Complete chloroplast genome of a widely distributed species in southwest China, *Hemiphragma heterophyllum* Wall. (Scrophulariaceae)

Xiaobo Wu and Dequan Zhang

*College of Pharmacy and Chemistry, Dali University, Dali, China; Institute of Materia Medica, Dali University, Dali, China; Key Laboratory of Yunnan Provincial Higher Education Institutions for Development of Yunnan Daodi Medicinal Materials Resources, Dali, China*

**ABSTRACT**

*Hemiphragma heterophyllum* Wall., a widely distributed species in southwest China, belongs to a monotypic genus, *Hemiphragma* Wall. in the Scrophulariaceae. To date, there has been no study on its complete chloroplast genome. Hence, we reported the first complete chloroplast genome sequence of *H. heterophyllum* here. The genome sequences of two individuals were extremely similar except slight differences on sequence lengths (152,707 bp and 152,700 bp, respectively). There was a typical circular quadripartite structure. A total of 113 genes were annotated, including 79 protein-coding genes, 29 tRNA genes, four rRNA genes, and one pseudogene. Among the annotated genes, 16 genes contained one intron, whereas another two genes (ycf3 and clpP) possessed two gene introns. Total GC content is 38.1% in the chloroplast genome. Moreover, a total of 63 simple sequence repeats (SSRs) with five types were detected. Phylogenetic analysis revealed that *Hemiphragma* was closely related to *Veronica* L. and *Veronicastrum* Heist. ex Fabricc.

*Hemiphragma heterophyllum* Wall. is a perennial herb belonging to the genus *Hemiphragma* Wall. in the family Scrophulariaceae and there is only one species in this genus (Hong et al. 1998). The species is widely distributed in Yunnan, Tibet, Sichuan, Guizhou, and adjacent regions in China, and also it could be found in Nepal, India, and the Philippines. It usually grows in alpine grassland or rock crevices with an altitude of 3000–4000 m (Hong et al. 1998). The whole plant of *H. heterophyllum* can be used for promoting blood circulation, heat-clearing and detoxification, as well as eliminating wind and dampness (Long and Li 2004; He et al. 2013). Therefore, it is listed as folk medicine by Bai and Dai Nationalities in western Yunnan, China (Lee et al. 2008). However, the current researches on this species mainly focussed on its chemical compositions, but rarely involved its molecular biology (Tian and Zhou 2004; Yang et al. 2004; Dai 2003). Hence, we reported the first complete chloroplast genome sequence of *H. heterophyllum* here. The genome sequences of two individuals were extremely similar except slight differences on sequence lengths (152,707 bp and 152,700 bp, respectively). There was a typical circular quadripartite structure. A total of 113 genes were annotated, including 79 protein-coding genes, 29 tRNA genes, four rRNA genes, and one pseudogene. Among the annotated genes, 16 genes contained one intron, whereas another two genes (ycf3 and clpP) possessed two gene introns. Total GC content is 38.1% in the chloroplast genome. Moreover, a total of 63 simple sequence repeats (SSRs) with five types were detected. Phylogenetic analysis revealed that *Hemiphragma* was closely related to *Veronica* L. and *Veronicastrum* Heist. ex Fabricc.

**KEYWORDS**

*Hemiphragma heterophyllum*; widely distributed species; complete chloroplast genome; phylogenetic analysis

**ARTICLE HISTORY**

Received 4 September 2019  
Accepted 23 September 2019

**CONTACT** Dequan Zhang  
zhangdeq2008@126.com  
College of Pharmacy and Chemistry, Dali University, Dali 671003, China; Key Laboratory of Yunnan Provincial Higher Education Institutions for Development of Yunnan Daodi Medicinal Materials Resources, Dali, China

