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PLASTOME ANNOUNCEMENT

The complete chloroplast genome of *Salvia liguliloba* Y. Z. Sun (Lamiaceae)

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ABSTRACT

Salvia liguliloba Y. Z. Sun is a plant species endemic to the Tianmu Mountains. In this study, we assembled the complete chloroplast genome of *S. liguliloba*. The chloroplast genome of *S. liguliloba* was 151,490 bp with quadripartite structure in length, which contained 124 encoded genes, including 79 protein-coding genes, eight ribosomal RNA genes, and 37 transfer RNA genes. Our phylogenetic analysis result based on 54 chloroplast genomes revealed that *S. liguliloba* was closely related to *S. miltiorrhiza* according to the current sampling extent in Lamiaceae.

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Salvia liguliloba; chloroplast genome; phylogenetic analysis

The genus *Salvia* encompasses more than 980 species and is the largest genus in the angiosperm family Lamiaceae (Will and Claßen-Bockhoff 2017; Hu et al. 2018). *Salvia liguliloba* Y. Z. Sun (1935) is one of the genus Salvia, a plant species endemic to the Tianmu Mountains, and is only distributed in Zhenjiang Province, China. *Salvia liguliloba* has a small corolla, short filament, two stamens with sterile and united lower thecae (Huang et al. 2015). As a Chinese herbal remedy, *S. liguliloba* was used to treat hematemesis, metrorrhagia, dysentery with bloody stools, and traumatic bleeding (Ran et al. 1993). However, the complete chloroplast (cp) genome sequence of *S. liguliloba* has not been reported so far. In this study, its cp genome was successfully assembled and annotated, and its relationship with closely related species was investigated.

The *S. liguliloba* individual was collected from Lin'an, Zhejiang, China (GPS: 30°23′45.00″N, 119°28′35.31″E, voucher S0747, contact person name: Yukun Wei, Email: ykwei76@hotmail.com). The specimen and extracted DNA were deposited at the Herbarium of Shanghai Chenshan Botanical Garden (CSH). The DNA Plantzol Reagent was used to extract DNA from its leaf (Invitrogen, Carlsbad, CA, USA). The Illumina platform was used to produce the raw data (Illumina Inc., San Diego, CA, USA). All research reported in this paper has been conducted ethically and responsibly and is in full compliance with all relevant codes of experimentation and legislation. Ethical approval has been obtained from the appropriate local ethics committee or Institutional Review Board and where relevant, informed consent has been obtained. With adaptors removed, about 5.72 G high-quality clean reads (150 bp PE read length) were obtained. NOVOPlasty v2.7.2 (Dierckxsens et al. 2016) was used to assemble the complete chloroplast genome of *S. liguliloba* with default settings. GeSeq (Tillich et al. 2017) and Geneious Prime were used for alignments and annotation with *Salvia miltiorrhiza* plastome (GenBank: HF586694) as a reference (Biomatters Ltd., Auckland, New Zealand).

The whole chloroplast genome of *S. liguliloba* (GenBank accession No. MZ855771) is 151,490 base pairs, with a typical circle form and 38.0% GC content. It is composed of a large single-copy region (LSC with 82,717 bp, 36.2% GC content), a small single-copy region (SSC with 17,546 bp, 38.6% GC content), and two inverted repeat regions (IR, 25,613 bp, 39.4% GC content). *S. liguliloba* has a total of 133 genes, including 87 protein-coding genes, eight rRNA genes, and 37 tRNA genes. There are seven protein-coding genes (*rps12*, *rpl2*, *rpl23*, *ycf2*, *ycf15*, *ndhB*, and *rps7*), six tRNA genes (*trnI-CAU*, *trnL-CAA*, *trnV-GAC*, *trnI-GAU*, *trnA-UGC*, and *trnR-ACG*) and all four rRNA genes (*rrn*16, *rrn*23, *rrn*4.5, and *rrn*5) have two copies. Six protein-coding genes (*rps16*, *atpF*, *rpoC1*, *petB*, *petD*, and *rpl16*) have one intron each and five (*ndhB*, *rpl2*, *ndhA*, *ycf3*, and *clpP*) have two introns.

