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TECHNICAL NOTE

Characterization of the complete chloroplast genome of *Dalbergia odorifera* (Leguminosae), a rare and critically endangered legume endemic to China

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Abstract *Dalbergia odorifera* is a critically endangered tree species with high economic and medicinal value. In this study, its chloroplast genome was characterized using next generation Illumina pair-end sequencing dataset. The chloroplast genome has a quadripartite structure with 156,064 bp in length and contains a pair of 25,702 bp inverted repeat (IR) regions, which were separated by the large single copy (LSC: 85,805 bp) region and small single copy (SSC: 18,856 bp) region. The plastid genome harbors 111 unique genes, including 77 protein-coding genes (PCGs), 30 tRNAs and 4 rRNAs. The overall GC content of the whole genome was 36.1%. The Phylogenetic analysis showed a close relationship between *D. odorifera* and *Arachis hypogaea* species of Dalbergieae in our sampled species. The complete chloroplast genome provides fundamental information for genetic and conservation studies of *D. odorifera*.

Keywords *Dalbergia odorifera* · Endangered species · Plastome · Phylogenetic analysis

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Dalbergia odorifera T. Chen, is medium sized evergreen tree, native to Hainan Island, southern China (Yu et al. 2007). The heartwood of *D. odorifera* known as "Jiangxiang" in traditional Chinese medicine (TCM) possess diverse pharmacological activities including antioxidant, anti-microbial and anti-inflammatory (Lee et al. 2014; Lee and Jeong 2014; Yun et al. 2017). It is well known and valued for the quality and beauty of its heartwood and is sought after for use in luxury furniture and crafts owing to the sweet fragrance and economic value of the heartwood (Yu et al. 2007). This plant species is under serious threat by human activities and overexploitation for medicinal and economic uses. It has been classified as a critically endangered plant listed in the category of key protected wild plants in China (http://www.zhb.gov.cn/gkml/hbb/bgg/201309/t20130912_260061.htm) and is listed in the "Red List of Threatened Species" (World Conservation Monitoring Centre 1998). There is an urgent need for incentives and regulations for the protection and conservation of this important species. Some measures have been taken already, for example, over the last decade, large scale plantations of *D. odorifera* in southern China have been encouraged by the local and central Chinese governments. In this context, an improved understanding of its genetics would contribute to the formulation of conservation and management strategies (Yang et al. 2017; Wariss et al. 2017). In this study, we reconstructed the complete chloroplast genome of *D. odorifera* based on the whole-genome Illumina sequencing dataset. The annotated chloroplast genome of *D. odorifera* has been deposited into the GenBank with the Accession number MF668133.

Fresh leaves of *D. odorifera* were collected from Ledong County, Hainan Province, China and voucher specimen (Yi15518) were deposited in Herbarium, Kunming Institute of Botany, Chinese Academy of Sciences. Genomic DNA was isolated with the improved CTAB protocol (Doyle 1987)

and sent to the Beijing Genomics Institute (BGI), Shenzhen, China for library construction and sequencing. The reads were assembled using Linux-OS SPAdes genome assembler v3.10.1 (Bankevich et al. 2012) with k-mer = 115. Contigs were filtered by customized python script and later connected into plastome using Bandage Ubuntu dynamic v.8.0 (Wick et al. 2015). PE reads were mapped to the plastome using Bowtie2 (Langmead and Salzberg 2012) implemented in Geneious v.9.1.4 (Kearse et al. 2012). Annotation was performed using GeSeq (Tillich et al. 2017), coupled with manual adjustment. The tRNAs sequences were confirmed using online Search Service tRNAscan-SE (Schattner et al. 2005). The final genome map of *D. odorifera* were generated using OrganellarGenomeDRAW (http://ogdraw.mpimp-golm.mpg.de/cgi-bin/ogdraw.pl; Lohse et al. 2013).

