The first complete chloroplast genome of Briggsia chienii W. Y. Chun and its phylogenetic position within Gesneriaceae

Xiaolan Xu, Mengmeng Shi, Linchun Shi, Wujun Zhang, Jinxin Liu and Xinle Duan

ABSTRACT
Briggsia chienii W. Y. Chun 1946 is an endemic herbaceous perennial species distributed in southern China. In this study, we firstly characterized the complete chloroplast genome sequence of B. chienii and provided new molecular resources for promoting its conservation and taxonomic assignment. Its complete chloroplast genome is 154,082 bp in length and contains the typical quadripartite structure of angiosperm plastome, including two inverted repeat (IR) regions of 25,447 bp, a large single-copy (LSC) region of 85,035 bp, and a small single-copy (SSC) region of 18,153 bp. The plastome contains 114 genes, consisting of 80 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. The overall GC content in the plastome of B. chienii is 37.4%, which is lower than lots of angiosperm plastome. The phylogenetic result indicated that B. chienii exhibited the closest relationship with Oreocharis cotinifolia W. T. Wang 1983, and provided new information for the phylogeny relationship of genus Briggsia.
the organelle assembler GetOrganelle v1.7.3.5 with the parameters ‘-R 15 -k 21,45,85,105 -F embplant_pt’ (Jin et al. 2020), and validated by reads mapping using bowtie2 (Langmead and Salzberg 2012). The protein-coding, rRNA, and tRNA genes of B. chienii chloroplast genome were annotated by using the CPGAVAS2 online webserver (www.herbalgenomics.org/cpgavas2) (Shi et al. 2019). The complete chloroplast genome sequence of B. chienii was submitted to GenBank (Accession number: MZ868555).

The length of the B. chienii complete chloroplast genome sequence was 154,082 bp, and the total GC content was 37.4%. The genome displayed a typical quadripartite structure, including large single-copy (LSC) region (85,035 bp), small single-copy (SSC) region (18,153 bp) and a pair of inverted repeats IR regions (25,447 bp). There are 114 unique genes in the whole chloroplast genome sequence of B. chienii, including 80 protein-coding genes, 30 represented tRNA genes, and four denoted rRNA genes (rrn23S, rrn16S, rrn5S, and rrn4.5S). Among them, 19 genes were annotated as containing introns. Nine protein-coding genes and seven tRNA genes (tmA-UGC, tmG-UCC, tmI-GAU, tmK-UUU, tmL-UAA, tmR-UCU, tmV-UAC) contained one intron, and three protein-coding genes (clpP, ycf3, and rps12) contained two introns. In addition, small exons were annotated in petB, petD, and rpl16 genes, and the length of their small exons were 6 bp, 8 bp and 9 bp, respectively. Moreover, rps12 was identified as a trans-splicing gene.

To confirm the phylogenetic position of B. chienii in Gesneriaceae, a total of 18 complete chloroplast genomes were used for phylogenetic analysis based on the Maximum Likelihood (ML) method using RAxML v8.2.12 with 1000 bootstrap replicates (Stamatakis 2014). Salvia mekongensis E. Peter 1936 and S. umbratica Hance 1884 were used as the out groups. The phylogenetic result indicated that B. chienii exhibited the closest relationship with Oreocharis cotinifolia (Figure 1), and was consistent with the prior taxonomic suggestion (Möller et al. 2014). This study provided a useful molecular resource for its conservation and the phylogenetic studies of genus Briggsia.

**Author contributions**

X.X., J.L. and X.D. conceived and designed the experiments; M.S and L.S. performed the experiments; M.S and C.S. analyzed the data; M.S., L.S. and W.Z. contributed reagents/materials/analysis tools; X.X., J.L. and X.D. wrote the paper.

**Disclosure statement**

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

**Funding**

This research was supported by the Natural Science Foundation of Fujian Province [No. 2020J01538].

![Figure 1](attachment:phylogenogram.png)
**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under the accession no. MZ868555. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA682118, SRR16930608, and SAMN23005362, respectively.

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