

EVALUATION OF SALT STRESS RESISTANCE IN DIPLOID WHEAT SPECIES

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The National Gene Bank of the Genetic Resources Institute of Azerbaijan houses over 2,000 wheat accessions, vital for breeding plants resilient to environmental stresses. This study focuses on comparing the salinity stress resistance of three diploid wheat species: *Triticum monococcum* L., *Triticum boeoticum* (L.) Boiss, and *Triticum urartu* Thum. ex Gandil., comprising 170 accessions from the ICARDA gene bank. Salinity stress resistance was assessed according to the capacity of the genotypes to exclude Na⁺ ions from leaves. A wide variation was observed among accessions for stress response, allowing for classification them into resistant, moderately resistant, and susceptible groups within each species. Analysis revealed differing resistance percentages among species. *T. boeoticum* had 61% resistant, 20.8% moderately resistant, and 18.2% susceptible accessions. *T. monococcum* showed 40%, 33.3%, 26.7%, and *T. urartu* had 23%, 50.6%, 26.4% respectively. Notably, *T. boeoticum* exhibited greater resistance than *T. monococcum* and *T. urartu*, attributed to its wild-growing nature and distinct biomorphological, biochemical, and molecular features. Salt-tolerant accessions are recommended for breeding programs and stored in both the National Gene Bank of Azerbaijan and the ICARDA Gene Bank. These findings highlight the potential of

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utilizing salt-tolerant accessions, particularly *Triticum boeoticum* genotypes, in targeted breeding programs to enhance wheat's resilience to salinity stress.

Keywords: salinity stress, tolerance, diploid wheat, sodium exclusion

INTRODUCTION

Over 800 million hectares of global land face the impacts of salinity, which represents 6% of the total landmass and 20% of the land used for cultivation (MUNNS and TESTER, 2008; SANDHU *et al.*, 2020; ZHANG *et al.*, 2021). Predictions warn of a potentially drastic rise in salinized arable land, with estimates suggesting nearly half of all arable land could be impacted by 2050 (LIU *et al.*, 2020; CHAURASIA *et al.*, 2022). This poses a substantial threat to global food security in light of our growing population. The increase in saline land is anticipated due to the use of high-salt irrigation water, a result of insufficient rainfall and inadequate agricultural practices (LUO *et al.*, 2017; ZHANG *et al.*, 2021; LIU *et al.*, 2020). Arid and semi-arid regions are particularly susceptible to salinization due to these factors (KASHYAP *et al.*, 2017; JHA *et al.*, 2019).

It is widely recognized that soil salinity leads to disruptions in mineral uptake and plant nutrition (BEHDAD *et al.*, 2021), with the initial impact of salinity manifesting as a decrease in the ability to absorb water in the root zone (ZHAO *et al.*, 2020).

Salinity tolerance is a complex trait, encompassing a range of physiological and genetic components, each with varying roles and contributions to total tolerance, which can differ among species and at different stages of plant development (ASHRAF and ASHRAF, 2016; DAOUD *et al.*, 2018; ZHANG *et al.*, 2019; JHA *et al.*, 2019). Several physiological traits have been consistently identified as valuable indicators for wheat breeders aiming to enhance salinity stress tolerance. These include tissue Na^+ concentration, the ability of plants to preferentially uptake K^+ over Na^+ to achieve a higher K^+/Na^+ ratio (MUNNS *et al.*, 2006; ZOUBEIR *et al.*, 2022). Many researchers have also pointed out that plants have evolved various strategies to cope with salt stress, such as osmotic tolerance, Na^+ exclusion, and tissue tolerance (RAZA, 2020; CHAVARRIA *et al.*, 2020). Approximately 98% of the Na^+ taken up by roots is actively extruded back into the rhizosphere via several processes (ZHAO *et al.*, 2020).

