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ARAŞTIRMA MAKALESİ **RESEARCH ARTICLE**

Evaluation of germination responses on the some barley genotypes under saline conditions

Bazı arpa genotiplerinin tuzlu koşullarda çimlenme tepkilerinin değerlendirilmesi

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Ö Z E T / A B S T R A C T

Aims: The aim of this research was to determine the responses of some barley genotypes to salinity stress at the germination period.
Methods and Results: Barley seeds provided from the Osman Tosun Gene Bank at Ankara University. Eight six-row barley genotypes (33, 64, 159, 184, 200, 202, 220 and 231) and two six-row barley cultivars (cv Avcı-2002 and cv Cetin-2000) were used in this study. Salinity stress was applied to the seeds in four different doses of NaCl (distilled water (0), 75 mM, 150 mM and 225 mM). The experiments were carried out at 25±1°C and dark conditions with triplicate according to completely randomized plot design. In order to determine the salinity tolerance of genotypes in the study; germination speed (%), germination power (%), root length (cm), shoot length (cm), shoot fresh weight (g), shoot dry weight (g), root fresh weight (g) and root dry weight (g) parameters were measured.
Conclusions: As results of these measures, all parameters were found to be statistically significant ($p \leq 0.01$) except for germination power and shoot dry weight. Genotype × NaCl dose interaction was found significantly different at $p \leq 0.01$ level for germination speed and root fresh weight.
Significance and Impact of the Study: Genotype 200 and 220 showed better performance under salinity stress than other genotypes. Also, it can be used as a parental genitor in future breeding studies.

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INTRODUCTION

Salinity and drought are the most common and influential abiotic stress factors that cause significantly plant production losses in the world. More than 800 million hectares of arable land are affected by salinity worldwide (FAO, 2008). This area constitutes more than 6% of the total arable land area in the world. Most of these areas are due to natural causes as a result of the long accumulation of salt in arid and semi-arid regions (Rengasamy, 2002). Salt stress poses a great threat to agricultural production in the future. Salt stress in plants causes basically two types of damage by inhibiting the water intake of the roots and causing ion toxicity (Munns and Tester, 2008). In plants that exceed their salt carrying capacity in their cytoplasm, leaf injuries then deaths occur (Munns et al., 2006). Thus, the crop yield decreases, and the nutritional and calorie values of the products reduce (Yokoi et al., 2002). During their evolution, plants have developed several defense mechanisms to combat excess salt. Osmotic adjustments, halting of shoot growth, reducing photosynthesis, closure of stomata, sodium transport from leaves to roots are some of these mechanisms (Wu et al., 2013).

Barley is the fourth most produced grain in the world. Hence, barley has many uses, including livestock feed and forage, human food, and malt beverages (Horsley et

al., 2009). It is more tolerant to the salinity than the other cereal crops (Colmer et al., 2006). However, barley is still exposed to significant yield losses due to cultivating marginal lands such as saline areas (Munns and Tester, 2008; Mahmood, 2011). Therefore, examining salt tolerance mechanisms and characterizing high tolerance barley gene resources are crucial for future barley breeding programs (Mian et al., 2011). On the other hand, using elite lines in barley breeding programs resulted in narrowed and uniformed barley germplasm pools that are inadequate to develop new varieties with high tolerance to salt stress. Modern varieties, old varieties, landraces, and closely related species were defined as primary germplasm pools (Harlan and deWet, 1971; von Bothmer et al., 2003) to expand the germplasm resource. In particular, plant breeders show special attention on landraces because of their adaptation ability to particular areas. Barley landraces evaluated at the vegetative growth stage (Chikha et al., 2016), at the germination, early seedling, and maturation stage (Abdel-Ghani et al., 2020), and at the reproductive stage (Allel et al., 2019) were identified as a primary gene resource to enhance the salt tolerance in barley.

Multivariate analysis is the most commonly used method to illustrate the variation in collected germplasm or genotypes. Principal component analysis (PCA) and cluster analysis (CA) are preferred tools for screening morphological traits of genotypes and grouping them in accordance with their similaries and differences (Mohammadi and Prasanna, 2003; Peeters and Martinelli, 1989). PCA is a multivariate statistical method that provides important information by transforming the obtained data into its basic components and making it a new data series. PCA can be successfully used to analyze big data from experiments to evaluate genotypes (Chikha et al., 2016; Allel et al., 2016; Raza et al., 2017; Sivakumar et al., 2020). The present study was undertaken with the objective to assess and determine the salinity tolerant barley genotypes based on germination traits via multivariate analysis.

