

The complete chloroplast genome of a medical herb, *Halenia elliptica* D. Don (Gentianaceae), from Qinghai-Tibet Plateau in China

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ABSTRACT

Halenia elliptica D. Don (Gentianaceae) is one of the genuine medicinal species in Qinghai-Tibet Plateau, China. Here we report the first chloroplast (cp) genome of *H. elliptica* using Illumina HiSeq X Ten platform. The length of its complete cp genome is 153,341 bp, containing four sub-regions; a large single-copy region (LSC) of 82,811 bp and a small single-copy region (SSC) of 18,278 bp, which are separated by a pair of inverted repeat regions (IRs) of 26,126 bp each. The complete cp genome of *H. elliptica* contains 129 genes, including 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The overall GC content of the cp genome is 38.1%. The phylogenetic analysis, based on 15 cp genomes, suggested that *H. elliptica* is closely related to *Halenia corniculata* (L.) Cornaz and *Swertia* species.

ARTICLE HISTORY

Received 31 August 2019
Accepted 23 September 2019

KEYWORDS

Halenia elliptica; chloroplast genome; Gentianaceae; Qinghai-Tibet Plateau; phylogenetic trees

Halenia Borkh. (Gentianaceae) includes about 40 species distributed in the Americas, Eastern Europe, and East Asia (von Hagen and Kadereit 2003). There are only two *Halenia* species distributed in China, *Halenia corniculata* (L.) Cornaz and *Halenia elliptica* D. Don. *Halenia elliptica*, known as the 'Tibetan capillaris,' is one of the common Tibetan herbal

medicines used in the treatment of liver and gallbladder diseases (Song 1986). It is mainly distributed in mountain area (altitude 2600–4600 m) in Tibet, Qinghai, Sichuan Provinces and other places in China (Yang 1991; Jia and Li 2005).

To study the systematic position and genetic background of *H. elliptica*, we sequenced the *H. elliptica* DNA and

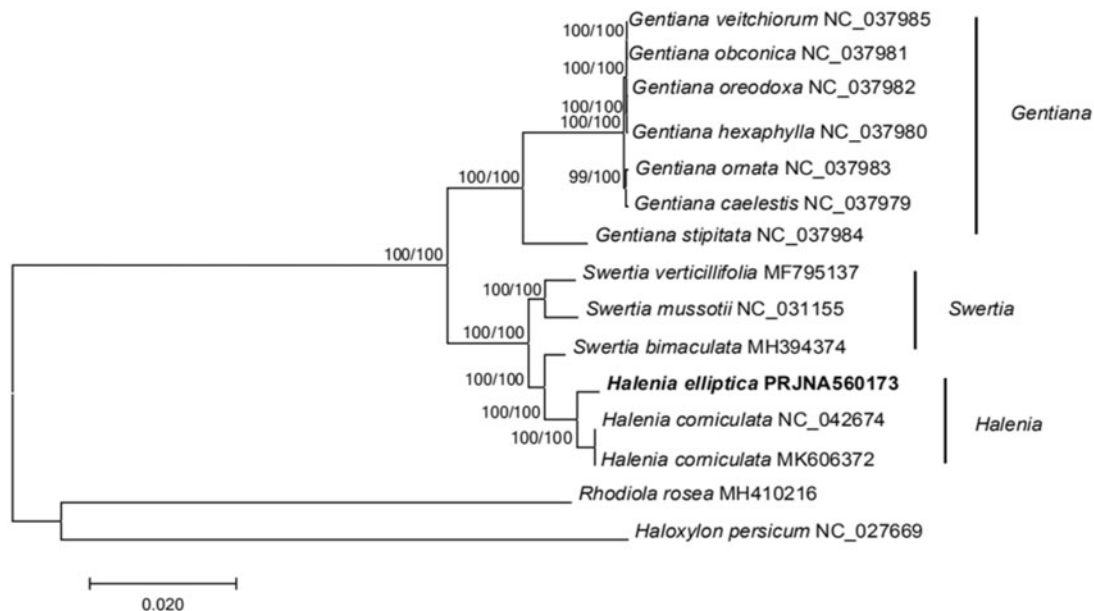


Figure 1. Phylogenetic tree of 15 species based on complete chloroplast (cp) genome sequences using NJ (with 1000 replicates) and ML (with 1000 replicates) methods. The numbers below the branches indicate the corresponding bootstrap support values from the NJ and ML trees. *Haloxylon persicum* (NC_027669) and *Rhodiola rosea* (MH410216) are outgroups.

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obtained its complete chloroplast (cp) genome. The voucher specimen of *H. elliptica* was collected from the meadow in the West Zhang Line (G227) in Datong Hui Autonomous County, Qinghai Province, China, on 24th July in 2017 (alt. 2762 m, E101°53'87.89", N37°20'4.7"). The total DNA was isolated from leaf materials of the voucher specimen using the plant genomic DNA extraction kit (Solarbio LIFE SCIENCES, China). The DNA concentration and quality were then measured by NanoDrop2000c micro-uv spectrophotometer (Thermo Scientific, Waltham, MA). The DNA was sequenced at Novogene Biotech Co. (Beijing, China) using the Illumina HiSeq X Ten platform (Illumina, San Diego, CA) with a 150-bp shotgun library. In the end, 1.63 G of 150-bp paired-end raw reads of *H. elliptica* were obtained, processed, and assembled following the method of Bakker et al. (2016) and Wei et al. (2017). The assembled contigs were mapped to the reference cp genome (*H. corniculata*, GenBank accession no. NC_042674) and annotated using Geneious Prime software (<https://www.geneious.com>). The border regions between the large single-copy region (LSC), the small single-copy region (SSC) and two inverted repeat regions (IRs) were validated by PCR amplifications and Sanger sequencing. The complete cp genome of *H. elliptica* is 153,341 bp in length (GenBank accession no. PRJNA560173). It contains two IRs of 26,126 bp each, separated by an LSC of 82,811 bp and a small SSC of 18,278 bp. The cp genome of *H. elliptica* is comprised of 136 genes, including 91 protein-coding genes (2 duplicated), 8 rRNA genes, and 37 tRNA genes (8 duplicated). There are 19 genes containing one intron, and 2 genes have two introns. The overall GC content of the cp genome is 38.1%, while the corresponding values of the LSC, SSC, and IR regions are 36.2, 32.1, and 43.3%, respectively.

The cp genome of *H. elliptica* and 14 cp genome sequences (downloaded from GenBank) were aligned using MAFFT (Katoh and Standley 2013) and then constructed phylogenetic trees using neighbor-joining (NJ) and maximum-likelihood (ML) methods in MEGA7 (Kumar et al. 2016). *Haloxylon persicum* (Chenopodiaceae) and *Rhodiola rosea* (Crassulaceae) were selected as outgroups. The results showed that *H. elliptica* was sister group to *H. corniculata* and they were closely related to *Swertia bimaculate* (Figure 1). The phylogenetic

analysis was consistent with previous studies (Chassot et al. 2001; Park et al. 2019).

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the Natural Science Foundation of Qinghai Provincial Science and Technology Department, China [2017-ZJ-742].

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