


## Characterization of the complete chloroplast genome of *Trachycarpus fortunei*

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### ABSTRACT

*Trachycarpus fortunei* (Hook.) H. Wendl. (Fam.: Palmae; Gen.: *Trachycarpus*) is an evergreen tree that is widely distributed in China. In this study, *T. fortunei* complete chloroplast (cp) genome was assembled. The total cp genome size of *T. fortunei* was 158,613 bp in length, containing a large single-copy region of 86,422 bp, a small single-copy region of 17,847 bp, and a pair of inverted repeat regions of 27,172 bp. The overall GC-content of *T. fortunei* cp genome was 37.21%. It encodes a total of 109 unique genes, including 79 protein-coding genes, 26 tRNA genes, four rRNA genes. Twelve genes contain a single intron and 11 genes have two introns. Phylogenetic analysis results reveal that *T. fortunei* was closely related to *Chamaerops humilis*.

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*Trachycarpus fortunei* (Hook.) H. Wendl. (Fam.: Palmae; Gen.: *Trachycarpus*) is an evergreen tree that is widely distributed in China, where its leaf sheath fiber is often used as a rope and its unopened flower buds, also known as ‘brown fish,’ are edible and consumed (Yunfa 2005).

The cp genome contains a large amount of genetic information and has highly conservative characteristics.

*Trachycarpus fortunei* seeds were collected in Guiding County, Guizhou Province, China (E: 107°07'42", N: 26°13'19"). The seeds were germinated and nursed in the laboratory (the seed specimen is accessible at the Institute for Forest Resources & Environment of Guizhou, Guizhou University (accessions No. TF-001-2)), total genome DNA of collected annual new needles was extracted with EasyPure<sup>®</sup> Plant

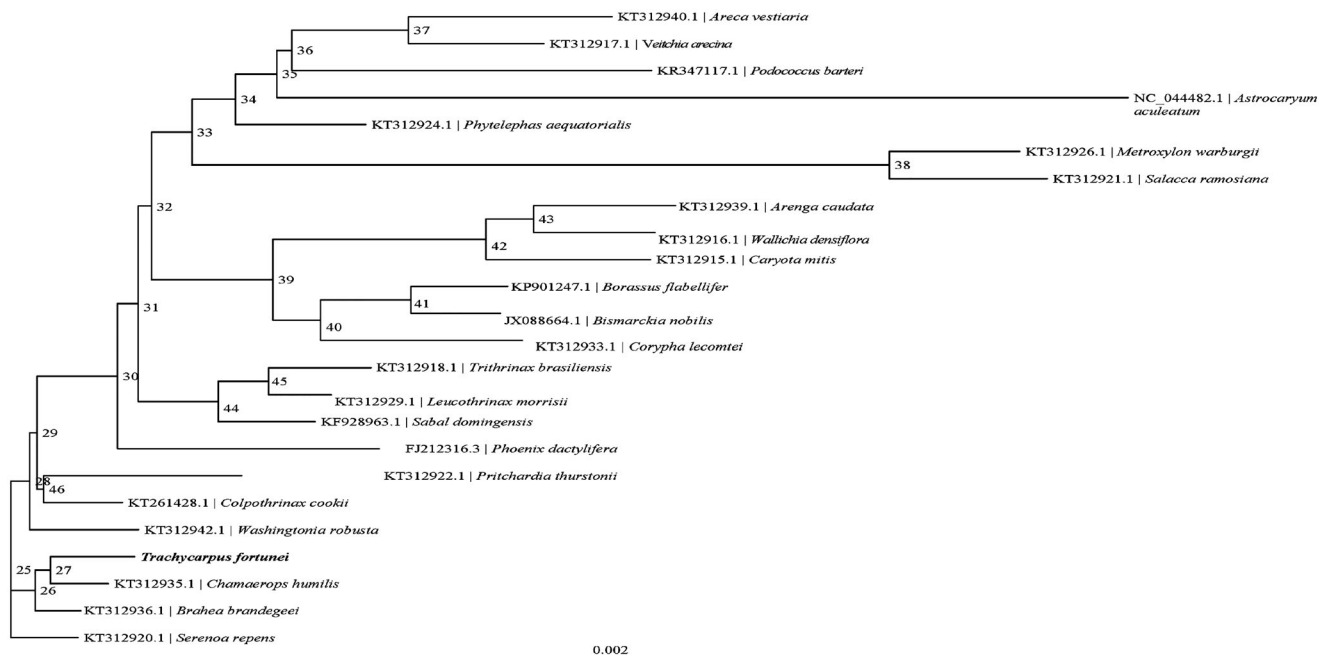




Figure 1. Phylogenetic relationships of 24 species based on the maximum-likelihood (ML) analysis of *T. fortunei*.

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Genomic DNA Kit (TransGen Biotech, Beijing, China). Total DNA was used to generate libraries with an average insert size of 400 bp, which were sequenced using the Illumina NovaSeq platform. *Trachycarpus fortunei* cp genome sequence was assembled by SPAdes (Bankevich et al. 2012) and A5-miseq (Coil et al. 2015) fragment assembly. The complete cp genome of *T. fortunei* was annotated in CPGAVAS2 (<http://47.96.249.172:16019/analyzer/home>, Shi et al. 2019). The annotated cp genome sequence has been deposited into the Genbank (accession number: MT712077).

*Trachycarpus fortunei* cp genome exhibited a general quadripartite structure of plants, with two reverse repeated regions (IRa and IRb) of 27,172 bp in length. The repeat regions divided the genome into two single-copy regions, SSC and LSC with 17,847 and 86,422 bp, respectively. The overall GC-content of the *T. fortunei* cp genome is 37.21%. It encodes a total of 109 unique genes, including 79 protein-coding genes, 26 *tRNA* genes, four *rRNA* genes. Twelve genes (*rps16*, *atpF*, *rpoC2*, ...) contain a single intron, and 11 genes (*trnk-UUU*, *trnS-CGA*, *ycf3*, ...) have two introns.

Phylogenetic analysis suggested that *T. fortunei* is closely clustered with *Chamaerops humilis* (Figure 1), which was generated based on the 24 complete cp genomes. The sequences were initially aligned using MAFFT (Katoh and Standley 2013). The phylogenetic tree was built using IQ-TREE (Nguyen et al. 2015) with 1000 bootstrap. The result shows a foundation for chloroplast genome engineering of *T. fortunei* in the future.

## Disclosure statement

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

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## Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI at <http://www.ncbi.nlm.nih.gov>, reference number MT712077.

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