

## Complete chloroplast genome sequence of *Stachys japonica* (Labiatae)

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### ABSTRACT

The complete chloroplast genome of *Stachys japonica* was reconstructed by reference-based assembly using Illumina paired-end data. The assembled plastome is 150,599 base pairs (bp) in length, including a pair of inverted repeat regions (IRs) of 25,654 bp each, a large single-copy region (LSC) of 81,701 bp and a small single-copy region (SSC) of 17,590 bp. A total of 131 genes were predicted from the chloroplast genome, including 86 protein coding genes, 37 tRNA genes and 8 rRNA genes. The overall GC content of *S. japonica* chloroplast genome was 38.5%. Phylogenetic analysis with several reported chloroplast genomes showed that *S. japonica* is closely clustered with *S. sylvatica*. The complete chloroplast genome of *S. japonica* provides new insight into Labiatae evolutionary and genomic studies.

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*Stachys japonica*; chloroplast genome; phylogenetic analyses

The perennial herb *Stachys japonica* is widely distributed in China, Japan and Russia. It has been used in traditional Chinese medicine for the treatment of dysentery, laryngitis and a few other diseases. To date, the phylogenetic position of *S. japonica* in the genus *Stachys* is still unclear. In this study, we first reported the complete chloroplast (cp)

genome of *S. japonica* and reconstructed a plastome phylogeny for the genus *Stachys*.

The mature and healthy leaves of a single individual of *S. japonica* was sampled from the field of Haiyuan county in south Ningxia, NW China (36°12'43"N, 105°37'9"E). The voucher specimen was deposited in the Herbarium of Sichuan

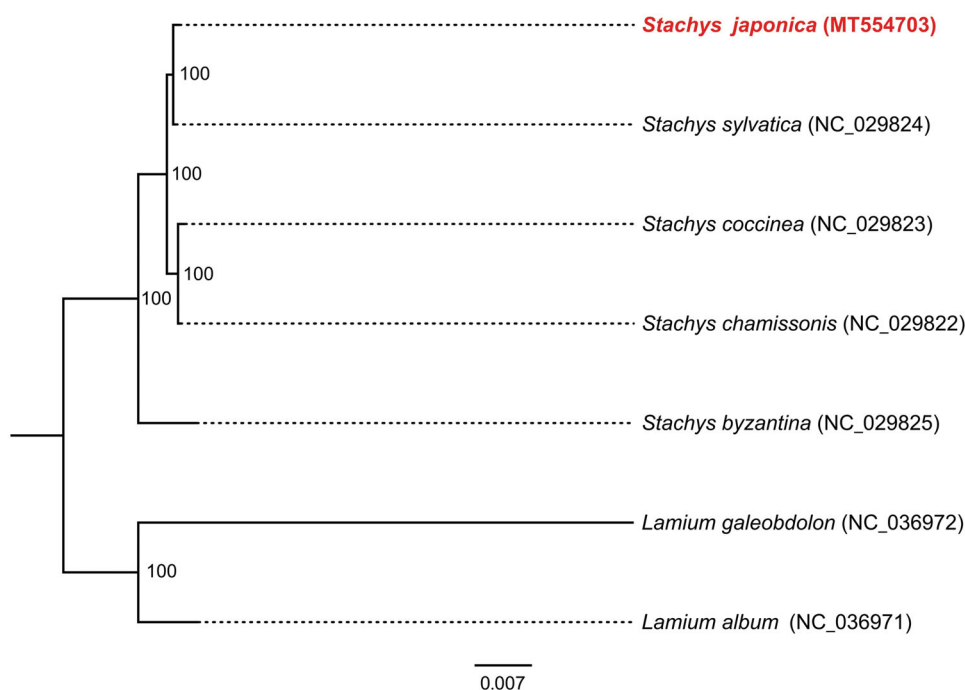


Figure 1. Phylogenetic relationships of seven species based on chloroplast genome sequences. Bootstrap support is indicated for each branch.

University (accession number: QTPLJQ14383116). The total genomic DNA was extracted from silica gel dried leaves using a modified CTAB method (Doyle and Doyle 1987) and sequenced based on the Illumina pair-end technology. The filtered reads were assembled using the program NOVOPlasty (Dierckxsens et al. 2017) with complete cp genome of *S. coc-cinea* as the reference (GenBank accession no. NC\_029823). The assembled cp genome was annotated using Plann (Huang and Cronk 2015), and the annotation was corrected using Geneious (Kearse et al. 2012). To examine the phylogenetic position of *S. japonica*, a multiple sequence alignment (MSA) analyses was performed using MAFFT v7.313 (Kato and Standley 2013) based on seven cp genomes in Labiatae. Finally, a maximum likelihood (ML) tree was constructed by RAxML v8.2.11 (Stamatakis 2006) with 500 bootstrap replicates based on the alignments, using two species from the genus *Lamium* as outgroup.

The complete cp genome of *S. japonica* was a circular molecular genome with a size of 150,599 bp in length, which presented a typical quadripartite structure containing two inverted repeat (IR) regions of 25,654 bp separated by the large single-copy (LSC) region of 81,701 bp and small single-copy (SSC) region of 17,590 bp. The cp genome consists of 131 genes including 86 protein coding genes, 37 tRNA genes, and 8 rRNA genes. The overall GC content was about 38.5%. In the plastome phylogeny, *S. japonica* shows the closest genetic relationship to *S. sylvatica*. (100% bootstrap support) (Figure 1). The *S. japonica* cp genome can be further used for population genomic studies, phylogenetic analyses, genetic engineering studies of Labiatae.

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## Disclosure statement

None of the coauthors has any conflict of interest to declare. The authors alone are responsible for the content and writing of the paper.

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## Data availability statement

The data that support the findings of this study are openly available in NCBI GenBank database at <https://www.ncbi.nlm.nih.gov/> with the accession number is MT554703 or available in [figshare.com] at <https://doi.org/10.6084/m9.figshare.12443378>.

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