MATERIALS and METHODS

Eight six-row barley genotypes preserved in Osman Tosun Gene Bank at Ankara University (register number 33, 64, 159, 184, 200, 202, 220, 231) and two salt-tolerant six-row barley cultivar (cv Cetin-2000 and cv Avcı-2002) (Anonymous, 2021) were used as plant materials (Table 1). In order to obtain salt-tolerant barley genotypes, morphological traits were measured at the germination stage. Salt concentrations were applied to seeds at 75 mM, 150 mM, and 225 mM doses, with 0 mM for the control group.

Table 1. Locations of genotypes

Gene Bank No.	Accession No.	Spike Type	Origin
33	63A0912	Short, thick	USA
64	67A06	Long, thick	USA
159	CI6251	Short, thick	Finlandia
184	CI0995	Short, thick	USA
200	CI0997	Short, thick	USA
202	CI1010	Long, sparse	USA
220	CI11025	Long, sparse	USA
231	CI8159	Long, sparse	Argentina
Avcı-2002	Registered Cultivar	Long, large	Turkey
Çetin-2000	Registered Cultivar	Long, large	Turkey

Seeds were first sterilized with 2% sodium hypochlorite for 30 min before the germination stage. The germination test was carried out as described by Kaya et al. (2006). Briefly, 25 seeds per genotype were placed between double-layered filter paper with dimensions 25 cm $\times$ 25 cm. After applying 10 mL of respective test solutions to each double-layered filter paper with seeds, filter papers were rolled and put into sealed plastic bags to avoid moisture loss. To prevent salt accumulation, the papers were replaced every two days. The seeds were kept at 25 ° C for 7 days in darkness and treated with the same solutions whenever necessary. The germinated seeds on the 3rd day were counted to calculate germination speed. The germination tests were terminated on the 7th day as described by International Seed Testing Association (ISTA) (ISTA, 2017). The seeds were considered germinated with the emergence of the radicle (≥ 2 mm). The germination experiments were repeated three times with 25 seeds per treatment. Germination power, shoot length, root length, shoot fresh weight, and root fresh weight were measured. In order to determine shoot dry weight and root dry

weight, the fresh weights of the plant materials were kept at 60 ° C for 72 hours, then weighted.

The data obtained in the study were subjected to analysis of variance (ANONA) for the completely randomized design with triplicate using JMP v 13.0 (SAS, 2017) statistics package program to evaluate significant differences among treatments. Duncan's multiple range test was applied to compare the means if there were any significant differences. Percentage data were transformed to arcsine before the analysis of variance. Morphological traits were analyzed as multivariate by using procedures of principal component analysis (PCA) and cluster analysis (CA) with the assist of computer software JMP v 13.0 (SAS, 2017). The other multivariate analysis the most widely used clustering technique, hierarchical clustering was used to determine similarity and dissimilarity in the genotypes. CA was designed on the average distance k-means. Then genotypes in each cluster were analyzed for informative statistics.

RESULTS and DISCUSSION

The distribution of germination speed, germination power, shoot length, root length, shoot fresh weight, root fresh weight, shoot dry weight, root dry weight at four different salinity levels showed wide fluctuations. The results from the analysis of variance (ANOVA) are given in Table 2. The difference among genotypes was significant in germination speed, root length, shoot length, shoot fresh weight, and root fresh weight at p≤0.01 level (Table 2). Additionally, root dry weight was significantly different at p≤0.05 level. The difference among genotypes on germination power and shoot dry weight were insignificant. The difference between salt levels at different concentrations was statistically significant (p≤0.01 and p≤0.05) in all parameters except for germination power. It was determined that genotype × NaCl interaction was significant for germination speed and root fresh weight at p≤0.01 level, but genotype × NaCl interaction was insignificant in other parameters examined (Table 2).

Table 2. Analysis of variance and mean square of different salt stress levels in barley genotypes

		Mean Square							
V.R.	**dF**	**Germination Speed**	**Germination Power**	**Root Length**	**Shoot Length**	**Shoot Fresh Weight**	**Shoot Dry Weight**	**Root Fresh Weight**	**Root Dry Weight**
G	9	333.54**	35.30 **ns**	8.836**	5.418**	0.001645**	0.0002 **ns**	0.002361**	0.00007*
S	3	3106.46**	24.31 **ns**	306.842**	357.021**	0.020328**	0.00033*	0.010749**	0.00011**
G × S	27	216.03**	31.06 **ns**	1.141 **ns**	2.627 **ns**	0.000578 **ns**	0.0001 **ns**	0.000608**	0.00002 **ns**
Error	80	465.49	31.50	26.432	30.532	0.00235	0.0001	0.00179	0.00004
Total	119	107.76	29.90	2.173	1.623	0.00039	0.0001	0.00029	0.00003

Genotype: G, Salinity level: S, **, *: Significantly different from zero at p≤0.01 and p≤0.05, ns: non significant.

