**The complete chloroplast genome sequence of *Stachys sieboldii* Miquel. (Labiatae), a kind of vegetable crop and Chinese medicinal material plant**

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**ABSTRACT**

*Stachys sieboldii* Miquel, belongs to the *Stachys* of the Labiatae family. It is a good vegetable and widely cultivated in China. In this study, the complete chloroplast genome of the *S. sieboldii* was sequenced, assembled and annotated, which contains 132 unique genes, including 87 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. A maximum likelihood phylogenetic tree based on 17 complete chloroplast genomes revealed that *S. sieboldii* is closely related to *Stachys* genus. These data could be used for variety identification and genetic improvement.

The *Stachys sieboldii* Miquel, belongs to genus *Stachys* of the family Labiatae. It is indigenous to China and widely cultivated in China, Japan and Korea (Yamahara et al. 1990). As a Chinese favorable vegetable, it provides a lot of oligosaccharides, proteins, and water-soluble vitamins (Yin et al. 2006). Dried whole grass of *S. sieboldii* used as Chinese herbal medicines could treat cold and against infections, promoting blood circulation. Several studies revealed that *S. sieboldii* has many benefits for human body, such as anti-inflammatory activity, antinephritic activity, antioxidant and memory improvement (Yin et al. 2006; Vijaya Abinaya et al. 2017).

To date (3/10/2020), more than 30 species belonging to 15 different genus of Labiatae chloroplast genome have been deposited in the National Center for Biotechnology Information (NCBI) and released. These data include four species of *Stachys* genus come from Hawaii (Roy et al. 2013). However, the chloroplast genome of the *Stachys* of China has not been reported. In this study, we first reported the complete chloroplast genomes of *S. sieboldii* based on Illumina Hiseq pair-end sequence assemble.

Fresh and clean leaf materials of *S. sieboldii* were collected from Yabai Town, Zhouzhi County, Shaanxi Province (34°11′5″N, 108°4'34″E), frozen and preserved at the Northwest A&F University. The specimen (No. 61012419082010LY) was deposited in the herbarium of Shaanxi University of Chinese Medicine. Total genomic DNA was extracted with the modified CTAB method (Stefanova et al. 2013). Genome sequencing was performed by HiSeqX at Biomarker Technologies Corporation. Low-quality sequences were filtered by NGSQC Toolkit with Q30 (base Phred quality score of ≥30)(Patel and Jain 2012). Total high-quality reads were mapped to reference (*Stachys chamissonis* chloroplast genome: NC_029822) using Bowtie2 (Langmead and Salzberg 2012) and the mapped reads were extracted and assembled by SPAdes (Bankevich et al. 2012) and CAP3 (Huang and Madan 1999). A total of 199,499 reads have been assembled with an average coverage of 200.0×. The assembled chloroplast genome was annotated and manually corrected using Geneious (Kearse et al. 2012), and was deposited into the GenBank (accession No. MT 241264).

The complete chloroplast genome of *S. sieboldii* is 149,523 bp in length, containing a large single-copy (LSC: 81,155 bp), two inverted repeats (IRa and IRb: 25,656 bp), and a small single-copy (SSC: 17,056 bp). 132 genes were annotated in total, including 87 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The GC content of the complete genome is 38.6%.

The maximum likelihood method were adopted to construct the molecular phylogenetic tree, so as to elucidate the taxonomic status and the evolutionary relationship of *S. sieboldii*. A total of 17 complete chloroplast genome, including *S. sieboldii* and 14 other Labiatae species were multiple aligned by MAFFT (Katoh et al. 2002). *Rosa chinensis* and *Arabidopsis thaliana* were used as outgroup, and then the maximum likelihood phylogenetic tree was generated by RAxML v7.2.8 (Stamatakis 2006) with 1000 bootstrap replicates (Figure 1). The results showed that *S. sieboldii* was closely related to the same genus species of *S. chamissonis*, *S. cocinea*, *S. sylvatica* and *S. byzantine*. Sequences of the complete chloroplast genome of *S. sieboldii* would lay foundation for medicinal material and species identification, genetic improvement, and cultivation.
Disclosure statement

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

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