Fifty-four species of Lamiaceae with accessible complete chloroplast genomes were chosen to confirm the phylogenetic position of *S. liguliloba* (Figure 1). The complete cp sequences were aligned using MAFFT version 1.3 (Katoh and Standley 2013). The maximum likelihood (ML) phylogenetic analyses were constructed using the program IQ-TREE (Nguyen et al. 2015) with 5000 bootstrap repetitions under the TVM + F + R3 model. Phylogenetic research revealed that *S. liguliloba* was closely related to *S. miltiorrhiza* according to the current sampling extent.

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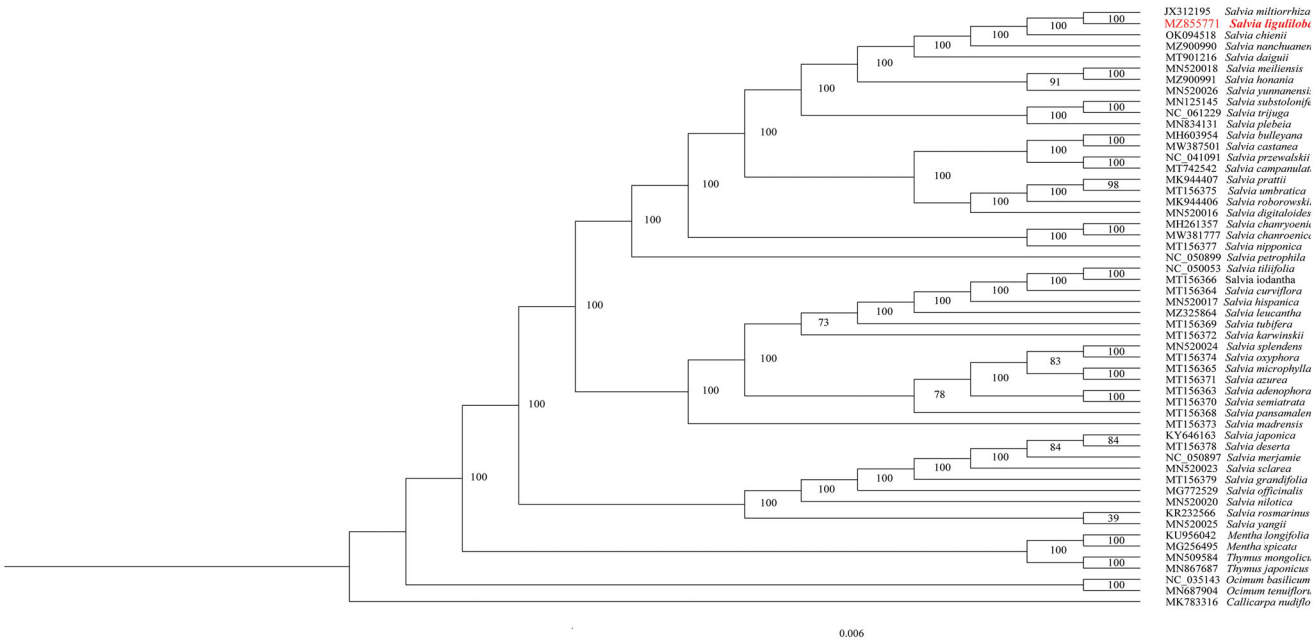

Figure 1. Phylogenetic relationship of *Salvia liguliloba* in Lamiaceae using maximum likelihood (ML) method based on 54 species complete chloroplast genomes (accession numbers were listed behind each taxon. Statistical support values were shown on nodes).

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Ethical approval

Research and collection of plant material were conducted according to the guidelines provided by the Herbarium of Shanghai Chenshan Botanical Garden. Permission was granted by the Hangzhou Academy of Agricultural Sciences to carry out research on the species. This article does not contain any studies on endangered or protected species performed by any of the authors. Experiments were performed in accordance with the recommendations of the Ethics Committee of Zhejiang Sci-Tech University.

Author contributions

The experiments were conceived and organized by Yukun Wei and Dongfeng Yang. Yue Chen, Zewei Du, and Ying Cheng performed the bioinformatics analysis. Fuhai Yuan, Yanbo Huang, and Yukun Wei contributed to the collection of plant material. The paper was written by Yue Chen and Dongfeng Yang. The final approval of the version to be published and that all authors agree to be accountable for all aspects of the final manuscript.

Disclosure statement

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

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Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov, reference number MZ855771. Raw Illumina data is available at the Sequence Read Archive (SRA) under accession SRR15533979. BioProject (PRJNA756452), BioSample accession: SAMN20866468.

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