Germination speed and germination power (%)

Average germination speed of genotype 33 and 64 (92.71%) were the highest under salt stress levels, while genotype 159 was the lowest. Genotype 184 (100%) had maximum germination percentage, while genotype 200 (94.79%) had minimum germination percentage under salt stress levels (Table 3). Germination speed (96.67-73.16%) and germination percentage (98.33-96.25%) were decreased under increasing salt levels (Table 4). The germination speed of barley genotypes varied from 87.5% to 100% at 0 mM, 87.5% to 100% at 75 mM, 66.6% to 95.8% at 150 mM, 50% to 91.7% at 225 mM, in the same order. Germination power ranged from 87.5% to 100% at 0 mM, 91.7% to 100% at 75 mM, 91.7% to 100% at 150 mM, and 91.7% to 100% at 225 mM (data not shown).

It was observed that salinity has a delayed germination effect on barley genotypes, but it does not significantly affect germination rate. It can be speculated that these parameters were insufficient in determining the tolerance level of genotypes by protecting the germination of genotypes at high salt levels. Genotype 159 and 184 showed 100% germination under all stress doses. In previous studies, germination power decreased with increasing salt level (Zhang et al., 2010, Kirmizi and Bell, 2012; Kanbar and El-Drussi, 2014). However, some genotypes in these studies seem to maintained germination under increased salt levels. Thus, it can be interpreted that the genetic structure controls germination under salinity stress.

Table 3. Mean values of germination traits in accordance with genotypes

L No.	GS (%)	GP(%)	RL (cm)	SL(cm)	SFW (g)	SDW(g)	RFW (g)	RDW (g)
33	92.71 a	96.88	10.65 a	8.61 ab	0.0854 bc	0.0076	0.0558 d-f	0.0056 c
64	92.71 a	98.96	9.69 a-c	7.70 b-d	0.1015 a	0.0093	0.0582 d-f	0.0064 c
159	75.00 c	98.96	10.19 a-c	8.69 ab	0.0797 c	0.0095	0.0723 bc	0.0110 ab
184	87.50 ab	100.0	10.38 ab	8.20 b-d	0.1065 a	0.0124	0.0893 a	0.0115 a
200	87.50 ab	94.79	10.17 a-c	8.72 ab	0.0918 a-c	0.0090	0.0694 b-d	0.0064 c
202	88.54 ab	95.83	9.36 bc	7.49 cd	0.1032 a	0.0082	0.0831 ab	0.0072 bc
220	89.58 ab	97.92	9.99 a-c	9.49 a	0.1067 a	0.0086	0.0672 c-e	0.0057 c
231	85.42 ab	96.88	7.64 d	7.22 d	0.1008 ab	0.0196	0.0535 ef	0.0056 c
2000	83.96 b	95.83	9.98 a-c	8.29 bc	0.0790 c	0.0072	0.0486 f	0.0046 c
2002	91.67 ab	98.96	9.18 c	8.07 b-d	0.0790 c	0.0075	0.0493 f	0.0052 c

GS: Germination speed; GP: Germination percentage; RL: Root length; SL: Shoot Length; SFW: Shoot fresh weight; SDW: Shoot dry weight; RFW: Root fresh weight; RDW: Root dry weight.

Table 4. Mean values of germination traits in accordance under different salinity levels

L No.	GS (%)	GP(%)	RL (cm)	SL(cm)	SFW (g)	SDW(g)	RFW (g)	RDW (g)
0	96.67 a	97.50	13.74 a	12.43 a	0.0996 a	0.0080 a	0.0800 a	0.0095 a
75	92.08 ab	98.33	10.47 b	9.58 b	0.1204 a	0.0146 a	0.0801 a	0.0070 ab
150	87.91 b	97.91	8.50 c	6.30 c	0.0955 b	0.0097 ab	0.0573 b	0.062 ab
225	73.16 c	96.25	6.19 d	4.69 d	0.0579 c	0.0072 b	0.0413 c	0.0050 b

GS: Germination speed; GP: Germination percentage; RL: Root length; SL: Shoot Length; SFW: Shoot fresh weight; SDW: Shoot dry weight; RFW: Root fresh weight; RDW: Root dry weight.

