The complete chloroplast genome sequence of the medicinal plant *Stephania epigaea* H. S. Lo, 1978 (Menispermaceae) from Yunnan, China

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**ABSTRACT**

*Stephania epigaea* H. S. Lo, 1978 is a medicinal plant commonly used in southwest China. This study characterized the first complete chloroplast (cp) genome sequence of this species. The complete cp was 157,738 bp in length, containing a large single-copy region (LSC) of 88,460 bp, a small single-copy region (SSC) of 19,778 bp, and a pair of inverted repeat regions (IRs) of 24,750 bp. It encoded 130 genes, including 85 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The GC content of the complete genome was 36.7%. Phylogenetic analysis of complete cp sequences revealed that *S. epigaea* was clustered with *S. japonica* from the Menispermaceae family.

This article is licensed under the Regulations of Yunnan Province on Biodiversity Protection and is not require any ethical or institutional approvals. Healthy and fresh leaves of *S. epigaea* were collected from Dali county (25°44’59” N, 100°11’6” E) and deposited in the Herbarium of Dali University (http://yxy.dali.edu.cn/yhxy/, Min Fan, fanmin@dali.edu.cn) under the voucher number LJ2020060607. The total genomic DNA was extracted using the improved CTAB method (Doyle and Doyle 1986) and sequenced by the Illumina NovaSeq 6000 platform (Chang et al. 2021). In total, 19,098,862 clean reads (https://github.com/ndierckx/novoplasty) were de novo assembled by NOVOPlast (Wang et al. 2020; Xia et al. 2021) and annotated by GeSeq with default settings (Tillich et al. 2017; Wei and Li 2021). The GenBank accession number is MZ678241.

The length of the *S. epigaea* cp genome was 157,738 bp with a typical quadripartite circular structure (Zhou et al. 2017), which contained a pair of inverted repeat regions (IRa and IRb, 24,750 bp), a large single-copy region (LSC, 88,460 bp), and a small single-copy region (SSC, 19,778 bp). All 130 genes were identified, including 85 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The overall GC content of the cp genome was 36.7%.

To evaluate the phylogenetic relationship of *S. epigaea*, 5 Menispermaceae, 10 Berberidaceae, and 9 Ranunculaceae complete cp genomes were downloaded from the NCBI database and aligned by MAFFT v7 (https://mafft.cbrc.jp/alignment/server/index.html) (Katoh and Standley 2013; Yamada et al. 2016). A maximum-likelihood tree with 1,000 bootstrap replicates was inferred using IQ-TREE v2.1.2 (Nguyen et al. 2015; Liu et al. 2021), with *Aristolochia debilis* (NC 036153.1) and *Aristolochia kwangsiensis* (NC 052833.1) as outgroups. The phylogenetic analysis revealed that *S. epigaea* was closely related to *S. japonica* (Figure 1). The cp genome of *S. epigaea* will be helpful for a comprehensive understanding of phylogenetic relationships among the genus *Stephania* and provide a valuable reference for the conservation genetics of this species.
Author contributions statement

Qin Guan analyzed the data, prepared figures, authored drafts of the paper and approved the final draft. Danping Feng collected materials and performed the experiments. Min Fan designed the experiments, contributed reagents/materials/analysis tools, revised the content and approved the final draft. All authors 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, supporting the findings of this study, are openly available in GenBank of NCBI (https://www.ncbi.nlm.nih.gov) with the accession number is MZ678241, which permits unrestricted use, distribution and reproduction in any medium provided the original work is cited correctly. The associated BioProject, Bio-Sample and SRA numbers are PRJNA759697, SAMN21188258 and SRR15693952, respectively.

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