

The complete chloroplast genome sequence of *Ligularia stenocephala* (Maxim.) Matsum. & Koidz. (Asteraceae: Senecioneae)

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ABSTRACT

Ligularia stenocephala (Maxim.) Matsum. & Koidz is a widely known edible plant species in Korea. It contains various useful antioxidant compounds and has been developed as a horticultural cultivar blooming showy inflorescence. We report the complete plastid genome (plastome) of *Ligularia stenocephala*, a collection from Korea. The plastome of *L. stenocephala* is 151,158 base pairs (bp) long and includes a pair of inverted repeat (IR) regions (24,830 bp each) that are separated by a large single copy (LSC) region (83,265 bp) and a small single copy (SSC) region (18,233 bp). The phylogenetic tree shows that *L. stenocephala* is closely related to *L. fischeri* with strong bootstrap support.

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The genus *Ligularia* Cass., belonging to the tribe Senecioneae of Asteraceae, comprises approximately 140 species. It is widely distributed in Europe and Asia, with a primary distribution center in southwestern China (Liu 1989; Liu and Illarionova 2011). The genus *Ligularia* is used as a folk medicine to treat influenza, asthma, cough, ulcers, arthritis and tuberculosis in some region of eastern and western Asia (Debnath et al. 2017). Therefore, much research has been conducted on the ingredients and efficacy of these medicines. Many phylogenetic studies have shown that *Ligularia* is a non-monophyletic taxon, demonstrating a common ancestor sharing *Cremanthodium* and *Parasenecio* (LCP complex) (Liu et al. 2006; Pelsner et al. 2007; Ren et al. 2017). Phylogenomics is a good solution to this phylogenetic conundrum; however, we need more evolutionary evidence of the complex members.

In Korea, *Ligularia stenocephala* (Maxim.) Matsum. & Koidz. (1910), is commonly known as 'Gondalbi'. The species is perennial herb and its leaves are consumed as an edible vegetable. It grows on wet, grassy slopes and forest understories, mainly distributed in China, central and southern parts of Japan, the northern part of Taiwan, and several southwestern islands in Korea (Liu 1989; Koyama 1995). In this study, we report the complete chloroplast (cp) genome sequence of *L. stenocephala* to provide genomic and genetic sources for further research.

Genomic DNA was extracted from fresh leaves (34°03'42.7"N 125°07'19.9"E; Gageodo, Jeollanam-do Province, Korea) using the DNeasy Plant Mini Kit (Qiagen). The voucher

specimen was deposited at the Herbarium of the Kongju National University (KNH, accession number: PMS_180805_001, collected by Minsu Park, E-mail: lacmyo14@gmail.com), Kongju, Korea. The DNA library was constructed and sequenced on the MGISEQ-2000 platform (LAS, Seoul, Korea) with paired-end reads (150 bp paired-end). The Sequencing generated a total of 88,552,680 raw reads, it was deposited into Sequence Read Archive (SRA) database (<https://www.ncbi.nlm.nih.gov/sra/>) with the accession no. SRR13950043. The cp genome sequence of *L. stenocephala* was constructed by using NOVOPlasty 4.1 (Dierckxsens et al. 2017), and for validation the obtained data were mapped with the reference *rbcl* gene sequence for *L. intermedia* (Chen et al. 2018; MF539930), using Geneious 11.0.4 (Kearse et al. 2012). On this genome, 916,240 reads were assembled with a 906.5 × coverage. The annotation was separately performed in Geneious 11.0.4 (Kearse et al. 2012), and was manually corrected for the start and stop codons and for the intron/exon boundaries. The annotated cp genome sequence was submitted to GenBank with the accession number of NC_056964.1. A phylogenetic analysis was conducted on the complete chloroplast genome sequences of *L. stenocephala* and 22 other related species (including 4 outgroups) from the NCBI database and alignments were performed with MAFFT (Katoh and Toh 2010). The maximum likelihood (ML) analysis was performed with RAXML v.8.0 (Stamatakis 2014) using default parameters and 1,000 bootstrap replicates.