Root length (cm) and shoot length (cm)

Root and shoot length of the barley genotypes were found to significantly decrease with increasing NaCl concentrations from 13.74 cm at 0 mM NaCl to 6.19 cm at 225 mM NaCl for root length and from 12.43 cm at 0 mM NaCl to 4.69 cm at 225 mM NaCl for shoot length (Table 4). Genotype 33 had the longest root length (10.65cm), while genotype 231 had the shortest root length (7.64cm) under salt stress levels. Genotype 220 and 231 were the highest (9.49cm) and lowest (7.22cm) shoot length under salt stress levels, respectively (Table 3). Root length ranged from 11.4 cm to 14.7 cm at 0 mM, 8.4 cm to 11.9 cm at 75 mM, 6.4 cm to 9.9 cm at 150 mM, and 5.4 cm to 7.7 cm at 225 mM. The shoot length ranged from 9.8 cm to 14.8 cm at 0 mM, 7.7 cm to 11.6 cm at 75 mM, 4.5 cm to 7.4 cm at 150 mM, and 3.9 cm to 6.5 cm at 225 mM (data not shown).

Significant reductions in the root-forming capacities of barley genotypes have occurred. The mean root length, which was 13.7 cm in the control group, was reduced by approximately 51.1% at a dose of 225 mM, and then it was measured as 6.2 cm. Genotype 33, 64, 159, 184, and 200 formed more roots by performing superior performance than those in the control group at doses of 75 mM, 150 mM, and 225 mM NaCl. It was emphasized that the root development of plants decreased significantly with the increasing salt concentration (Zhang et al., 2010, Kirmizi and Bell, 2012; Benlioglu and Ozkan, 2015).

Significant decreases occurred in the shoot length of barley genotypes as a result of the increasing salt level. While the average shoot length of the genotypes in the control group (0 mM) was 12.43 cm, the average shoot length at the highest salt dose (225 mM) was calculated as 4.69 cm. Salt concentration at 250 mM caused a 62.3% reduction in shoot length compared to the control treatment. It has been determined that the shoot length is the one of the most affected parameters by salt stress (Benlioglu and Ozkan, 2015; Benlioglu and Ozkan, 2021). It was determined that the mean shoot length formed by the genotypes 159 (7.48 cm) and 220 (8.00 cm) under stress doses were higher than the shoot length mean of cv Cetin-2000 (7.35 cm) and cv Avcı-2002 (6.66 cm) cultivars. In studies conducted to determine the tolerance of salt in the germination stage, the shoot length is significantly affected by salt concentration (El Madidi et al., 2004; Patterson et al., 2009; Kirmizi and Bell, 2012; Benlioglu and Ozkan, 2015; Benlioglu and Ozkan, 2021) with identical results of this study. In accordance with the results in this study, root and shoot length are very important and selective criteria for determining the salt tolerant of genotypes.

Shoot fresh (g) and dry weight (g)

Genotype 220 had the heaviest shoot fresh weight (0.1067g), while cv Avci 2002 and cv Cetin 2000 had the lightest shoot fresh weight (0.0790g) under salt stress levels. Genotype 231 were the heviest shoot dry weight (0.0196g) and lightest (0.0072g) under salt stress levels (Table 3). 75 mM salt level was the heaviest shoot fresh weight (0.1204g), while 225 mM was the lightest shoot fresh weight (0.0579g). Similar to shoot fresh weight, 75 mM salt level was the heaviest shoot dry weight (0.0146g) (Table 4). The shoot fresh weight ranged from 0.126 g to 0.076 g at 0 mM, from 0.149 g to 0.098 g at 75 mM, from 0.071 g to 0.122 g at 150 mM, from 0.488 g to 0.073 g at 225 mM. Shoot dry weight ranged from 0.005 g to 0.012 g at 0 mM, from 0.008 g to 0.049 g at 75 mM, from 0.007 g to 0.015 g at 150 mM, from 0.006 g to 0.008 g at 225 mM (data not shown).

Shoot fresh weights of barley genotypes increased by approximately 20% in 75 mM NaCl stress compared to the control dose (0 mM). However, with the increase of salt level, significant decreases occurred in each unit. It can be demonstrated that the reason of that the Na+ and Cl- ions that do not have a toxic effect have a stimulating effect on germination and seedling development. Indeed, low concentrations of NaCl might positively affect germination. Chickha et. al. (2016), Hellal et al. (2018), Dogru and Kacar (2019), Benlioglu and Ozkan (2020), Ebrahim et al. (2020), Narimani et al. (2020), Benlioglu and Ozkan (2021) agreed with this knowledge. At the highest stress level; the genotype 33, 159, 184, 202, 220 and 231, gained more shoot fresh weight than the cultivars used as controls. It is determined that an increase occurs in shoot fresh weight in 75 mM salt level compared to the control group. However, shoot dry weights decreased at 150 mM and 225 mM NaCl dose. Genotype 64, 159, 184, 200, 202, 220 and 231 produced heavier shoot dry weight than cv Cetin 2000 and cv Avcı 2002 at the highest salinity level (225 mM).

