

The complete chloroplast genome sequence of *Aristolochia manshuriensis* Kom. (Aristolochiaceae)

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ABSTRACT

Aristolochia manshuriensis is a medicinal plant belonging to the family Aristolochiaceae. In this study, complete chloroplast (cp) genome sequence of *A. manshuriensis* was characterized through *de novo* assembly with next-generation sequencing data. The cp genome is 160,182 bp long and has a typical quadripartite organization consisting of a large single-copy (LSC), a small single-copy (SSC), and a pair of inverted repeats (IRs). The cp genome harboured 79 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. Phylogenetic analysis revealed that *A. manshuriensis* has close relationship with *Aristolochia macrophylla*.

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The genus *Aristolochia* L. sensu lato (Aristolochiaceae), which consists of ~400 species, is distributed from temperate to tropical regions around the world (Ohi-Toma et al. 2006). In Korea, only two species are distributed; *Aristolochia contorta* and *Aristolochia manshuriensis* (Oh 2007). For thousands of years, *Aristolochia* species have been used as medicinal plants in East Asia including China, Korea, and Japan (Chinese Company of Medicinal Materials 1995; Hu et al. 2004). In particular, aristolochic acid (AA) from root, rootstock or stem of *Aristolochia* species is used to treat gout, rheumatoid arthritis, wound festering, or to reduce inflammation (Negi et al. 2003; Heinrich et al. 2009; Nie et al. 2015). However, AA is also reported as mutagenic, nephrotoxic, and carcinogenic to animals and humans (Arlt et al. 2002, 2007; International Agency for Research on Cancer 2002; Cheng et al. 2006; Huang et al. 2007; Nie et al. 2015). Recently, it has been banned to utilize AA for medicinal purposes in many countries (International Agency for Research on Cancer 2002; Cheng et al. 2006; Arlt et al. 2007; Martena et al. 2007; Lai et al. 2010).

In this study, we determined the chloroplast (cp) genome of *A. manshuriensis* to contribute to the classification and development of DNA markers for the authentication of *Aristolochia* species. The specimen was collected from Samil-ri, Sanae-myeon, Hwacheon-gun, Gangwon-do, South Korea (38°0'23.5"N, 127°31'22.2"E) and deposited at NIBR herbarium (KB) with the accession number NIBR-VP0000575956. Total genomic DNA was prepared and sequenced by the Illumina MiSeq platform (Illumina Inc., San Diego, CA) and

obtained high-quality paired-end reads of ca. 2.5 Gb. The complete cp genome of *A. manshuriensis* was revealed to GenBank (Accession no. MN132862), as described previously (Kim et al. 2015).

The cp genome was 160,182 bp in length with 38.7% overall GC content. The cp genome structure of *A. manshuriensis* has the typical quadripartite organization featuring two copies (IRa and IRb) of inverted repeat (IR) regions (25,691 bp) that are separated by a large single-copy (LSC) region (89,503 bp), and a small single-copy (SSC) region (19,297 bp). The total number of identified encoded genes is 113 with 79 protein-coding genes, 30 tRNA genes, and 4 rRNA genes.

To understand the phylogenetic relationship of *A. manshuriensis* with relative taxa, a maximum-likelihood (ML) tree was constructed using 75 common protein-coding genes of *A. manshuriensis* and 11 taxa in Aristolochiaceae. Outgroup includes two species of *Piper* (*Piper austrittum* and *Piper kadsura*) in Piperaceae, which is the most likely sister group of Aristolochiaceae (Figure 1). The *Aristolochia* clade comprised well-supported monophyletic group (pp = 100), and the two major subclades were circumscribed; these include (1) subgn. *Aristolochia*, and (2) subgn. *Siphisia* (Murata et al. 2001) (Figure 1). *Aristolochia manshuriensis* was contained in subgn. *Siphisia* clade with *Aristolochia kaempferi*, *Aristolochia kunmingensis*, *Aristolochia macrophylla*, *Aristolochia mollissima*, and *Aristolochia moupinensis*. Among those species, *A. manshuriensis* has more close relationship with *A. macrophylla* (Figure 1).

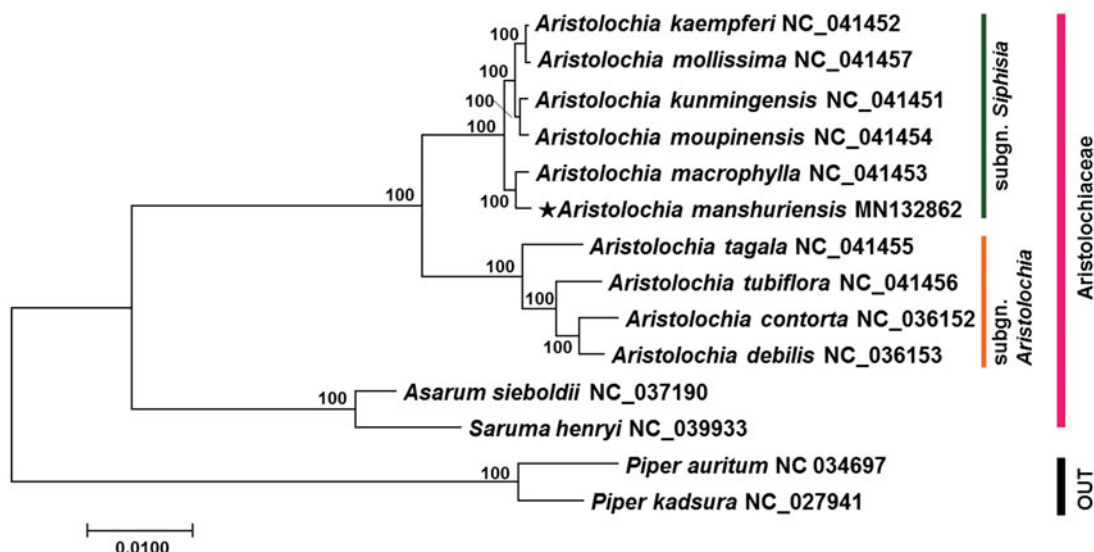


Figure 1. Maximum-likelihood (ML) tree based on the 75 chloroplast protein-coding genes of 14 taxa including *A. manshuriensis*. Sequences of 75 chloroplast protein-coding gene from 14 taxa were aligned using MAFFT (<http://mafft.cbrc.jp/alignment/server/index.html>) and used to generate ML phylogenetic tree by MEGA 7.0 (Kumar et al. 2016).

Disclosure statement

None of the authors report any conflict of interest. The authors alone are responsible for the content and writing of the paper.

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