Characterization of the complete chloroplast genome of *Macleaya cordata* and its phylogenomic position within the subfamily Papaveroideae

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**ABSTRACT**

*Macleaya cordata* (Willd.) is a perennial herb with significant antimicrobial and anti-inflammatory activities. In this study, we report the complete chloroplast genome sequence of *M. cordata*. The total genome size was 163,179 bp in length, containing two inverted repeated (IR) regions of 28,329 bp each, a large single copy (LSC) region of 87,933 bp and a small single copy (SSC) region of 18,588 bp. The genome contains 114 genes, including 79 protein genes, 4 rRNA genes, 28 tRNA genes and 3 pseudo genes. The overall GC content of *M. cordata* is 38.59%, with the highest GC content of 42.79% in IR region. A total of 49 simple sequence repeats are identified in the cp genome of *M. cordata*. Phylogenetic analysis demonstrated that *M. cordata* clustered together with *M. microcarpa*, further forming a monophyletic group with the genuses Hylomecon and Coreanomecon. This work provides basic genetic resources for developing robust markers and investigating the population genetics diversities for this famous medicinal species.

*Macleaya cordata* is a medicinal plant species from the subfamily Papaveroideae, which is typically prescribed as a traditional antibacterial medicine (Sai et al. 2015). This species has been used as a natural additive in livestock because of its antimicrobial, anti-fungal and anti-inflammatory activity (Li et al. 2018). Furthermore, *M. cordata* provides a safe resource for the bioactive compound sanguinarine, which could potentially improve the growth performance and intestinal morphology of early-weaned piglets via modifying the intestinal luminal environment (Chen et al. 2018). The extract of *M. cordata* plays a preventative role with respect to *Escherichia coli* infection (Guan et al. 2019). The complete chloroplast genome information would contribute to the species identification and cultivation research of this important medicinal plant. Here, we report the complete chloroplast genome of *M. cordata* to provide a genomic resource for molecular marker development and clarify the phylogenetic position of this plant within the subfamily Papaveroideae.

The sample of *Macleaya cordata* was collected from Fuyang area of Zhejiang Province (30°05′2.4″N, 119°53′20.4″E) and deposited in the collection center of Zhejiang Chinese Medical University with the specific identifying number of BLH-1932. Total genomic DNA was extracted and sequenced using the Illumina Hiseq Platform according to the previous reprot (Ying et al. 2019; Gao et al. 2020). The chloroplast genome of *M. cordata* was assembled by metaSPAdes with the chloroplast sequence of *M. microcarpa* as reference (Nurk et al. 2017). The chloroplast was annotated using GeSqe and further confirmed by BLAST (Tillich et al. 2017). The complete cp genome of *M. cordata* was submitted to GenBank with the accession number of MT178411.

The length of the complete chloroplast genome sequence of *M. cordata* was 163,179 bp, with a large single copy (LSC) region of 87,933 bp, a small single copy (SSC) region of 18,588 bp, and two separated inverted repeated (IR) regions of 28,329 bp each. A total of 114 genes were identified in the cp of *M. cordata*, including 79 protein-coding genes, 28 tRNA genes, 4 rRNA genes and 3 putative pseudo genes. The overall GC content was 38.59%, and the corresponding contents for LSC, SSC and IR regions were 37.04%, 33.12% and 42.79%, respectively. The genome included 19 duplicated genes in the IR region and exhibited 51.1% protein-coding sequences. Moreover, a total of 49 small single repeats (SSR) are identified in the cp of *M. cordata*, ranging from 10 bp to 36 bp.

The complete genome sequences of *M. cordata* and other 17 representative species from the subfamily Papaveroideae were analyzed using MEGA 7.0 by maximum-likelihood (ML) method to confirm its phylogenetic position. The result demonstrated that a sister relationship between *M. cordata* and *M. microcarpa*, indicating a close genetic relationship between the two species (Figure 1). Furthermore, the monophyletic group of Macleaya displayed a sister-relationship with the combined clade of genuses Hylomecon and...
Coreanomecon, forming the Group II in the the subfamily Papaveroideae (Figure 1). These results would contribute the development of molecular markers and understanding of evolutionary history and cultivation strategy for Macleaya cordata.

Disclosure statement
No potential conflict of interest was reported by the author(s).

Funding
This work was financially supported by the Opening Project of Zhejiang Provincial Preponderant and Characteristic Subject of Key University (Traditional Chinese Pharmacology), Zhejiang Chinese Medical University [No. ZYAOX2018033] and Project of Quality Guarantee System of Chinese Herbal Medicines [Grant No. 201507002-4].

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