The complete chloroplast genome sequence of Potentilla tanacetifolia Willd. ex Schltdl.

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ABSTRACT

Potentilla tanacetifolia Willd. ex Schltdl. is a perennial herb in China, which has high ecological and economic values. Its complete chloroplast genome was reported in this study for the first time. The whole chloroplast genome was 157,051 base pairs in length with 129 genes, including 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. In addition, phylogenetic analysis showed a sister relationship between P. tanacetifolia and P. chinensis.

The fresh leaves of P. tanacetifolia were collected from Duolun County (42°02’N, 116°17’E, 1324 m asl), Inner Mongolia Autonomous Region of China. The leaf samples were silica-dried and taken to the laboratory until DNA extraction. The voucher specimen (HF2019002) was laid in the Herbarium of Xi’an Botanical Garden of Shaanxi Province, China. The total genomic DNA was isolated according to a modified CTAB method (Doyle and Doyle 1987). Total genome DNA of P. tanacetifolia was sequenced by Illumina Hiseq 2500 Sequencing System (Illumina, Hayward, CA) to construct the shotgun library. The qualified clean reads were assembled by NOVOPlasty (Dierckxsens et al. 2017), with P. stolonifera (NC_044418) as a reference. The low-quality sequences were filtered out using CLC Genomics Workbench v8.0 (CLC Bio, Aarhus, Denmark). The complete chloroplast genome of P. tanacetifolia was annotated by Geneious ver. 10.1 (http://www.geneious.com, Kearse et al. 2012) and online program Chloroplast Genome Annotation, Visualization, Analysis, and GenBank Submission (CPGAVAS) (Institute of Medicinal Plant development, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China) (Zuo et al. 2017). Finally, the validated complete chloroplast genome of P. tanacetifolia was deposited in Genbank (Accession number MW125592).

The complete chloroplast genome of P. tanacetifolia was 157,051 bp in length, containing a large single-copy region (LSC) of 86,147 bp, a small single-copy region (SSC) of 18,883 bp, and two inverted repeat (IR) regions of 26,010 bp. The overall GC content is 36.8%. The genome contains 129 complete genes, including 84 protein-coding genes, 37 tRNA genes and 8 rRNA genes.

To identify the phylogenetic position of P. tanacetifolia, 8 complete chloroplast genomes sequence of Potentilla were obtained from NCBI GenBank, and Agrimonia pilosa and Sanguisorba officinalis was used as out-group for phylogenetic analysis. The 11 chloroplast genome sequences were aligned with MAFFT (Katoh and Standley 2013) and then the maximum likelihood (ML) tree was constructed by RAxML (Stamatakis 2014). The results confirmed that P. tanacetifolia was clustered with P. chinensis (Figure 1).
Disclosure statement

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

Funding

This work was supported by the Scientific Research Program of Shaanxi Province under Grant [2019QJ-436]; Scientific Research Program of Xi’an City under Grant [2019112913CXSFO07SF017, 20NYFY0003]; Science and Technology Program of the Shaanxi Academy of Sciences under Grant [2021K-18, 2016K-16].

Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov] under the accession no. MW125592. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA678424, SRR13062013, and SAMN16796184 respectively.

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