RESEARCH ARTICLE

SABRAO Journal of Breeding and Genetics
57 (4) 1389-1398, 2025
http://doi.org/10.54910/sabrao2025.57.4.5
http://sabraojournal.org/
pISSN 1029-7073; eISSN 2224-8978

GENETIC DIVERSITY IN MAIZE (*ZEA MAYS* L.) GENOTYPES AGAINST SALINITY TOLERANCE AT SEEDLING STAGE

M. KHAN[1], N. AKHTAR[1*], M. ARSHAD[2], M. KAUSAR[1], S. GUL[1], U. SALEEM[1], and M.I. YOUSAF[3]

[1]Department of Plant Breeding and Genetics, College of Agriculture, University of Sargodha, Sargodha, Pakistan
[2]Maize & Millets Research Institute, Yousafwala, Sahiwal, Pakistan
[3]Cotton Research Station, Bahawalpur, Punjab, Pakistan
*Corresponding author's email: naeem.siraj@uos.edu.pk
Email addresses of co-authors: mariak364@gmail.com, directormmri@gmail.com, samringulpbg@gmail.com, maria_kausar12@yahoo.com, usman.saleem@uos.edu.pk, irfanpbg.uaf@gmail.com

SUMMARY

Salinity is one of the major threats to sustainable maize (*Zea mays* L.) production. The presented study sought to compare 50 maize inbred lines in pots filled with sand under three salinity levels: T_1 = NaCl @ 0 dsm^{-1} (control), T_2 = NaCl @ 8 dsm^{-1}, and T_3 = NaCl @ 12 dsm^{-1} at the seedling stage, held in the College of Agriculture, University of Sargodha, Sargodha, Pakistan. The NaCl solutions of 0, 8, and 12 dsm^{-1} salt concentrations served to irrigate the pots. Data collection of maize seedling traits continued after 28 days of seed sowing. The results have shown a significant differences among genotypes, NaCl levels, and their interaction effects on all studied plant traits. Statistical means comparison and principal component analysis indicated inbred lines G-2 (ILYL-19), G-11 (ILYL-30), G-26 (ILYL-7), and G-45 (DDR-15) showed high values for cell membrane stability under studied salt-stress conditions. Meanwhile, G-2 (ILYL-19), G-3 (PEIL-6), G-11 (ILYL-30), G-13 (ILYL-34), G-32 (ILYL-44), G-33 (ILYL-45), G-35 (PEIL-20), and G-45 (DDR-15) exhibited high mean values for shoot and root length, potassium contents, and root and shoot dry weights. They proved to be salt-tolerant maize inbred lines under all treatments at the seedling stage.

Keywords: Maize (*Z. mays* L.), genetic variability, salinity, salt tolerance, cell membrane stability

Key findings: The presence of genetic variability of maize (*Z. mays* L.) inbred lines for salinity tolerance and cell membrane stability under saline conditions indicated maize inbred lines G-3 (PEIL-6), G-11 (ILYL-30), G-33 (ILYL-45), G-35, and G-45 could be desirable for breeding salt-tolerant hybrids to enhance maize production in saline soils.

Communicating Editor: Dr. Anita Restu Puji Raharjeng

Manuscript received: December 02, 2024; Accepted: May 17, 2025.

Citation: Khan M, Akhtar N, Arshad M, Kausar M, Gul S, Saleem U, Yousaf MI (2025). Genetic diversity in maize (*Zea mays* L.) genotypes against salinity tolerance at seedling stage. *SABRAO J. Breed. Genet.* 57(4): 1389-1398. http://doi.org/10.54910/sabrao2025.57.4.5.

INTRODUCTION

Maize (*Zea mays* L**.**) is the third most important cereal crop in the world, known as the king of cereals, with a total production of 1099.61 million metric tons (Zahra *et al.,* 2020). Nutritionally, maize contains 72%–73% starch, 8%–11% protein, 3%–18% oil content, and vitamins and minerals in trace amounts (FAO, 2019). In Pakistan, its cultivation covers an area of 1.6 million hectares, with a production of 9.8 million tons, showing a decrease of 4.5% in area and 10.4% in production from the previous year (Economic Survey of Pakistan, 2023–2024). Salinity is one of the chief threats to agricultural production worldwide. In Pakistan, where major source of irrigation is canal water with high amounts of sodium and chlorine in it, salinity is a continuous hazard for field crops. General reports state salinity is common in irrigated soils. Globally, 15% of arable land is under salinity, with 50% of the cultivated land expected to be saline by 2050 (Akram *et al.,* 2010; Ren *et al.,* 2025).

