



MORPHOLOGICAL CHARACTERIZATION AND PHYLOGENETIC STRUCTURE OF *TULIPA GREIGII* L. IN THE TURKESTAN REGION, KAZAKHSTAN

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SUMMARY

Kazakhstan has become widely regarded as one of the primary centers of origin and genetic diversity of wild tulips (*Tulipa*). Among them, *Tulipa greigii* Regel is a prominent species distributed across Central Asia and protected in Kazakhstan due to its slow development and threats from illegal harvesting. This study investigated the plant density, morphological characteristics, and phylogenetic structure of *T. greigii* L. populations in the Shubaykyzyl area, Turkestan Region, Kazakhstan. Plant density assessment used the quadrat method, while the conduct of morphological analysis focused on diagnostic traits observed in natural populations. Phylogenetic relationships' evaluation employed ITS, matK, rbcL, and psbA sequences. The density varied from nine to 36 plants (per square meter) across different sites. Morphological observations showed the species has the feature of a single erect stem, 35–50 cm tall, and large solitary red flowers 10–12 cm in diameter, with a black or yellow basal spot. Phylogenetic analysis of ITS sequences revealed that *T. greigii* L. shares the highest genetic similarity with *T. patens*, *T. alberti*, and *T. kaufmanniana*, forming a distinct clade. These results indicate close regional genetic relationships among Central Asian tulip species and suggest a relatively recent divergence of local wild populations.

Keywords: *Tulipa greigii* L., genetic diversity, morphology, population density, phylogenetic analysis, ITS, chloroplast DNA

Key findings: *T. greigii* L. populations exhibited variable densities while retaining key diagnostic traits. Phylogenetic analysis showed the highest genetic similarity and clustered the species *T. greigii* L. with three closely related species (*T. patens*, *T. alberti* L., and *T. kaufmanniana*), exhibiting recent regional divergence in Central Asia.

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INTRODUCTION

The *Tulipa* is one of the largest genera in the family *Liliaceae*, showing a broader geographic distribution across the Middle East, Southern Europe, Northern Africa, and Central Asia. Several species of *Tulipa* are dominant in Central Asia, Iran, and Afghanistan, and most of them are endemic, revealing it as one of the centers of speciation for the genus (Tojibaev *et al.*, 2022). In Central Asia, the Tian Shan and Pamir-Alay mountains were the widely recognized main centers of *Tulipa* species diversity (Zonneveld, 2009; Wilson *et al.*, 2021; Asatulloev *et al.*, 2023). Tulips typically grow well in areas with hot, dry summers; relatively cold winters; and low rainfall in spring and autumn. Similarly, Kazakhstan has become recognized as one of the key centers of origin and diversity of wild tulips (Zonneveld and De-Groot, 2012). The genus *Tulipa* shows characteristics of significant taxonomic diversity, with 90 to 120 species worldwide (Eker *et al.*, 2014, 2024; Li *et al.*, 2021; Beshko *et al.*, 2023; Dekhkonov *et al.*, 2023).

Similarly, the tulip's composition varied from 32 to 42 species, depending on the source in Kazakhstan. As a result of the species diversity, field observations, and analysis of an extensive herbarium, this confirmed the presence of 42 *Tulipa* taxa in Kazakhstan, of which 13 are endemic, revealing the highest adaptability to diverse ecological conditions (Kubentayev *et al.*, 2024). The country is considerably the home of various endemic and rare species that can play a vital role in preserving biodiversity for future breeding programs. These factors highlighted the importance of tulips not only as elements of flora but also as objects for future research and nature conservation (Akhmetova and Dunets, 2025).

