

## The complete chloroplast genome and phylogenetic analysis of *Syringa reticulata* subsp. *amurensis* (Rupr.) P.S.Green & M.C.Chang from Qinghai Province, China

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### ABSTRACT

*Syringa reticulata* subsp. *amurensis* (Rupr.) P. S. Green & M. C. Chang (Oleaceae) is a shrub or tree with high medicinal value as well as great ecological significance as an urban garden plant. To better understand the molecular genetics and evolutionary of *S. reticulata* subsp. *amurensis*, its complete chloroplast genome was sequenced and annotated. The assembled chloroplast genome is a circular 156,141 bp sequence, consisting of 87,108 bp large single copy (LSC) region and 17,239 bp small single copy (SSC) region, which were flanked by a pair of 25,897 bp inverted repeats (IRs). The GC content of the chloroplast genome is 36.14%. Moreover, a total of 132 functional genes were annotated, including 88 protein-coding, 36 tRNA, and eight rRNA genes. Phylogenetic analysis showed that *S. reticulata* subsp. *amurensis* was most closely related to *S. reticulata* subsp. *pekinensis* and the genus *Syringa* is paraphyletic group. This study provides important information for further phylogenetic studies on *S. reticulata* subsp. *amurensis* and its allies.

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*Syringa reticulata* subsp. *amurensis* (Oleaceae: Syringaceae), is a shrub or tree with high medicinal and horticultural values. Its flowers are white, luxuriant, and fragrant. *Syringa reticulata* subsp. *amurensis* can also be used to treat respiratory diseases (Zhu et al. 2021). In addition, with its excellent adaptation to the strong environmental stress in northwest China, this species is considered a high-quality garden plant with great potential to improve urban ecology. Wild individuals of *S. reticulata* subsp. *amurensis* grow mainly in mixed forests on slopes and grasslands, or near gullies, 100–1200 m above sea level (Chang et al. 1996). The plant is usually cultivated as an ornamental in northern China (Chang et al. 1996). The chloroplast genome is particularly useful in studies on the maternal evolutionary history of angiosperms for its matrilineal inheritance without recombination (Nock et al. 2019). However, no studies on the complete chloroplast genome of *S. reticulata* subsp. *amurensis* have been published. In the present study, the complete chloroplast genome of *S. reticulata* subsp. *amurensis* was obtained using the next-generation sequencing (NGS) technologies and a phylogenetic analysis of *S. reticulata* subsp. *amurensis* and its allies was carried out.

The samples of *S. reticulata* subsp. *amurensis* were collected from Xining Botanical Garden, Xining City, Qinghai Province, China (36.62°N, 101.75°E). The experiment and data

analysis followed Wang et al. (2019). The DNA was extracted from silica gel dried young leaves (about 0.4 g) with a modified CTAB method (Doyle and Doyle 1987). The voucher specimen (specimen accession number: WangJL2019236, <http://www.nwipb.cas.cn/znbm/qzgzswbbg/bbgjj/>, Shilong Chen, [herbarium@nwipb.cas.cn](mailto:herbarium@nwipb.cas.cn)) was kept at the Qinghai-Tibetan Plateau Museum of Biology, Chinese Academy of Sciences (QTPMB). The genome sequencing was performed on an Illumina HiSeq Platform (Illumina, San Diego, CA) by Genepioneer Biotechnologies Inc. (Nanjing, China). Approximately, 5 GB of clean data were yielded. The sequencing reads were mapped to the reference chloroplast genomes using the Bowtie2 software (Langmead and Salzberg 2012). The SPAdes version 3.10.1 (Bankevich et al. 2012) and SSPACE version 2.0 (Boetzer et al. 2011) were used to assemble the chloroplast genome. The chloroplast genes were annotated with CpGAVAS (Liu et al. 2012) and the sequence coordinates for the genes were verified by BLAST search against the *Syringa reticulata* subsp. *pekinensis* (GenBank accession number: MN901632.1) reference chloroplast genome. Annotation errors were manually corrected.

The phylogenetic relationships of *S. reticulata* subsp. *amurensis* and its allies were inferred using the maximum-likelihood (ML) method based on the General Time Reversible

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the number of substitutions per site. The analysis involved 39 complete chloroplast genome sequences. There was a total of 202,491 positions in the final dataset.

The complete chloroplast genome of *S. reticulata* subsp. *amurensis* was 156,141 bp in length and has a typical quadripartite structure, containing a pair of IR regions of 25,897 bp, a large single copy (LSC) region of 87,108 bp, and a small single copy (SSC) region of 17,239 bp. The two IRs were separated by the LSC and the SSC. The GC content of the complete chloroplast genome was 38.03%. A total of 132 functional genes were annotated, including eight rRNA genes, 36 tRNA genes, and 88 protein-coding genes. The rRNA, tRNA, and protein-coding genes account for 6.06%, 27.27%, and 66.67% of all annotated genes, respectively.

The phylogenetic analysis fully resolved *S. reticulata* subsp. *amurensis* in a clade with *S. reticulata* subsp. *pekinensis* (Figure 1). The phylogenetic tree suggested that *S. reticulata* subsp. *amurensis* and *S. reticulata* subsp. *pekinensis* are polyphyletic with respect to *Ligustrum* spp. and other species classified to the genus *Syringa*. This result is consistent with previous studies (Li et al. 2002; Dupin et al. 2020; Wang et al. 2020). The present study provides important information for further molecular studies on *S. reticulata* subsp. *amurensis* and its allies.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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## Data availability statement

The genome sequence data obtained in this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov/> under the accession

number MW525283. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA692790, SRR13480493, and SAMN17717949, respectively.

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