Numerous studies have focused on identifying salt-tolerant wheat accessions based on Na^+ content and the underlying genes involved in this mechanism. FENG *et al.* (2018) assessed 30 morphological and physiological traits in both wild emmer and durum wheat accessions, uncovering notable variations in salt tolerance index among studied genotypes, which showed a correlation with both shoot K^+/Na^+ ratio and Na^+ concentration (FENG *et al.*, 2018). Munns and colleagues observed that a durum wheat variety named Line 149 possesses the capacity to extract salt from its roots (MUNNS *et al.*, 2006). In their investigation of salt tolerance across numerous durum wheat accessions, the researchers noted that the Line 149 cultivar exhibited greater tolerance compared to others and had low levels of Na^+ ions in its leaves, similar to common wheat.

Sodium ions are the primary substances responsible for salinity effects, impacting the yield potential of wheat. Therefore, plants employ a series of mechanisms, including genetic pathways, to mitigate the negative effects of Na^+ (CHAVARRIA *et al.*, 2020). SHARMA *et al.* (2020) identified and characterized four Na^+ sequestration genes in wheat, while JAMES *et al.*

(2023) demonstrated that the introduction of the *Nax* gene into bread wheat varieties resulted in decreased leaf Na^+ levels, leading to 10%–20% higher yields in field conditions (SHARMA *et al.*, 2020; JAMES *et al.*, 2023).

The National Gene Bank of the Genetic Resources Institute of Azerbaijan currently houses over 2,000 wheat accessions. These accessions constitute a crucial genetic resource that can be utilized in breeding programs to enhance the available genetic diversity for adaptation to various environmental conditions and to enhance crop quality.

Different cultivated species and plant varieties vary in their sensitivity to abiotic stress (MAMMADOVA *et al.*, 2015). Developing plants that are resistant to abiotic stresses necessitates a thorough understanding of the source materials and their intentional integration into breeding programs. Wild relatives of wheat contain a wealth of genetic resources for stress resistance, including genes from halophytes known for salt tolerance (ZENG *et al.*, 2023). From this perspective, studying the salt tolerance of wheat collections, which include wild relatives, and identifying new sources of resistant genes is of utmost importance.

The primary objective of this study was to comparatively assess the level of resistance to salinity stress among three diploid wheat species.

MATERIALS AND METHODS

We used 170 accessions of three species of diploid wheat (*Triticum monococcum* L., *Triticum boeoticum* (L.) Boiss, and *Triticum urartu* Thum. ex Gandil.), which were collected from various countries worldwide and stored at the ICARDA gene bank. These accessions were brought to Azerbaijan for our study, with some of them being propagated, while the majority was included into the National Gene Bank.

The diploid wheat genotypes under investigation were analyzed phenotypically for their capacity to exclude Na^+ ions from the leaves. To achieve this, the seeds underwent sterilization with a 1% hypochlorite solution for 15 minutes and were then germinated in Petri dishes for 3 days. The germinated seeds were subsequently transferred to hydroponic systems with 5-fold replication (Fig. 1). To induce stress, 75 mM NaCl was added to the irrigation solution twice a day, starting 10 days after germination. After 20 days, leaf samples were collected and the levels of Na^+ and K^+ were measured (MUNNS and JAMES, 2003).



Fig.1. Hydroponic systems used in the study

RESULTS AND DISCUSSION

Creating new salt-tolerant wheat varieties through wheat breeding methods is essential to tackle this challenge, ensuring the sustainability and productivity of wheat production systems under current climate conditions (KOTULA et al., 2024). However, advancements in breeding for wheat salt tolerance are hindered by the limited genetic diversity in existing germplasm and the absence of precise indicators for physiological and agronomic traits associated with salt stress (MIRANSARI and SMITH, 2019).

In this study, we evaluated the salt tolerance of diploid wheat germplasm by analyzing the accumulation of Na⁺ and K⁺ ions in the leaves. The findings are presented separately for each species.

Salt tolerance in T. monococcum genotypes.

Among the 31 *T. monococcum* accessions examined, 11 originated from Turkey, 5 from Bulgaria, 2 from Italy, 3 from Albania, 1 from Romania, 1 from Serbia, 1 from Morocco, 1 from Greece, and 4 from Georgia. The samples were cultivated in a hydroponic system and incrementally exposed to NaCl salt stress until reaching a final concentration of 75 mM. Subsequently, the levels of Na⁺ and K⁺ ions accumulated in the leaves were quantified.

