Complete chloroplast genome of medicinal plant *Sabia parviflora* Wall. ex Roxb. (Sabiaceae)

Qiuyu Chen, Wenfen Xu, Chao Zhao, Bo Wang, Chunling Chen, Qu Liu, Qingwen Sun and Yuan Huang

College of Pharmacy, Guizhou University of Traditional Chinese Medicine, Guiyang, PR China

**ABSTRACT**

*Sabia parviflora* Wall. ex Roxb., an evergreen climbing woody vine, is a Chinese herbal medicine commonly used by ethnic minorities in some areas of China. In this study, the chloroplast genome of *S. parviflora* was sequenced for the first time. Its genome is 162,054 bp in length with 38.6% of GC content. The genome consists of a large single copy (LSC) region of 90,001 bp, a small single copy (SSC) region of 18,887 bp, and two inverted repeat (IRa and IRb) regions of 26,583 bp each. A total of 130 genes were annotated, including 85 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Phylogenetic analysis was conducted by nine species from order Proteales, which demonstrated a close relationship between the family Sabiaceae and Nelumboaceae.
The whole chloroplast genomes of nine species in four families of Proteales were used for phylogenetic analysis. After sequence alignment by MAFFT (Katoh and Standley 2013), MEGA X (Kumar et al. 2018) was used to perform maximum likelihood (ML) tree with the Tamura Nei model. The bootstrap method was used to test the reliability of phylogeny with 1000 replicates. Two species from Sabia showed a cognate relationship, and the family Sabiaceae have a closer relationship with family Nelumbonaceae than that of Platanaceae and Proteaceae (Figure 1). These relationships are congruent with previous report (Sun et al. 2016).

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the National Natural Science Foundation of China [Grant No. 81560707], First class discipline construction project in Guizhou Province [Grant No. GNYL [2017]008], Project of Engineering Research Center of Guizhou University [Grant No. KY [2017]018], and Excellent young scientific and Technological Talents Project of Guizhou Province [Grant No. [2019]5658].

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](https://www.ncbi.nlm.nih.gov) under the accession no. MW566751. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA727714, SRR14455320, and SAMN19030660 respectively.

References

Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics. 30(15):2114–2120.

Chen YR, Pan GJ, Xu WF, Sun QW, Wang B, Zhang Y, Yang TJ. 2020. Spectrum-effect relationship study between HPLC fingerprints and antioxidant activity of Sabia parviflora. J Chromatogr B-Anal Technol Biomed Life Sci. 1140:121970.

Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. Nucleic Acids Res. 45(4):e18.

Editorial Committee of Flora of China (ECFC). 1988. Flora republicae popularis sinicae. Beijing: Science Press.

Guo LX, Anthony RB. 2007. Flora of China (Sabiaceae) Vol. 12. Beijing: Science Press.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30(4):772–780.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing Platforms. Mol Biol Evol. 35(6):1547–1549.

Luo YC, Sun QW. 2013. Natural medicines commonly used by ethnic groups in Guizhou. Vol. 2. Guiyang (China): Guizhou Science and Technology Publishing House.

Shi LC, Chen HM, Jiang M, Wang LQ, Wu X, Huang LF, Liu C. 2019. CPGAVAS2, an integrated plastome sequence annotator and analyzer. Nucleic Acids Res. 47(W1):W65–W73.

Sun QW, Pan GJ, Xu WF, Lu X, Bai CH, Liu MG, Chen YR. 2019. Isolation and structure elucidation of a new flavonol glycoside from Sabia Parviflora. Nat Prod Res. 29:1–6

Sun YX, Moore MJ, Zhang SJ, Solitis PS, Solitis DE, Zhao TT, Meng AP, Li XD, Li JQ, Wang HC. 2016. Phylogenomic and structural analyses of 18 complete plastomes across nearly all families of early-diverging eudicots, including an angiosperm-wide analysis of IR gene content evolution. Mol Phylogenet Evol. 96:93–101.