First record of the complete chloroplast genome of *Syneilesis aconitifolia* (Asteraceae)

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**ABSTRACT**

*Syneilesis aconitifolia* is an herbaceous perennial of the Asteraceae family native to forests in China, Korea, Japan, and eastern Russia. In Korea, the young leaves of the plant are edible and the extract is known to have antitumor effects. The length of the complete plastome was found to be 150,773 bp, including 130 genes, consisting of 85 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The assembled plastome showed typical structure and gene content of the angiosperm plastome, which includes two inverted repeats (IR) regions of 24839 bp, a large single copy (LSC) region of 82911 bp, and a small single-copy (SSC) region of 18184 bp. The total G/C content in the *S. aconitifolia* plastome was 37.5%. The maximum likelihood (ML) phylogenetic tree strongly supports that *S. aconitifolia* is closely related to the hosts of *Ligularia Fischeri*. This study reports the first complete chloroplast genome of the genus *Syneilesis* and will contribute to the phylogenetics of the family Asteraceae.

**Introduction**

*Syneilesis aconitifolia* (Bunge) Maxim. 1859 (Maximowicz 1859), commonly known as the shredded umbrella plant, is an herbaceous perennial of the Asteraceae family that is native to forests in China, Korea, Japan, and eastern Russia. In Korea, the young leaves of the plant are edible and the extract is known to have antitumor effects (Wu et al. 2011). The genus *Syneilesis* contains seven species in the world, which are known to have antitumor effects. The length of the complete plastome was found to be 150,773 bp, separated into a large single-copy region of 82,911 bp, a small single-copy region of 18,184 bp, and a pair of inverted repeats (IRs) of 24,839 bp. The genome contained 130 genes, including 85 protein-coding genes, 37 tRNA genes, and eight rRNA genes, and showed a GC content of 37.5% (LSC: 35.6%, SSC: 30.8%, IRs: 43.0%). Among the identified genes, six protein-coding genes, seven tRNA genes, and four rRNA genes were completely duplicated in the IR regions. Eight tRNA genes and ten protein-coding genes contained one intron, and two protein-coding genes (clpP1 and *paf*) contained two introns. The complete chloroplast genome of *S. aconitifolia* was submitted to GenBank with the accession number OM622255, which is the first reported chloroplast genome sequence in the genus *Syneilesis*.

Phylogenetic analysis of *S. aconitifolia* was performed by comparing with 79 protein-coding gene sequences derived from the chloroplast genome sequences of other 11 species in the family Asteraceae and two outgroups (family Menyanthaceae). 79 protein-coding gene sequences were aligned using MAFFT in PhyloSuite (Katoh et al. 2005; Zhang et al. 2020), and ModelFinder (Kalyaanamoorthy et al. 2017) within the PhyloSuite program was used to determine
the optimal alternative model. ML analysis was performed using IQ-tree and TVM + F+R3 models (Nguyen et al. 2015). *S. aconitifolia* was a sister group of the genus *Ligularia*. In addition, within Senecioneae, Tussilagininae and Senecioninae were distinguished.

### Ethical approval

The materials used in this study are not included IUCN red list, the collection area is not a protected area. And this article was conducted in compliance with the regulations of the Act on the creation and furtherance of arboretums and gardens.

### Author contributions

Hyuk-Jin and Kyung conceived the original structure of the review. Sang-Chul and Young-Ho have made collecting and experimentation, Sang-Chul prepared the manuscript. All authors have read and agreed to the published version of the manuscript.

### Disclosure statement

No potential conflict of interest was reported by the authors.

### Funding

This study was supported by grants from the Scientific Research (KNA1-1-13, 14-1) of the Korea National Arboretum.

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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](https://www.ncbi.nlm.nih.gov/) under accession no. OM622255. The associated BioProject, SRA, and Bio-Sample numbers were PRJNA804266, SRR17927967, and SAMN23721206, respectively.

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