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The complete chloroplast genome sequence of *Syringa oblata* Lindl. var. *alba* Hort. ex Rehd. 1763 (Oleaceae)

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ABSTRACT

Syringa oblata var. *alba* is a shrub or a small tree from China with high ornamental, medicinal, and edible value. Here, we present its first complete chloroplast genome. The entire circular genome is 155,648 bp in length, with large single-copy (LSC) length of 86,247, small single-copy (SSC) length of 17,937, inverted repeat (IR) length of 25,732, and GC content of 37.9%. One hundred and thirty-two genes, including 88 protein-coding, 36 tRNA, and eight rRNA genes were predicted. A phylogenetic tree of 25 plant species was constructed based on the maximum-likelihood method, indicating that *S. oblata* var. *alba*, *S. vulgaris*, and *S. oblata* form a sister group. This study will provide valuable basic information for phylogeny, species identification, and varieties breeding of this species.

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Oleaceae; chloroplast genome; *Syringa oblata* var. *alba*; phylogenetic analysis

1. Introduction

Syringa oblata Lindl. var. *alba* Hort. ex Rehd. 1763, a shrub or a small tree in *Syringa* genus, has strong adaptability to cold, drought, barren environment, and resistance to diseases and insect pests. It is distributed in the north of the Yangtze River Basin in China, with flowering period from April to May and fruit period from June to October, according to the record of Flora Reipublicae Popularis Sinicae (FRPS). *S. oblata* var. *alba* is generally used for garden cultivation and ornamental for its lush branches and leaves, elegant flowers and fragrant smell. Moreover, the flowers of many *Syringa* plants are the materials of spices and clove oil which can be used in cosmetics, drugs, and food (Cheng et al. 2021). Taxonomically, *Syringa* is closely related to *Ligustrum*. Sect. Ligustrina of Syringa possesses similar floral and seed characteristics to some species of Ligustrum. This finding is consistent with the report of nuclear ribosomal DNA ITS and ETS region sequencing to test Syringa and Ligustrum relationship (Li et al. 2002). In addition, a study of *S. oblata* genome pointed out that segment and tandem duplications could contribute to the odor formation in the woody aromatic species (Wang et al. 2022). In this study, the complete chloroplast (cp) genome of *S. oblata* var. *alba* was assembled and characterized for the first time, which would enrich the genomic resources of Oleaceae and contribute to the identification and application of *Syringa*.

2. Materials and methods

S. oblata var. *alba* (Figure 1) was sampled from Dalian, Liaoning, China (E 121°35′39″, N 38°58′13″) and identified by professor Ting-guo Kang. The voucher specimen and genomic DNA were deposited at the herbarium of Liaoning University of Traditional Chinese Medicine (Liang Xu 861364054@qq.com, plant number: 10162210515096LY). All operations are carried out in accordance with guidelines in Specification on Good Agriculture and Collection Practices for Medicinal Plants (GACP; Number: T/CCCMHPIE 2.1-2018). The extraction of total genomic DNA from fresh leaves was achieved by Magbead Plant DNA Kit (CWBIO, Taizhou, China) and sequenced on Illumina Novaseq 6000 platform. Data were processed and assembled by NGS QC toolkit (Patel and Jain 2012) and SPAdes v3.14.1 (Bankevich et al. 2012), respectively. The protein-coding sequences of cp genome were compared with NR (RefSeq