The salt tolerance of the accessions was evaluated by comparing them with known salinity-resistant (*T. monococcum* CV 68-101, Line 149 cultivar) and salinity-sensitive (Tamoroi cultivar) accessions.

In the leaves of the *T. monococcum* C68-101, used as a control, the accumulated amount of Na⁺ ions was 31 mM, with an average value of 195 mM for K⁺ ions. Similar results were observed in the durum wheat variety Line 149, where the accumulated Na⁺ ions measured 40 mM and K⁺ ions measured 216 mM. In contrast, the durum wheat variety Tamoroi, included as a salinity-sensitive genotype, showed higher levels of accumulated Na⁺ ions at an average of 154 mM, with K⁺ ions at 140 mM.

From the data presented in Table 1, it is evident that the Na⁺ ion levels in the leaves of the *T. monococcum* accessions ranged from 11.5 mM to 175.6 mM.

It is well recognized that an elevated Na⁺ content can have adverse effects on cell metabolism. Ideally, this should be kept at a low level, or, alternatively, balanced by a high cytosolic K⁺ retention capacity (WU et al., 2018; RUBIO et al., 2020).

Based on their Na⁺ ion removal capability, the studied samples can be classified into 3 groups. The first group consisted of 12 accessions from various origins, where the Na⁺ ion accumulation in the leaves was less than 40 mM. In other words, these accessions expelled more Na⁺ ions than the salt-tolerant Line 149 variety. These accessions in the group did not share a common geographical range, representing nearly all regions. Among them, 1 genotype was from Morocco, 3 from Albania, 1 from Greece, 3 from Turkey, and 3 from Georgia. K⁺ ions are smaller than Na⁺ ions and have greater absorption potential. It is noteworthy that in the leaves of these 12 selected accessions, there was no significant difference in the amount of K⁺ ions; their concentration ranged from 198 to 254 mM, with the K⁺/Na⁺ ratio varying from 5.2 to 21.8.

The resistance of samples to stress determines their ability to maintain normal metabolic levels across a wider range of unfavorable conditions and a higher rate of developing

protective metabolic changes. Resistant plants, compared to less stable ones, completely restructure their essential functions towards adapting to adverse environmental conditions.

Table 1. The amount of Na^+ and K^+ ions in the leaves of *T. monococcum* accessions

№	Catalog number	Species	Na^+ (mM)	K^+ (mM)	K^+/Na^+
1	44852	<i>T. monococcum</i>	75	168,7	2,2
2	44913	<i>T. monococcum</i>	49	0,17	0,0
3	44914	<i>T. monococcum</i>	89	197	2,2
4	44915	<i>T. monococcum</i>	54	206,3	3,8
5	44916	<i>T. monococcum</i>	50	213,4	4,3
6	44918	<i>T. monococcum</i>	43	254,2	5,9
7	44931	<i>T. monococcum</i>	44	295,9	6,7
8	44932	<i>T. monococcum</i>	46	238,1	5,2
9	45085	<i>T. monococcum</i>	130	198,8	1,5
10	45086	<i>T. monococcum</i>	63	232,4	3,7
11	45092	<i>T. monococcum</i>	16	245,3	15,1
12	45093	<i>T. monococcum</i>	65	200,7	3,1
13	45110	<i>T. monococcum</i>	38	253,5	6,7
14	45231	<i>T. monococcum</i>	28	245,5	8,9
15	45232	<i>T. monococcum</i>	39	234,2	6,0
16	45234	<i>T. monococcum</i>	26	246,8	9,4
17	45235	<i>T. monococcum</i>	98	219,5	2,2
18	45255	<i>T. monococcum</i>	115	201,8	1,8
19	45256	<i>T. monococcum</i>	91	196,6	2,2
20	45257	<i>T. monococcum</i>	29	226	7,9
21	45258	<i>T. monococcum</i>	49	200,4	4,1
22	45259	<i>T. monococcum</i>	18	264,2	14,4
23	45461	<i>T. monococcum</i>	176	93,8	0,5
24	132841	<i>T. monococcum</i>	57	211,7	3,7
25	132869	<i>T. monococcum</i>	37	197,5	5,3
26	132870	<i>T. monococcum</i>	34	207,1	6,1
27	132873	<i>T. monococcum</i>	34	199,3	5,9
28	139090	<i>T. monococcum</i>	18	240,7	13,2
29	141291	<i>T. monococcum</i>	12	251,2	21,8
30		<i>T. monococcum</i> CV 68-101	31	195,3	6,3
31		Line 149	40	216	5,5
32		Tamaroi	154	140	0,9