Plants have several mechanisms to reduce the extreme effects of salinity. Ion toxicity, poor uptake of nutrients, imbalanced osmotic adjustment, reduced chlorophyll contents, and membrane disintegrity are some major issues related to salinity. Maize is an essential C_4 plant that is moderately salt sensitive. The maize plant responds against salinity in two phases—in the first phase of imbalanced osmotic adjustment and ion toxicity with stunted growth in the second phase. Nutritional imbalance due to increased uptake of sodium and chloride ions by rhizospheres in maize under salinity was evident (Farooq *et al.,* 2015). Accounts of low uptake of nitrogen, phosphorus, and potassium occur under salinity (Katerji *et al.,* 2000). Salt stress has adversely affected the photosynthetic activity of maize plants, leading toward reduced yields (Jattan *et al.,* 2023). Maize production bears more ills from sodium augmentation than chloride accumulation, while irrigation water has high electrical conductivity and high sodium concentration. Na^+ alters the photochemical activity of photosystem II (PS II), which interferes with photosynthetic activities in maize, while penetration of Cl^- and Na^+ in hydration shells leads to conformational change in the proteins (Dionisiosese and Tobita, 2000; Hussain *et al.,* 2010). The presented study aimed to detect the genetic variability for salt tolerance in maize inbred lines at different salinity levels. It intends to benefit future selection of suitable parents for hybridization, which will ultimately develop salt-resilient maize hybrids.

MATERIALS AND METHODS

The experiment commenced at the College of Agriculture, University of Sargodha, Sargodha, Pakistan, in the year 2018 to evaluate 50 maize inbred genotypes (Table 1), with one control and two levels of salinity as treatments. Pots (14 cm × 8 cm) contained sieved sand (500 g in each pot). Electric conductivity (EC) of sand, as measured by an EC meter, was 0.89 dsm^{-1} for the control, with salt solutions made accordingly, as described by the US Salinity Lab (Richards, 1954). The research trial was in a two-factor layout under completely randomized design (CRD) and three repeats in the screening house. Salinity treatments' designations were T_1 = NaCl @ 0 dsm^{-1} (control), T_2 = NaCl @ 8 dsm^{-1}, and T_3 = NaCl @ 12 dsm^{-1}. Salinity levels' maintenance was by adding exact amounts of NaCl salt in the sand, as described by the US Salinity Lab (Richards, 1954).

$$\text{NaCl salt (g) per kg of soil} = \frac{\text{TSS} \times \text{Eq. wt. of NaCl salt} \times \text{SP}}{1000 \times 100}$$

Where: TSS = Total soluble salts, Eq. wt. = Equivalent weight, and SP = Saturation percentage of soil.

Evaluation of maize genotypes

At the age of 28 days of seedlings, the recorded data comprised root length (cm), shoot length (cm), root dry weight (g), shoot dry weight (g), and cell membrane thermostability, following the formula formulated by Sairam (1994). Measurements

Table 1. List of maize genotypes along with names and codes used in research trials.

Inbred code	Inbred name	Inbred code	Inbred name	Inbred code	Inbred name	Inbred code	Inbred name	Inbred code	Inbred name
G1	ILYL-41	G11	ILYL-30	G21	PEIL-7	G31	PEIL-16	G41	DDR-4
G2	ILYL-19	G12	ILYL-36	G22	PEIL-8	G32	ILYL-44	G42	ILYL-8
G3	PEIL-6	G13	ILYL-34	G23	PEIL-9	G33	ILYL-45	G43	DDR-5
G4	DDR-25	G14	ILYL-17	G24	ILYL-6	G34	PEIL-18	G44	DDR-6
G5	ILYL-12	G15	ILYL-48	G25	PEIL-10	G35	PEIL-20	G45	DDR-15
G6	ILYL-7	G16	ILYL-49	G26	ILYL-7	G36	PEIL-55	G46	DDR-21
G7	ILYL-23	G17	ILYL-5	G27	PEIL-19	G37	ILYL-38	G47	DDR-22
G8	ILYL-14	G18	ILYL-50	G28	PEIL-11	G38	PEIL-21	G48	DDR-23
G9	ILYL-16	G19	PEIL-1	G29	PEIL-12	G39	PEIL-22	G49	DDR-24
G10	ILYL-32	G20	PEIL-23	G30	PEIL-15	G40	DDR-3	G50	ILYL-15

Source: Maize and Millet Research Institute, Yousafwala, Sahiwal, Punjab, Pakistan.

Table 2. The mean sum of squares of seedling traits of maize genotypes at different salinity levels.

