Lilium davidii var. unicolor, also called Lanzhou lily (Shang et al. 2014), one important genus in Liliaceae that is originated in China. The bulb of L. davidii var. unicolor is widely used in the food industry. Moreover, it has medicinal value on heart and lung diseases (Li et al. 2014). Most of the studies on L. davidii var. unicolor focused on cultivation and flower chemical component for its ornamental and economic values (Li et al. 2014; Shang et al. 2016). None researches had put the focus on the chloroplast genome of L. davidii var. unicolor. In the present study, we sequenced the complete chloroplast genome of L. davidii var. unicolor and explore its internal relationships within the family Liliaceae.

Plantlets of L. davidii var. unicolor (voucher number: SD_JBZDZ) was obtained from in vitro Shandandan germplasm preserved at the Conversation and Utilization of Regional Biological Resources, Yan’an, China. L. davidii var. unicolor was obtained in tube seedling form and were originally from Bali Town, Qilihe District, Lanzhou, Gansu, China (N35°09′91.84″, E103°83′51.67″).

Approximately 10 mg fresh young leaf tissue was used for DNA extraction through Plant Chloroplast DNA Column Extraction Kit (BNT120406, Baiao Laibo Technology Co., Ltd. Beijing, China). More than 15 μg DNA was used for the SMRTbell sequencing (8 kb-10 kb) and high-throughput sequencing library preparation. Initially, the Illumina sequencing data was assembled usingSOAPdenovo v2.04 (Luo et al. 2012). Then, the sequencing data were subsequently aligned to PacBio RS sequencing data to remove single base and compilation errors using the blasR software (Sergey et al. 2012). After that, the corrected data were assembled using Canu v1.5 (https://canu.es/) (Sergey et al. 2012). The whole chloroplast genome sequence of L. davidii var. unicolor was deposited to NCBI (https://www.ncbi.nlm.nih.gov/genbank/) database with the accession number of MK954110.

The result showed that the L. davidii var. unicolor chloroplast genome size was 152,659 bp, with typical quadripartite structure: one large single copy (LSC, 82,060 bp), one small single copy (SSC, 17603 bp), and two inverted repeats (IRs, 26,498 bp). The overall GC content was 37.02%. After removing the duplicate genes, 78 protein-coding genes, 28 tRNA genes, and 4 rRNA genes remained. Most of the genes did not contain the introns, whereas 19 contained one intron, and four genes (clpP, rps12, rps12-D2, and ycf3) contained two introns. The gene rps12 is a trans-spliced gene with its 5′ end located in the LSC region and the duplicated 3′ end in the IR region.

The phylogenetic tree of L. davidii var. unicolor was constructed using the whole chloroplast genome, in combination with other 22 Lilium species and four outgroup species. The phylogenomic relationship was inferred by the Maximum-Likelihood (ML) method based on the general time-reversible (GTR) + G substitution model in PhyML 3.0 (Larkin et al. 2007; Guindon et al. 2010), with 1000 bootstrap replicates (Letunic and Bork, 2016). The phylogenetic tree showed that L. davidii var. unicolor was related to L. callosum, L. amabile, L. lancifolium, L. sp., L. tsingtauense, L. hansonii, and L. cernuum (Figure 1).
**Disclosure statement**

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

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**Figure 1.** A phylogenetic tree of the *Lilium* species based on the completed chloroplast genomes of 23 species and 4 outgroup species. We downloaded all the other sequences from NCBI GenBank.