Root fresh (g) and dry weight (g)

Genotype 202 had the heaviest root fresh weight (0.0831g), while cv Avci 2002 had the lightest root fresh weight (0.0486g) under salt stress levels. Genotype 184 and cv Avci 2002 were the heaviest (0.0115g) and lightest root dry weight (0.0046g) under salt stress levels, in the same order (Table 3). The heaviest root fresh weight was measured at 75 mM salt level (0.0801g), while the lightest was at 225 mM salt level (0.0413g). Root dry weight was decreased under increasing salt levels (0.0095-0.0050g) (Table 4). Root fresh weight ranged from 0.123 g to 0.049 g at 0 mM, from 0.129 g to 0.059 g at 75 mM, from 0.089 g to 0.040 g at 150 mM, from 0.068 g to 0.025 g at 225 mM. Root dry weight ranged from 0.006 g to 0.024 g at 0 mM, from 0.005 g to 0.011 g at 75 mM, from 0.004 g to 0.009 g at 150 mM, from 0.004 g to 0.009 g at 225 mM (data not shown).

It is observed that root fresh weights of the barley genotypes were not significantly affected by the salt dose at 75 mM compared to those in the control group. However, a sharp decreases occurred in root fresh weight at increasing stress levels. Genotype 159, 184, 200, and 202 had more root fresh weights than cultivars at all stress levels. Root fresh weights of the genotypes did not change between the control group (0 mM) and 75 mM NaCl dose, but root dry weights decreased. The reason of this situation may be explained that relatively low NaCl dose creates ion toxicity in the roots of barley genotypes before osmotic stress. When the average root dry weights of genotypes under all stress doses were examined, it was determined that genotypes 159 and 184 got the highest values. When the root dry weights are examined, with the onset of salt stress, the amount of dry weight formed in the roots of the genotypes has decreased. Genotype 64, 159, 184, 200, 202, 220 and 231 had more root dry weight than cv Cetin 2000 and cv Avci 2002 at all stress levels. Several previous studies noted that increasing salt concentration adversely affects the root fresh and dry weight (Chickha et al., 2016; Hellal et al., 2018; Dogru and Kacar, 2019; Benlioglu and Ozkan, 2020; Ebrahim et al., 2020; Narimani et al., 2020; Benlioglu and Ozkan, 2021).

Multivariate analysis of genotypes

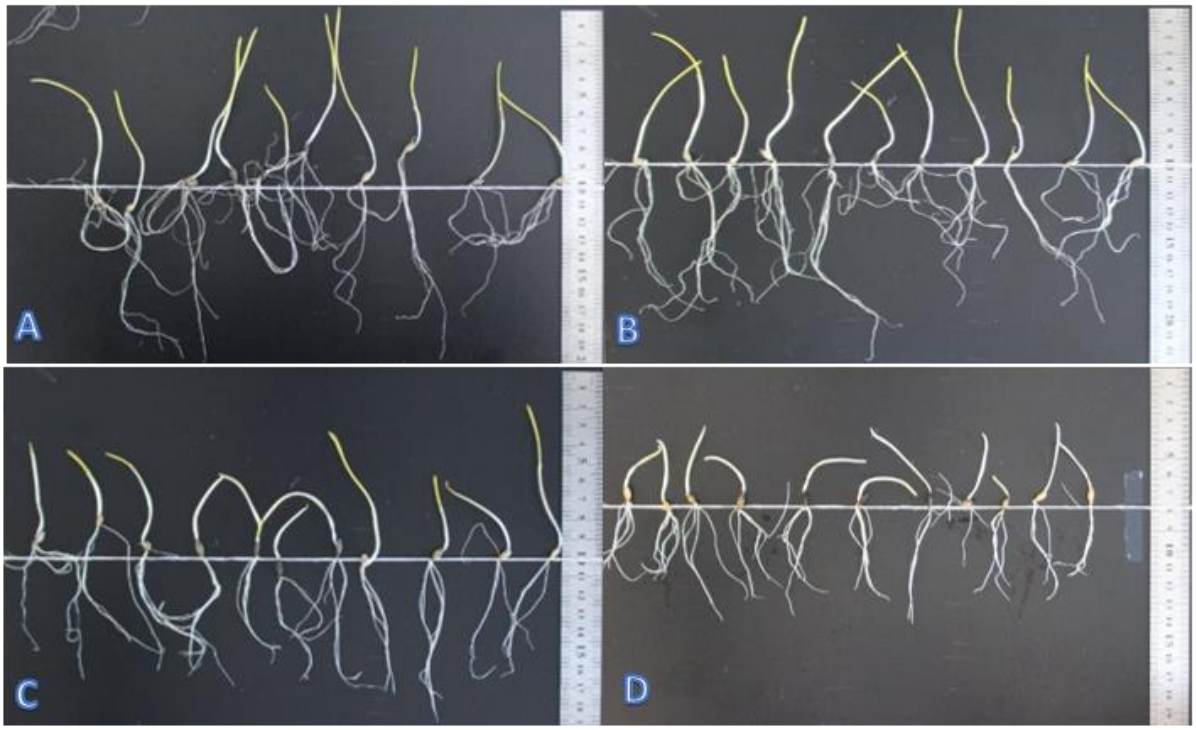
Multivariate analysis has many benefits, such as improved efficiency for genotypic distinction as various characteristics are exposed to analysis together (Aslam et al. 2017). The distinction of genotypes is also made simultaneously under different salt stress to evaluate salt tolerance that generally provides tolerance to more comprehensive salt stress levels (Zeng et al., 2002). The principal component analysis is a multivariate data analysis method that can be applied to identify the similarities and differences among several factors for salt tolerance (Rana et al. 2015).

