The first complete chloroplast genome of *Tetradium daniellii* (Benn.) T. G. Hartley

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**ABSTRACT**
*Tetradium daniellii* (Benn.) T. G. Hartley is an important medicinal, ornamental, and timber tree species and belongs to genus *Tetradium* in family Rutaceae. It is widely distributed in warm temperate deciduous broad-leaved forest areas in northern China, Korean Peninsula and Japan. In this study, we sequenced its sample and determined complete chloroplast genome. The CP genome of *T. daniellii* has a circle structure with the length of 158,446 bp, includes a small single copy region (17,972 bp), a large single copy (86,478 bp) and two inverted repeats (6,2998 bp). There were 131 genes, including 86 protein-coding genes, 8 rRNA and 37 tRNA, and overall GC content covered by 38.3%. The gene *trnK-UUU*, *rps16*, *trnG-UCC*, *atpB*, *rpoC1*, *trnL-UAA*, *trn-V-UAC*, *petB*, *petD*, *rpl16*, *rpl2*, *ndhB*, *trnL-GAU*, *trnA-UGC* and *ndhA* contained an intron; gene *clpP*, *ycf3* contained 2 introns. The phylogenetic result showed that *T. daniellii* had the closest relationship with *Tetradium ruticarpum* (NC_052830).

1.57 Gb clean sequence data was assembled by de novo assembler SPAdes v3.11.0 (Bankevich et al. 2012) with the reference genome *Phellodendron amurense* (NC_035551). Finally the complete chloroplast genome was annotated by PGA (Qu et al. 2019). We submitted the assembled genome DNA to GenBank under the accession number of MZ145060, and SRA submitted to NCBI under the BioProject No. PRJNA732282 and SRA number: SRR14663312

The chloroplast genome of *T. daniellii* has a circle structure with the size of 158,446 bp in length that contains a large single copy (LSC: 86,478 bp) region, a small single copy (SSC: 17,972 bp) and two inverted repeats (IRs: 26,998 bp) region. The overall GC content was 38.3%. There were 131 genes including 86 protein-coding genes, 37 tRNA and 8 rRNA. Each of *trnK-UUU*, *rps16*, *trnG-UCC*, *atpB*, *rpoC1*, *trnL-UAA*, *trn-V-UAC*, *petB*, *petD*, *rpl16*, *rpl2*, *ndhB*, *trnL-GAU*, *trnA-UGC* and *ndhA* contained one intron respectively, *clpP* and *ycf3* had two introns respectively. While *rps12* had Trans splicing.

To determine the phylogenetic position of *T. daniellii* in family Rutaceae, we selected 19 complete chloroplast genomes from NCBI and aligned with *T. daniellii* by using Mafft 7.473 (Katoh and Standley 2013) with strategy of FFT-NS-2. Then we used model finder to selecte TVM+F+I+G4 model (Subha et al. 2017) and constructed the phylogenomic tree (Figure 1) by IQtree 2.0 (Minh et al. 2020) with 1000
bootstrap and Maximum-likelihood method. During the ML tree construction, the complete chloroplast genomes of Murraya koenigii (MT806177) was used as outgroup. Then the result showed that T. daniellii had the closest relationship with Tetradium ruticarpum (NC_052830).

Disclosure statement

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

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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/] under the accession no. MZ145060. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA732282, SRR14663312, and SAMN19316631 respectively.

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Figure 1. Maximum-likelihood phylogenetic tree for T. daniellii based on 20 complete chloroplast genomes.