SOV	DF	RL	SL	RDW	SDW	CMS	Na	K
Genotypes	49	69.1^*	58.2^*	0.05^*	0.03^*	32^*	50^*	101.5^*
Salinity	3	38419.2^*	18164.3^*	1.18^*	1.32^*	103887^*	295726^*	23855.5^*
Genotype × Salinity	147	18.2^*	11.6^*	0.0042^*	0.012^*	16^*	12^*	16.5^*
Error	400	0.8	2.3	0.0013	0.004	1.4	1.9	1.1

*denotes significant difference ($P < 0.05$), RL = Root Length, SL = Shoot Length, RDW = Root Dry Weight, SDW = Shoot Dry Weight, CMS = Cell Membrane Stability, Na = Sodium Contents, K = Potassium Contents.

for sodium (Na^+) and potassium (K^+) contents (mol m^{-3}) followed the method described by Noiur *et al*., (1978), while cell membrane stability (%) employed the approach as reported by Sairam (1994).

Biometrical analysis

The analysis of variance (ANOVA) of seedling traits progressed as described by Steel *et al.,* (1997), using the window-based statistical software Statistix 8.1. It assessed the genetic variability among inbred lines. Biplot analysis also took place for all studied traits for the control and each treatment separately. Biplot analysis employed the window-based statistical package XLSTAT 17.0.

RESULTS

Analysis of variance

The results of ANOVA for seedling traits indicated all maize genotypes showed significant differences ($P < 0.05$) among them for all studied plant attributes. The similar pattern was also evident for treatments and treatment × genotypic interaction effects, where substantial ($P < 0.05$) changes appeared for studied traits (Table 2). This revealed the presence of ample genetic variation among maize inbred lines for salt tolerance.

Mean comparisons

Means of plant traits for salinity stress provided the basis of bifurcation of genotypes as salt tolerant and salt susceptible. Mean comparisons of maize genotypes (Table 3) displayed maximum shoot dry weight (1.27 g) and potassium contents (53.7 mol m^{-3}) in G-2 at T_1 = 0.89 dSm^{-1} (control). Similarly, maize genotypes G-11 and G-35 performed better than others for root length (36 cm). The maximum value for shoot length (49 cm) resulted in G-26. Maize lines G-3 and G-26 remained the best performing in the seedling experiment, with high mean values for root dry weight (1.34 g each) and cell membrane stability (96% and 95%, respectively) and low

Table 3. Mean performance of maize genotypes for seedling traits under Treatment-I (T_1 = 0.89dsm^{-1}).

Geno	RL	SL	RDW	SDW	CMS	Na	K	Geno	RL	SL	RDW	SDW	CMS	Na	K
G1	31	38	0.81	0.98	94	18.3	44.1	G26	37	49	1.34	0.93	95	16.2	49.9
G2	33	42	1.19	1.27	95	15.7	53.7	G27	33	40	0.96	0.81	90	18.2	39.1
G3	31	42	1.34	1.19	96	15.4	43.4	G28	26	35	0.76	0.83	93	17.7	43.1
G4	25	32	0.96	0.97	93	18.1	39.2	G29	23	43	0.76	0.87	95	17.4	42.8
G5	32	41	0.76	0.91	92	17.6	42.7	G30	32	38	0.56	0.91	96	17.2	41.6
G6	30	35	0.76	0.94	94	16.7	43.1	G31	28	39	0.74	0.88	92	17.7	38.2
G7	31	36	0.56	0.74	93	19.1	35.3	G32	39	41	0.68	0.83	95	16.2	46.8
G8	36	41	0.74	0.81	93	16.1	41.6	G33	29	34	0.77	0.94	96	16.5	48.2
G9	34	38	0.68	0.74	92	17.5	38.2	G34	27	33	0.79	0.86	95	18.3	38.4
G10	27	32	0.77	0.87	93	18.1	39.1	G35	36	38	0.78	0.88	92	16.5	48.7
G11	36	43	0.79	0.91	94	17.9	51.3	G36	28	35	0.89	0.91	91	16.2	41.1
G12	27	33	0.78	0.88	93	18.7	49.4	G37	27	33	1.10	0.94	88	18.9	38.9
G13	28	32	0.89	0.83	94	16.1	51.9	G38	27	37	0.67	0.87	89	16.3	41.2
G14	34	42	1.29	1.31	96	17.5	52.4	G39	30	32	0.88	0.79	95	17.4	41.7
G15	30	38	0.67	0.86	94	18.1	43.1	G40	31	36	0.67	0.81	95	17.3	40.9
G16	27	36	0.88	0.88	96	16.7	38.1	G41	27	31	0.78	0.87	96	18.1	44.7
+G17	31	38	0.67	0.91	95	16.3	42.7	G42	30	43	0.59	0.98	89	16.9	45.3
G18	30	35	0.78	0.94	95	18.1	42.6	G43	35	47	0.67	0.88	95	18.1	43.2
G19	30	36	0.59	0.87	95	18.1	43.4	G44	35	47	0.67	0.93	96	17.7	44.1
G20	34	34	0.67	0.98	95	16.4	38.1	G45	31	43	0.79	0.95	95	14.2	45.4
G21	25	35	0.67	0.87	95	17.8	38.5	G46	35	29	0.78	0.97	96	16.4	43.2
G22	33	34	0.79	0.79	95	17.5	38.3	G47	31	33	0.79	0.88	91	18.8	36.3
G23	26	38	0.87	0.87	95	18.8	43.1	G48	28	35	0.68	0.87	95	17.2	41.2
G24	32	34	0.81	0.91	95	15.1	51.1	G49	28	33	0.69	0.91	95	18.1	40.9
G25	28	32	1.19	0.94	94	16.9	42.7	G50	29	36	0.78	0.71	93	18.4	43.1

