**The complete chloroplast genome of *Aesculus chinensis***

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**ABSTRACT**

The complete chloroplast genome of *Aesculus chinensis* was obtained with Illumina HiSeq X Ten. The chloroplast genome is 155,528 bp in length, including a pair of inverted repeat (IR) regions of 25,656 bp, a large single-copy (LSC) region of 85,489 bp, and a small single-copy (SSC) region of 18,727 bp. It contains 115 genes, including 80 protein-coding genes, 31 transfer RNAs, and four ribosomal RNAs. The total GC content is 37.9%, whereas the corresponding values of the LSC, SSC, and IR regions are 36.1%, 31.8%, and 43.2%, separately. Phylogenetic analysis of the protein-coding genes showed a close relationship with *Aesculus wangii* in Hippocastanaceae.

*Aesculus chinensis* (Hippocastanaceae), abundant in the northwestern China, is a widely used medicinal plant rich of escins (Cheng et al. 2018). Modern pharmacological studies show that *A. chinensis* possess diverse biologic activities such as antiviral (Yang et al. 1999), anti-inflammatory (Zhao et al. 2001; Wei et al. 2004), antitumor (Wang et al. 2017), antioxidative (Sato et al. 2005; Cheng et al. 2018), and antigenotoxic properties (Sato et al. 2005; Cheng et al. 2018). Its dried ripe seeds have been used as a stomachic and analgesic in the treatment of ditation and pain in the chest and abdomen (Wei et al. 2004). *Aesculus chinensis* has high prospects to be further developed for tree cultivation.

The chloroplast genome sequences have been utilized as reliable tools for phylogenetic and evolutionary research (Wang et al. 2018). In recently, many chloroplast genomes of valuable plants have been reported (Chen et al. 2018; Liu and Han, 2018; Zheng et al. 2018; Wang et al. 2018; Kwon et al. 2019; Yang et al. 2019; Zhu and Sun 2019). To facilitate its genetic research and contribute to its utilization, we reported the complete chloroplast genome sequence of *A. chinensis* based on Illumina HiSeq X Ten. The annotated genomic sequence has been submitted to GenBank with the accession number MK737939. Phylogenetic evolution analysis revealed that its phylogenetic placement within the family Hippocastanaceae.

The pattern specimens were taken from Shaanxi Province in Southwest of China, located at 105°59'40"E, 33°11'57"N and were stored in the Herbarium of Neijiang Normal University (accession number: 20190122AC02). Chloroplast DNA (cpDNA) extracted following the directions of DNeasy Plant Mini Kit (Qiagen, CA, USA). The whole genome sequencing was conducted on the Illumina HiSeq X Ten Sequencing System in Novogene Bioinformatics Technology Co., Ltd. (Beijing, China). The complete chloroplast genome was assembled using the baiting and iterative mapping approach (Hahn et al. 2013), with that of its congener *Aesculus wangii* (GenBank: MF583747) as the initial reference genome. A total of 4,323,520 individual chloroplast reads yielded an average coverage of 141.3-fold. The chloroplast genome was annotated in GENEIOUS R11 (Biomatters Ltd., Auckland, New Zealand) and was drawn to the circular chloroplast genome sequence map of OGDRAW.

The chloroplast genome of *A. chinensis* is 155,528 bp in length (GenBank accession number: MK737939) and exhibits a typical quadripartite structure of the large (LSC, 85,489 bp) and small (SSC, 18,727 bp) single-copy regions, separated by a pair of inverted repeat regions (IRs, 25,656 bp each). The total GC content is 37.9%, whereas the corresponding values of the LSC, SSC, and IR regions are 36.1%, 31.8%, and 43.2%, respectively. The complete chloroplast genome of *A. chinensis* contains 115 unique genes, including 80 protein-coding genes, 31 transfer RNA genes, and four ribosomal RNA genes. Intron-exon structure analysis indicated that 97 (84.3%) genes had no introns, whereas 16 (13.9%) genes contained a single intron and two protein-coding genes had two introns.

In order to verify the evolutionary relationship, maximum-likelihood phylogenetic tree was generated using the whole chloroplast DNA alignment from 20 published plant species in *Sapindaceae* using MEGA 7.0 (Kumar et al. 2016), which showed that *A. chinensis* has a close relationship with *Aesculus wangii* in Hippocastanaceae (Figure 1). The results will provide a foundation for further investigation of chloroplast genome evolution in Hippocastanaceae.
Disclosure statement

No potential conflict of interest was reported by the authors.

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