T. greigii L. has the quality of the highest morphological variability, especially in flower color, which varies from red to orange, yellow, and cream, often with a contrasting spot at the base of the perianth (Tojibaev *et al.*, 2022). The *T. greigii* L. reproduction can occur under natural conditions mainly by seed, while vegetative reproduction is extremely

rare, which may limit the rate of natural population renewal. The said species has a wide ecological range and grows on foothill plains, in foothills, and on mountain slopes with clay, shallow, and stony-gravelly substrates at altitudes of up to 2,400 meters above sea level (Dekhkonov *et al.*, 2021). Flowering occurs from early spring to early summer, and fruiting happens in early to mid-summer. The ecological plasticity allows *T. greigii* L. to exist in arid and semi-arid landscapes. In Kazakhstan, the species *T. greigii* L. range extends from the northern deserts (around Kyzylorda) through the mountain systems and foothills of the Tien Shan to the Kurdai Pass, covering the Zhambyl, Turkestan, and Kyzylorda regions (Tojibaev *et al.*, 2022; Tussipkan *et al.*, 2024). The wide but uneven distribution of the species, in integration with enhanced anthropogenic pressure on natural ecosystems, highlighted the importance of comprehensive studies in investigating morphological diversity, population structure, adaptive potential, and effective conservation measures of *T. greigii* L.

In the present era, molecular genetics and phylogenetic approaches have become an essential component of comprehensive studies of the genus *Tulipa*, especially in studying natural and ornamental diversity, as well as the use of wild species for breeding purposes (Haerinasab *et al.*, 2021). The application of nuclear and chloroplast DNA markers allows for a more accurate assessment of the genetic diversity in populations and the reconstruction of evolutionary relationships among the closely related taxa (Zhou *et al.*, 2019; Ju *et al.*, 2020a, 2020b, and 2021; Yuan *et al.*, 2022; and Xing *et al.*, 2023). Molecular studies using EST-SSR (expressed sequence tag-simple sequence repeat) and other DNA markers have shown that the *T. greigii* L. populations attained characterization by relatively high levels of intrapopulation genetic variability. This reflected the species' considerable adaptive potential and confirmed its role as a valuable genetic resource for *Tulipa* breeding and biodiversity conservation (Li *et al.*, 2021; Yermagambetova *et al.*, 2024).

The comparative analysis of complete chloroplast genomes of representatives of the genus *Tulipa*, including the species *T. greigii* L., also revealed additional data. These studies enunciated a conserved chloroplast genome structure and identified informative regions suitable for phylogenetic and taxonomic studies (Abduraimov *et al.*, 2020; Tussipkan *et al.*, 2024; Yermagambetova *et al.*, 2024; Almerekova *et al.*, 2024a; and Sutula *et al.*, 2024). Therefore, the integrated use of morphological and molecular data allows for complete characterization of the intraspecific structure of the species *T. greigii* L. and classification of its position within the phylogenetic system of the genus.

The presented study focuses on the assessment of the natural population of species *T. greigii* L. in the Shubaykzyl, Turkestan Region, Kazakhstan based on the plant density, morphological characterization, and phylogenetic structure. The research sought to identify the distribution patterns and phylogenetic affiliation of the species, as well as to justify measures for its monitoring and habitat conservation.

MATERIALS AND METHODS

Population density and morphological description

The study conducted on the natural population of *T. greigii* L. was within the Shubaykzyl, Turkestan Region, Kazakhstan (42°35'01"N 70°19'43"E) during the active flowering period in May 2023 and 2024. It ensured the highest visibility of the plants. The population size estimation used the quadrat method, a standard approach widely applied for assessing rare and seasonal plant species. The plant density, as estimated, counted individuals within randomly placed square quadrats (1 m × 1 m). Plant density calculation was the total number of individuals of species *T. greigii* L. divided by the total number of quadrats surveyed.

$$\text{Plant density (D): } D = N / S$$

Where N is the total number of plants in all quadrants, and S is the total area of the quadrants (m²).

The collection of plant materials of *T. greigii* L. came from Shubaykzyl, Turkestan Region, Kazakhstan. Tulip plant materials entailed sampling from generative individuals without harming natural populations, with permission from the Committee of Forestry and Wildlife of the Ministry of Ecology, Geology, and Natural Resources, Kazakhstan. Morphological description of various characteristics (leaf shape and size, flower color and size, and fruit structure) proceeded in accordance with generally accepted methods of floristic research and plant morphology standards (Dekhkonov *et al.*, 2022). Morphological methods allow for identifying the patterns in the structure of plant organs and assessing the morphological diversity of species *T. greigii* L. populations under natural conditions.

