

The complete chloroplast genome of *Celtis julianae* (Ulmaceae)

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ABSTRACT

Celtis julianae C.K. Schneid. is a large deciduous tree of Ulmaceae. In this study, the chloroplast genome sequence of *C. julianae* was 159,064 bp in length, consisting of a large single-copy (LSC) region with 86,139 bp, a small single-copy (SSC) region with 19,137 bp, and two inverted repeat regions (IRs) with 26,894 bp. The GC content in the chloroplast genome of *C. julianae* was 36.3%. The chloroplast genome of *C. julianae* contained 127 genes, including 86 protein-coding genes, 37 tRNA genes, and four rRNA genes. Phylogenetic tree showed that *C. julianae* was clustered with *C. tetrandra*.

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Celtis julianae; chloroplast genome; Illumina sequencing; phylogenetic tree

Celtis is a genus of Ulmaceae, including more than 60 species, widely distributed in tropical and warm regions of the world. *Celtis julianae* C.K. Schneid. is a large deciduous tree, more than 25 m in height, with deep green leaf and red flower (Huang and Zhao 2004). It also has good economic value because of its high oil content in the kernel. *Celtis* has many questions in relation to its genetic phylogeny and species identification.

The fresh leaf samples of *C. julianae* were collected in Green Expo Garden, Zhengzhou, China (N347591.8300; E1139260.3300). The voucher specimen was deposited at the Herbarium of Henan Agricultural University (voucher number: CJ-20-0715). The total genomic DNA was extracted from fresh leaves of *C. julianae* using a modified CTAB method (Doyle and Doyle 1987). Sequencing was performed with an Illumina HiSeq2500 Platform (San Diego, CA). The raw reads were

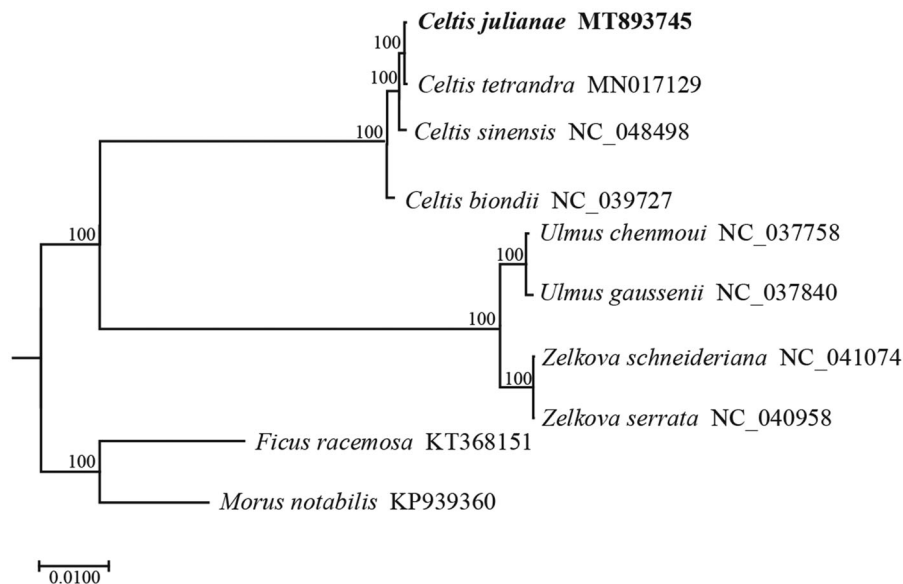


Figure 1. Maximum-likelihood (ML) phylogenetic tree inferred from 10 plant chloroplast genomes. Numbers next to the branches are bootstrap support percentages.

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generated by Illumina paired-end sequencing after removing adapters. The low quality sequences of raw reads used Fastp (<https://github.com/OpenGene/Fastp>) for quality control. Resultant clean reads were assembled using GetOrganelle pipeline v1.6.3a (<https://github.com/Kinggerm/GetOrganelle>) with the gene from *Celtis sinensis* (GenBank accession no. NC_048498) as the reference sequence. The genome was automatically annotated by using the CpGAVAS2 pipeline (<http://www.herbalgenomics.org/cpgavas>) (Shi et al. 2019) and start/stop codons and intron/exon boundaries were adjusted in Geneious 20.2.2 (<https://www.geneious.com/>).

The chloroplast genome sequences of *C. julianae* were submitted to NCBI, and the accession number was MT893745. The genome sequence of *C. julianae* was 159,064 bp in length, consisting of a large single-copy (LSC) region with 86,139 bp, a small single-copy (SSC) region with 19,137 bp, and two inverted repeat regions (IRs) with 26,894 bp. The GC content in the chloroplast genome of *C. julianae* was 36.3%. The chloroplast genome of *C. julianae* contained 127 genes, including 86 protein-coding genes, 37 tRNA genes, and four rRNA genes.

The phylogenetic tree was constructed based on the genome sequences of *C. julianae* in RAxML v8.2 (Stamatakis 2006) with 1000 bootstrap replicates. A total of 10 species were used, including four *Celtis* species, two *Ulmus* species, two *Zelkova* species, one *Ficus* species, and one *Morus* species as outgroup (Chen et al. 2016; Mao and Bi 2016).

As shown in the phylogenetic tree (Figure 1), the 10 Ulmaceae species were organized into three clusters. One of the clusters was comprised of four genus *Celtis* species, which *C. julianae* was closely related to *C. tetrandra*. This result was similar to the previous phylogenetic trees based on chloroplast genome sequences of Ulmaceae (Li et al. 2020).

Disclosure statement

No potential conflict of interest was reported by the authors.

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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. MT893745. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA670186, SRA: SRS7853389, and SAMN17035257, respectively.

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