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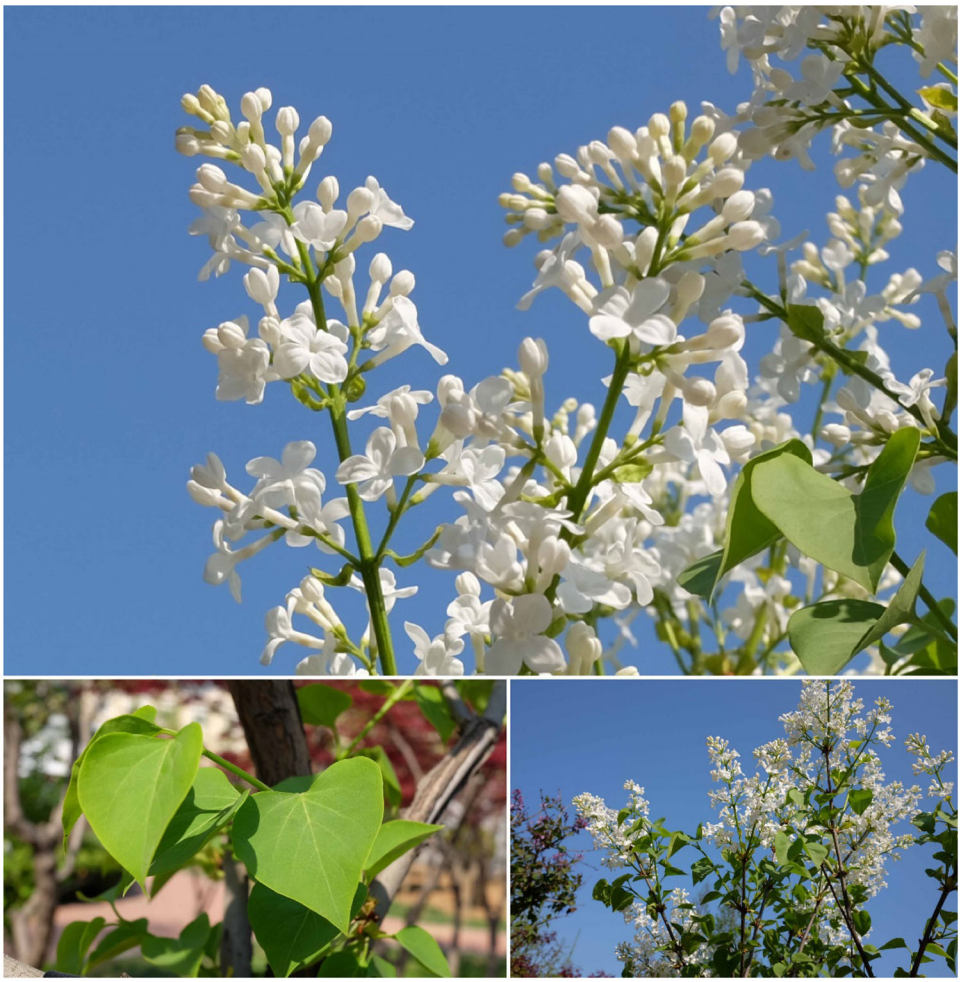

Figure 1. *S. oblata* var. *alba* from Dalian, Liaoning, China (E 121°35′39″, N 38°58′13″). Small tree, white flowers not fully expanded at anthesis, small blade, base subcordate or truncate to broadly cuneate. Photo was taken by Zhang Shumei.

non-redundant proteins) databases for the gene prediction and annotation.

3. Results and discussion

The cp genome of *S. oblata* var. *alba* was 155,648 bp in length with a GC content of 37.9%. One hundred and thirty-two genes were predicted, including 88 protein-coding, 36 tRNA, and eight rRNA genes. The genome had a large single-copy (LSC) region with a length of 86,247 bp, a small single-copy (SSC) region of 17,937 bp, and a pair of inverted repeats (IRs) regions of 25,732 bp. In addition, trnK-UUU, *rps*16, trnG-GCC, *atp*F, *rpo*C1, trnL-UAA, *pet*B, *pet*D, *rpl*16, *rpl*2, *ndh*B, trnI-GAU, trnA-UGC, and *ndh*A contain a single intron, *clp*P and *ycf*3 genes contain two introns, and *rps*12 gene has trans splicing. As the evidence for correct assembly of the genome, coverage depth figure was provided in Supplemental Figure S1. The maps of annotated cp genome, cis-splicing genes, and trans-splicing genes of *S. oblata* var. *alba* were processed by CPGview (Liu et al. 2023) and shown in Figure 2, Supplemental Figures S2 and S3, respectively.

Maximum-likelihood (ML) phylogenetic tree was conducted on 25 species of plant. The ML analysis was performed by IQ-TREE 1.6.12 software (http://www.iqtree.org/) with 1000 bootstrap replicates (Nguyen et al. 2015). According to the Bayesian information criterion (BIC), the best evolutionary model was chosen as JTT + F + R3. Based on this phylogenetic tree, all selected species in Ligustrum are located in a branch within Syringa branches, indicating the close relationship between Ligustrum and Syringa. *S. oblata* var. *alba*, *S. vulgaris*, and *S. oblata* are sister groups, and the relationship between the latter two is consistent with a previous study (Zhao et al. 2020). *Crocus sativus*, as an outgroup, is far from the other species (Figure 3).

