

## Characterization of the complete chloroplast genome of *Pterocarya macroptera* var. *delavayi* (Juglandaceae)

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### ABSTRACT

In this study, the complete chloroplast genome sequence of *Pterocarya macroptera* var. *delavayi* was reported and characterized. The chloroplast genome is 160,168 bp in length, and consists the typical quadripartite structure, a pair of inverted repeats (IRs, 26,007 bp) separated by a large single-copy region (89,701 bp) and a small single-copy region (18,453 bp). A total of 136 unique genes were predicted, including 88 protein-coding genes, 40 tRNA genes, and 8 rRNA genes. The GC content of the chloroplast genome is 36.2%. Phylogenetic analysis confirmed the close relationship between *Pterocarya* and *Juglans*.

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*Pterocarya macroptera* var. *delavayi*; chloroplast genome; phylogenetic analysis

*Pterocarya macroptera* var. *delavayi* distributes in western Hubei, western Sichuan, and northwest Yunnan of China (Lu et al. 1999). It is a riparian dominant tree, and its bark can be used as fiber raw material (Lu et al. 1999; Ying and Chen 2011). *P. macroptera* var. *delavayi* is a variety of *P. macroptera*, which is morphologically different from *P. macroptera* var. *macroptera* by its mature leaves with exclusively solitary trichomes (Song et al. 2020). Based on RAD-seq data, Song et al. (2020) showed that the genus *Pterocarya* is monophyletic and close to *Juglans*. *P. macroptera* var. *delavayi* was sister to the other two varieties (*P. macroptera* var. *macroptera* and *P. macroptera* var. *insignis*) (Song et al. 2020).

Here, the complete chloroplast genome of *P. macroptera* var. *delavayi* was determined, annotated, and analyzed. The sample was collected from the Botanical Garden Edinburgh (UK) (55°56'54.56"N, 3°1'57.59" W) by Jianfei Ye. The DNA sample (RBGE 2019-08-27) was deposited in the Institute of Life Science, Nanchang University (JXU). Total genomic DNA was extracted from silica gel-dried leaves using the modified CTAB method (Doyle 1987) and sequenced using MGI MGISEQ-2000 High-throughput Sequencing Set. In total, 3 Gb of 150-bp paired-end raw reads were generated and used for chloroplast genome assembly. Trimmomatic version 0.39 (Bolger et al. 2014) was used to organize and trim overrepresented sequences for getting the clean reads. The clean reads were assembled by using GetOrganelle version 1.5 (Jin et al. 2020). The chloroplast genome of *P. macroptera* var. *delavayi* was annotated used Geneious version 9.05 (<http://www.geneious.com/>) with *P. stenoptera* (NC\_046428) as reference. The annotated complete chloroplast genome of *P. macroptera* var. *delavayi* was deposited in GenBank (the accession number MW194257).

