

MITOGENOME ANNOUNCEMENT

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The complete chloroplast genome sequence of *Ligularia fischeri* (Ledeb.) Turcz. (Asteraceae)

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ABSTRACT

We characterized the complete chloroplast genome sequence of *Ligularia fischeri*, a collection from Halla Mountain in Jeju Island, Korea. The plants are utilized as edible functional plant species harbouring useful antioxidant compounds in family Asteraceae. *De novo* assembly with whole genome sequencing data of *L. fischeri* completed the chloroplast genome of 151 133 bp long, which included two inverted repeats (IRs) blocks of 24 831 bp, separated by the large single-copy block of 83 238 bp and small single-copy block of 18 233 bp. The genome encoded 113 genes consisting of 80 protein-coding genes, 29 tRNA genes and 4 rRNA genes. Phylogenetic analysis with protein coding gene sequences of reported Asteraceae chloroplast genomes revealed a close relationship of *L. fischeri* with *Jacobaea vulgaris*, a weed species world-widely distributed.

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Chloroplast; *Ligularia fischeri*; whole genome sequence

Introduction

Ligularia fischeri, called *Gomchi* in Korea, is a perennial herbal plant belonging to family Asteraceae. In Korea, this plant has been used as a wild edible herbal plant and is mainly distributed in damp shady regions of high altitudes more than at least 600 m in the eastern part of Korea (Choi et al. 2007; Shang et al. 2010; Song et al. 2014). In addition, the leaves of this species have been used in Korea for medicinal purposes such as treatment of jaundice, scarlet fever, rheumatoid arthritis and hepatic function failure, owing to their antioxidant compounds, like Korean ginseng (Jeong et al. 1998; Lee et al. 2002, 2015; Park & Choi 2007; Bae et al. 2009). Nevertheless, large cultivation of *L. fischeri* in farm field is difficult, due to the limitation of cultivatable regions (Song et al. 2014). In this study, we characterized the complete chloroplast genome sequence of *L. fischeri* to contribute to further physiological, molecular and phylogenetical studies of this plant.

A plant material of *L. fischeri*, endemic in Jeju Island Korea, was provided by Hantaek Botanical Garden (<http://www.hantaek.co.kr/>), Yongin, Korea. Genomic DNA was extracted from fresh leaves following a modified cetyltrimethylammonium bromide (CTAB) protocol (Allen et al. 2006). The quality and quantity of the DNA were examined using a NonDrop ND-1000 (NanoDrop Technologies, Inc., Wilmington, DE, USA). A pair-end (PE) library was constructed and sequenced using an Illumina MiSeq platform by Lab Genomics, Inc. (Seongnam,

Korea). Approximately 1.01 Gb of sequencing data were obtained, and *de novo* assembled by a CLC genome assembler (v. beta 4.6, CLC Inc., Aarhus, Denmark), as reported in Kim et al. (2015a, 2015b). Compared with the chloroplast sequence of *Artemisia frigida* (NC_020607) as a reference, eight representative chloroplast contigs were selected and joined into a single draft sequence. The draft sequence was validated and corrected by PE read mapping. DOGMA software was used for annotation of protein-coding genes in the chloroplast genome (Wyman et al. 2004), and manual confirmation process was carried out by BLAST searches.

The complete chloroplast genome of *L. fischeri* was circular DNA molecule of 151 133 bp in length, which was separated into a large single copy region of 83 238 bp, a small single copy region of 18 233 bp and a pair of inverted repeats (IRa and IRb) of 24 831 bp. The genome contained a total of 113 genes including 80 protein-coding genes, 29 tRNA genes and 4 rRNA genes, and showed the GC content of 37.5%. Among the genes identified, 7 protein-coding, 7 tRNA and 4 rRNA genes were completely duplicated in the IR regions. The complete chloroplast genome of *L. fischeri* was submitted into GenBank with accession number KT988070, which is firstly reported chloroplast genome sequence in genus *Ligularia*.