Syringa vulgaris MG255768, *S. oblata* NC057990, *S. pinnatifolia* NCO41119 (Zhang et al. 2019), *S. persica* NC042280 (Olofsson et al. 2019), *S. komarowii* subsp. *reflexa* MT648823, *S. villosa* NC061378, *S. yunnanensis* NC042468 (Olofsson et al. 2019), *S. wolfii* NC049090 (Liu et al. 2020), *S. pubescens* subsp. *microphylla* MT872641, *S. reticulata* subsp. *pekinensis* MN901632 (Wang et al. 2020), *S. reticulata* subsp. *amurensis* MT872640, *Ligustrum vulgare* NC042274 (Olofsson et al. 2019), *L. gracile* NC042425 (Olofsson et al. 2019), *L. lucidum*

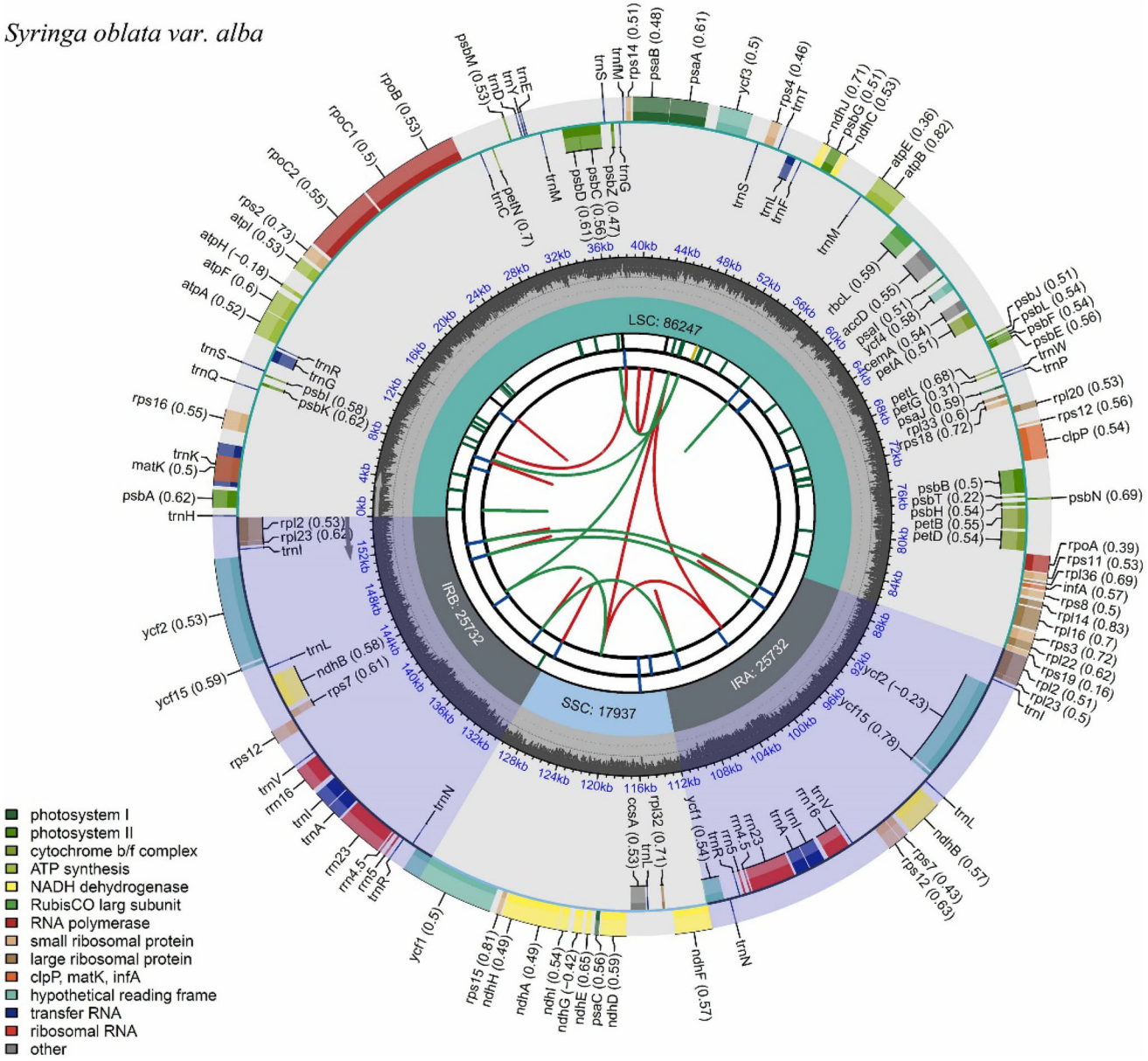

Figure 2. The annotated chloroplast genome map of *S. oblata* var. *alba*. From the center outward, the forward and reverse repeats were shown in the first track and connected with green and red arcs, respectively. The tandem repeats and microsatellite sequences were shown in the second and third tracks with different colors. Genes are colored in the outer track by their functional classification listed in the bottom left.

NC056243, *L. quihoui* NC057246 (Wang et al. 2019), *L. japonicum* NCO42454 (Olofsson et al. 2019), *L. ovalifolium* NC056242, *Fraxinus chinensis* MW599993, *F. pennsylvanica* NCO43874 (Yi et al. 2019), *F. americana* NCO42449 (Olofsson et al. 2019), *Forsythia suspensa* NC036367 (Wang et al. 2017), *F. mira* M. C. Chang NC046065 (Gao et al. 2019), *F. mandschurica* NC048504 (Olofsson et al. 2019), and *Crocus sativus* NC041460 (Nemati et al. 2019).

