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The complete plastid genome sequence of *Begonia guangxiensis*

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ABSTRACT

Begonia guangxiensis was assessed as endangered according to Red List of Chinese Plants. In this study, we described the complete plastid genome of *B. guangxiensis*. The plastid genome sequence of *B. guangxiensis* is 157,648 bp in size, having a large single-copy region (LSC) of 86,514 bp, a small single-copy region (SSC) of 18,076 bp, and two inverted repeat (IR) regions of 26,529 bp. The complete plastid genome of *B. guangxiensis* encoding 112 unique genes including 79 protein-coding genes, 29 tRNA genes, and four rRNA genes. The overall GC content of the plastid genome is 35.9%. Phylogenetic analysis confirmed that *B. guangxiensis* is closely related to *B. varipeltata*.

Begonia guangxiensis C.Y. Wu belongs to sect. *Coelocentrum* in the genera *Begonia* L. of the family Begoniaceae. This species was assessed as endangered according to Red List of Chinese Plants (Qin et al. 2013) and endemic to limestone area in Guangxi of China (Wu and Ku 1997). Because of the destruction of habitats and over-collection, the species is facing serious threat. Thus, we reported the plastid genome sequences of *B. guangxiensis*, which will contribute to conservation and further study of this species

Total DNA was extracted from fresh leaves of a single individual of *B. guangxiensis* in greenhouse (102°44′40.9″E, 25°08′06.3″N), which is cultivated in Kunming Institute of Botany, Chinese Academy of Sciences. The voucher specimen of *B. guangxiensis* was stored at Guangxi Institute of Botany (IBK 00418686).

Illumina paired-end (PE) library of *ca.* 500 bp was constructed and sequenced with *ca.* 200 bp PE read length, following the standard protocols on the Illumina HiSeq 2500 platform in Kunming Institute of Botany in Kunming, China. Approximately 2.0 Gb of clean data were obtained. *De novo* assemblies were constructed with SPAdes 3.9.1 (Bankevich et al. 2012). GetOrganelle (Jin et al. 2018) was also used to improve accuracy and efficiency in *de novo* assembly. Reference-guided connecting and annotation were subsequently conducted using Bandage 0.8.1(Wick et al. 2015) and Geneious 9.1.4 (Kearse et al. 2012), based on previously published plastomes.

The assembled plastid genome of *B. guangxiensis* is 157,648 bp in length (MN480848). The plastid genome shows a typical quadripartite structure with one large single copy region (LSC) of 86,514 bp, one small single copy region (SSC)
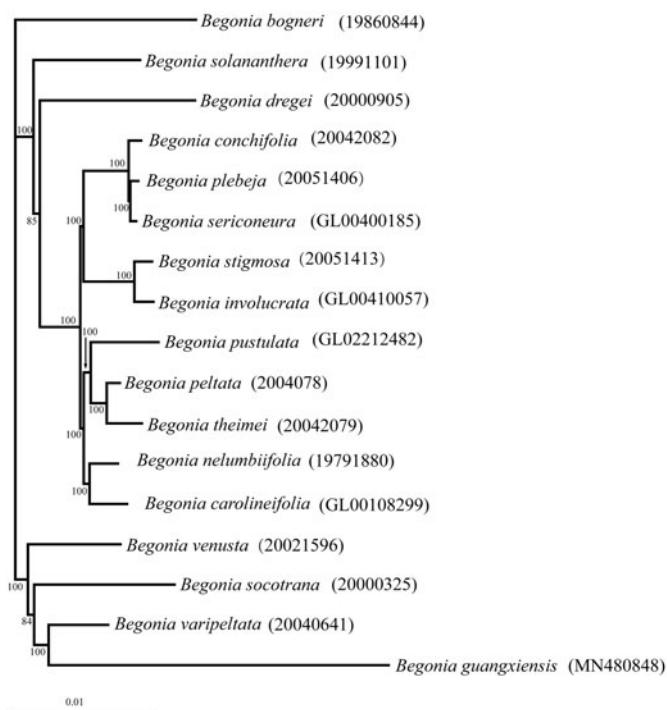

Figure 1. The phylogenetic relationship of *Begonia guangxiensis* that reconstructed with 17 complete plastid genome sequences of *Begonia*.

of 18,076 bp and a pair of inverted repeat regions (IRs) of 26,529 bp. There was a small gap between psbD gene and trnE-UUC gene within LSC, mainly due to multiple mononucleotide repeats. A total of 112 unique genes were encoded by the plastid genome, which including 79 protein-coding genes, four ribosomal RNA genes and 29 transfer RNA genes.

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The overall GC content of the plastid genome is 35.9% and coding sequences (CDS) amounted to 49.8% in size (78,504 bp).

The phylogenetic analysis was performed with additional 16 plastid genomes of the genera *Begonia* available on Dryad (Harrison et al. 2016) using W-IQ-TREE (Trifinopoulos et al. 2016). The result showed that *B. guangxiensis* is closely related to *B. varipeltata* (Figure 1).

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