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The complete chloroplast genome sequence of the medicinal plant, *Angelica gigas* (Apiaceae)

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ABSTRACT

The complete chloroplast genome sequence of *Angelica* gigas, a traditional herbal plant used in treating diseases, was obtained by de novo assembly using illumina sequencing data (Illumina Inc., San Diego, CA). The circular molecule of the genome was constructed of four parts, with a size of 146,916 bp in total – a large single copy (LSC) region of 93,118 bp, a small single copy (SSC) region of 17,582 bp and two inverted repeat (IRa and IRb) regions of 18,108 bp each. There were a total of 113 annotated genes, including 80 protein-coding genes, 29 tRNA genes and four rRNA genes. The phylogenetic result acquired through maximum parsimony analysis showed that *A. gigas* is closely related with *A. decursiva* and *Seseli montanum*.

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Angelica gigas; Apiaceae; chloroplast; genome sequence; medicinal plant

Angelica gigas Nakai belongs to the family Apiaceae, and is a perennial herb found in Korea, China and Japan (Zehui & Watson 2005). The roots of this plant, called Dang-gui in Korea (Korea Food and Drug Administration, 2013), have been well used as a traditional medicinal plant for gynaecological diseases, haematopoiesis and anti-inflammation (Ahn et al. 1996; Yoon et al. 2007). The material plants for Dang-gui differ among countries depending on their regulations, with *A. sinensis* (Oliv.) Diels in China (Pharmacopoeia Commission of the People's Republic of China, 2010) and *A. acutiloba* Kitagawa or *A. acutiloba* Kitagawa var. *sugiyamana* Hikino in Japan (The Ministry of Health, Labour and Welfare, 2011). However, *A. acutiloba* and *A. acutiloba* var. *sugiyamana* are prescribed as Il-dang-gui in Korea. Because of the similar medicinal names and closely related species in the genus *Angelica* among herbal materials, mixes or misuses could occur in the market place. We, therefore, assembled the complete chloroplast genome of *A. gigas*, to provide a genomic resource for fair trade and harmony in the regulation of herbal medicines through correct discrimination among species.

The leaves of *A. gigas* was obtained from a farmhouse in Jecheon-si, Korea (37°11′22.10″N, 128°15′32.99″E), and extracted by DNeasy Plant Mini Kit (QIAGEN Inc., Valencia, CA). The isolated genomic DNA was manufactured to 300 bp paired-end (PE) library using the Illumina Hiseq library kit (Illumina, San Diego, CA), and sequenced by Illumina genome analyzer (Hiseq2000). Acquired high-quality reads were conducted by *de novo* assembly using CLC genome assembler (ver. 4.06 beta, CLC Inc, Rarhus, Denmark). The assembled structures and genes of the complete chloroplast genome were annotated by DOGMA (http://dogma.ccbb.utexas.edu/) (Wyman et al. 2004), and manually corrected by Blast search. The chloroplast genome map was drawn with OGDRAW v 1.2 (http://ogdraw.mpimp-golm.mpg.de/) (Lohse et al. 2007). The complete chloroplast genome sequence was deposited in GenBank under accession no. KT963098. Sample was deposited at the National Center for Herbal Medicine Resources, NIFDS, and MFDS, of Korea under accession no. 13E-39.

The chloroplast genome of *A. gigas* was a circular molecule with a size of 146,916 bp comprising four structures, with 93,118 bp in the large single copy (LSC) region, 17,582 bp in the small single copy (SSC) region and 18,108 bp in each of duplicated inverted repeat (IRa and IRb) regions. The overall GC content was 37.56%, with the GC contests of the IRs the highest at 44.81% and followed by those of the LSC (35.97) and the SSC (31.01). The chloroplast genome contained a total of 113 genes – 80 protein-coding genes, 29 tRNA genes and four rRNA genes.

To analyze the phylogenetic relationships between *A. gigas* and related species in Apiaceae, the chloroplast genome sequences of a total of nine taxa were aligned by MAFFT (http://mafft.cbrc.jp/alignment/software/) (Katoh et al.

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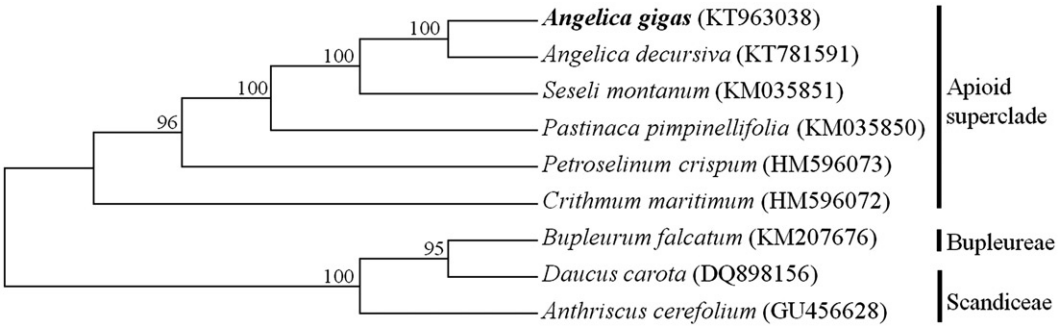

Figure 1. Phylogenetic trees based on maximum parsimony analysis of *A. gigas* with related species in Apiaceae. The numbers above the branches are the bootstrap statistics values from 1000 replications.

2002). Maximum parsimony (MP) analysis was performed based on tree bisection reconnection (TBR) branch swapping with 1000 replications in MEGA6 (Tamura et al. 2013). The phylogenetic tree was divided into two groups, which were Apioid superclade with *Angelica*, and two other tribes, Bupleureae and Scandiceae (Figure 1). *A. gigas* showed a close relationship to the same genus species *A. decursiva* and *Seseli montanum*.

Disclosure statement

The authors declare that there is no conflict of interest. The authors alone are responsible for the content and writing of the paper.

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