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Complete chloroplast genome sequences of *Debregeasia orientalis* (Urticaceae)

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ABSTRACT

Debregeasia orientalis is an economically and ecologically important species, which belongs to the genus *Debregeasia* within the family Urticaceae. The complete chloroplast genome size of *D. orientalis* is 155,894 bp in length, including a large single copy (LSC) region of 85,558 bp, a small single copy (SSC) region of 19,064 bp, and a pair of inverted repeats (IRs) of 25,636 bp. The genome contains 112 genes, including 78 protein-coding genes, 30 tRNA genes, and four rRNA genes. The GC content in chloroplast genome, LSC region, SSC region, and IR region were 36.3%, 34.0%, 29.4%, and 42.7%, respectively. A total of 15 species are used to construct the phylogenetic tree of Rosales, employing the maximum likelihood (ML), and the results showed that *D. orientalis* is closely related to *Debregeasia saeneb*.

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Debregeasia orientalis is an economically and ecologically important species in Urticaceae, and it is usually distributed in the shaded, wet places by streams of mountain valleys in East Asia (Chen et al. 2003). Previous studies of this species have mainly focused on the chemical constituents (Xiao et al. 2008), phylogeny, and biogeography (Wu et al. 2013, 2015, 2018). In this study, we sequenced and assembled the complete chloroplast genome (cpDNA) of *D. orientalis*, and revealed its closest relative species. The annotated cpDNA of

D. orientalis has been deposited into the GenBank with the accession number MH196364.

In this study, young, fresh, and healthy leaves were collected from *D. orientalis* in Lancang county (Yunnan, China; N 23.238902°, E 99.700676°; Alt. 857m). The voucher specimen was deposited in herbarium KUN (collection numbers is Liuj166488). Total genomic DNA was extracted using CTAB method (Doyle and Doyle 1987) and sequenced with Illumina HiSeq 2500 platform. All raw reads were trimmed using

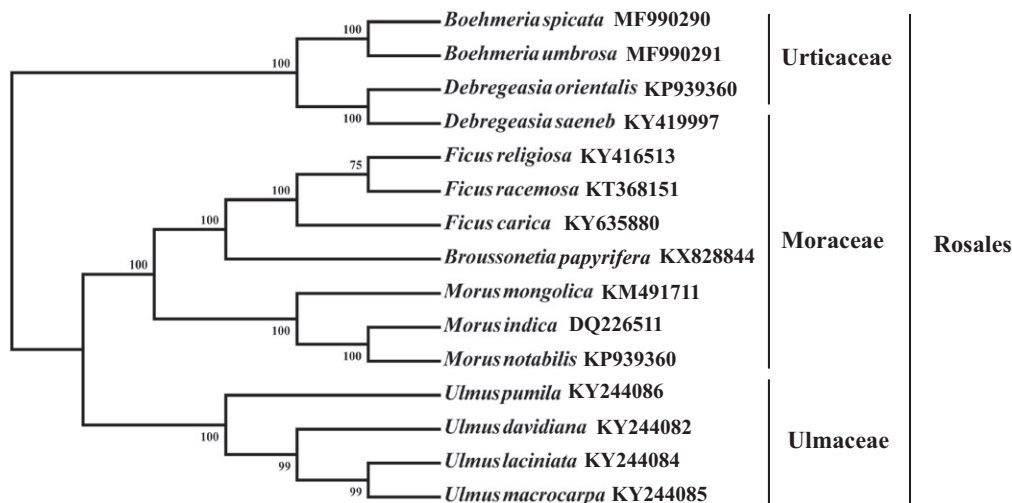





Figure 1. Phylogenetic tree produced by Maximum Likelihood (ML) analysis based on chloroplast genome sequences from 15 species of Rosales, numbers associated with branched are assessed by Maximum Likelihood bootstrap.

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NGSQCToolkit_v2.3.3 (Patel and Jain 2012). After dislodged the low quality reads, the clean reads were assembled using MIRA v4.0.2 (Chevreux et al. 2004) and MITObim v1.8 (Hahn et al. 2013) using the chloroplast genome of *Morus notabilis* (KP939360) as the reference sequences.

The complete chloroplast genome of *D. orientalis* is 160,621 bp in length, including a large single copy (LSC) region of 88,580 bp, a small single copy (SSC) region of 20,049 bp, and a pair of inverted repeats (IRs) of 25,996 bp (Figure 1). The GC content in chloroplast genome, LSC region, SSC region, and IR region were 36.2%, 33.9%, 29.0%, and 42.8%, respectively. The complete chloroplast genome of *D. orientalis* contains 112 genes, including 78 protein-coding genes, 30 tRNA genes, and four rRNA genes. A total of 15 genes (*tRNA-Lys(UUU)*, *tRNA-Gly(UCC)*, *tRNA-Leu(UAA)*, *tRNA-Val(UAC)*, *tRNA-Ile(GAU)*, *tRNA-Ala(UGC)*, *rps16*, *atpF*, *rpoC1*, *petB*, *petD*, *rps16*, *rpl2*, *ndhB*, and *ndhA*) contains a single intron, and three genes (*clpP*, *rps12*, and *ycf3*) contains two introns.

A total of 15 species were used to reconstruct the phylogenetic tree of Rosales (Figure 1). Modeltest v3.7 (Posada and Crandall 1998) was used to determine the best-fitting model. Maximum likelihood analysis was performed using MEGA7 (Kumar et al. 2016) with 1000 bootstrap replicates. The results showed that *D. orientalis* was closely related to *D. saeneb*.

Disclosure statement

No potential conflict of interest was reported by the authors.

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