Our results are in line with CHENG *et al.*'s (2015) findings, who subjected the seeds of two contrasting bread wheat cultivars, one sensitive and one tolerant, to six NaCl concentrations. They observed that the reduction in K^+ or the increase in Na^+ content due to salinity stress was

considerably smaller in the tolerant cultivar compared to the susceptible. CHENG *et al.* (2015) propose that a higher-affinity K⁺ uptake mechanism may play a crucial role in enhancing salt tolerance, suggesting it as a reliable indicator for breeding new salt-tolerant wheat varieties (CHENG *et al.*, 2015).

The genotypes in the second group exhibited lower activity in removing Na⁺ ions compared to the first group. The Na⁺ ion accumulation in the leaves of these samples ranged from 43.3 to 64.5 mM. These accessions in the second group also originated from different regions. Among the 10 samples, 5 were from Turkey, 2 from Italy, 1 from Georgia, 1 from Bulgaria, and 1 from Romania. These samples in this group can be classified as moderately salt-tolerant.

In this regard, the sample under catalog number 45461 is characterized as salt sensitive. Unstable plants under the influence of a negative environmental factor are more conservative and are not capable of rapidly changing their vital functions, as a result of which they often die. Among the studied accessions, 7 genotypes exhibited higher Na⁺ ion accumulation than the others. Specifically, the Na⁺ ion levels in their leaves ranged from 75.4 to 175.6 mM. Out of these, 4 accessions were originated from Turkey, 2 from Bulgaria, and 1 from Serbia. Notably, accession number 45461 from Serbia showed the highest Na⁺ ion content at 175 mM. The amount of K⁺ ions present in the leaves of this accession was relatively low. As a result, sample 45461 is categorized as salt-sensitive.

While the wheat genome possesses significant genetic diversity for salt tolerance, contemporary elite cultivars struggle to thrive in high soil salinity conditions. Many genotypes exhibit low grain yield when subjected to salinity levels of L-1 (ZHU *et al.*, 2016). Unstable plants, when faced with adverse environmental conditions, tend to be more conservative and are unable to swiftly adjust their essential functions, often leading to their demise.

Salt tolerance in T. boeoticum genotypes.

The study focused on 77 accessions of *T. boeoticum* collected at various times and locations. Among these samples, 47 exhibited a notable capacity for Na⁺ ion removal. The accumulated Na⁺ ion levels in their leaves ranged from 7.69 to 40.9 mM. These accessions, identified as salt-tolerant, are suggested for further breeding efforts aimed at enhancing salt tolerance (Table 2).

The amount of Na⁺ ions accumulated in the 16 studied accessions (catalog numbers: 44936, 131176, 44832, 113280, 44878, 137477, 137341, 44868, 113288, 113284, 137391, 110789, 44822, 116134, 140980, 44955) ranged from 44.2 to 58 mM. These samples were classified as moderately tolerant to salinity.

In the investigation, it was observed that the salt tolerance varied greatly among 14 accessions from the *T. boeoticum* collection (catalog numbers: 113286, 113277, 44856, 44870, 116153, 44866, 44887, 116139, 44857, 139313, 44895, 110749, 113273). The leaves of these samples contained Na⁺ ions in the range of 63.8–181.9 mM. Among these accessions, 3 were from Iran, 2 from Bulgaria, 6 from Turkey, and 3 from Syria. These particular samples were classified as sensitive to salt stress.

