Characterization of the complete chloroplast genome sequence of *Pueraria montana* var. *lobata* and its phylogenetic implications

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**ABSTRACT**

*Pueraria montana* var. *lobata* is a traditional Chinese herb with various medicinal purposes. In this study, the complete chloroplast genome of the *P. montana* var. *lobata* was obtained by using Illumina HiSeq X Ten. The chloroplast genome was 153,411 bp long, with 2 large single-copy (LSC) regions of 84,131 bp and 17,990 bp separated by a pair of inverted repeat (IR) regions of 25,645 bp each. The whole chloroplast genome contained 111 gene species including 77 protein-coding genes (PCG), 30 tRNA, and 4 rRNA species, with 19 of them occurring in double copies. Intron detection was conducted in 12 PCG and 6 tRNA species. The overall GC content is 35.4%. Phylogenetic analysis indicated that *P. montana* var. *lobata* was relatively close to *Pachyrhizus erosus* in phylogeny.

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*Pueraria montana* var. *lobata* is a semi-woody, perennial liana belonging to the family Leguminosae in possession of a variety of beneficial health effects. It was usually used as traditional Chinese medicine with various medicinal purposes (Li 2015; Heo et al. 2019). The dry root of *P. montana* var. *lobata* was full of secondary metabolites such as isoflavonoids (Rong et al. 1998; Joung et al. 2003), flavones (Kinjo et al. 1988), triterpenoids (Arao et al. 1995, 1997), and dibenzyl butyrolactones (Hirakura et al. 1997). It had the efficacy of antidiabetes (Cui et al. 2018), relieving muscles analgesia, reducing fever and antidiarrheal (Li 2015), treating diabetes and cardiovascular diseases (Wong et al. 2011; Liu et al. 2019), and so on. The isoflavonoids are also common constituents in human diets (Joung et al. 2003). To facilitate its genetic research and contribute to its utilization, the complete chloroplast genome of the *P. montana* var. *lobata* was assembled from the whole genome Illumina sequencing data and phylogenetic analysis was conducted using the neighbor-joining (NJ) method.

DNA samples were extracted from the fresh leaves collected from a single individual of *P. montana* var. *lobate* in Enshi, Hubei Province of China (109°32′23″E, 29°57′33″N) and stored in the Herbarium of Neijiang Normal University (accession number: 20190225PM04). The Illumina sequencing was conducted on Illumina HiSeq X Ten platform by Beijing Novogene Bioinformatics Technology Co., Ltd (Beijing, China). The complete chloroplast genome was assembled using the baiting and iterative mapping approach (Hahn et al. 2013). * Cajanus cajan* (GenBank accession number KU729879) within the subfamily *Papilionoideae* was used as a reference for assembling and annotation (Kaila et al. 2016). The annotated chloroplast DNA (cpDNA) sequence has been deposited into GenBank with the accession number MK820065.

The complete cpDNA of *P. montana* var. *lobate* was a circular molecule of 153,411 bp in length including an LSC region of 84,131 bp and an SSC region of 17,990 bp separated by a pair of IR regions of 25,645 bp each. It encodes a total of 111 genes including 77 protein-coding genes, 30 tRNA, and 4 rRNA species, in which 19 of them were with double copies (8 protein-coding genes, 7 tRNA, and 4 rRNA genes). Introns detected were 71 (83.8%) genes, whereas 18 (16.2%) genes (12 PCG and 6 tRNA genes) contained a single intron and 2 PCG (atP and ycf3) had two introns. The total GC content is 35.4%, while the corresponding values of the LSC, SSC, and IR regions are 32.8%, 28.9%, and 41.9%, respectively.

To identify the phylogenetic position of *P. montana* var. *lobata*, phylogenetic analysis was conducted using 38 complete chloroplast sequences in *Papilionoideae* and other 3 species within the subfamily *Caesalpinioideae* as outgroup taxa by MEGA 7.0 (Kumar et al. 2016). The neighbor-joining (NJ) tree indicated that *P. montana* var. *lobata* was closely related to *Pachyrhizus erosus* (Figure 1). The results will provide a foundation for further investigation of chloroplast genome evolution in *Pueraria*.
Disclosure statement

No potential conflict of interest was reported by the authors.

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