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PLASTOME ANNOUNCEMENT

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The complete chloroplast genome of *Bauhinia racemosa* Lam. (Fabaceae): a versatile tropical medicinal plant

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ABSTRACT

Bauhinia racemosa Lam. (1783), a versatile medicinal plant, belongs to the family Fabaceae (subfamily Cercidoideae). In this study, we analyzed the complete chloroplast genome to facilitate its use in genetic research. The complete chloroplast genome of *B. racemosa* was found to be 155,501 bp long, including two inverted repeat (IR) regions of 25,446 bp, which are separated by a small single-copy (SSC) region of 18,295 bp and a large single-copy (LSC) region of 86,314 bp. The overall GC content is 36.4%. The genome of *B. racemosa* contains 129 genes, including 83 protein-coding genes, 37 tRNAs, 8 rRNAs, and 1 pseudogene (rps19). Phylogenetic analysis suggests that *B. racemosa* forms a monophyletic clade with the other four *Bauhinia* species (*B. brachycarpa*, *B. purpurea*, *B. blakeana* and *B. variegata* var. *variegata*).

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Bauhinia racemosa Lam., commonly known as the bidi leaf tree, is a small (up to 12 metres) deciduous species of tree with dark scabrous bark and is widely distributed in tropical areas of South, Southeast and East Asia, which are characterized by harsh climatic conditions (Panda et al. 2015). The tree is important nutritionally and economically, with its leaves serving as fodder for livestock and its hard and heavy wood being used as fuel (Panda et al. 2015). More significantly, *B. racemosa* is also used in traditional medicine with almost every part of the plant having some medicinal value. The flower buds have anti-ulcerogenic properties (Akhtar and Ahmad 1995), the seeds can be exploited for their antibacterial benefits (Kumar et al. 2005), and the isolated compounds from the roots exhibit profound antibacterial and antifungal activity (Jain et al. 2008). In addition, its leaf extracts have antihyperglycemic and anthelmintic properties (Prusty et al. 2012), and its stem bark is reported to be medicinally important for treating a range of ailments, e.g. headache, fever, skin diseases, and diarrhea (Borikar et al. 2009). Although the plant is known to be important for human use, there has only been a limited number of genomic studies on this species.

In this analysis, young leaves of *B. racemosa* were collected from Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Yunnan Province, China (XTBG, 21°41′N, 101°25′E). A voucher specimen, reference number F2020012, was deposited at the Herbarium of Xishuangbanna Tropical Botanical Garden (HITBC) (http://hitbc.xtbg.ac.cn, Jianwu Li, ljw@xtbg.org.cn). DNA sequencing was performed by the Personal Biotechnology Co., Ltd (Shanghai, China), where the CTAB method (Doyle 1987) was used to extract the total genomic DNA of leaves, and the Illumina NovaSeq 6000 sequencing platform was used to generate 2×150 bp paired-end reads. A total of 3.46 G bases of raw data were trimmed and filtered by Fastp software (Chen et al. 2018). The chloroplast genome of *B. racemosa* was assembled and annotated using default parameters of the GetOrganelle toolkit (Jin et al. 2020) and the web server CPGAVAS2 (Shi et al. 2019), respectively. In addition, Geneious v.8.1.3 software (Kearse et al. 2012) was used to check and correct erroneous gene names after an auto-annotation. The annotated sequence was submitted to Genbank with the accession number ON456405.

The annotation results show that the complete chloroplast genome of *B. racemosa* is a circular DNA molecule with a length of 155,501 bp, which is 47 bp shorter than *B. brachycarpa* (NC037762). The plastome of *B. racemosa* contains a small single-copy region (SSC) of 18,295 bp, a large single-copy region (LSC) of 86,314 bp, and two inverted repeat (IR) regions of 25,446 bp. The overall GC content is 36.4%. The GC content is the highest in IR regions (42.5%), the corresponding values of the SSC and LSC are 30.5% and 34.1%, respectively. The complete chloroplast genome encoded 129 genes, including 83 protein-coding genes, 37 tRNA genes, 8 rRNA genes, and 1 pseudogene (rps19).