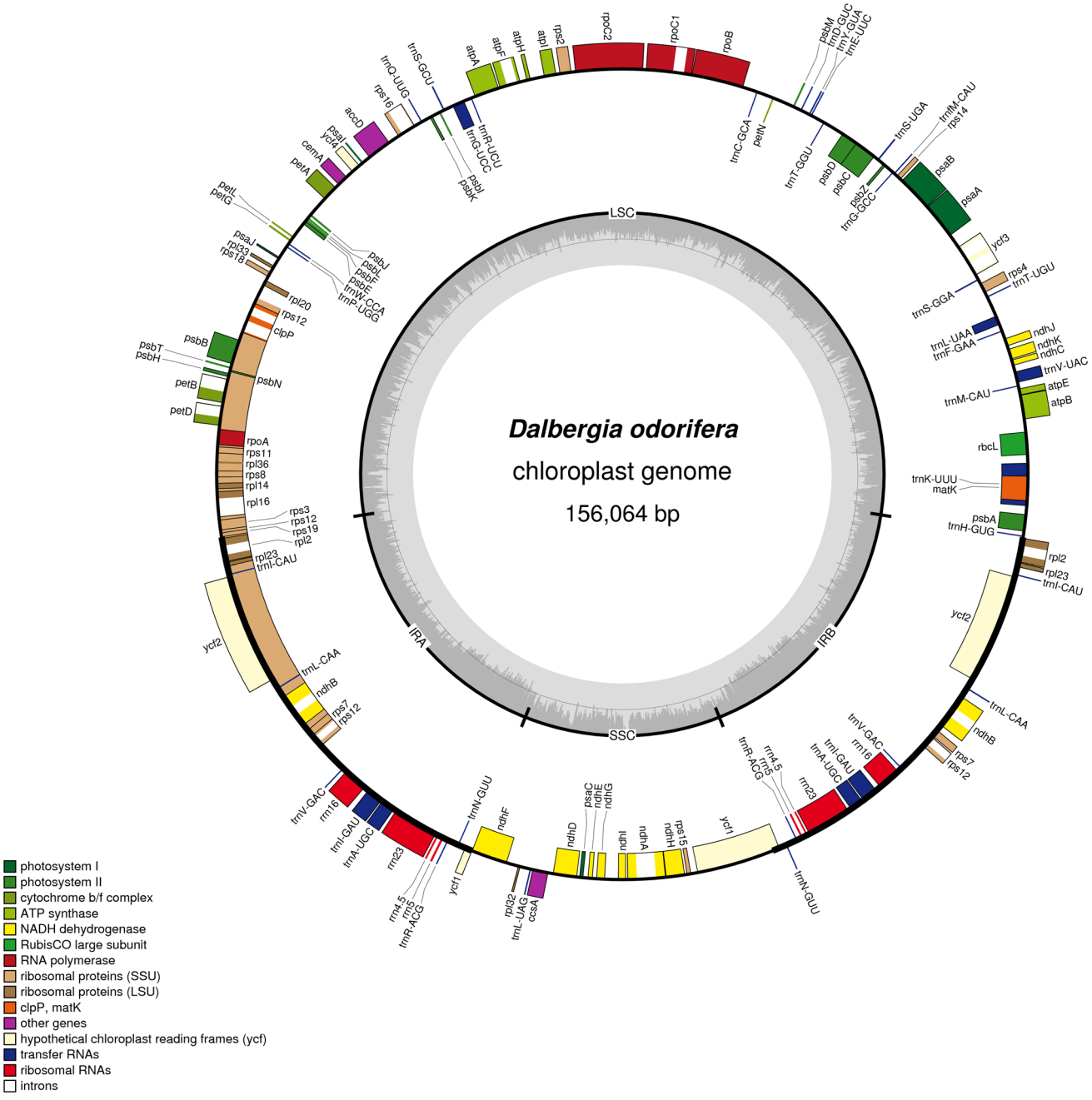

Fig. 1 The gene map of the complete plastome of *Dalbergia odorifera*. Genes are indicated by boxes on the inside (clockwise transcription) and outside (counterclockwise transcription) of the outermost circle. Genes belonging to different functional groups are color coded. Dashed area in the inner circle indicates the GC content of the plastome

