**MITOGENOME ANNOUNCEMENT**

**The complete chloroplast genome sequence of *Gentiana atropurpurea* and phylogenetic analysis**

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**ABSTRACT**

*Gentiana atropurpurea* T. N. Ho is an annual herb belonging to section Microsperma T.N. Ho series Suborbisepalae Marquand. This species is endemic to China with its distribution limited to the southeast of the QTP. In this study, the complete chloroplast genome sequence of *G. atropurpurea* was characterized from Illumina pair-end sequencing. The chloroplast genome of *G. atropurpurea* was 145,757 bp in length, containing a large single-copy region (LSC) of 78,287 bp, a small single-copy region (SSC) of 16,750 bp, and two inverted repeat (IR) regions of 25,360 bp. The overall GC content is 37.90%, while the corresponding values of the LSC, SSC, and IR regions are 35.8, 31.7, and 43.4%, respectively. The genome contains 132 complete genes, including 86 protein-coding genes (62 protein-coding gene species), 37 rRNA genes (29 rRNA species), and eight tRNA genes. Phylogenetic analysis based on complete chloroplast genomes showed that *G. atropurpurea* and *G. tongolensis* clustered together as sisters to other related species.

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values of the LSC, SSC, and IR regions are 35.8, 31.7, and 43.4%, respectively. The genome contains 132 complete genes, including 86 protein-coding genes (62 protein-coding gene species), 37 tRNA genes (29 tRNA species), and eight rRNA genes (four rRNA species). To further investigate its taxonomic status, a maximum-likelihood (ML) tree was constructed based on complete chloroplast genome sequences using MEGA version 7.0 (Kumar et al. 2016) with 1000 replicates. The program operating parameters were set as follows: a Tamura 3-parameter (T92) nucleotide substitution model with 1000 bootstrap repetitions, accompanied by Gamma distributed with Invariant site (G + I) rates, and partial deletion of gaps/missing data. We used the complete chloroplast genomes sequence of *G. atropurpurea* and 22 other related species to construct phylogenetic tree. The 23 chloroplast genome sequences were aligned with MAFFT (Katoh and Standley 2013), and then the ML tree was constructed (Figure 1). The phylogenetic analysis revealed that *G. atropurpurea* and *Gentiana tongolensis* clustered together as sisters to other related species.

**Disclosure statement**

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

**Data availability statement**

The data that support the findings of this study are available in GenBank at https://www.ncbi.nlm.nih.gov, reference number MT593367.

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