PLASTID GENOME SEQUENCING OF *TULIPA* SPECIES FROM KAZAKHSTAN: INSIGHTS INTO GENOMIC STRUCTURE, REPEATS, NUCLEOTIDE DIVERSITY, AND PHYLOGENETIC RELATIONSHIPS

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We sequenced and analyzed the plastid genomes of *Tulipa* species using the Illumina NovaSeq 6000 platform. The plastomes exhibited a typical quadripartite structure with LSC, SSC, and IR regions, displaying a GC content ranging from 36.63% to 36.69%. Gene annotation revealed 136 genes across all species, including 80 protein-coding, 30 tRNA, and 4 rRNA genes. Repeat sequence analysis identified simple sequence repeats, predominantly mononucleotide repeats, and long repeat types, with palindromic repeats being the most abundant. Nucleotide diversity analysis indicated protein-coding genes with high variability. Phylogenetic analysis based on nucleotide sequences of complete plastid genomes grouped the species into three main clades corresponding to *Tulipa* subgenera. This study provides insights into the plastid genome structure, repeat sequences, and phylogenetic relationships in *Tulipa*, highlighting the potential of the *ycf1* gene as a DNA barcode for *Tulipa* species.

This research was funded by the Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan (Grant No. AP14870612).