Principal component analysis (PCA) revealed a high level of variation among the genotypes. The variation studied with PCA showed that the first two principal components contributed 54.23% of the total variance among the nine germination traits under non-stress conditions. The first two principal components contributed 57.00%, 60.58% and 64.91% of the total variance among the nine germination traits for 75 mM, 150 mM and 225 mM salinity stress levels respectively (Table 5). The first two

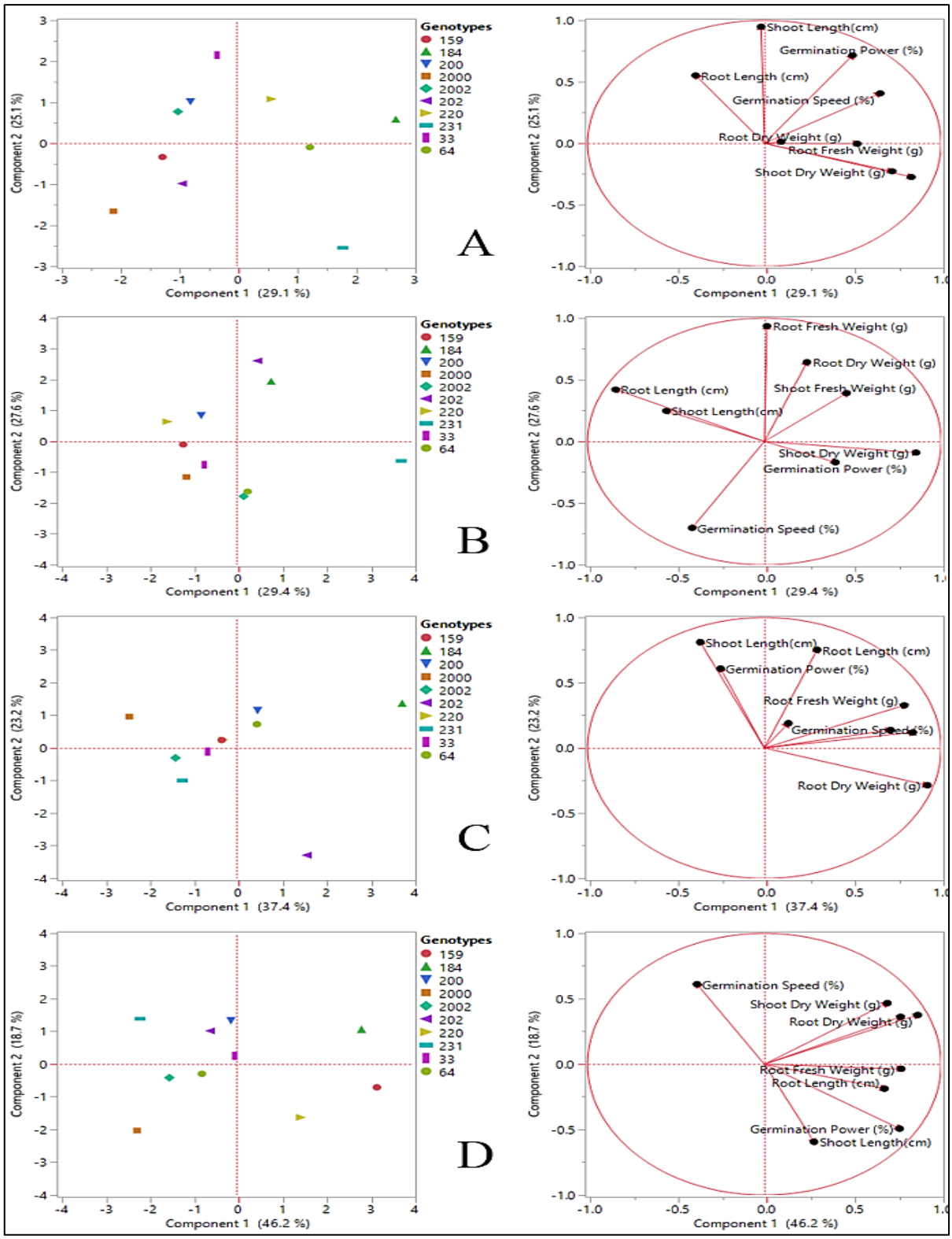
principal components were plotted graphically to show the similarities among genotypes at different salinity levels (Figure 2). The graphs were designed by computing each trait individually to separate stress level. Besides, the graphs showed the variability of genotypes for the nine germination parameters in the study. It can be concluded that wide genetic variability exists among the genotypes based on the distribution model of the under the different salinity stress levels of genotypes on the PCA graphs (Figure 2).