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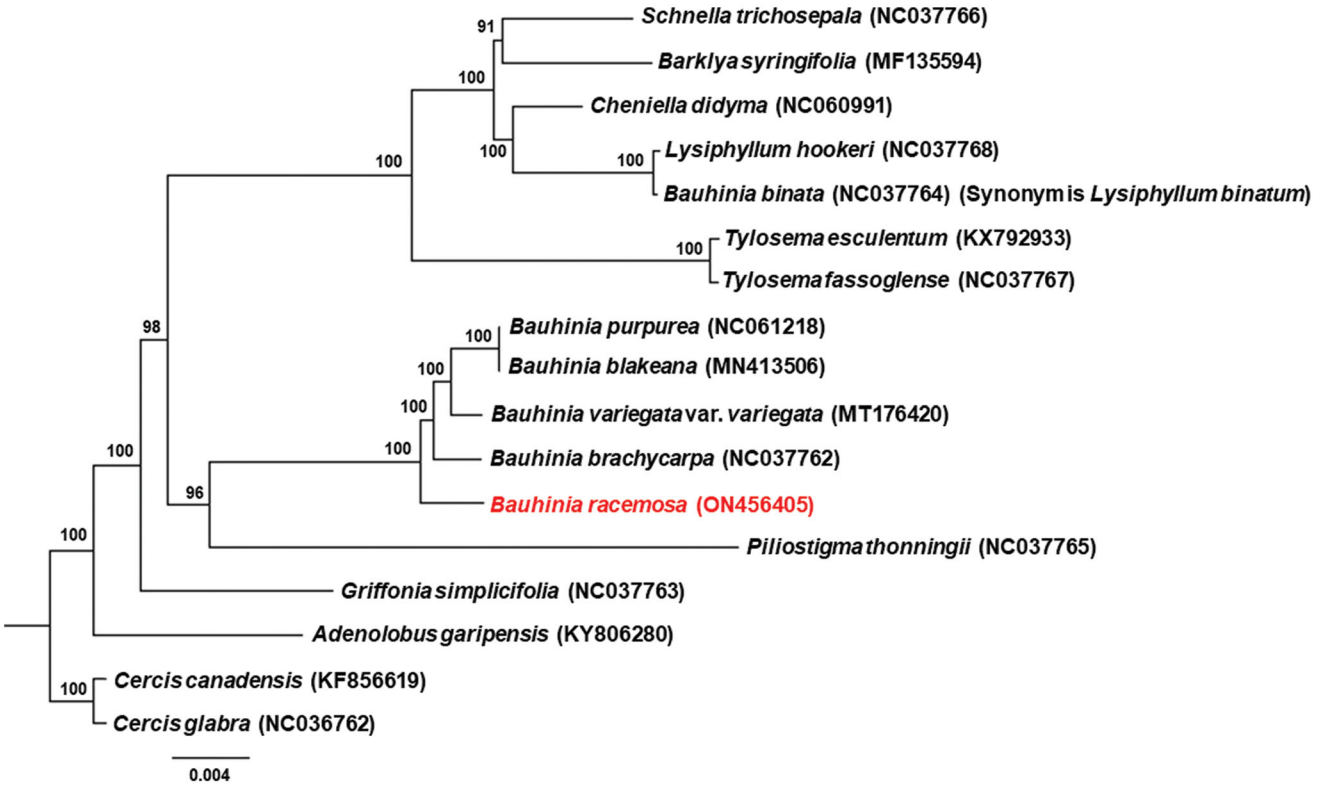

Figure 1. The maximum-likelihood phylogenetic tree for *B. racemosa* based on 71 protein-coding genes from the plastomes of 16 other Cercidoideae species. The outgroup species are *Cercis canadensis* and *C. glabra*.

To determine the phylogenetic position of *B. racemosa*, the complete chloroplast genomes of 16 additional Fabaceae species from the subfamily Cercidoideae were downloaded from GenBank and all protein coding gene sequences were compared using the MAFFT alignment method by Geneious v.8.1.3 software (Kearse et al. 2012). A maximum-likelihood analysis was performed with IQ-TREE v.1.6.7 (Nguyen et al. 2015) with the best-fit model TVM + F+R2 automatically selected by ModelFinder (Kalyaanamoorthy et al. 2017). *Cercis canadensis* (KF856619) and *C. glabra* (NC036762) were selected as the outgroups. Phylogenetic analysis suggests that *B. racemosa* forms a monophyletic clade with the other four *Bauhinia* species (*B. brachycarpa*, *B. purpurea*, *B. blakeana* and *B. variegata* var. *variegata*) (Figure 1). The basic structure of our phylogenetic tree was consistent with that seen in a previous study (Gu et al. 2020).

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Ethical approval

Research and collection of plant material was conducted according to the guidelines provided by Xishuangbanna Tropical Botanical Garden. Permission was granted by the Center for Horticulture Gardening of Xishuangbanna Tropical Botanical Garden to carry out research on the species.

Authors' contributions

YX, YYQ and JLZ conceived the research. YX collected the samples. YX, YYQ, CHH and LT performed data analysis. YX wrote original draft of the manuscript. JLZ revised the manuscript. All authors have read and approved the final manuscript.

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 finding of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov) under the accession no. ON456405. The associated BioProject, SRA, and Bio-Sample number are PRJNA843449, SRS13209563, and SAMN28742914, respectively (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA843449).

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