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MITOGENOME ANNOUNCEMENT

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The complete chloroplast genome of *Schizonepeta tenuifolia* (Benth.) Briq., a traditional Chinese herb

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ABSTRACT

Schizonepeta tenuifolia (Benth.) Briq. is a traditional Chinese medicinal herb. The complete chloroplast genome sequence of *S. tenuifolia* was obtained by high-throughput sequencing platform. The chloroplast genome of *S. tenuifolia* is a circular form of 151,254 bp in length, with an average GC content of 37.85%. The genome contains a set of 132 genes, including 87 protein-coding genes, 37 tRNA genes, and eight rRNA genes. Phylogenetic analysis based on complete chloroplast genome sequences indicates that *S. tenuifolia* has a close relationship with *Dracocephalum palmatum*. This study provides a molecular basis for the classification of *S. tenuifolia*.

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Schizonepeta tenuifolia; chloroplast genome; phylogenetic tree

Schizonepeta tenuifolia (Benth.) Briq., a species of Lamiaceae, has been used as an herbal constituent of traditional Chinese medicine and a common herb in landscaping. As a medicinal plant, it is widely cultivated in China, Korea, and Japan. It is commonly used to treat headaches, colds, allergies, and eczema (Liu et al. 2018; Jeon et al. 2019). Previous studies have shown that this herb had multiple pharmacological properties for anti-inflammatory, immunomodulatory, analgesic, hemostatic, antioxidant, and antipruritic activities (Fung and Lau 2002). The complete chloroplast (cp) genome of *S. tenuifolia* was reported herein, which is helpful for further studies on its taxonomy and population genetics.

Fresh leaves of *S. tenuifolia* were collected from the herb nursery of Xianyang (108.69E, 34.35 N), Shaanxi Province, China. The voucher specimen was deposited in Herbarium of the Microbiology Institute of Shaanxi, Microbiology Institute of Shaanxi (http://sxim.xab.cas.cn/, Yan Wang, Wangy@xab.ac.cn) under the voucher number zw2020004. Total genomic DNA was extracted using the CTAB method (Dolye 1987). The library with an insert size of about 400 bp fragments was prepared and then sequenced by an Illumina Novaseq Sequencing System in Personal Biotechnology (Shanghai, China). Through 150 bp paired-end sequencing model, it generated 1.79 G bp high-quality reads data after adapters were removed. After trimming, the paired-end reads were assembled with programs SPAdes v3.9.0 (Bankevich et al. 2012) and A5-MiSeq v20150522 (Coil et al. 2015), with complete cp genome of *Mentha x piperita* (NCBI accession No. NC_047475.1) as the reference. The chloroplast genome annotation was performed by program CPGAVAS2 (Shi et al. 2019). The positions of start and stop codons and intron/exon boundaries were manually checked. The chloroplast genome sequence was submitted to NCBI database (accession number MW013765).

The complete chloroplast genome of *S. tenuifolia* was a circular form of 151,254 bp in length. It was divided into four distinct regions, including a large single-copy region (LSC) of 82,662 bp, a small single-copy region (SSC) of 17,338 bp, and a pair of inverted repeat regions (IR) of 25,627 bp. The genome contained 132 annotated genes with 87 protein-coding genes, 37 tRNA genes, and eight rRNA genes. The overall GC content was 37.85%.

To ascertain the phylogenetic position of *S. tenuifolia,* the cp genome sequences of 23 species from Lamiaceae family and *Catalpa bungei* from Bignoniaceae family (out-group) were downloaded from NCBI. The phylogenetic analysis was inferred using the maximum likelihood (ML) method based on the complete cp genomes, which was performed using IQtree v1.6.12 (Nguyen et al. 2015) under parameters "-nt AUTO -m MFP -bb 1000 –bnni." The TVM + F + R3 model was chosen according to BIC and the bootstrap probability of each branch was calculated by 1000 replications. The phylogenetic tree showed that the *S. tenuifolia* was most closely

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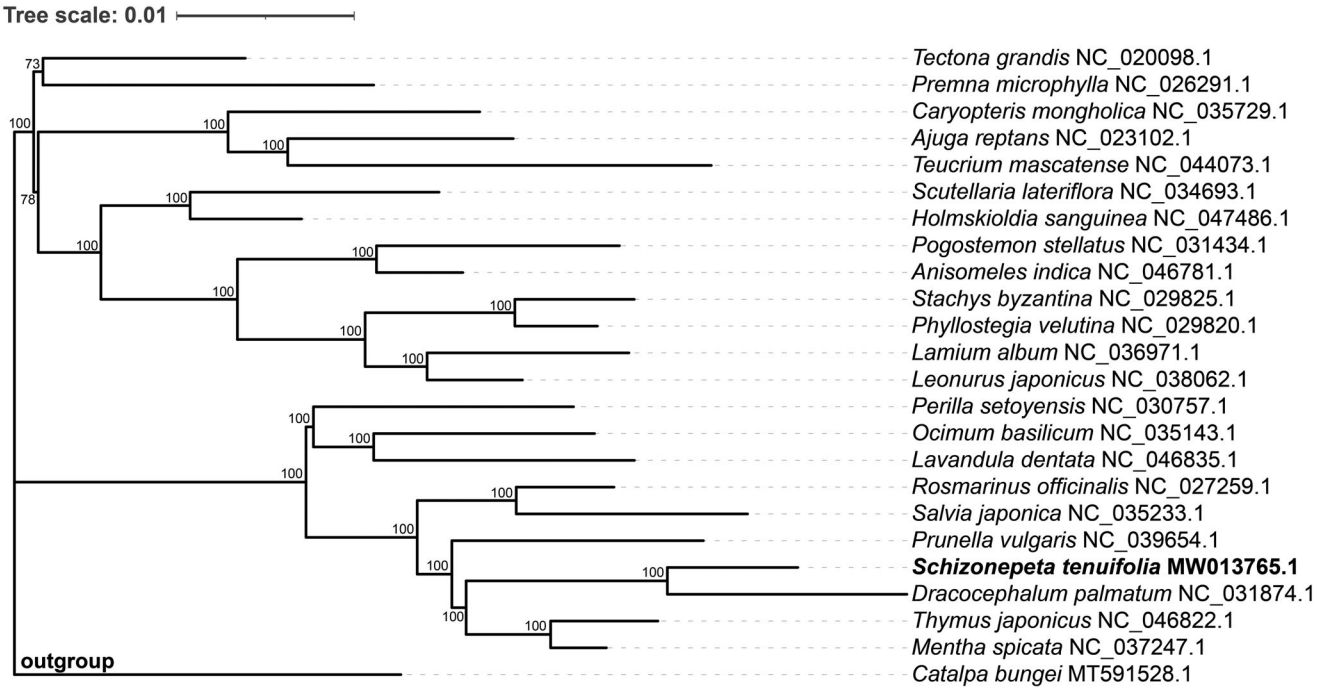

Figure 1. Phylogenetic analysis of 24 complete chloroplast genomes. The bootstrap support values are marked at the nodes.

related to *Dracocephalum palmatum* with 100% bootstrap support (Figure 1).

Disclosure statement

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

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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/ under the accession no. MW013765. The associated BioProject, BioSample and SRA numbers are PRJNA687557, SAMN17150321 and SRR13313686 respectively.

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