Schisandra chinensis is a deciduous woody vine plant that has been used in traditional medicine for thousands of years in China. In this study, we researched the complete chloroplast genome of S. chinensis. The complete chloroplast genome length is 147,779 bp, containing a large single-copy region (LSC) of 97,352bp, a small single-copy region (SSC) of 20,313 bp, and a pair of inverted repeat (IR) regions of 15,057 bp. The overall nucleotide composition is: A of 29.8%, T of 30.8%, C of 20.2%, and G of 19.2%, with a total GC-content of the chloroplast genome 39.4% and AT of 60.6%. Whole chloroplast genome of S. chinensis contains 126 genes, including 83 protein-coding genes (PCG), 35 transfer RNA (tRNAs) genes, and 8 ribosome RNA (rRNAs) genes. Phylogenetic and genetic analysis based on 30 herbal species confirmed the position of S. chinensis closely related to S. sphenanthera. The complete chloroplast genome of S. chinensis provides more molecular data for the genetic diversity and genetic evolutionary relationship of this species in China.

**ABSTRACT**

*Schisandra chinensis* is a deciduous woody vine plant that has been used in traditional medicine for thousands of years in China. In this study, we researched the complete chloroplast genome of *S. chinensis*. The complete chloroplast genome length is 147,779 bp, containing a large single-copy region (LSC) of 97,352 bp, a small single-copy region (SSC) of 20,313 bp, and a pair of inverted repeat (IR) regions of 15,057 bp. The overall nucleotide composition is: A of 29.8%, T of 30.8%, C of 20.2%, and G of 19.2%, with a total GC-content of the chloroplast genome 39.4% and AT of 60.6%. Whole chloroplast genome of *S. chinensis* contains 126 genes, including 83 protein-coding genes (PCG), 35 transfer RNA (tRNAs) genes, and 8 ribosome RNA (rRNAs) genes. Phylogenetic and genetic analysis based on 30 herbal species confirmed the position of *S. chinensis* closely related to *S. sphenanthera*. The complete chloroplast genome of *S. chinensis* provides more molecular data for the genetic diversity and genetic evolutionary relationship of this species in China.
model and used the number of bootstrap replicates with 5000. All of the nodes were inferred with strong support by the ML methods. The phylogenetic ML tree was represented using MEGA X (Kumar et al. 2018) and edited using iTOL Version 4 (Ivica and Peer 2019). The result (Figure 1) showed that the chloroplast genome of *S. chinensis* is clustered and the one closest to *S. sphenanthera* (No. NC_037145.1) provides more molecular data for the genetic diversity and genetic evolutionary relationship of herbal medicine in China.

**Disclosure statement**

No potential conflict of interest was reported by the author.

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