mean values for sodium contents in leaf sap at 15.4 and 16.2 mol m^{-3}, respectively.

Mean comparison for seedling traits under T_2 = 8 dSm^{-1} salinity level exhibited that G-26 had the highest mean value for root length (34 cm) and shoot length (45 cm). Inbred G-2 emerged to have the highest mean values for root dry weight and shoot dry weight (1.19 g and 1.07 g, respectively). The lowest value for cell membrane stability (55%) was notable for G-37, and the maximum value (78%) was evident in G-2. However, mean values for cell membrane stability decreased significantly even at low salinity levels. Regarding sodium content in leaf sap, G-33 appeared to have the lowest value of 32 mol m^{-3}, while the premiere value (41 mol m^{-3}) emerged for G-7 and G-20. Two maize genotypes, G-33 and G-35, surfaced with the highest value (33 mol m^{-3}) of potassium content in leaf sap. Meanwhile, G-27 resulted in the lowest value of 21 mol m^{-3} under T_2 = 8 dSm^{-1}, as shown in Table 4.

In the case of the T_3 = 12 dSm^{-1} salinity level, maize genotype G-35 gained the highest mean values for root length (27 cm) and shoot length (31 cm), while maize genotype G-3 had the topmost mean value for root dry weight (0.89 g). The maximum mean value for potassium content (21 mol m^{-3}) occurred in G-45 and G-14 at T_3 = 12 dSm^{-1} salinity. Regarding cell membrane stability, a maximum value (24%) was available in the G-35 genotype (Table 5). Thus, maize genotypes G-2, G-3, G-13, G-26, G-32, G-33, and G-35 proved to be salt-tolerant under all treatments in the seedling experiment.

Principal component analysis

The results of the biplot indicated that high genetic variability was present in the studied 50 maize genotypes under control and salt stress conditions. Maize inbred lines away from the origin were good performers for relative traits as compared with the genotypes nearer

Table 4. Mean performance of maize genotypes for seedling traits under Treatment-II (T_2 = 8 dSm^{-1}).

Geno	RL	SL	RDW	SDW	CMS	Na	K	Geno	RL	SL	RDW	SDW	CMS	Na	K
G1	26	34	0.71	0.73	66	39	23	G26	34	45	0.67	0.99	75	36	31
G2	28	40	0.94	1.02	78	34	31	G27	21	36	0.62	0.31	64	37	21
G3	28	39	1.19	1.07	72	39	32	G28	23	31	0.73	0.69	74	40	27
G4	24	28	0.86	0.18	66	37	26	G29	23	35	0.71	0.83	74	40	28
G5	27	36	0.67	0.75	66	37	24	G30	27	34	0.69	0.67	73	40	28
G6	25	31	0.61	0.53	70	36	23	G31	23	35	0.75	0.54	73	33	29
G7	21	30	0.51	0.28	64	41	22	G32	34	37	0.89	0.71	74	34	31
G8	22	38	0.67	0.34	66	35	24	G33	26	38	0.81	0.53	73	32	33
G9	23	34	0.62	0.89	70	36	25	G34	22	29	0.75	0.71	71	40	26
G10	22	28	0.73	0.31	71	37	26	G35	31	34	0.89	0.82	69	32	33
G11	31	40	0.71	0.94	74	36	31	G36	23	31	0.78	0.63	73	34	24
G12	22	29	0.69	0.49	77	37	29	G37	21	29	0.45	0.36	55	35	21
G13	23	37	0.97	0.57	74	37	26	G38	22	33	0.92	0.52	59	36	26
G14	29	39	1.09	0.98	77	35	34	G39	25	28	0.91	0.61	61	36	25
G15	25	34	0.64	0.24	69	40	24	G40	26	32	0.81	0.55	59	37	24
G16	22	32	0.75	0.12	74	39	24	G41	22	27	0.67	0.46	63	36	26
G17	24	32	0.74	0.87	73	37	25	G42	25	35	0.67	0.79	65	36	29
G18	25	31	0.78	0.94	71	39	25	G43	29	35	0.61	0.52	70	36	23
G19	25	32	0.45	0.5	69	38	23	G44	28	34	0.51	0.62	66	40	25
G20	20	27	0.68	0.26	66	41	24	G45	30	40	0.67	0.97	71	31	31
G21	22	31	0.87	0.79	65	37	25	G46	27	25	0.62	0.7	75	40	24
G22	28	30	0.86	0.22	70	36	26	G47	26	29	0.56	0.65	72	39	24
G23	23	34	0.67	0.69	71	37	26	G48	23	31	0.61	0.43	69	37	23
G24	27	30	0.61	0.36	66	39	26	G49	23	29	0.69	0.68	71	38	23
G25	23	28	0.58	0.78	75	36	27	G50	24	32	0.65	0.51	57	37	25

