


The complete chloroplast genome sequence of *Cinnamomum kotoense*

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ABSTRACT

The first complete chloroplast genome (cpDNA) sequence of *Cinnamomum kotoense* was determined from Illumina HiSeq pair-end sequencing data in this study. The cpDNA is 154,010 bp in length, contains a large single copy region (LSC) of 93,676 bp and a small single copy region (SSC) of 18,830 bp, which were separated by a pair of inverted repeats (IR) regions of 20,752 bp. The genome contains 127 genes, including 82 protein-coding genes, 8 ribosomal RNA genes, and 36 transfer RNA genes. The overall GC content of the whole genome is 39.2%, and the corresponding values of the LSC, SSC, and IR regions are 37.9%, 33.9%, and 44.3%, respectively. Further phylogenomic analysis showed that *C. kotoense* and *Cinnamomum bodinieri* clustered in a clade in *Cinnamomum* genus.

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Cinnamomum kotoense Kanehira & Sasaki is an important small evergreen tree indigenous to Lanyu Island of Taiwan Province in China (Chen et al. 2006). *Cinnamomum kotoense* belongs to the species of genus *Cinnamomum* within the family Lauraceae, and is a kind of plant endowed with high pharmaceutical value and ornamental value (Cheng et al. 2010). The chemical constituents of *C. kotoense* possessed bioactive activities of anticancer, antioxidation and antibacterial (Chen et al. 2007; Kuo et al. 2008; Wang et al. 2010). In recent years, it has been widely cultivated for pot landscape plants in Taiwan, Yunnan, Guangxi, Guangdong and Fujian because of its bright evergreen leaves and beautiful tree shape (Yi et al. 2017). However, there has not found yet genomic report about *C. kotoense*.

Herein, we reported and characterized the complete *C. kotoense* plastid genome (MN698964). One *C. kotoense* individual (specimen number: 5309270232) was collected from Kunming botanical garden, Kunming, Yunnan Province of China (25°14'16"N, 102°75'13"E). The specimen is stored at Yunnan Academy of Forestry Herbarium, Kunming, China and the accession number is YAFH0012766. DNA was extracted from its fresh leaves using DNA Plantzol Reagent (Invitrogen, Carlsbad, CA).

Paired-end reads were sequenced by using Illumina HiSeq system (Illumina, San Diego, CA). In total, about 21.2 million high-quality clean reads were generated with adaptors trimmed. Aligning, assembly, and annotation were conducted by CLC de novo assembler (CLC Bio, Aarhus, Denmark), BLAST, GeSeq (Tillich et al. 2017), and GENEIOUS v 11.0.5 (Biomatters Ltd, Auckland, New Zealand). To confirm the phylogenetic position of *C. kotoense*, other five species of *Cinnamomum* genus from NCBI were aligned using MAFFT

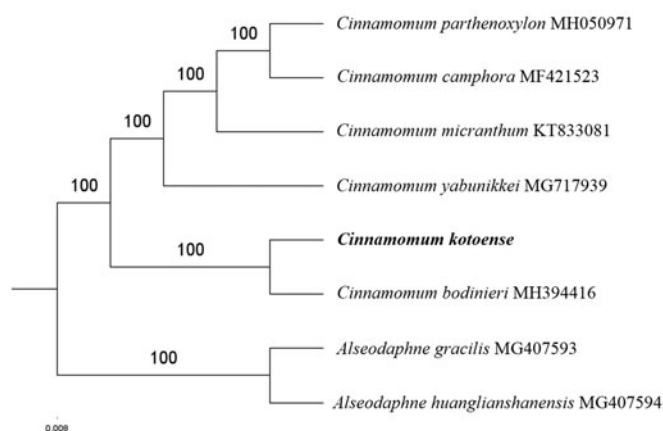


Figure 1. The maximum-likelihood tree based on the six chloroplast genomes of *Cinnamomum* genus. The bootstrap value based on 1000 replicates is shown on each node.

v.7 (Katoh and Standley 2013). The Auto algorithm in the MAFFT alignment software was used to align the six complete genome sequences and the G-INS-i algorithm was used to align the partial complex sequences. The maximum-likelihood (ML) bootstrap analysis was conducted using RAxML (Stamatakis 2006); bootstrap probability values were calculated from 1000 replicates. *Alseodaphne gracilis* (MG407593) and *Alseodaphne huanglianshanensis* (MG407594) were served as the out-group.

The complete *C. kotoense* plastid genome is a circular DNA molecule with the length of 154,010 bp, contains a large single copy region (LSC) of 93,676 bp and a small single copy region (SSC) of 18,830 bp, which were separated by a pair of inverted repeats (IR) regions of 20,752 bp. The overall GC content of the whole genome is 39.2%, and the

corresponding values of the LSC, SSC, and IR regions are 37.9%, 33.9%, and 44.3%, respectively. The plastid genome contained 127 genes, including 82 protein-coding genes, 8 ribosomal RNA genes, and 36 transfer RNA genes. Phylogenetic analysis showed that *C. kotoense* and *Cinnamomum bodinieri* clustered in a unique clade in *Cinnamomum* genus (Figure 1). The determination of the complete plastid genome sequences provided new molecular data to illuminate the *Cinnamomum* genus evolution.

Disclosure statement

No potential conflict of interest was reported by the authors.

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