Table 5. Principal component analysis of morphological variation of barley genotypes. Eigenvectors and eigenvalues of the principal components, total variance (%) and cumulatives (%) of germination traits

Stress Level	Principal Components	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8
Control	**Eigenvalue**	2.33	2.01	1.46	0.86	0.81	0.36	0.13	0.05
	Variance (%)	29.10	25.13	18.22	10.77	10.08	4.50	1.61	0.59
	Cumulative (%)	29.10	54.23	72.46	83.23	93.30	97.80	99.41	100.00
75 mM	**Eigenvalue**	2.35	2.21	1.29	1.03	0.85	0.21	0.05	0.00
	Variance (%)	29.41	27.59	16.17	12.88	10.65	2.68	0.61	0.02
	Cumulative (%)	29.41	57.00	73.17	86.05	96.69	99.37	99.98	100.00
150 mM	**Eigenvalue**	2.99	1.85	1.48	0.89	0.64	0.10	0.03	0.01
	Variance (%)	37.42	23.17	18.49	11.17	8.03	1.25	0.35	0.12
	Cumulative (%)	37.42	60.58	79.07	90.25	98.28	99.53	99.88	100.00
225 mM	**Eigenvalue**	3.70	1.49	1.04	0.79	0.70	0.19	0.06	0.02
	Variance (%)	46.24	18.67	13.06	9.92	8.80	2.41	0.71	0.19
	Cumulative (%)	46.24	64.91	77.97	87.89	96.69	99.10	99.81	100.00



A: control group of all genotypes (0 mM); B: 75 mM; C:150 mM; D:225 mM
Figure 1. Distribution of root and shoot length in different salt levels



A: control group of all genotypes (0 mM); B: 75 mM; C:150 mM; D:225 mM

Figure 2. Classification of barley genotypes along the first and second principal components based on characterization of germination traits under different salinity levels

Chikha et al. (2016) applied NaCl at 0 mM, 200 mM and 250 mM levels to barley genotypes during vegetative development periods. The responses of genotypes to salt stress were evaluated by PCA. The effect of the first two principal components on the total variation, respectively; they stated that it was 43.92%, 64.99% and 59.46% and that the genotypes with high tolerance were located close to the tolerance indicators in the PCA

graphs. Aslan et al (2016) determined the salt stress tolerance of bread wheat and einkorn genotypes during the germination period. In the PC analysis, they reported that the first PC1 had an effect on the total variation at the rate of 71.946% and the PC2 at the rate of 11.098%. Aslam et al. (2017) investigated the tolerances of 15 lentil genotypes to different salt stresses in the early period using the PCA technique. They determined that the total variation in NaCl stress of the first two principal components; 0 mM, 50 mM, 100 mM and 150 mM accounted for 61.57%, 63.05%, 66.44% and 58.39%, respectively. Gungor et al. (2021) screened the salt stress tolerance of oat genotypes during germination by PCA method. It was stated that the first two principal components accounted for 50.3% of the total variation in the traits studied in stress-treated oat genotypes. The results we obtained from this study were in parallel with these studies. The phylogenetic tree of barley genotypes for germination traits was presented in Figure 3. The closest genotypes were 33 and 202, while the furthest genotypes are 33 and 159, according to the cluster grouping.