The size of the cp genome of *L. stenocephala* was 151,158 bp in length, including a large single copy region

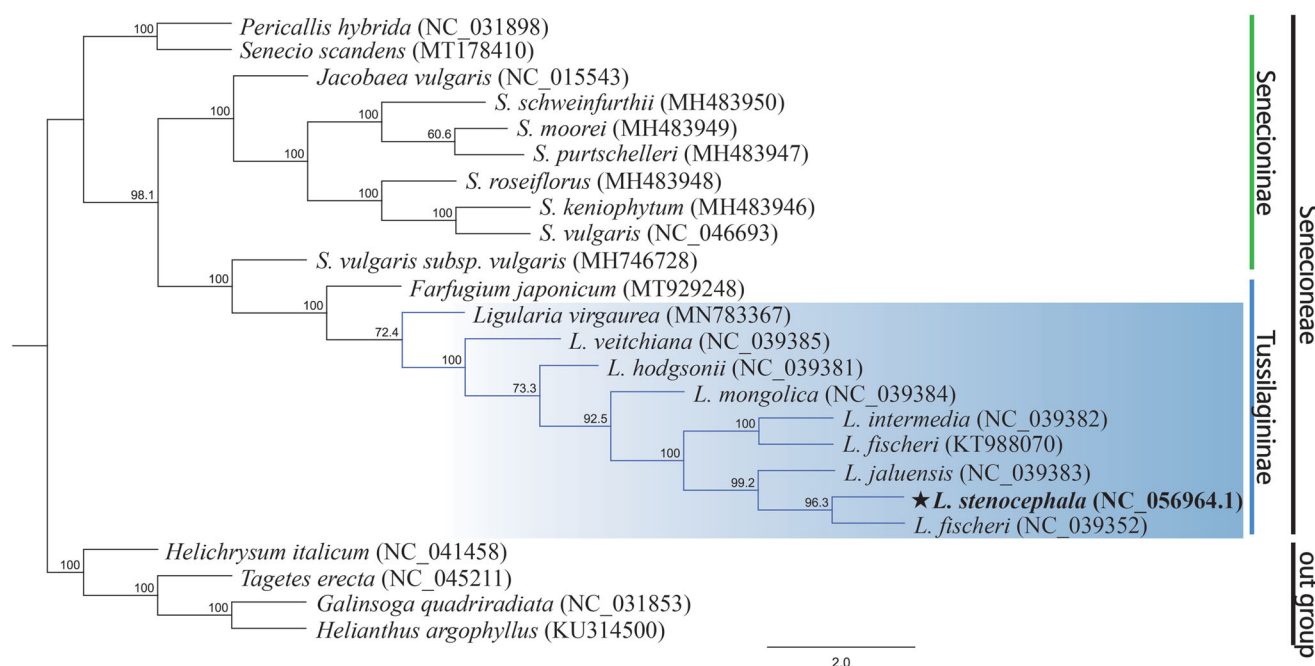


Figure 1. Maximum-likelihood phylogenetic tree based on complete chloroplast genomes of 23 species. Numbers above nodes indicate bootstrap values with 1,000 replicates. The bottom scale bar represents the number of substitutions per site. The species highlighted is *Ligularia* species.

(LSC) of 83,265 bp, a small single copy region (SSC) of 18,233 bp, and a pair of inverted repeat regions (IRs) of 24,830 bp each. The gene content and order were comparable to other published *Ligularia* cp genomes (Chen et al. 2018). The cp genome contains 132 genes, including 87 protein-coding genes, 8 rRNA genes, and 37 tRNA genes. The overall G+C content of the genome is 37.5, 35.6% in the LSC region, 30.7% in the SSC region, and 43.0% in the IR regions. The phylogenetic tree shows that *L. stenocephala* is closely related to *L. fischeri*, with strong bootstrap support (Figure 1). These data are useful for the phylogenetic and evolutionary studies of LCP complex and Asteraceae.

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 National Institute of Biological Resources (NIBR).

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. NC_056964.1. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA713916, SRR13950043, and SAMN18275096 respectively.

Author contributions

Min-Su Park: sample collection, the drafting of the paper.
Won-Bum Cho: data analysis.
Hyun-Do Jang: conception and design of the article.
Chang-gee Jang: literature research and phylogenetic discussion.

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