**ABSTRACT**

*Waldheimia glabra* (Decne.) Rgl. 1879 (family Asteraceae) is a perennial herb with high economic and medicinal values. In this study, we sequenced the complete chloroplast (cp) genome of *W. glabra* by high-throughput Illumina sequencing. The size of the *W. glabra* cp genome is 151,499 bp, with overall GC content of 37.3%. It contains a large single copy and a small single copy region of 83,078 bp and 18,457 bp, respectively, separated by a pair of inverted repeats regions of 24,982 bp. We also discovered 131 genes, including 86 protein-coding genes, 37 transfer RNA genes, and 8 ribosomal RNA genes in the genome. The maximum-likelihood phylogenetic tree demonstrated that *W. glabra* is closely related to *Leucanthemella linearis*.

Novaseq platform. The results were stored in the FASTQ file format.

Approximately 4.25 Gb of clean data were generated after filtering. The GetOrganelle (Jin et al. 2018) and SOAPdenovo software (Luo et al. 2012) assessed and assembled the paired-end reads. We used OGDRAW program to draw circular chloroplast genome map (Marc et al. 2013). The cp genome sequence of *W. glabra* has been submitted to GenBank (accession number: MW628520).

The cp DNA of *W. glabra* is 151,499 bp long, with an average sequencing depth of 467x. It contains a large single-copy (LSC) region of 83,078 bp and a small single-copy (SSC) region of 18,457 bp, which is separated by a pair of inverted repeats (IR) regions (24,982 bp). The overall GC content of the cp genome is 37.3%. We annotated a total of 131 functional genes, including 86 protein-coding genes, 8 ribosomal RNA (rRNA) genes, and 37 transfer RNA (tRNA) genes. Among them, 15 genes contain only one intron and 2 genes contain two introns. In addition, one ribosomal-protein gene has trans-splicing. Gene duplication was found in the IR regions, including one protein-coding gene, four tRNA genes, and four rRNA genes. Our result is consistent with those obtained from other Asteraceae species (Zhang et al. 2016).

Since reports on the floristic study of this high-altitude plant species are limited, its interspecific relationship with other members of the Asteraceae family is still unclear. A phylogenetic analysis compared the cp genome of *W. glabra* with those from 21 Asteraceae species, including *Chrysanthemum, Artimisia, Crossostephium, Opisthopappus*, and other genera. *Arabidopsis thaliana* was used as an outgroup for the study. The maximum-likelihood phylogenetic tree demonstrated that *W. glabra* is closely related to *Leucanthemella linearis*. 

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likelihood phylogenetic tree shows that *W. glabra* is most closely related to *Leucanthemella linearis* with high bootstrap values. It clusters with *Stilpnolepis centiflora*, *Chrysanthemum*, and *Artimisia*. *Chrysanthemum* and *Artimisia* are grouped together (Figure 1). Our result is consistent with previous studies on the phylogenetic relationship of Asteraceae species (Panero and Crozier 2016; Wang et al. 2020). Our research lays the foundation for the study of genetic diversity and phylogeny of *W. glabra*.

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**Disclosure statement**

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

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**Data availability statement**

The genome sequence data that support the findings of this study are openly available in the GenBank of NCBI at (https://www.ncbi.nlm.nih.gov) under the accession no. MW628520 (https://www.ncbi.nlm.nih.gov/nuccore/MW628520.1/). The associated BioProject, SRA and Bio-Sample number are PRJNA702561 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA702561), SRR14664915 and SAMN19356817 respectively.
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