MITOCHONDRIAL DNA PART B
2019, VOL. 4, NO. 2, 2562–2563
https://doi.org/10.1080/23802359.2019.1642156

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MITOGENOME ANNOUNCEMENT

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Complete chloroplast genome of *Sorbaria sorbifolia* var. *stellipila*

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ABSTRACT

The complete plastid genome of *Sorbaria sorbifolia* var. *stellipila* was sequenced and analyzed in this study. It was found to be 160,820 bp and consisted of a large (88,869 bp) and small (20,853 bp) single-copy regions, separated by a pair of identical inverted repeats (25,549 bp). The GC content of the whole genome was 37.8%, and there were 84 unique protein-coding genes, 37 tRNAs, and 8 rRNAs. The gene order and organization were consistent with those of other complete plastid genomes from the Rosaceae. The phylogenetic tree construct was based on 76 protein-coding genes and demonstrated a sister relationship with the Rosaceae.

ARTICLE HISTORY
Received 19 June 2019
Accepted 22 June 2019

KEYWORDS
Sorbaria sorbifolia var. *stellipila*; Rosaceae; complete chloroplast genome; phylogenetic analysis

There are seven species in the genus *Sorbaria* (Ser.) A. Braun, a member of the Rosaceae group (https://www.theplantlist.org [cited 2019 Jun 20]. *Sorbaria sorbifolia* var. *stellipila* Maxim. is a deciduous shrub that grows naturally in the mountain valleys and wetlands of northeastern East Asia and reaches 2 m in height (Lee 1989). It is reported to be used medicinally to relieve the pain from fractures and bruises (Ahn 2000). In addition, the fruit of *S. sorbifolia* var. *stellipila* are known to have antioxidant activities that are three times greater than those of vitamin E owing to the complex actions of their active antioxidant ingredients (Park et al. 2011). However, molecular studies of this species have not yet been