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The whole cp genome sequence was 152,707 bp in length with a typical circular quadripartite structure, consisting of a pair of inverted repeat regions (IRa and IRb) of 25,808 bp, which were separated by a large single copy (LSC) region of 83,268 bp and a small single copy (SSC) region of 17,823 bp. A total of 113 genes were annotated in the *H. heterophyllum* cp genome, including 79 protein-coding genes, 29 tRNA genes, four rRNA genes, and one gene was inferred to be pseudogene. Among the annotated genes, 16 genes (*atpF, ndhA, ndhB, petB, petD, rpl2, rpl16, rpoC1, rps12, rps16, trnA-UGC, trnG-UCC, trnI-CAU, trnK-UUU, trnL-UAA, and trnV-UAC*) contained one intron, whereas another two genes (*ycf3* and *clpP*) possessed two introns. Total GC content was 38.1%, and the corresponding values in LSC, SSC, and IR regions are 36.2%, 32.1%, and 43.2%, respectively. Furthermore, a total of 63 simple sequence repeats (SSRs) with five types were detected in the *H. heterophyllum* cp genome, including 42 mononucleotide repeats, eight dinucleotide repeats and 13 other types of SSR loci.

The phylogenetic tree showed that two individuals of *H. heterophyllum* were clustered together with *Veronica nakaiana*, *Veronica persica* and *Veronicastrum sibiricum*. The results revealed that the genus *Hemiphragma* was closely related to *Veronica* and *Veronicastrum*. Compared with *Veronica*, the genus was closer to *Veronicastrum* in molecular phylogenetics (*Figure 1*). On the contrary, the monotypic genus was obviously more distant to *Brandisia*, *Lindenbergia* and *Pedicularis* than other genus. Consequently, this study accurately revealed phylogenetic position of *H. heterophyllum* in the Scrophulariaceae, which would be beneficial to further phylogenetic studies on the related species or genera in the family.

**Disclosure statement**
The authors are highly grateful to the published genome data in the public database. The authors declare no conflicts of interest and are responsible for the content.

**Funding**
This study was co-supported by National Natural Science Foundation of China [31660081], Yunnan Provincial Science and Technology Department [Grant No. 2016FB144] as well as Innovation Team Project.
for Traditional Chinese Medicine Resources and Ethnic Medicine of Dali University [ZKLX2019318].

References

Bolger AM, Marc L, Bjoern U. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics. 30(15):2114–2120.

Dai JM, Li YH, Pu XY, Yang C, Sun JX, Ruan R, Li XN, Tian K, Huang XZ. 2019. Chemical constituents from the whole herb of Hemiphragma heterophyllum. J Asian Nat Prod Res. 21(6):551–558.

Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochem Bull. 19:11–15.

He KQ, Lu WY, Yang Q, Zhao YZ. 2013. Determination of total flavonoids content in Hemiphragma heterophyllum Wall. Med Plant. 4:16–18.

Hong DY, Yang HB, Jin CL, Holmgren NH. 1998. Scrophulariaceae. In: Wu ZY and Raven PH, editors. Flora of China (18th). Beijing: Science Press.

Jin JJ, Yu WB, Yang JB, Song Y, Yi TS, Li DZ. 2018. GetOrganelle: a simple and fast pipeline for de novo assembly of a complete circular chloroplast genome using genome skimming data. bioRxiv:256479.

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

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12):1647–1649.

Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol. 33(7):1870–1874.

Lee SW, Xiao CJ, Pei SJ. 2008. Ethnobotanical survey of medicinal plants at periodic markets of Honghe Prefecture in Yunnan Province, SW China. J Ethnopharmacol. 117(2):362–377.

Long CL, Li R. 2004. Ethnobotanical studies on medicinal plants used by the Red-headed Yao People in Jinping, Yunnan Province, China. J Ethnopharmacol. 90(2–3):389–395.

Lu Y, Pu XY, Tian K, Sun JX, Wang W, Liu HC, Shao JL, Huang XZ, Li YH. 2019. On the phenolic compounds from Hemiphragma heterophyllum Wall. J Yunnan Minzu Univ (Nat Sci Ed). 28:16–19.

Thiel T, Michalek W, Varshney RK, Graner A. 2003. Exploiting EST databases for the development and characterization of gene-derived SSR-markers in barley (Hordeum vulgare L.). Theor Appl Genet. 106(3):411–422.

Tian L, Zhou JY. 2004. Studies on chemical constituents from herb of Hemiphragma heterophyllum. China J Chin Mater Med. 29(6):528–531.

Yang MF, Li YY, Li BG, Zhang GL. 2004. A new monoterpenoid glycoside from Hemiphragma heterophyllum. Acta Botanica Yunnanica. 46:1454–1456.