DNA extraction and PCR amplification

DNA extraction continued from *T. greigii* L. samples using the commercial Monarch® Spin gDNA Extraction Kit (New England Biolabs, Ipswich, USA) in accordance with the manufacturer's instructions, with amplification carried out using the matK, rbcL, and psbA markers. The preparation of a 25 µl reaction mixture has the following composition: 2.5 µl of 10× Taq polymerase buffer (final concentration 1×), 0.5 µl dNTP (final concentration 0.2 mM of each nucleotide), 0.2 µM of forward and reverse primers, 0.2 µl Taq DNA polymerase, and approximately 50 ng of DNA template. The performance of PCR ensued on a SimpliAmp™ thermal cycler (Thermo Fisher Scientific, Waltham, USA) using the following program: predenaturation at 95 °C for 3 min, followed by 35 cycles comprising denaturation at 95 °C for 30 s, annealing at an individual temperature for each marker (ITS, matK, rbcL, psbA) for 30 s (Table 1), elongation at 72 °C for 1 min, and final elongation at 72 °C for 5 min (Sutula *et al.*, 2024).

Table 1. Characterization of the molecular markers.

Primer Name	Barcoding Locus	Primer Sequence (5'-3')	Annealing temperature (°C)
ITS4	ITS1 and ITS2	TCCTCCGCTTATTGATATGC	55
ITS5	ITS1 and ITS2	GGAAGTAAAAGTCGTAACAAG	55
3F_KIMf	matK	CGTACAGTACTTTTGTGTTTACGAG	50
1R_KIMr	matK	ACCCCATTCATCTGGAAATCCTTGGTTC	50
rbcLa_F	rbcL	ATGTCACCAACAAACAGAGACTAAAGC	58
rbcLa_R	rbcL	GTAAAATCAAGTCCACCRG	58
psbA3f	psbA	GTTATGCATGGTGGATTACAATCC	53
trnHf_05	psbA	CGCGCATGGTGGATTACAATCC	53

Library preparation, sequencing, and data processing

Libraries' preparation for sequencing used the SQK-RBK114.96 kit (Oxford Nanopore Technologies, Oxford, UK) in accordance with the manufacturer's protocol. Sequencing took place on the PromethION platform (Oxford Nanopore Technologies, Oxford, UK) using MinKNOW software (v25.05.14). The obtained reads underwent filtering for quality using the NanoFilt program with a value of $Q > 15$, and a consensus sequence was the output.

Phylogenetic analysis

The construction of a phylogenetic tree in Geneious Prime (v2025.2.1) used the Neighbor-Joining method, with a bootstrap value of 500, sequences of 10 closely related species of the genus *Tulipa* obtained using BLAST analysis. Multiple alignment performance of nucleotide sequences engaged the Clustal W algorithm. *Tulipa sylvestris*, a species predominantly distributed in Europe, served as an outgroup, which allowed for the correct determination of the root position of the tree and the evaluation of the phylogenetic relationships among the studied taxa.

RESULTS

Population density of *T. greigii* L.

The survey results enunciated that the plant density of the species *T. greigii* L. significantly varied in different locations of the population, reflecting the influence of local microclimatic conditions and relief. Plant density data for the

area of the surveyed plots made it possible to estimate population sizes, which ranged from nine to 36 plants at different places in Shubaykyzyl (Table 2). The results indicated a fragmented distribution of population, with individual clusters of *T. greigii* L. plants differing in density and size. Such variability in plant density of the species *T. greigii* L. under arid and semi-arid conditions of the Turkestan region can be because of the combined effects of natural factors and anthropogenic impacts (Zhumanova *et al.*, 2021).