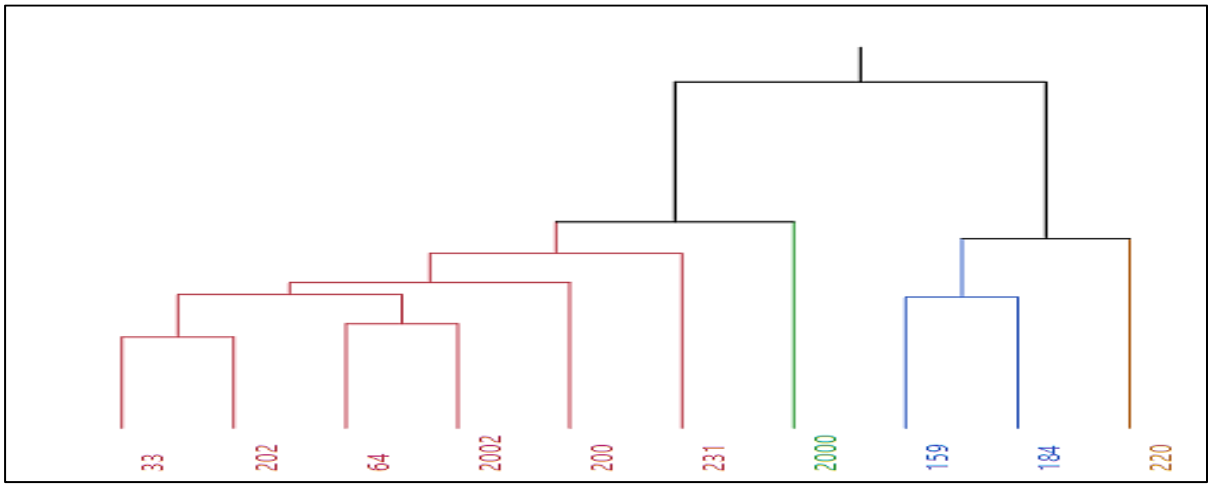


Figure 3. Phylogenetic tree for barley genotypes for germination traits under 225 mM NaCl salinity level

In conclusion, genotype 200 and 220 showed prominent characters in all examined parameters than in registered cultivars. Genotype 33 and 159 obtained higher values in all parameters except germination speed and germination power than those of in registered cultivars. According to the parameters examined, genotype 202 and 231 had lower values than registered cultivars. Confirming to these results, the tolerances of barley genotypes to salt stress was determined; Genotype 200 and 220 were high tolerant, genotype 33 and 159 were moderate tolerant, and genotype 202 and 231 were salt sensitive. It was concluded that the more comprehensive studies conducted on the barley genotypes preserved in the Osman Tosun Gene Bank could be revealed new gene resources against salt tolerance in barley.

ÖZET

Amaç: Bu araştırmanın amacı, bazı arpa genotiplerinin çimlenme döneminde tuzluluk stresine karşı tepkilerini belirlemektir.

Yöntemler ve Bulgular: Arpa tohumları Ankara Üniversitesi Osman Tosun Gen Bankası'ndan temin edilmiştir. Bu çalışmada sekiz adet altı sıralı arpa genotipi (33, 64, 159, 184, 200, 202, 220 ve 231) ve iki adet altı sıralı arpa çeşidi (Avcı-2002 ve Çetin-2000) kullanılmıştır. Tohumlara dört farklı NaCl dozunda saf su (0), 75 mM, 150 mM ve 225 mM tuzluluk stresi uygulanmıştır. Deneme tesadüf parseller deneme desenine göre, 25±1°C'de ve karanlık koşullarda üç tekrarlamalı olarak uygulanmıştır. Çalışmada yer alan genotiplerin tuzluluk toleransını belirlemek için; çimlenme hızı (%), çimlenme gücü (%), kök uzunluğu (cm), fide uzunluğu (cm), fide yaş ağırlığı (g), fide kuru ağırlığı (g), kök yaş ağırlığı (g) ve kök kuru ağırlığı (g) parametreleri ölmüştür.

Genel Yorumlar: Bu ölçümler sonucunda çimlenme gücü ve fide kuru ağırlığı dışındaki tüm parametreler istatistiksel olarak anlamlı ($p \leq 0.01$) bulunmuştur. Genotip × NaCl doz interaksiyonu, çimlenme hızı ve kök yaş ağırlığı için $p \leq 0.01$ seviyesinde önemli bulunmuştur.

Çalışmanın Önemi ve Etkisi: Genotip 200 ve 220, diğer genotiplere göre tuzluluk stresi altında daha iyi performans göstermiştir. Ayrıca gelecekteki ıslah çalışmalarında ebeveyn genitoru olarak kullanılabileceği düşünülmektedir.

Anahtar Kelimeler: Arpa, tuzluluk stresi, çimlenme, temel bileşenler analizi, gen bankası materyali

CONFLICT OF INTEREST

We have no conflict of interest to declare.

AUTHOR'S CONTRIBUTIONS

The contribution of the authors is equal.

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