Complete chloroplast genome sequence of medicinal plant *Potentilla lineata* Treviranus (Rosaceae) from Yunnan, China

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**ABSTRACT**

*Potentilla lineata* Treviranus is a common medicinal plant distributed in the southwest of China. In this study, we sequenced the complete chloroplast genome sequence of *P. lineata* and investigated its phylogenetic relationship within *Potentilla* and related genera. The total length of the chloroplast genome is 156,985 bp. The genome exhibits a typical quadripartite structure containing a pair of IRs (inverted repeats) of 25,974 bp separated by a single small copy (SSC) region of 18,859 bp and a large single copy (LSC) region of 86,178 bp. The chloroplast genome contained 112 genes, including 78 protein-coding genes, 30 tRNA genes, and four rRNA genes. The phylogenetic analysis indicates that *Potentilla* L. is a monophyletic taxon that is sister to *Potaninia* Maxim. *Potentilla lineata* is closely related to *P. centigrana* Maxim in the present study. This study provides a reference for the phylogeny and species evolution of the genus *Potentilla* and related genera.

*Potentilla lineata* Treviranus is classified in a complex genus with about 500 species, namely *Potentilla* in the Rosaceae (Xu and Podlech 2010). The species is mainly distributed in Yunnan, Guizhou and Tibet provinces of China. As a common medicinal plant, the root of *P. lineata* is used to treat enteritis and diarrhea, traumatic bleeding, and is an anti-inflammatory (Manju et al. 2006). The plant is widely used by Bai and Dai people due to its medicinal value (Duan 2017; Jiang 2017). Studies on this species have mainly focused on pharmacological effects and active ingredients (Chen et al. 2013; Toğrul et al. 2015). However, the chloroplast genome of *P. lineata* has not been analyzed. Here we sequenced the complete chloroplast genome sequence of *P. lineata*, as well as reconstructed a phylogenetic tree with other taxa classified in the Rosaceae to determine its evolutionary history.

Fresh and cleaned leaf materials of *P. lineata* were sampled from Dali, Yunnan, China (N 25\(^\circ\)52'38.91", E 100\(^\circ\)00'27.25")\(^c\)). A voucher specimen (No. ZDQ2021) was collected and deposited at the Herbarium of Medicinal Plants and Crude Drugs of the College of Pharmacy, Dali University (Professor Dequan Zhang, zhangdeq2008@126.com). The total genomic DNA was extracted using an improved CTAB method (Yang et al. 2014), and sequenced with Illumina Hiseq 2500 (Novogene, Tianjing, China) platform using a pair-end (2 \times 300 bp) library. The raw data were filtered using Trimmomatic v0.32 with the default settings (Bolger et al. 2014). The resulting paired-end reads were assembled into a circular contigs using GetOrganelle.py (Jin et al. 2020). The complete chloroplast genome was annotated with Geneious 8.0.2 software (Kearse et al. 2012) and the annotated results were obtained after manual correction.

The annotated chloroplast genome was submitted to the GenBank with an accession number MT677853. The complete chloroplast genome was 156,985 bp. It consists of a typical quadripartite structure with a pair of IRs (inverted repeats) of 25,974 bp that are separated by a small single copy (SSC) region of 18,859 bp and a large single copy (LSC) region of 86,178 bp. The overall GC content is 36.7%, while 34.4%, 30.5%, and 42.7% are respectively calculated for the LSC, SSC, and IR regions. The chloroplast genome contains 112 genes, including 78 protein coding, 30 tRNA, and four rRNA genes. Of these, 17 genes occur in duplicate in the inverted repeat regions, 9 genes (rpl2, rpl16, rps12, rps16, rpoC1, ndhB, ndhA, petD, petB) contained one intron, while two genes (ycf3 and cplp) have two introns.

For the phylogenetic analysis, 21 complete chloroplast genome sequences of Rosoideae were downloaded from the NCBI database. The sequences were aligned with MAFFT v7.149 using the default settings (Katoh and Standley 2013). The nucleotide substitution model was determined by jModelTest v2.1.7 (Darriba et al. 2012). A Bayesian inference (BI) analysis was performed by MrBayes v3.2.6 (Ronquist et al. 2012) with *Crataegus kansuensis* Wils. (No. NC_039374) designated as the outgroup (Figure 1). The phylogenetic analysis indicated *Potentilla* L. is a monophyletic genus, which is consistent with the previous phylogenetic analysis by Faghir et al. (2014) Li et al. (2020) and Li et al. (2021). In this analysis, *Potentilla* is sister to *Potaninia* Maxim. *Potentilla lineata* was fully resolved in a clade with *P. centigrana* Maxim., *P.
suavis and P. hebiichigo. This complete chloroplast genome of P. lineata provides a reference for further phylogenetic studies and the evolution of species in Potentilla and related genera, as well as for conservation and utilization of the resources.

Disclosure statement
The authors declare no conflicts of interest and are responsible for the content.

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Data availability statement
The genome sequence data that support the findings of this study are openly available in GenBank at [https://www.ncbi.nlm.nih.gov/] under the accession no. MT677853. The associated BioProject, SRA, and BioSample numbers are PRJNA737049, SRR14825541, and SAMN19698019 respectively.

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