**MITOGENOME ANNOUNCEMENT**

**The complete chloroplast genome of *Glaux maritima*, a monotypic species**

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**ABSTRACT**

*Glaux maritima* Linnaeus (1753), the monotypic species of the genus *Glaux* in Primulaceae, with unique physiological characteristics—salt gland, is a typical salt-secreting plant. We sequenced and assembled the complete chloroplast genome of *Glaux maritima* with a length of 154,939 bp, consisting of a large single-copy region (LSC) of 84,808 bp, a small single-copy region (SSC) of 18,031 bp, and two inverted repeats (IR) region of 26,050 bp. The chloroplast genome contained 111 genes, including 77 protein-coding genes, 4 rRNA genes, and 30 tRNA genes. The phylogenetic tree exhibited that *Glaux maritima* is nested in the monophyletic clade of *Lysimachia hemsleyana*, *L. congestiflora*.

*Glaux maritima* Linnaeus (1753) is a low, subfleshy, saltmarsh perennial herb with opposite, oval leaves and tiny, white, pink, lavender, or crimson flowers rising from leaf axils, which is the monotypic species of the genus *Glaux* in Primulaceae. This species is widely distributed in the Northern temperate zone, growing in coastal marshes, tidal flats, beaches, also in brackish marshes and alkaline flats inland (Hu and Kelso 1996). *Glaux maritima* is tolerant to high salinity and is therefore considered as an indicator plant in saline alkali soil area (Joanna et al. 2011). It is also a typical salt-secreting plant. After absorbing salt, it is actively excreted to the surface of stem and leaves by salt glands or salt hairs, and then washed off (Rozema et al. 1977). So, it is the dominant plant in improving saline-alkali land. Cattle, sheep and other animals enjoy eating it, which can be used as pasture.

In this study, we sequenced and assembled the complete chloroplast genome of *G. maritima*. Fresh leaves of *G. maritima* were collected from Ali of Tibet (29°41′–35°52′N, 78°24′–86°20′E). A specimen was deposited in the Herbarium of Yunnan Normal University (Kunning, China; Prof. Yonghong Zhang, daphnecl@aliyun.com) under the voucher number HY-25. The modified CTAB method (Porebski 1997) was used to isolate chloroplast genome DNA, which was stored in the Huang’s Lab of Yunnan Normal University. The fragmented genomic DNA was used to construct short-insert libraries for Illumina paired-end (PE) sequencing on the Illumina Hiseq X Ten sequencer. A total of ca. 6.7 million reads generated and were assembled by program NOVOPlasty v2.7.2 using a seed-and-extend algorithm that assembles organelle genome in one circular high quality contig (Dierckxsens et al. 2016). The whole-genome sequence was corrected based on Illumina sequencing data using BWA software (Wang et al. 2018). The raw data has been uploaded to the NCBI Sequence Read Archive (SRA) with accession number SAMN17312054. Geneious V2020.1.1 software (Kearse et al. 2012) was used to annotate the chloroplast genome of *Glaux maritima* using *Lysimachia hemsleyana* as reference. The genes or other feature-encoding regions were identified by BLAT-based homology searches and additionally, by profile HMM searches for protein and rRNA coding genes and two de novo predictors for tRNA genes. Then *Lysimachia congestiflora* is used as a reference for modification and correction. The complete chloroplast genome of *Glaux maritima* is 154,939 bp in length GC content of 36.9% (GenBank Accession No. MW029425), containing a large single-copy (LSC) region of 84,808 bp, a small single-copy (SSC) region of 18,031 bp, and two inverted repeats (IR) region of 26,050 bp. In total, the chloroplast genome contains 111 genes, including 77 protein-coding genes, 30 tRNA genes, and 4 rRNA genes.

In order to explore the phylogenetic relationship, the chloroplast genome sequences of relative 30 species of Primulaceae family in GenBank were aligned using software MAFFT v7.47 (Katoh and Standley 2013). Then IQ_TREE v1.6.10 software was used to construct the maximum likelihood phylogenetic tree with 10,000 replicates (Nguyen et al. 2015). The best-fit model according to Bayesian information criterion (BIC) is TVM + F + R4 (Kalyaanamoorthy et al. 2017). The phylogenetic tree exhibited that *Glaux maritima* is nested in the monophyletic clade of *Lysimachia hemsleyana*, *L. congestiflora*, being consistent with former taxonomic studies of *G. maritima* treated as a species of *Lysimachia* (Hu and Kelso 1996) (Figure 1). Moreover, the topologic structure of phylogenetic tree showed the relationship of other genus of Primulaceae in agreement with previously phylogenetic studies of Primulaceae (Mast et al. 2001).
Disclosure statement
The authors declare that they have no competing interests.

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Data availability statement
The genome sequence data that support the findings of this study are openly available in GenBank of NCBI under the accession no. MW029425. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA692040, SRX9848770, and SAMN17312054, respectively.

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