Table 5. Mean performance of maize genotypes for seedling traits under Treatment-III (T_3 = 12 dSm^{-1}).

Geno	RL	SL	RDW	SDW	CMS	Na	K	Geno	RL	SL	RDW	SDW	CMS	Na	K
G1	16	24	0.49	0.33	11	84	12	G26	22	27	0.72	0.49	18	77	12
G2	23	29	0.71	0.48	21	79	16	G27	17	29	0.41	0.01	3	90	19
G3	22	31	0.89	0.57	19	78	19	G28	14	20	0.45	0.19	12	85	11
G4	17	20	0.61	0.18	12	82	15	G29	19	23	0.47	0.33	14	85	11
G5	19	22	0.52	0.23	14	82	17	G30	16	22	0.61	0.17	19	87	11
G6	19	16	0.48	0.33	11	81	11	G31	21	29	0.56	0.14	16	78	16
G7	12	19	0.39	0.08	3	89	9	G32	22	26	0.71	0.21	20	79	18
G8	16	29	0.41	0.14	12	83	10	G33	23	22	0.89	0.54	19	77	12
G9	14	19	0.49	0.39	12	84	10	G34	19	24	0.47	0.51	16	86	11
G10	16	20	0.56	0.11	19	84	11	G35	27	31	0.69	0.52	24	79	20
G11	26	26	0.64	0.34	21	79	13	G36	16	21	0.59	0.23	14	79	12
G12	19	28	0.53	0.19	5	80	16	G37	13	17	0.41	0.06	4	89	9
G13	26	21	0.61	0.11	19	77	12	G38	14	19	0.51	0.12	8	76	11
G14	21	23	0.84	0.68	21	77	21	G39	17	23	0.43	0.21	13	76	10
G15	19	26	0.59	0.14	11	85	12	G40	16	21	0.51	0.15	12	77	12
G16	17	20	0.59	0.12	10	84	14	G41	18	18	0.59	0.16	14	78	11
G17	14	21	0.48	0.27	14	88	11	G42	19	21	0.62	0.39	19	79	12
G18	15	23	0.61	0.34	19	77	11	G43	18	20	0.43	0.12	16	79	11
G19	18	23	0.29	0.21	16	76	12	G44	21	21	0.41	0.22	4	85	11
G20	13	23	0.58	0.06	4	84	11	G45	26	26	0.69	0.77	21	82	21
G21	14	22	0.49	0.39	13	82	13	G46	22	21	0.42	0.3	16	85	16
G22	14	22	0.59	0.12	16	81	11	G47	12	22	0.41	0.35	12	84	13
G23	15	19	0.61	0.29	12	82	12	G48	21	21	0.39	0.13	14	85	12
G24	16	18	0.63	0.06	14	84	11	G49	19	23	0.42	0.18	4	83	11
G25	16	22	0.51	0.38	4	79	12	G50	18	20	0.41	0.11	8	85	11

to the origin. Maize genotypes' response for seedling traits was recognizable by plotting the three biplot in the studied saline environments (T_1 = 0.89 dSm^{-1}, T_2 = 8 dSm^{-1}, and T_3 = 12 dSm^{-1}). On the biplot for T_1 = 0.89 dSm^{-1} under the control condition, the first two components contributed collectively 56.2% of the variation, where PC1 contributed 38% and PC2 provided 18.2% individually for seedling samples (Figure 1).

Concerning the biplot for the T_2 = 8 dSm^{-1} genotypes under salt stress, the first two components contributed 63.4% variation, where PC1 contributed 49.2% and PC2 indicated 14.2% variation for seedling traits (Figure 2). Similarly, in the biplot for T_2 = 12 dSm^{-1}, the first two components had cumulative contributions of 56.2% variation, where PC1 contributed 38% and PC2 gave 18.2% variation for seedling traits (Figure 3). The opposite vectors of sodium contents displayed a strong negative association with dry root weight, dry shoot weight, root and shoot lengths, cell membrane stability, and potassium contents. At the normal condition (T_1 = 0.89 dSm^{-1}), maize genotypes represented high values of physio-morphological parameters, scattering opposite to sodium contents, and genotypes were closer in the biplot for the control treatment (Figure 1).