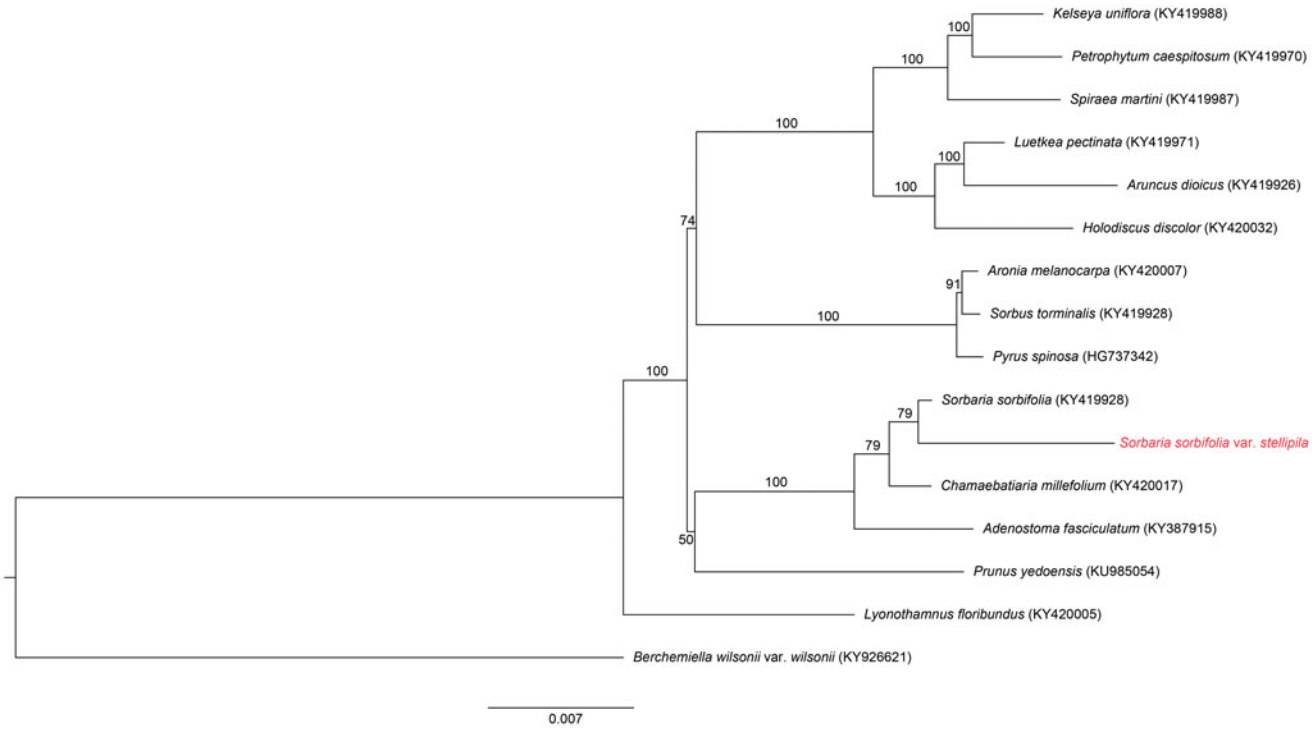

Figure 1. The maximum-likelihood (ML) tree based on the 16 representative chloroplast genomes of Rosaceae (with Rhamnaceae as the outgroup). The bootstrap value based on 100 replicates is shown on each node.

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conducted. In this study, we have reported for the first time, the entire sequence of the chloroplast genome of *S. sorbifolia* var. *stellipila* and constructed its phylogenic tree.

Fresh leaves were collected from Hongneung Arboretum (37°35′N, 127°2′E) and genomic DNA was isolated from fresh leaves by using a Plasmid SV mini kit (GeneAll, Seoul, Korea). Extracted DNA was stored in the Plant DNA Bank of the National Institute of Forest Science (No. 0335132685; Suwon, Korea). Whole genome sequencing was conducted using the Ion Torrent sequencing platform (Life Technologies, Carlsbad, CA). Filtered sequences were assembled using *Prunus yedoensis* as the reference sequence (GenBank accession number KU985054). The sequenced fragments were assembled using Geneious R10 (Biomatters Ltd, Auckland, New Zealand; Kearse et al. 2012). Annotation was performed using DOGMA (http://dogma.ccbb.utexas.edu/) and BLAST searches. All of the tRNA sequences were confirmed using the web-based tool tRNAScan-SE (Schattner et al. 2005) with the default settings to corroborate the tRNA boundaries identified using Geneious. The complete chloroplast genome of *S. sorbifolia* var. *stellipila* was submitted to the NCBI database under the accession number MN026875.

The plastid of *S. sorbifolia* var. *stellipila* was found to have a double-stranded, circular DNA, with 160,820 bp, and contained two inverted repeat regions (IRs) of 25,549 bp, each of which was separated by large single-copy (LSC) and small single-copy (SSC) regions of 88,869 and 20,853 bp, respectively. The genome contained 129 genes, including 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Six of the protein-coding genes, 8 tRNA genes, and 4 rRNA genes were duplicated in the IR regions. The overall GC content was 37.1% (LSC, 33.7%; SSC, 29.7%; IRs, 42.9%).

The maximum-likelihood (ML) tree searches and ML bootstrap searches were performed using the RAxML BlackBox web-server (https://raxml-ng.vital-it.ch/#/, Stamatakis et al. 2008) with 76 protein-coding genes, and 16 of which those were identified to be from the Rosaceae (with the outgroup being Rhamnaceae). The RAxML analyses were run with rapid bootstrap analysis using a random starting tree and 100 ML bootstrap replicates. The genus *Sorbaria* was found to be a sister to *Chamaebatiaria millefolium* (Torr.) Maxim. (Figure 1).

Disclosure statement

The authors report no declaration of interest. The authors alone are responsible for the content and writing of this article.

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