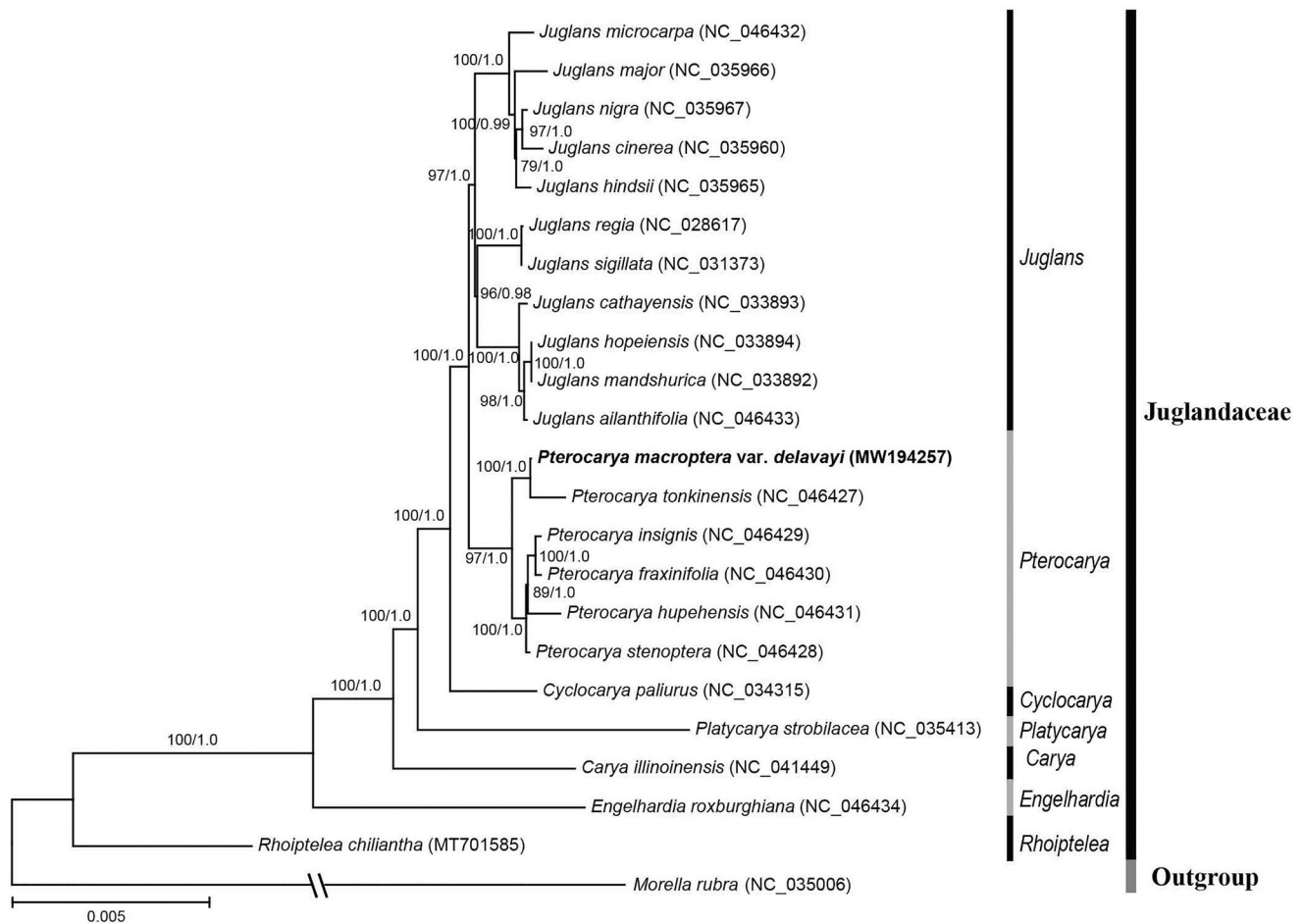
The complete chloroplast genome of *P. macroptera* var. *delavayi* is 160,168 bp in length, with a large single-copy region (LSC) of 89,701 bp, a small single-copy region (SSC) of 18,453 bp, and a pair of inverted repeat regions (IRs) of 26,007 bp, and forms a typical quadripartite structure. A total of 136 genes were annotated from the chloroplast genome of *P. macroptera* var. *delavayi*, including 88 protein-coding genes, 40 transfer RNA (tRNA) genes, and 8 ribosomal RNA (rRNA) genes. The GC content of the chloroplast genome is 36.2%, meanwhile, the corresponding value of LSC, SSC, and IR regions is 33.8%, 29.8%, and 42.6%, respectively.

In order to analyze the phylogenetic position of *P. macroptera* var. *delavayi*, another 22 complete chloroplast genomes were retrieved from NCBI, and *Morella rubra* from Myricaceae was set as the outgroup (Figure 1). All sequences were aligned by MAFFT version 7.409 (Katoh and Toh 2010). The maximum likelihood tree and Bayesian tree were constructed using RAXML version 8.2.12 (Stamatakis 2014) and MrBayes version 3.2.6 (Ronquist and Huelsenbeck 2003), respectively. The phylogenetic tree showed that *Pterocarya* is formed a clade with the *Juglans* with high support (ML-PP = 100%, BI-PP = 1.0), and *P. macroptera* var. *delavayi* is sister to *P. tonkinensis* with strongly supported values (ML-PP = 100%, BI-PP = 1.0, Figure 1). The phylogenetic relationships among

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**Figure 1.** The maximum likelihood (ML) tree of 23 species inferred from the complete chloroplast genome sequences. Numbers associated with branches are ML bootstrap values and Bayesian posterior probabilities.

Juglandaceae were consistent with the results of Xiang et al. (2014) and Mu et al. (2020) based on chloroplast genome data.

## 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.MW194257. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA692030, SRR13434420, and SAMN17304756, respectively.

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