The results explored that *T. greigii* L. population has an uneven distribution with often fragmentation. However, the highest plant density was dominant in protected areas with minimal human impact, while the lowest density resulted in open, arid areas, revealing the vulnerability of this population and the need for conservation measures. Quantitative assessment of plant density is an important tool for evaluating the population status and planning measures for their conservation and sustainable use. The results emphasized the importance of regular monitoring and the development of conservation strategies for species *T. greigii* L. under natural arid and semi-arid ecosystems.

Morphological characterization

The plant population of *T. greigii* L. reveals characteristics of an oblong to oval bulb, approximately 2–4 cm in diameter, covered with leathery and brownish-red scales. The stem was typically solitary, erect, and slightly pubescent, reaching a height of about 35–50 cm with a fluffy peduncle (Table 3). The leaves were usually three to five in number and observed with dark purple streaks. Flowers

Table 2. *T. greigii* L. population size density (per square meter) in Shubaykzyyl Region during 2023 and 2024.

Number of Sites	Quadrat 1	Quadrat 2	Quadrat 3	Quadrat 4	Quadrat 5	Quadrat 6	Quadrat 7	Quadrat 8	Quadrat 9	Quadrat 10	Total number of individual plants (N)	Total number of area (S)	Density (D)
2023													
Site 1	27	25	27	24	25	18	20	27	28	24	245	10	24.50
Site 2	25	19	26	18	28	35	25	31	31	25	263	10	26.30
Site 3	30	20	27	28	34	25	32	26	36	28	286	10	28.60
Site 4	20	18	15	21	19	14	10	15	14	21	167	10	16.70
Site 5	18	16	20	25	18	28	15	16	13	23	192	10	19.20
2024													
Site 1	9	16	17	21	11	31	25	25	24	35	214	10	21.40
Site 2	35	28	35	31	30	19	24	21	15	29	267	10	26.70
Site 3	21	25	25	24	19	25	18	20	18	18	213	10	21.30
Site 4	20	18	19	21	20	19	24	21	15	22	199	10	19.90
Site 5	20	19	25	25	18	25	18	19	22	20	211	10	21.10

Table 3. Morphological characteristics of *T. greigii* L.

Traits	Description
Bulb shape	Oblong to ovate, 2–4 cm in diameter. Covered with leathery reddish-brown scales.
Stems	Peduncle fluffy, 35–50 cm tall.
Leaves	3–5 per plant (occasionally 3–4), 2–5 cm wide. Leaves with dark purple streaks.
Flowers	Cup-shaped or goblet-shaped, 10–12 cm in diameter. Petal color is red, the outer tepals are pointed at a fluffy tip. The bottom of forms is black or yellow. Filaments and anthers are yellow, blackish, or maroon.
Fruits	The fruit is up to 8 cm long and 2.5 cm wide. The number of normally developed seeds is up to 313. Reproduction is seed, very rarely vegetative.
Flowering period	April – early June. Varies depending on altitude and microclimatic conditions.

were solitary, cup- and goblet-shaped, with a diameter of 10–12 cm. Petal color was red, with the outer petals pointed at the fluffy tip. The bottom of the forms was black or yellow. Filaments and anthers were yellow, blackish, and maroon. The fruit was 8 cm long and 2.5 cm wide. The number of normally developed seeds ranged from 1 to 313. Reproduction takes place through seeds,

which have the common dispersion from wind and animals and are very rarely vegetative. After flowering, the aboveground parts of the plant wither, and the plant survives the winter as a bulb. Flowering occurs in April to early June, depending on the altitude and local microclimatic conditions.

The *T. greigii* L. population in Shubaykzyl, Turkestan Region, may exhibit local morphological variations, such as reduced plant height, altered petal coloration, and smaller flower diameter, which have the likely influence of arid environmental conditions. Given its restricted distribution range and anthropogenic impacts, including land cultivation, flower collection, and trampling, the population of *T. greigii* L. often showed fragmentation, occurring in low numbers.

