The complete plastid genome of *Bauhinia variegata* L. var. variegata (Leguminosae)

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**ABSTRACT**

*Bauhinia variegata* L. var. *variegata* is a popular ornamental tree in the tropical and subtropical region. We herein report and characterize the complete plastid genome of *B. variegata* var. *variegata* in an effort to provide genomic resources for genetic utilization. The complete plastome is 155,415 bp in length and contains the typical quadripartite structure, including two inverted repeat (IR) regions of 25,549 bp, a large single-copy (LSC) region of 86,110 bp and a small single-copy (SSC) region of 18,207 bp. 130 genes are annotated, including 85 protein-coding genes, 37 transfer RNA genes, and four unique ribosomal RNA genes. The phylogenetic analysis based on the plastomes from *B. variegata* var. *variegata* and 12 previously reported species of Cercidioideae suggested a sister-relationship between *B. variegata* var. *variegata* and *B. × blakeana* with a strong bootstrap value.

*Bauhinia variegata* L. var. *variegata*, with large, fragrant flowers and long flowering time, is a well-known ornamental tree of the legume family in tropical and subtropical region. Evidence of morphology and Sanger sequencing suggests that it could be one of the parental species of the Hong Kong Orchid Tree, *Bauhinia × blakeana* Dunn (Lau et al. 2005; Mak et al. 2008; Kumari and Meenakshi 2013). *B. variegata* var. *variegata* and *B. × blakeana* are comparable in morphology by having five fertile stamens and leaves bifid to 1/3–1/2. Nevertheless *B. variegata* var. *variegata* has pink petals and linear legume, which is very different from the completely sterile *B. × blakeana* with purplish flowers. To better understand the plastid genome characterization of this plant, we generated the complete plastid genome of the species using the method of genome skimming.

The fresh leaf tissues were collected from South China Agricultural University, Guangzhou, China (113.35°E, 23.16°N). Voucher specimens (H1904242) were deposited in the herbarium of South China Botanical Garden (IBSC). We isolated the whole genomic DNA by a modified CTAB method (Doyle and Doyle 1987). We constructed a library for sequencing by fragmenting the total genomic DNA into 300–500 bp in length following the manufacturer’s manual (Illumina). Paired-end (PE) sequencing was conducted on the Illumina HiSeq X-Ten instrument at Beijing Genomics Institute (BGI) in Wuhan, China. We used GetOrganelle pipeline (Bankevich et al. 2012; Langmead and Salzberg 2012; Wick et al. 2015; Jin et al. 2018) to assemble the plastome from clean sequencing reads. We employed Geneious (Kearse et al. 2012) and Plastid Genome Annotator (PGA) (Qu et al. 2019) to verify the accuracy of the assembly and to annotate the plastome. The annotated plastome has been deposited in GenBank (accession number: MT176420).

To reconstruct the phylogenetic position of *B. variegata* var. *variegata*, we included 13 plastid genomes in previous publications and unpublished data in GenBank (Figure 1) (Sabir et al. 2014; Wang et al., 2017, 2018; Gu et al. 2019). We aligned the data matrix using MAFFT (Katoh and Standley 2013) as implemented in Geneious with default parameters. The maximum likelihood tree was built in IQ-tree (Trifinopoulos et al. 2016) using models recommended by ModelFinder (Kalyaanamoorthy et al. 2017) based on a data matrix of a concatenation of 77 CDS genes. The branch supports were estimated using 1000 replicates of bootstrap.

The complete plastid genome of *B. variegata* var. *variegata* was 155,415 bp in length and showed a typical quadripartite structure: a large single copy (LSC) region of 86,110 bp and a small single copy (SSC) region of 18,207 bp, respectively. These two regions were separated by two inverted repeat regions (IRa and IRb), each of 25,549 bp in length. A total of 130 functional genes were recovered, consisting of 85 protein-coding genes, 37 tRNA genes and four unique rRNA genes. The overall GC content was 36.5%. The phylogenetic analysis suggested that *B. variegata* var. *variegata* and *B. × blakeana* form a strongly supported clade, which is sister to *B. acuminata* L. with a strong bootstrap support value.

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The plastid genome of *B. variegata* var. *variegata* reported here could be helpful for answering questions regarding genetic diversity in Cercidoideae.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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(Figure 1). The plastid genome of *B. variegata* var. *variegata* reported here could be helpful for answering questions regarding genetic diversity in Cercidoideae.