The results showed a little depression of morphophysiological traits at the salinity level of T_2 = 8 dSm^{-1} (Figure 2), whereas genotypes moved toward the sodium-potassium ratio and sodium content vectors when salinity increased to T_3 = 12 dSm^{-1} (Figure 3). Genotypes G-2, G-14, G-3, G-11, G-13, G-26, G-32, G-33, G-35, and G-45 had shown positive responses toward root and shoot morphological traits under the T_2 = 8 dSm^{-1} level of salinity (Figure 2). At T_3 = 12 dSm^{-1}, Na^+ content has checked the physiological trait of maize plants, i.e., potassium content of most genotypes, and only a few, viz., G14, G3, G11, G32, and G45, responded a little comfortably. However, G-2, G-3, G-26, G-33, and G-35 had good root and shoot morphological attributes. Plant cell stability to retain K^+ is a key factor for salinity tolerance.

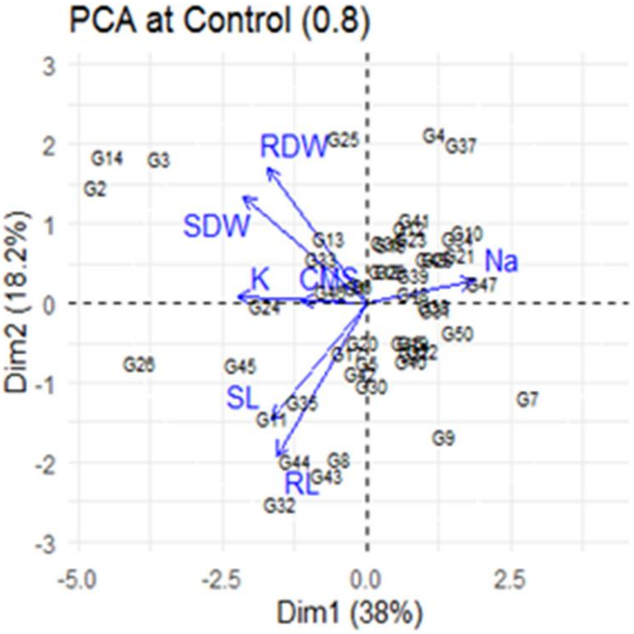

Figure 1. Biplot based on principal component analysis (PCA) of maize genotypes under Treatment-I (T_1 = 0.89 dSm^{-1}) for seedling traits.

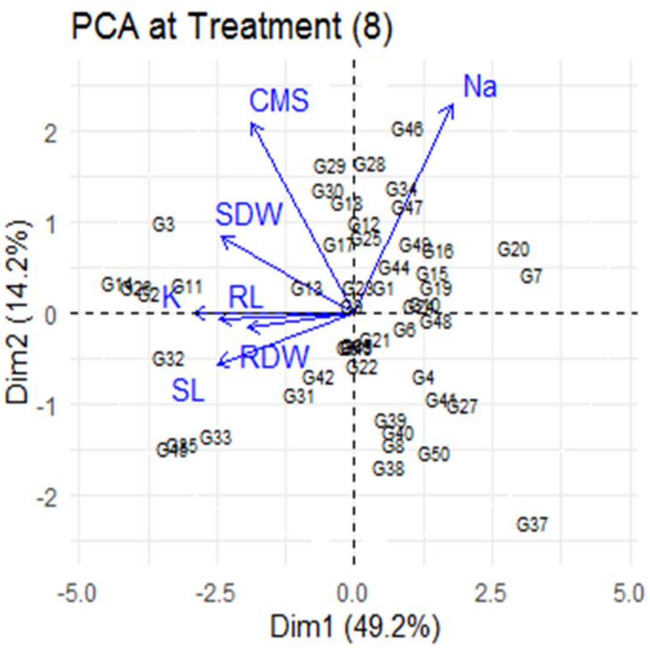

Figure 2. Biplot based on principal component analysis (PCA) of maize genotypes under Treatment-II (T_2 = 8 dSm^{-1}) for seedling traits.

