The complete chloroplast genome sequence of *Quercus chungii* (Fagaceae)

Xiao-Long Jiang*, Hong-Lin Mou*, Chang-Sha Luo and Gang-Biao Xu

The Laboratory of Forestry Genetics, Central South University of Forestry and Technology, Changsha, China

**ABSTRACT**

*Quercus chungii* F.P. Metcalf, a rare oak with endemic to southern China, belongs to the compound trichome base (CTB) lineage in the *Cyclobalanopsis* section. The complete chloroplast genome of the species was assembled and annotated in this study. The circular genome was 160,731 bp in size, presenting a typical quadripartite structure including one large single-copy region (LSC, 90,140 bp), one small single-copy region (SSC, 18,911 bp), and two copies of inverted repeat regions (IRs, 25,840 bp). It encoded a total of 113 unique genes, including 79 protein-coding genes, 30 tRNA genes, and four rRNA genes. The maximum-likelihood (ML) phylogenetic tree reconstructed by IQ-TREE indicated that *Q. chungii* was more closely related to *Q. myrsinifolia* and *Q. sichourensis*.

*Quercus chungii* is a rare and precious tree that is distributed in southern China at elevations ranging from 200 to 800 m. The species belongs to compound trichome base (CTB) lineage in the *Quercus* section *Cyclobalanopsis* (Deng et al. 2018). With the rapid changes in climate and intensification of human activities, the distribution of *Q. chungii* is rapidly reduced in recent decades. Understanding the spatial genetic pattern and demographic dynamics of the species can provide important guidelines for the protection and utilization of the species. Two species, *Trigonobalanus doichangensis* and *Fagus crenata*, were selected as outgroups. The sequences were aligned by MAFFT 7.475 (Rozewicki et al. 2019). The ML analyses were performed with IQ-TREE 1.6.12 (Chernomor et al. 2016). Node support was assessed by 1000 fast bootstrap replicates. Our result indicated that *Q. chungii* was more closely related to *Q. myrsinifolia* and *Q. sichourensis* with 83% bootstrap support (Figure 1).

CONTACT Gang-Biao Xu gangbiaoxu@163.com

The Laboratory of Forestry Genetics, Central South University of Forestry and Technology, Changsha, China

* Both authors contributed equally to this work.
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ORCID

Xiao-Long Jiang  http://orcid.org/0000-0003-3861-1109

Data availability statement

The complete chloroplast genome sequence of *Quercus chungii* is deposited in the GenBank database under the accession number MW401633 (https://www.ncbi.nlm.nih.gov/nuccore/MW401633). Raw sequencing reads used in this study were deposited in the public repository BioSample with accession number SAMN18499615 (https://www.ncbi.nlm.nih.gov/biosample/SAMN18499615).

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Figure 1. The maximum-likelihood (ML) phylogenetic tree of *Quercus chungii* and 19 relative species were reconstructed by IQ-TREE based on complete chloroplast genome sequences. The bootstrap support value is labeled for each node.