The phylogenetic analysis of *L. fischeri* was performed by comparison with 45 protein-coding gene sequences derived from chloroplast genome sequences of other 18 species in family Asteraceae. Phylogenetic tree was generated by a maximum

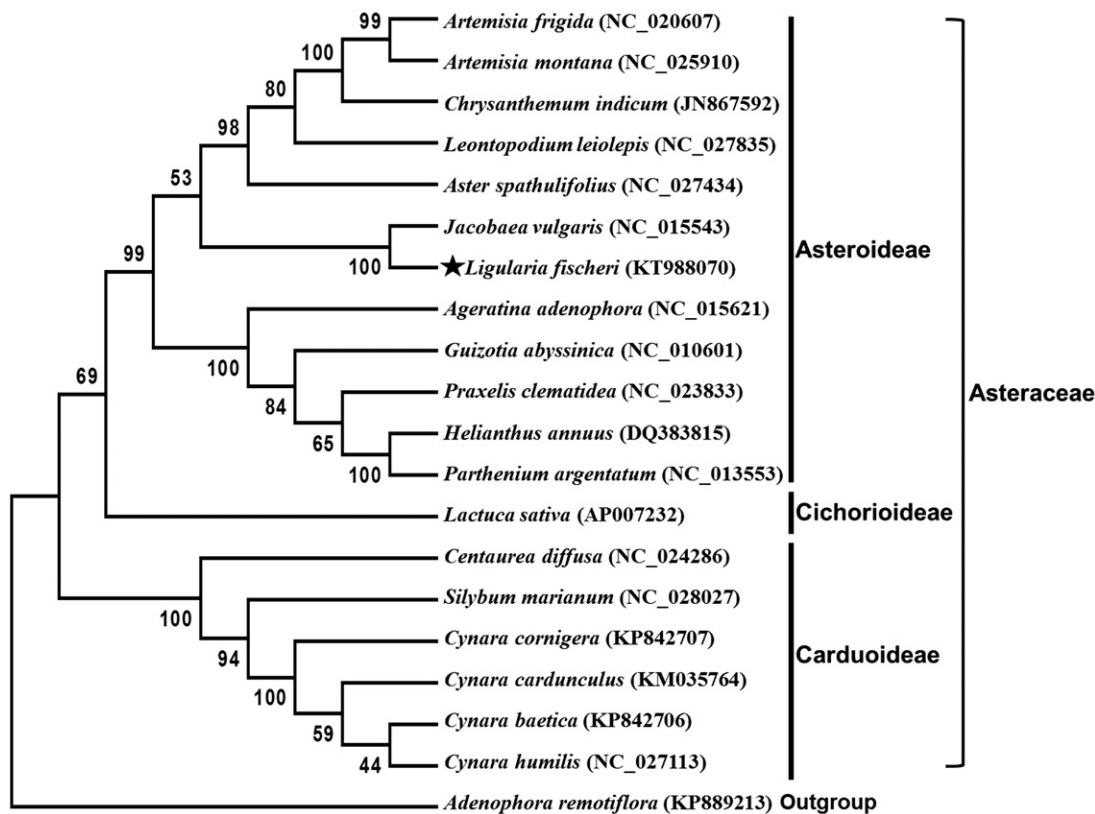


Figure 1. Maximum likelihood phylogenetic tree of *L. fischeri* with other 19 species based on 45 protein-coding gene sequences. Numbers in the nodes are the bootstrap values from 1000 replicates. The chloroplast sequence of *Adenophora remotiflora* (KP889213) in family Campanulaceae was set as an outgroup.

likelihood analysis of MEGA 6.0 program (Tamura et al. 2013) using 1000 bootstrap replicates and revealed that *L. fischeri* was placed mostly close to *Jacobaea vulgaris* (synonym *Senecio jacobaea*), a biennial or perennial Asteraceae weed widely distributed in Asia, Europe, America, Africa and Australia (McLaren et al. 2000; Jacobs & Sing 2009) (Figure 1).

Disclosure statement

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