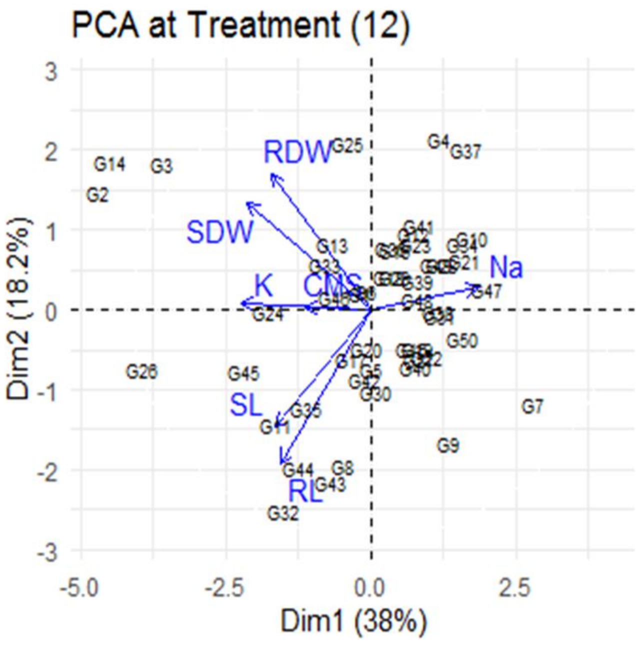

Figure 3. Biplot based on principal component analysis (PCA) of maize genotypes under Treatment-III (T_3 = 12 dSm^{-1}) for seedling traits

DISCUSSION

In this study, maize genotypes underwent screening against salinity to assess genetic diversity in available germplasm for the selection of genetically distant inbred lines under three treatments—T_1 = 0.89 dSm^{-1}, T_2 = 8 dSm^{-1}, and T_3 = 12 dSm^{-1}. Maize is a salt-sensitive crop, with reports of having maximum yield losses at 10 EC (FAO, 2019; Jattan *et al.,* 2023). Globally, abiotic stresses are emerging as a serious threat to agricultural production. Development of stress-resilient plants could be an effective tool to ensure sustainable productivity. A key factor to enhance stress tolerance is the assessment of genetic variability within existing germplasms (Bello *et al.,* 2012). A short way to develop salt-tolerant genotypes is the use of already available variations in existing germplasms. Genetic studies for salt tolerance had been progressing in many crops, including maize. The reported study sought to screen and discriminate salt-tolerant and susceptible maize inbred lines and their utilization for the development of salt-tolerant F_1 hybrids.

Better seedling growth showed a positive association with lateral plant developmental stages, resulting in high yields (Willenborg *et al.,* 2005). In this current study, 28-day-old seedlings received evaluation in sand pots under control and different salinity levels as practiced by Raza *et al.* (2017). Analysis of variance had shown that maize genotypes and salinity × genotypic interaction effects proved significant ($P < 0.05$) for all the studied standards against salinity for seedling traits (Table 2). Significant reductions in morphological and physiological parameters were also evident under high salt stress conditions due to an increase in Na^+ and a decrease in K^+ contents in plant cell sap, as described by Raza *et al., (*2017).

Significant reduction in root length and dry root weight appeared under salt stress conditions. Maize genotypes G-3, G-26, G-35, and G-45 performed excellently and gained high values for root length under salt stress levels T_2 = 8 dSm^{-1} and T_3 = 12 dSm^{-1}. Higher root length under salt stress conditions emerged to be linked with salt stress tolerance and helped to improve shoot length of maize seedlings under salt stress conditions (Mazhar *et al.,* 2020).

Salinity-induced reduction in shoot length and reduced root length had negative impacts on normal growth of the seedling. In the promising study, susceptible genotypes showed lesser shoot length, while tolerant genotypes attained higher shoot length, as genotypes G-3, G-26, and G-35 had shown longer shoot length than others under the studied salt-stressed conditions. Pessarakli and Kopec (2009) also reported higher salt concentrations reduced the shoot length significantly. Increasing salinity comes with a significant reduction in shoot length, as described in the past research (Ashraf *et al.,* 2010; Mazhar *et al.,* 2020). In literature, it is reported root growth is sensitive to high salt concentrations in the medium and rapidly reduced by salinity (Ashraf *et al.,* 2010). Under saline environments, the prime cause of decline in plant growth seemed either due to osmotic drop in water availability or too much accretion of ions (Chinnusamy *et al.,* 2005).

Potassium-retaining capability of plant cells is a key factor for salinity tolerance (Abbasi *et al.,* 2012). The ability of plant genotypes to maintain higher levels of K^+ and Ca^{2+} and low levels of Na^+ within the tissue is one of the crucial mechanisms contributing to the expression of high salt tolerance (Jamil *et al*., 2012; Hussain *et al.,* 2023). Our results indicated that more attention should focus on high uptake of K^+ by roots when testing a maize inbred line for salt stress tolerance. Ashraf *et al.,* (2010) reported an important emphasis should center on the ability of biomass production and ion contents for the categorization of maize hybrids for salt-stress tolerance.

