligned using MAFFT v7.307 (Kato and Standley 2013). The phylogenetic analysis revealed that *C. camphora* (MN326097) was most closely related to *C. camphora* (MF156716). Compared with the three previously reported genomes of *C. camphora* (MH050970; MF156716;

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**Figure 1.** Phylogenetic analysis of 13 species of Lauraceae and three other species (*Magnolia duclouxii*, *Magnolia cathcartii*, *Chloranthus japonicus*) as outgroup based on chloroplast genome sequences using RAxML, bootstrap support value near the branch.

LC228240) (Chen et al. 2017; Wu et al. 2017, 2019), the differences of the genome size, LSC, SSC, IR regions, and GC content were within 169 bp, 99 bp, 239 bp, 229 bp, and 0.08%, respectively, and their protein-coding genes, tRNAs and rRNAs were almost the same, indicating that there was less difference among the four genomes of *C. camphora*. Therefore, we speculate that the chloroplast genome of *C. camphora* may be relatively conserved.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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