4. Conclusions

The complete cp genome of *S. oblata* var. *alba* was determined in this study, which provides theoretical foundation for further study on the phylogenetic relationship of Oleaceae family.

Ethical approval

According to the Regulations of the People's Republic of China on Wild Plants Protection, *S. oblata* var. *alba* is not in the list of national key protection of wild plants. On-site and ex-situ protection of wild plants and scientific research on wild plants are supported in article five of the regulations. No ethical approval or specific permission was needed in this research.

Author contributions

L.X. designed the study. W.X.M., Y.Y.S., and C.B. collected the samples and performed the analyses; H.F.X. and Y.P.X. were involved in the data

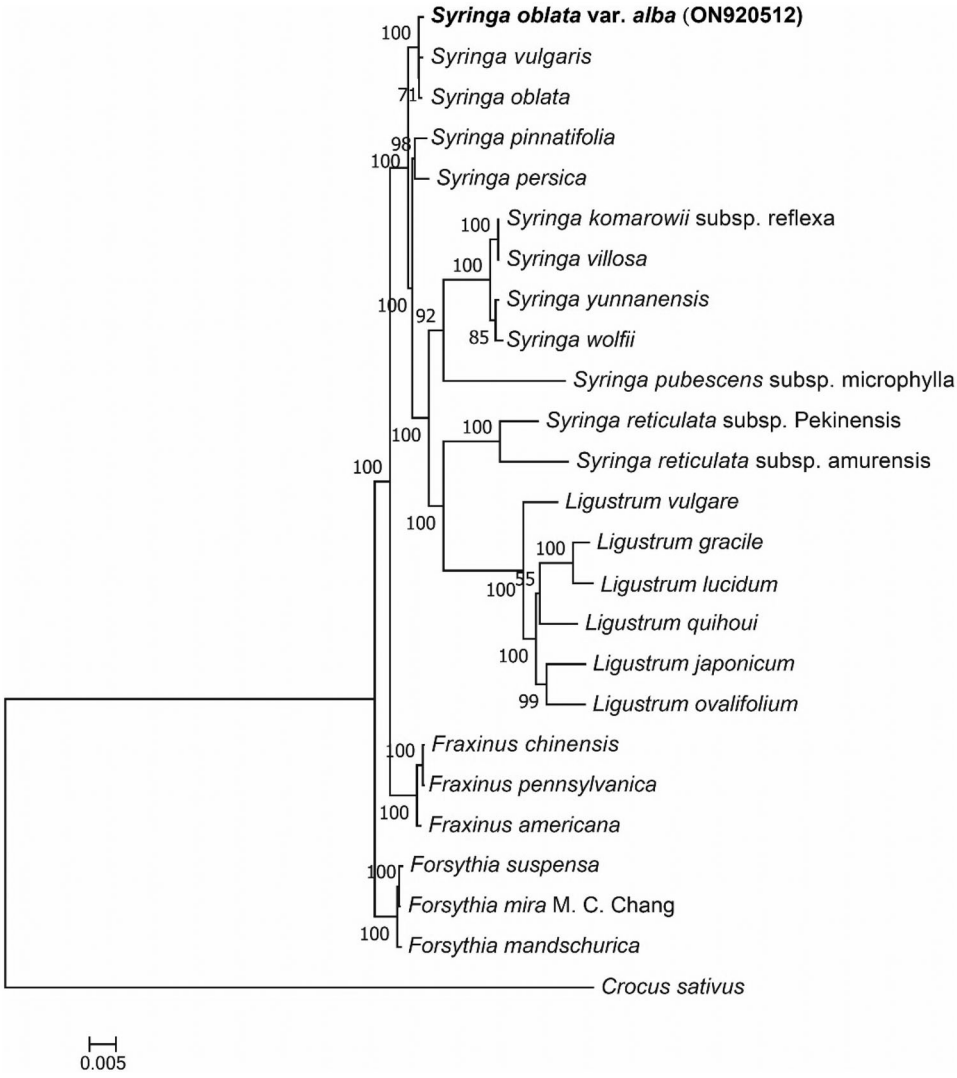

Figure 3. Maximum-likelihood (ML) phylogenetic tree based on the complete chloroplast genome of *S. oblata* var. *alba* and 24 other species. The following sequences were used.

interpretation; T.G.K. and M.X. participated in the verification and supervision; all authors contributed to the writing and revising of manuscript. All authors finally approved this version.

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. ON920512. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA854692, SRR19960680, and SAMN29446418, respectively.

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