The research revealed that under similar levels of extreme conditions, varieties of the same wheat species exhibit differences in the range of Na⁺ ion accumulation. This range depends

on the plant's resistance level, representing the heritable potential ability of the organism to adapt and manifest under the influence of extreme conditions.

Table 2. The amount of Na^+ and K^+ ions in the leaves of salt-resistant *T. boeoticum* samples

№	Catalog number	Na^+ (mM)	K^+ (mM)	K^+/Na^+	№	Catalog number	Na^+ (mM)	K^+ (mM)	K^+/Na^+
1	44821	7,69	230	29,908	25	109080	28,9	223	7,7162
2	137335	10,2	236	23,137	26	113266	29,3	208	7,0989
3	44919	10,9	291	26,697	27	116138	30,3	220	7,2607
4	44948	11,9	264	22,184	28	110826	30,5	193	6,3278
5	44833	13,6	217	15,955	29	44818	30,6	229	7,4836
6	137409	13,6	227	16,691	30	113282	30,7	189	6,1563
7	110820	15	213	14,2	31	113264	32	223	6,9687
8	116146	15,7	230	14,649	32	44941	32,2	227	7,0496
9	113283	15,8	204	12,911	33	44890	32,6	295	9,0490
10	44900	16	224	14	34	113275	33,1	217	6,5558
11	44861	16,7	254	15,209	35	109081	35,3	246,2	6,9745
12	113291	20,1	241	11,990	36	44855	35,6	201,8	5,6685
13	113311	20,4	212	10,392	37	44906	35,6	198,6	5,5786
14	44937	20,6	242	11,747	38	45103	36,1	250,4	6,9362
15	44899	21,2	261	12,311	39	44847	36,2	196,6	5,4309
16	113258	23	210	9,1304	40	44819	36,6	203,6	5,5628
17	126305	24,3	238	9,7942	41	44820	36,6	203,6	5,5628
18	44811	24,4	209	8,5655	42	44907	36,9	195,7	5,3035
19	44813	24,6	190	7,7235	43	113309	37,2	212,4	5,7096
20	113261	24,8	196	7,9032	44	113260	37,9	195	5,1451
21	109086	25,1	251	10	45	135341	39	221,5	5,6794
22	44921	25,4	277	10,905	46	44904	40,8	214	5,2450
23	113254	25,4	195	7,6771	47	44949	40,9	284,2	6,9486
24	44858	26,5	244	9,2075					

Salt tolerance in *T. urartu* genotypes.

Among the 87 samples of *T. urartu* studied, 20 exhibited high salt tolerance. The accumulated Na^+ ion levels in these samples ranged from 15.9 to 39.9 mM (Table 3). These samples included 1 from Iraq, 4 from Jordan, 2 from Lebanon, 4 from Turkey, and 9 from Syria. In another set of 44 *T. urartu* genotypes (catalog numbers: 116191, 45287, 139173, 116156, 115814, 116190, 135343, 45262, 109084), the Na^+ ion content was found to be in the range of 43–80.5 mM. These plants are categorized as moderately resistant.

Among the analyzed samples of *T. urartu*, 23 genotypes were identified as susceptible to salt stress, with their Na^+ ion accumulation ranging from 82.5 mM to 250.9 mM. It is advised to preserve these accessions (catalog numbers: 45484, 45476, 116196, 44827, 44942, 45462, 116160, 116200, 139317, 139969, 45285, 45293, 116198, 110766, 116194, 44911, 140058,

116202, 45300, 116192, 116199, 110753, 117911) for fundamental research in the field of salt tolerance.

