The complete chloroplast genome of *Isatis cappadocica* Desv. (Brassicaceae)

Zhen-Xi Fang*, Xiao-Jing Qin and Qing Li

*Research and Development Center of Chinese Medicine Resources and Biotechnology, Institute of Chinese Materia Medica, Shanghai University of Traditional Chinese Medicine, Shanghai, China; Department of Pharmacy, Second Affiliated Hospital of Naval Medical University, Shanghai, China

**ABSTRACT**

*Isatis cappadocica* Desv. is a vigorous perennial rosette plant and it can grow in highly arsenic-contaminated areas. In this study, the complete chloroplast genome of *I. cappadocica* was assembled and annotated. The total length of this genome is 153,800 bp and its GC content is 36.48%. It has a typical four-part structure: a pair of inverted repeat sequences (26,270 bp each), a small single-copy region (17,715 bp), and a large single-copy region (83,545 bp). The annotation results show that it contains 132 genes. The phylogenetic analysis of *I. cappadocica* and other 18 representative plants indicates that *I. cappadocica* is closely related to *Isatis tinctoria*.

The whole chloroplast genome of *I. cappadocica* is 153,800 bp in size and its GC content is 36.48%. The chloroplast genome has a typical four-part structure, with two inverted repeat regions (IR) of 26,270 bp each (42.33% GC content), separated by a small single-copy region (SSC) of 17,715 bp (29.68% GC content) and a large single-copy region (LSC) of 83,545 bp (34.25% GC content). The complete chloroplast genome of *I. cappadocica* contains 132 total genes, including 87 protein-coding genes, 8 rRNA genes, and 37 tRNA genes.

To investigate the phylogenetic relationship of *I. cappadocica*, the molecular phylogenetic tree was constructed based on the common genes of the complete chloroplast genome of *I. cappadocica* and other 18 plants, which were retrieved from GenBank. The chloroplast genomes were aligned by PhyloSuite v1.2.2 [Zhang et al. 2020, https://github.com/dongzhang0725/PhyloSuite/releases] and the maximum-likelihood (ML) analysis was conducted with a bootstrap of 1000 repetitions based on the GTR + F + I + G4 nucleotide substitution model [Nguyen et al. 2015]. The phylogenetic analysis
indicated that *I. cappadocica* has a close relationship with *Isatis tinctoria* (Figure 1), a famous indigo-producing plant.

**Ethical approval**

Research and collection of plant material were conducted according to the guidelines provided by the Shanghai University of Traditional Chinese Medicine. Permission was granted by the National Natural Science Foundation of China.

**Authors’ contributions**

ZF performed the experiments, evaluated the data, and wrote the manuscript. XQ helped to perform the experiments, and write and revise the manuscript. QL conceived the study, supervised the experiments, and made revisions to the manuscript. All authors read and approved the final manuscript.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Funding**

This work was supported by the National Natural Science Foundation of China under the grant numbers [32070327] and [31770329]; and the National Key Research and Development Program of China under the grant number [2019YFC1711100].

**Data availability statement**

The chloroplast genome sequence data that support the findings of this study are openly available in GenBank of NCBI (https://www.ncbi.nlm.nih.gov/) under the accession No. OL404951. The associated raw sequencing data have been deposited into the National Genomics Data Center, China National Center for Bioinformation/Beijing Institute of Genomics, Chinese Academy of Sciences, under the Genome Sequence Archive number CRA006127 with the BioProject number PRJCA008257 and the BioSample number SAMC606263 (https://ngdc.cnbc.ac.cn/).

**References**

Editorial Committee of the Flora of China. 1987. *Flora Reipublicae Popularis Sinicae*, Vol. 33. Beijing (China): Chinese Academy of Sciences; p. 846.

Güner M, Kanbolat S, Korkmaz N, Aliyazicioglu R, Abudayyak M, Kandemir A, Karaoglu SA, Kalaycioglu AT, Ozgen U. 2019. Evaluation of antioxidant, antimicrobial, antityrosinase and cytotoxic potentials of *Isatis cappadocica* subsp. *alyssifoli* as a potent pharmaceutical resource. J Pharma Res Int. 26(5):1–12.

Jin J-J, Yu W-B, Yang J-B, Song Y, dePamphilis CW, Yi T-S, Li D-Z. 2020. GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biol. 21(5):241.

Karimi N, Ghaderian SM, Maroofi H, Schat H. 2010. Analysis of arsenic in soil and vegetation of a contaminated area in Zarshuran, Iran. Int J Phytoremediation. 12(2):159–173.

Karimi N, Shayesteh LS, Ghasmpour H, Alavi M. 2013. Effects of arsenic on growth, photosynthetic activity, and accumulation in two new hyperaccumulating populations of *Isatis cappadocica* Desv. J Plant Growth Regul. 32(4):823–830.

Nguyen L-T, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32(1):268–274.

Souni Z, Karimi N, Sandalio LM. 2017. Arsenic hyperaccumulation strategies: an overview. Front Cell Dev Biol. 5:67.

Zhang D, Gao F, Jakovič I, Zou H, Zhang J, Li WX, Wang GT. 2020. PhyloSuite: an integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Mol Ecol Resour. 20(1):348–355.