Phylogenetic analysis

According to the phylogenetic analysis, the species *T. greigii* L. samples collected in the study area formed several distinct clades depending on the markers used. The marker-dependent clustering revealed considerable differences in phylogenetic resolution and evolutionary signals among the analyzed loci. Based on ITS sequences, the Kazakhstani samples appeared to be closely associated with *T. greigii* L. (GenBank accession OP279724.1) and also belonged to a separate clade with three other species. These are *T. patens*, *T. alberti*, and *T. kaufmanniana*, which are also widespread in Central Asia, detailing their regional genetic proximity and possible recent divergence within local wild populations (Figure 1).

According to the chloroplast genes *matK* and *rbcl*, the studied samples from Kazakhstan formed a well-supported clade with the species *T. greigii* L. and *T. patens* (Figure 2). Both these species belong to the Central Asian flora, found in Kazakhstan, which revealed their geographical and evolutionary relationship with the studied samples. This grouping exhibited that this taxon belongs to the same phylogenetic line that formed within the region.

As for the other *Tulipa* species, based on analysis of both genes, these species formed different, distinct clades, reflecting their genetic divergence and species isolation within the genus *Tulipa*. In contrast, analysis of the *psbA* region showed the species *T. greigii* L. created a separate branch, closer to *T. kaufmanniana* (Figure 3). This arrangement revealed the chloroplast similarity, which may

reflect both a common origin and hybridization events among the *Tulipa* lines of Central Asia.

Overall, the results exhibited that the wild species *T. greigii* L. population in Shubaykzyl, Turkestan Region, Kazakhstan, has the features of the integration of regionally conservative chloroplast haplotypes, reflecting a complex evolutionary history governed by hybridization and geographical isolation.

DISCUSSION

The potential study provides a comprehensive understanding of the plant population density, morphological characterization, and phylogenetic structure of *T. greigii* L. in Shubaykzyl, Turkestan Region, Kazakhstan. The survey results showed significant variability in plant density, which may be ascribable to microclimatic conditions and anthropogenic impacts. The highest plant density was evident on slopes and in sheltered areas, while open and anthropogenically impacted areas had the characterization of lower density. Population size estimates indicated a fragmented distribution (ranging from nine to 36 plants in the surveyed 1 m² area), revealing population vulnerability and an urgent need for protection and preservation (Dekhkonov *et al.*, 2021).

Past studies carried out in 2022 also demonstrated that during the spring plowing period, the natural habitats of the species *T. greigii* L. received significant disturbances because of field practices. In response to this impact, governmental monitoring and protective measures began operation in 2023 to prevent further habitat degradation (Akhmetova and Dunets, 2025). By 2024, the conservation efforts had been firm through the implementation of additional monitoring programs and ecological stabilization measures aimed at preserving the remaining populations of wild species *T. greigii* L. and improving habitat conditions.

The morphological features of the studied species *T. greigii* L. generally corresponded to the previously described diagnostic features of this taxon. A comparative study of seed morphology has



Figure 1. Phylogenetic tree based on the ITS gene sequences in the *Tulipa* species.

