Characterization of the complete chloroplast genome of *Ammopiptanthus mongolicus* (Papilionoideae), a rare and Endangered plant to China

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**ABSTRACT**

*Ammopiptanthus mongolicus* is a rare and Endangered plant of *Ammopiptanthus* (Papilionoideae) in China. It grows mainly in the arid and semi-arid regions. The complete chloroplast (cp) genome was assembled by Illumina paired-end reads data. The circular cp genome is 153,997 bp in size, including a large single copy (LSC) region of 83,957 bp, a small single copy (SSC) region of 18,008 bp and a pair of inverted repeat (IRs) regions of 26,016 bp. Besides, 5 genes possess a single intron, while another three genes ycf3, rps12, and clp have a couple of introns. The GC content of the entire *A. mongolicus* cp genome, LSC, SSC, and IR regions are 36.9, 34.6, 30.5, and 42.8%, respectively. Based on the concatenated coding sequences of cp PCGs, the phylogenetic analysis showed that *A. mongolicus* and *A. nanus* are closely related to each other within the family Leguminosae.

*Ammopiptanthus mongolicus* belongs to the family Papilionoideae, which is a traditional medicinal plant in China (Fu 1991). It grows mainly in the arid and semi-arid regions of Ningxia, Xinjiang, Inner Mongolia and so on (Liu et al., 1995). Previous studies had shown that the stem and leaf of the plant have commonly been used in traditional medicine, which was recorded as a famous and historic drug for its effects of flipping wind dehumidification and relieving muscle stasis. As an only evergreen broad-leaf shrub in the northwest desert of China, *A. mongolicus* shows very strong resistance to both drought and cold stresses (Huang et al. 2012).

The conserved quadripartite structure of a typical circular cp genome include a pair of inverted repeats (IRs), separated by a large single-copy region (LSC) and a small single-copy region (SSC) (Wolfe et al. 1992; Lee et al. 2007). This study will be very useful for the research on the phylogenetic relationships of *A. mongolicus* and Papilionoideae.

Fresh leaves of *A. mongolicus* were collected in the Yinchuan Botanical Garden (38°28′N, 106°16′E; Ningxia, NW China). A voucher specimen (PO2C) is deposited at the State Key Laboratory Seedling Bio-engineering in Ningxia Forestry Institute. We used the modified CTAB method to extract the total genomic DNA (Doyle and Doyle 1987). A shotgun library constructed following the manufacturer’s protocol for the Illumina HiSeq X Ten Sequencing System (Illumina, San Diego, CA, USA). We assembled the cp genome using the program MITObim v1.8 (DSM Nutritional Products Ltd, Kaiseraugst, Switzerland) (Hahn et al. 2013), with that of *Ammopiptanthus nanus* (GenBank: KF034454) as the initial reference. The web-based tool OGDRaw v1.2 (http://ogdraw.mpimp-golm.mpg.de/) was employed to generate a map of the complete cp genome (Lohse et al. 2013). The complete cp genome sequence has been submitted to GenBank (accession number MK704436).

The complete cp genome is a circular and double-stranded DNA molecule with a typical quadripartite structure, containing two inverted repeat (IRs) regions, a large single copy (LSC) region, and a small single copy (SSC) region. In all, we received 23,776,174 raw paired-end reads, which length distribution in 153,997 bp (GC, 36.9%), the length of LSC region, IRs regions and SSC region in 83,957 (GC, 34.6%), 26,016 (42.8%), and 18,008 (30.5%), respectively.

It encodes 130 complete genes, including 84 protein-coding genes, 37 transfer RNA genes, and 8 ribosomal RNA genes. In addition, 5 PCG genes (*atpF, ndhA, ndhB, rpl2*, and *rpoC1*) possess a single intron, 76 PCG genes no intron, 3 other genes (*clpP, rps12*, and *ycf3*) harbor two introns, 5 tRNA genes (*trnA-UGC, trnI-GAU, trnK-UUU, trnL-UAA, and trnV-UAC*) harbor a single intron.

To investigate the phylogenetic position of *A. mongolicus*, we constructed a neighbour-joining (NJ) phylogenetic tree
Figure 1. Maximum likelihood (ML) tree of *A. mongolicus* and its related relatives based on the complete chloroplast genome sequences.

(Figure 1) based on the concatenated coding sequences of 17 chloroplast PCGs for 17 plastid genomes from published species of Compositae using MEGA7 with 1000 bootstrap replicates (Kumar et al. 2016) ([http://www.megasoftware.net/](http://www.megasoftware.net/)). From the phylogenetic tree analysis, we find that *A. mongolicus* and *Ammopiptanthus nanus* (KY034454) are closely related to each other within the family Papilionoideae.

Disclosure statement

The authors report no conflicts of interest and are solely responsible for the content and writing of this paper.

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