Complete chloroplast genome sequences of *Sinosenecio baojingensis* Ying Liu & Q.E. Yang (Asteraceae)

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**ABSTRACT**

In this study, we assembled and described the complete chloroplast genome (cp) of *Sinosenecio baojingensis* Ying Liu & Q.E. Yang (Asteraceae) for the first time. The cp genome is 151,315 bp in length and exhibits a typical quadripartite structure, consisting of a large single-copy (LSC) region of 83,445 bp, a small single-copy (SSC) region of 18,172 bp, and a pair of inverted repeat regions (IRs) of 24,849 bp. A total of 133 genes were annotated, including 88 protein-coding genes (one pseudo gene), 37 tRNA genes (tRNAs), and eight ribosomal RNA genes (rRNAs). Further, the phylogenetic analysis based on eight complete chloroplast genomes indicates that *S. baojingensis* is shown to be a sister to *S. jishouensis*. The complete chloroplast genome of *S. baojingensis* provides significant molecular markers for the studies on phylogeny and species identification of this genus.

*S. baojingensis* Ying Liu & Q.E. Yang 2009, is a perennial herb belonging to Asteraceae (*Sinosenecio*), which mainly grows in the northwest of Hunan, China (Liu et al. 2009). *S. baojingensis* is distinguishable from *S. euosmus* and *S. denticulatus* in its taller stature, ovate-cordate undivided leaves, and basally expanded but never auriculate petioles. Jeffrey and Chen (1984) pointed out that the distribution area of most species of *Sinosenecio* was narrow in China and they were greatly affected by human activities. Therefore, the whole chloroplast gene analysis significantly contributes to future physiological and phylogenetic research. Here, we characterize the chloroplast whole genome of *S. baojingensis*.

Fresh leaves of *S. baojingensis* were collected from Hongping village, Jishou city (Hunan Province, China; 109°44′53″E, 28°23′58″N) and were dried with silica gel. The voucher specimen (JUU2021ZQ017) was deposited at the herbarium of Jishou University (Qiang Zhou, zhoutianzhi@jsu.edu.cn). High-quality total genomic DNA was extracted from the silica-dried leaf using Plant Genomic DNA Kit DP305 (Beijing, China) and the whole genome was sequenced by Biomarker Technologies Co. Ltd. (Beijing, China) on the Illumina Hiseq platform. The clean data was assembled by the Getorganelle program (Jin et al. 2018) with the following parameters (w: length multiples used to extract chloroplast gene reads, set to 0.6; R: rounds of extracting chloroplast gene reads, set to 15; t: 10; k: use spades for k-mer of de novo assembly, set to 75, 95, 115, 127) to obtain the complete chloroplast genome and annotated on the web page Geseq (https://chlorobox.mpimp-golm.mpg.de/geseq.html) (Tillich et al. 2017) with *Ligularia jaluensis* as the reference sequence. These annotations were also checked with other reference sequences for manual adjustment in Geneious-9.0.2 programme. Finally, the ultimate complete chloroplast genome of *S. baojingensis* was deposited in Genbank (MZ325394).

The complete chloroplast genome of *S. baojingensis* is 151,315 bp in length and exhibits a typical quadripartite structure, consisting of a large single copy (LSC) region of 83,445 bp, a small single copy (SSC) region of 18,172 bp, and a pair of inverted repeat regions (IRs) of 24,849 bp. The IRs regions are separated by the LSC and SSC. A total of 133 genes of this chloroplast genome were annotated, including 88 protein-coding genes (one pseudo gene), 37 tRNA genes (tRNAs), and eight ribosomal RNA genes (rRNAs). In addition, the overall GC content is 37.4%, while the corresponding values of the LSC, SSC, and IR regions are 35.50, 30.60, and 43.00%, respectively. It is worth noting that comparison among *S. baojingensis* and other two published species from *Sinosenecio* (*S. jishouensis* and *S. oldhamianus*) (Xu et al. 2019; Zhou et al. 2021) indicates the similarity in their genomic structure, gene number, and CG content of each region. This is congruent with the view of previous studies that most chloroplast genome of angiosperms is highly conserved (Cheng et al. 2017).

To further determine the phylogenetic position of *S. baojingensis*, the chloroplast genome sequences of seven other Asteraceae species were obtained from NCBI, including *Sinosenecio jishouensis* and *Sinosenecio oldhamianus* (Xu et al. 2019; Zhou et al. 2021). Sequences of these species were aligned by using MAFFT (Katoh and Standley 2013) and then RAxML-8.2.12 was used for maximum likelihood analysis on Cipres Portal (https://www.phylo.org/portal2) (Miller et al. 2010; Stamatakis 2014) with the recommended default model GTRCAT and 1000 bootstrap replicates. Finally, the ML phylogenetic tree

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was constructed and *Sonchus boulosii* (Asteraceae) was used as an outgroup. Two major clades (clade A and clade B) appear in this tree (Figure 1). The clade A includes *S. jishouensis*, *S. baojingensis*, *S. oldhamianus*, and *Ligularia hodgsonii*, and the other clade B consists of *Opisthopappus taihangensis*, *Chrysanthemum lucidum*, and *Artemisia selengensis*. Moreover, the support values of all nodes are 100% and such analysis result is consistent with the study of Xu et al. (2019). Our phylogenetic analysis indicates that *S. baojingensis* is shown to be a sister to *S. jishouensis* with the closest relationship, followed by *S. oldhamianus*. We consider that the chloroplast genome of *S. baojingensis* reported will provide significant molecular markers for the studies on phylogeny and species identification of this genus.

**Author contributions**

Jie-Nan Xie, Da Wang, and Jing-Yi Peng: data analysis and interpretation. Yi Wang: collection and identification of plant samples. Qiang Zhou: conceptualization (overarching experiment), funding acquisition, methodology (overarching experiment), resources, supervision, and writing (review and editing). The manuscript is written by Jie-Nan Xie and edited by Jing-Yi Peng and Yi Wang. All authors have approved the final version of this manuscript and agree to be accountable for all aspects of the work.

**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 findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/ under the accession no. MZ325394. The associated BioProject, SRA, and BioSample numbers are PRJNA695131, SRR13568816, and SAMN17602145, respectively.

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