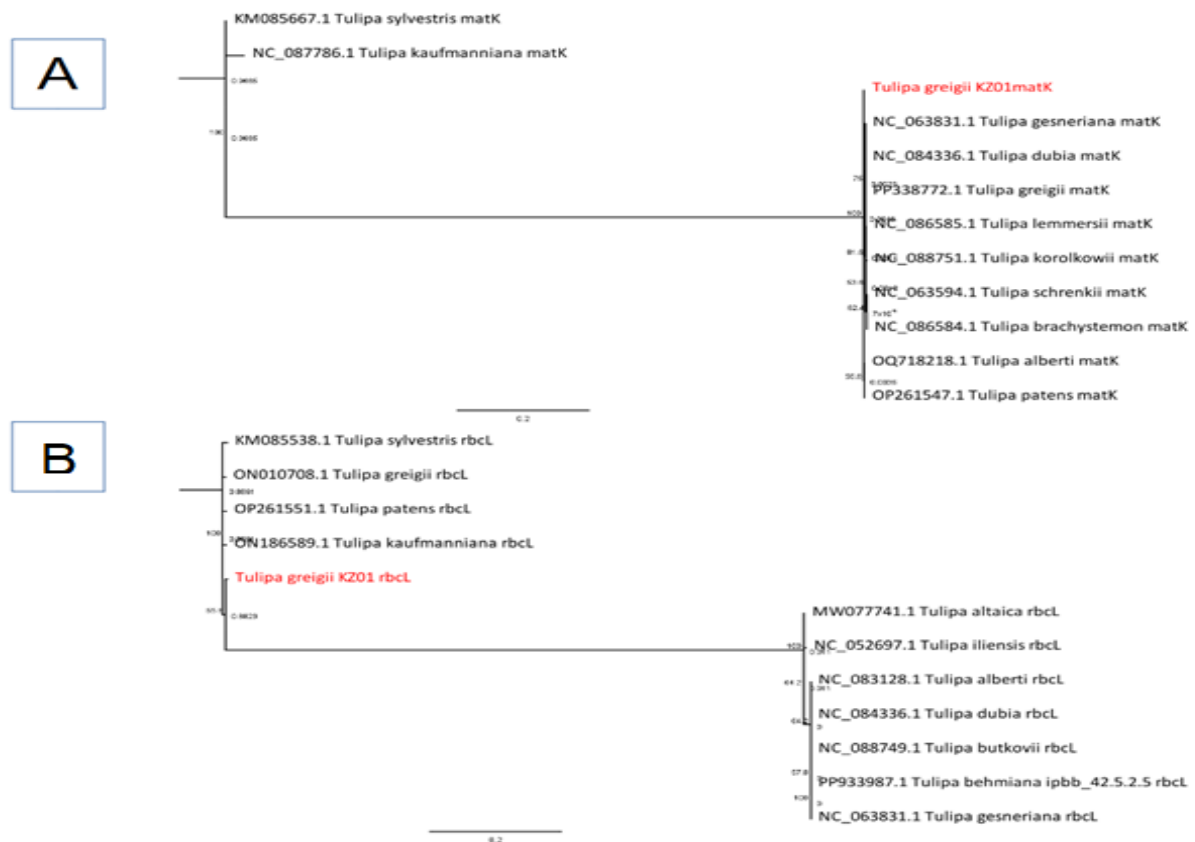


Figure 2. Phylogenetic trees based on chloroplast gene sequences: A) *matK*, and B) *rbcL* of the *Tulipa* species.