Table 3. The amount of Na^+ and K^+ ions in the leaves of salt-tolerant *T. urartu* accessions

№	Catalog number	Species	Na^+ (mM)	K^+ (mM)	K^+/Na^+
1	45278	<i>T. urartu</i>	15,9	209,2	13,16
2	139175	<i>T. urartu</i>	18,2	254,2	13,97
3	109087	<i>T. urartu</i>	20,5	215,5	10,51
4	45288	<i>T. urartu</i>	21,2	222	10,47
5	140061	<i>T. urartu</i>	22,9	233,6	10,21
6	116201	<i>T. urartu</i>	23,8	258	10,84
7	45475	<i>T. urartu</i>	27,2	225,9	8,31
8	45218	<i>T. urartu</i>	28,2	220,3	7,81
9	139317	<i>T. urartu</i>	31,3	228,7	7,31
10	45301	<i>T. urartu</i>	31,8	193,2	6,08
11	45286	<i>T. urartu</i>	32,5	203,4	6,26
12	110784	<i>T. urartu</i>	33,9	247,9	7,31
13	116203	<i>T. urartu</i>	35,2	240,6	6,84
14	45284	<i>T. urartu</i>	36,7	212,9	5,80
15	115815	<i>T. urartu</i>	37,1	235	6,33
16	44943	<i>T. urartu</i>	37,4	237,4	6,35
17	45292	<i>T. urartu</i>	38,2	192	5,03
18	116204	<i>T. urartu</i>	38,3	242,8	6,34
19	45290	<i>T. urartu</i>	39,5	221,2	5,60
20	45489	<i>T. urartu</i>	39,9	237,2	5,94

Adaptation, the process by which a plant adjusts to specific environmental conditions, occurs through physiological mechanisms (physiological adaptation). In a population of organisms (species), adaptation occurs through genetic variability, heredity, and selection (genetic adaptation). Each plant species develops characteristic resistance mechanisms, which encompass a range of morphophysiological and biochemical adaptations that define their adaptive strategy.

An analysis of the percentage distribution of resistance levels to salinity among the studied wheat species revealed differences. In *T. boeoticum*, 61% of the studied accessions were resistant to salt stress, 20.8% were moderately resistant, and 18.2% were sensitive. For *T. monococcum*, the ratio was 40%, 33.3%, and 26.7% respectively, while for *T. urartu* it was 23%, 50.6%, and 26.4% respectively. The variation in the resistance ratio to salt stress among wheat species is depicted in Figure 2.

The figure clearly illustrates that the wheat species *T. boeoticum* exhibits greater resilience to the negative impact of abiotic environmental factors compared to *T. monococcum* and *T. urartu*. This difference in resistance to abiotic stress can be attributed to the fact that diploid wheat

comprises two wild-growing species - *T. boeoticum* (AbAb) and *T. urartu* (AuAu) - which differ in biomorphological, biochemical, and molecular markers. *T. boeoticum*, originating from the Karachadag region of Southeastern Turkey, is the progenitor of *T. monococcum* (AmAm) (HEUN *et al.*, 2008). It is evident that a plant's requirements for a range of external conditions during its development are influenced by the species' previous evolutionary history.

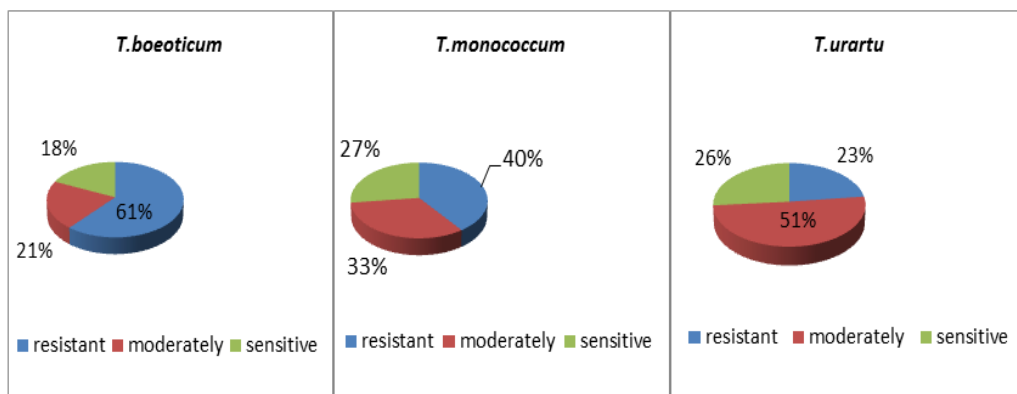


Fig.2. The ratio of the degree of resistance of different types of wheat to salinity stress