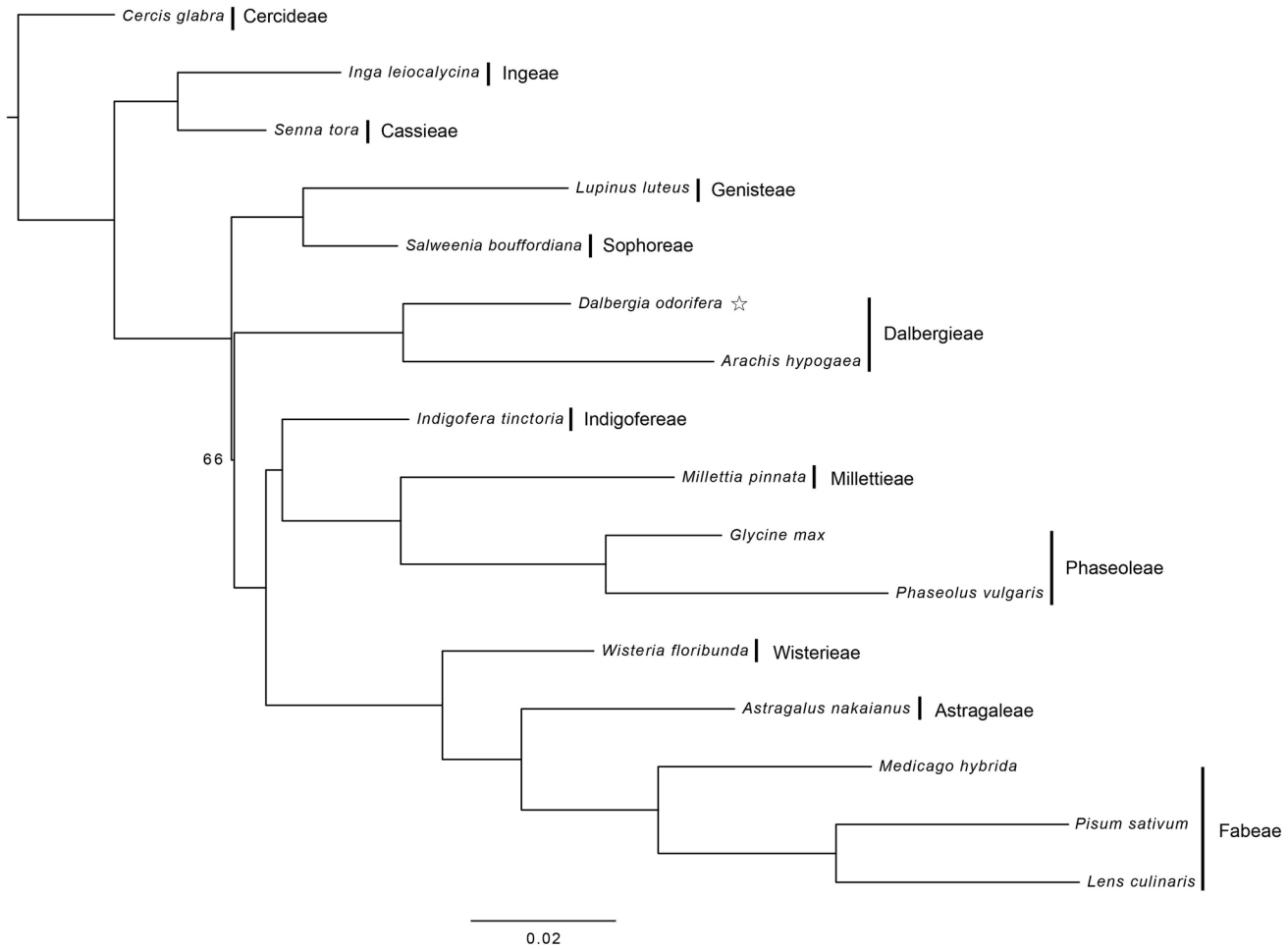

Fig. 2 The phylogenetic tree inferred using maximum likelihood (ML) analyses from 77 chloroplast PCGs of 16 complete chloroplast genomes. The bootstrap values were based on 1000 replicates, and the values of <100% are given beside nodes. *Cercis glabra, Senna tora* and *Inga leiocalycina* as outgroup species

The complete chloroplast genome is 156,064 bp in length, contains a quadripartite structure that consists of a large single copy (LSC) region of 85,805 bp and a small single copy (SSC) region of 18,856 bp with two inverted repeat (IR) regions of 25,702 bp (Fig. 1). The overall GC content was 36.1%, higher than that of the IR regions (16.47%) and SSC (12.08%) region but lower than those of the LSC (54.98%) region. It encodes 111 genes, including 77 PCGs, 30 tRNAs and four rRNAs. Among these, nine genes (*atpF, ndhA, ndhB, petB, petD, rpl2, rpl16, rpoC1* and *rps16*) contain a single intron while three genes (*clpP, rps12* and *ycf3*) possess two introns. Six PCGs (*ndhB, rpl2, rpl23, rps7, rps12* and *ycf2*), 7 tRNAs genes (*trnA-UGC, trnI-CAU, trnI-GAU, trnL-CAA, trnN-GUU, trnR-ACG* and *trnV-GAC*) and 4 rRNAs genes (*rrn4.5, rrn5, rrn16* and *rrn23*) are duplicated in both IR regions (Supplementary file 1).

The phylogenetic tree was constructed based on 77 PCGs of 16 complete chloroplast genomes of the Fabaceae (the Online Resource 1 shows the details of sampled taxa information) with *Cercis glabra*, *Senna tora* and *Inga leiocalycina* as outgroup species (Fig. 2). All sequences were aligned using MAFFT (Katoh and Standley 2013) in Geneious v.9.1.4 and maximum likelihood (ML) analysis was performed using RAxML v7.2.8 (Stamatakis 2006) in Linux OS, including tree robustness assessment using 1000 replicates of rapid bootstrap with the GTRCAT substitution model. The phylogeny reconstructed based on the complete genome sequences of our sampled 16 Fabaceae species strongly supports the sister relationship between *D. odorifera* and *Arachis hypogea* species. The complete plastid genome will provide a useful resource for studying the genetic diversity of *D. odorifera* and conservation of this valuable and critically endangered species.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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