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Complete chloroplast genome of *Tulipa buhseana* (Liliaceae)

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ABSTRACT

The complete chloroplast genome of *Tulipa buhseana* was sequenced and reported here. The circular genome of *T. buhseana* is 152,062 bp in length and contains 133 functional genes consisting of 87 coding sequences, 38 tRNA genes, and 8 rRNA genes. With 1 species from Smilacaceae and 1 species from Alstroemeriaceae as outgroup, phylogenetic relationships of 8 Liliaceae species based on their chloroplast genomes indicated that *T. buhseana* is closest to *T. altaica*.
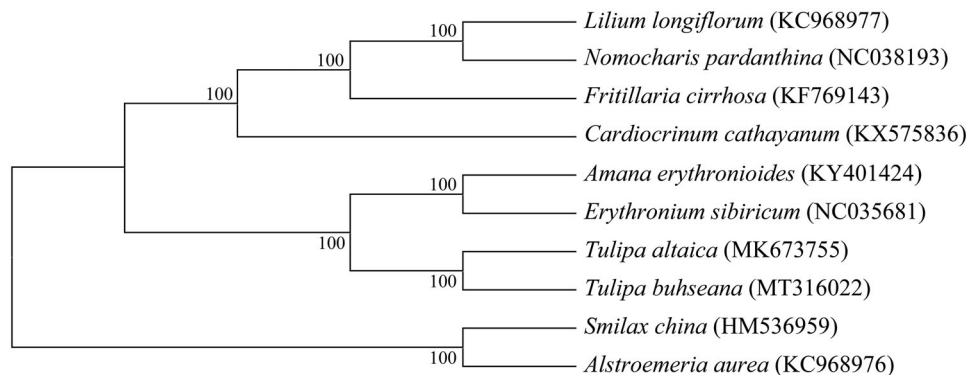
Tulipa L. belongs to the Liliaceae family and includes approximately 139 species in the world (Zhou et al. 2019), which is one of the world's most well-known, beloved, and economically important flowering plants (Li et al. 2017). *Tulipa* L. is widely distributed in Central Asia, the Mediterranean, Europe and North Africa (Xing et al. 2017). Here, we sequenced the complete chloroplast genome of *Tulipa buhseana* to provide more fundamental data to the development of the DNA barcoding system.

In this study, *T. buhseana* were collected from Altay Region, Buerjing County, Xinjiang Province, China (48°41′48″N, 87°02′03″E) in September 2018. The specimen was kept in the Key Laboratory of Landscape Plants Lab, College of Agriculture and Animal Husbandry, Qinghai University, Xining, China (accession number: JXT-2018-YJX016). Genomic DNA was extracted using leaves from the same plant. Genomic sequencing was performed on the Illumina HiSeq Platform (Illumina, San Diego, CA) with a read length of 150 bp. The software SPAdes v.3.14.0 (Bankevich, et al. 2012) was employed to assemble the chloroplast genome. Then, Prodigal v2.6.3 (https://www.github.com/hyattpd/Prodigal), Hmmer v3.1b2 (http://www.hmmer.org/) and Aragorn v1.2.38 (http://130.235.244.92/ARAGORN/) were respectively used to annotate the coding sequences (CDs), transfer RNA (tRNA) genes, and ribosomal RNA (rRNA) genes.

A circularized DNA assembly was 152,062 bp in length. It was harvested and deposited in the GenBank with accession number of MT316022. Totally, 133 functional genes are recognized in this chloroplast genome: 87 CDs, 38 tRNA genes, and 8 rRNA genes. The rRNA genes, tRNA genes, and protein-coding genes account for 6.02%, 28.57%, and 65.41% of all annotated genes, respectively. The GC content of the complete chloroplast genome was 36.61%.

Based on chloroplast genomes assembled here and downloaded from GenBank, phylogenetic relationships of 8 Liliaceae species were resolved by means of neighbor-joining with 1 species from Smilacaceae and 1 species from Alstroemeriaceae as outgroup (Figure 1). After aligned using MAFFT (Katoh and Standley 2013), the neighbor-joining tree

Figure 1. The neighbor-joining tree based on 10 chloroplast genome sequences.

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was built using MEGA7 (Kumar et al. 2016) with bootstrap set to 1000. In the phylogenetic tree, *T. buhseana* and *T. altaica* went to an independent clade with a 100% node support rate.

Disclosure statement

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

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Data availability statement

The data that support the findings of this study are openly available in Genbank at https://www.ncbi.nlm.nih.gov/genbank/, reference number MT316022.

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