The obtained results are in accordance with AHMADI *et al.* (2018), who conducted a screening of 179 Aegilops and Triticum accessions, including diploid species such as *T. boeoticum* and *T. urartu*, to identify the most salt-tolerant wild relatives. Among the diploid species, two Aegilops species exhibited the highest leaf K^+ under saline conditions, followed by *T. boeoticum*, while *T. urartu* showed the lowest leaf K^+ . The study also found that activities of superoxide dismutase (SOD) and catalase (CAT) in *T. boeoticum* increased under salinity stress. The salt-tolerant accessions identified from all three species can be utilized more effectively in breeding programs aimed at enhancing resistance.

CONCLUSION

In this study, we investigated the sodium (Na^+) and potassium (K^+) content in the leaves of three diploid wheat species under salinity stress. The analysis of the resistance levels to salinity among these species revealed notable differences. *T. boeoticum* showed the highest proportion of accessions resistant to salt stress (61%), followed by *T. monococcum* (40%) and *T. urartu* (23%). Additionally, *T. boeoticum* had a lower percentage of moderately resistant accessions compared to *T. monococcum* and *T. urartu*, suggesting its overall greater resilience to salinity stress.

These findings provide valuable insights into the salt tolerance mechanisms of these diploid wheat species. Higher proportion of salt-tolerant accessions in *T. boeoticum* highlights its potential as a genetic resource for breeding new salt-tolerant wheat varieties. Breeding programs could benefit from targeting *T. boeoticum* for its favorable traits under salinity stress.

Furthermore, understanding the varying levels of salt tolerance among these three species can aid in the development of tailored management strategies for different environments.

The identified patterns of Na⁺ and K⁺ accumulation under salinity stress in these diploid wheat species offer a foundation for further research into the genetic and physiological mechanisms underlying salt tolerance. Identified salt-tolerant accessions from all three species are included into the trait collection of the National Gene Bank of Azerbaijan and of the ICARDA Gene Bank. This knowledge could be applied in breeding programs to develop wheat varieties better equipped to thrive in saline conditions, ultimately contributing to sustainable agriculture practices in regions affected by soil salinity.

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PROCENA OTPORNOSTI NA STRES SOLI KOD DIPLOIDNIH VRSTA PŠENICE

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Izvod

U Nacionalnoj banci gena Instituta za genetičke resurse Azerbejdžana nalazi se preko 2.000 uzoraka pšenice, vitalnih za oplemenjivanje biljaka otpornih na stresove životne sredine. Ova studija se fokusira na poređenje otpornosti na stres soli tri diploidne vrste pšenice: *Triticum monococcum* L., *Triticum boeoticum* (L.) Boiss i *Triticum urartu* Thum. ex Gandil., koji obuhvata 170 uzoraka iz banke gena ICARDA. Otpornost na stres saliniteta procenjena je na osnovu sposobnosti genotipova da isključe Na⁺ jone iz listova. Uočene su velike varijacije među uzorcima za odgovor na stres, što je omogućilo njihovu klasifikaciju u otporne, umereno otporne i osetljive grupe unutar svake vrste. Analiza je otkrila različite procenete otpornosti među vrstama. *T. boeoticum* je imao 61% rezistentnih, 20,8% umereno rezistentnih i 18,2% osetljivih uzoraka. *T. monococcum* je imao 40%, 33,3%, 26,7%, a *T. urartu* 23%, 50,6%, 26,4% respektivno. Primetno je da je *T. boeoticum* pokazao veću otpornost od *T. monococcum* i *T. urartu*, što se pripisuje njegovom divljem rastu i različitim biomorfološkim, biohemijskim i molekularnim karakteristikama. Uzorci otporni na stres soli preporučuju se za programe oplemenjivanja čuvaju se u Nacionalnoj banci gena Azerbejdžana i ICARDA banci gena. Ovi rezultati naglašavaju potencijal korišćenja uzoraka otpornih na salinitet, posebno genotipova *Triticum boeoticum*, u ciljanim programima oplemenjivanja kako bi se povećala otpornost pšenice na ovaj stres.

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