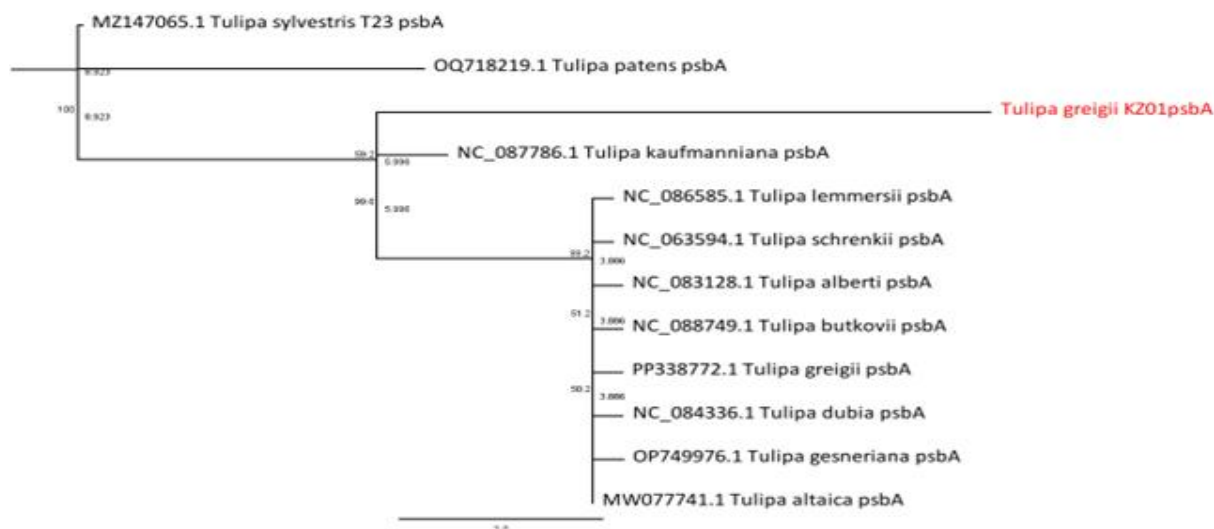


Figure 3. Phylogenetic tree based on the *psbA* gene sequences of *Tulipa* species.

revealed a set of diagnostic features for specifying species affiliation. However, no universal seed marker for all species in the genus has succeeded in its identification, underscoring the urgent need for an integrative approach that combines morphological and molecular data (Dekhkono^v *et al.*, 2022).

Phylogenetic analyses based on the nuclear marker ITS and chloroplast markers (*matK*, *rbcl*, *psbA*, *trnL-trnF*) revealed well-supported clades reflecting species differences and regional genetic structure (Hajdari *et al.*, 2021; Li *et al.*, 2021; Sutula *et al.*, 2024). The Kazakhstani samples proved closely associated with the species *T. greigii* L., *T. patens*, *T. alberti*, and *T. kaufmanniana*, indicating their regional genetic proximity and possible recent divergence. Chloroplast markers confirmed the conservatism of Central Asian lines, while *psbA* exhibited the proximity of Kazakhstani samples to the species *T. kaufmanniana*, which could indicate the chloroplast introgression or a common origin (Tussipkan *et al.*, 2024; Hajdari *et al.*, 2021).

The analysis of complete plastid genomes from several *Tulipa* species in Kazakhstan revealed the highest structural conservatism, with hypervariable regions (*ycf1*, *petD*, and *ndhH*) suitable for developing molecular markers. Phylogenetic analysis of the complete plastid genome confirmed three

main clades corresponding to the subgenera *Tulipa*, *Eriostemon*, and *Orithyia*, expressing the complex intrasubgeneric relationships (Haerinasab *et al.*, 2021). Likewise, this details evolutionary relationships among the *Tulipa* species, such as *T. sylvestris*, *T. iliensis*, *T. thianschanica*, *T. altaica*, *T. sinkiangensis*, *T. buhseana*, *T. biebersteiniana*, *T. patens*, *T. scytica*, and *T. riparia*, in other studies (Ju *et al.*, 2020a, 2020b, 2021; Li *et al.*, 2021; Yuan *et al.*, 2022; Xing *et al.*, 2023; Sarsen *et al.*, 2023).

The genetic diversity of the species *T. greigii* L., assessed using SSR and EST-SSR markers, revealed the highest intrapopulation variability (75%–77%) and three genetic clusters (Yermagambetova *et al.*, 2024; Almerekova *et al.*, 2024b). It also highlighted the importance of the most diverse populations for preserving the genetic potential of the said species.

CONCLUSIONS

The study based on the wild population of the species *T. greigii* L. in the Shubaykyzyl, Turkestan Region, Kazakhstan, showed the said species with characteristics of fragmentation and uneven distribution due to a combination of natural factors and

anthropogenic impacts. Plant density varied among the studied sites and was relatively higher in the protected habitats, revealing the highest sensitivity of the population to environmental pressure. The morphological characteristics of the *T. greigii* L. population generally correspond to the species' diagnosis, but local adaptive variations associated with arid conditions have been notable. Phylogenetic structure analysis confirmed the studied samples belong to the species *T. greigii* L. and are in a close association with the Central Asian group of species. These include *T. patens*, *T. alberti*, and *T. kaufmanniana*, reflecting a regionally determined evolutionary history. The results disclosed the ecological specialization and vulnerability of *T. greigii* L. in the arid ecosystems of Southern Kazakhstan and underscored the urgent need to monitor its population and preserve key habitats.

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