Accumulation of sodium in plant parts hinders the availability of essential elements (K and Ca), which causes damage to biological membranes, having negative impacts on the normal functioning of cellular organelles (Quintero *et al.,* 2007). The results of this study indicated physiological traits due to their high sensitivity toward salinity acquired adverse effects from salt treatments. However, significant genetic variation resulted in the performance of maize genotypes at different salinity levels. Maize genotypes G-2, G-11, and G-45 showed higher values for cell membrane stability under salt stress conditions. Thus, maize genotypes G-2, G-3, G-11, G-13, G-32, G-33, G-35, and G-45 had displayed high mean values for shoot and root lengths, potassium contents, root dry weight, and shoot dry weight. They proved to be salt tolerant under all treatments at the seedling stage.

In the principal component analysis, at the normal condition (T_1 = 0.89 dSm^{-1}), maize genotypes represented high values for morphophysiological traits, as they scattered opposite to sodium contents (Na^+), and genotypes were closer in the biplot for the control treatment. This showed a little depression of morphophysiological traits at the salinity level of T_2 = 8 dSm^{-1}, whereas genotypes moved toward sodium-potassium ratio and sodium content vectors when salinity increased to T_3 = 12 dSm^{-1}. Genotypes G-2, G-3, G-11, G-13, G-32, G-33, G-35, and G-45 had exhibited positive responses toward root and shoot morphological traits under the T_2 = 8 dSm^{-1} level of salinity. Ashraf *et al.* (2010) reported that an important emphasis is necessary on the ability of biomass production and ion contents for the categorization of maize genotypes for salt-stress tolerance.

The higher root length under salt-stress conditions revealed an association with salt tolerance, which facilitated shoot length of maize seedlings under salt-stress conditions. Ahmad *et al*., (2010), Mustafa *et al*. (2013), and Mazhar *et al*., (2020) also observed more root and shoot dry weight in salt-tolerant genotypes. Differential selectivity for K^+ over Na^+ of genotypes under salinity is a determinant of the magnitude of dry matter production in plants. At T_3 = 12 dSm^{-1}, Na^+ had checked the physiological trait, potassium contents of most genotypes, with only a few, such as G-2, G-3, G-33, and G-35, gaining good root and shoot morphological attributes.

CONCLUSIONS

Maize genotypes G-3 (PEIL-6), G-11 (ILYL-30), G-33 (ILYL-45), G-35 (PEIL-20), and G-45 (DDR-15) emerged as salt-tolerant genotypes at 10 dSm^{-1} and 12 dSm^{-1} levels for most studied traits. Thus, the study suggests that these genotypes should be most suitable in maize breeding programs to develop salt-tolerant hybrids and open-pollinated varieties for saline soils.

ACKNOWLEDGMENTS

This paper is the part of Ph.D. Thesis research of first author, conducted at the College of Agriculture, University of Sargodha, Sargodha, Pakistan. The authors are pleased to acknowledge Higher Education Commission (HEC), Pakistan for financial support under HEC Indigenous Scholarship Program Phase II and Hi-Tech Laboratory University of Sargodha.

REFERENCES

Abbasi GH, Akhtar J, Anwar-ul-Haq M, Ahmad N (2012). Screening of maize hybrids for salt tolerance at seedling stage under hydroponic condition. *Soil Environ.* 31(1): 83-90.

Ahmad P, Jaleel CA, Salem MA, Nabi G, Sharma S (2010). Roles of enzymatic and nonenzymatic antioxidants in plants during abiotic stress. *Crit. Rev. Biotechnol.* 30(3): 161-175.

Akram M, Ashraf MY, Ahmad R, Waraich EA, Iqbal J, Mohsan M (2010). Screening for salt tolerance in maize (*Zea mays* L.) hybrids at an early seedling stage. *Pak. J. Bot.* 42: 141-154.

Ashraf M, Akram NA, Arteca RN, Foolad MR (2010). The physiological, biochemical and molecular roles of brassinosteroids and salicylic acid in plant processes and salt tolerance. *Crit. Rev. Plant Sci.* 29(3): 162-190.

Economic Survey of Pakistan (2023). Economic Survey of Pakistan, Finance Division, Islamabad, Pakistan.

Food and Agriculture Organization (2019). FAO scales up fight against Fall Army worm. https: //www.fao.org/news/story/en/item/1253916/icode/.

Farooq M, Hussain M, Wakeel A, Siddique KH (2015). Salt stress in maize: Effects, resistance mechanisms, and management. *Agron. Sustain Dev.* 35(2): 461-481.

Hussain K, Majeed A, Nawaz K, Nisar MF (2010). Changes in morphological attributes of maize (*Zea mays* L.) under NaCl salinity. *Am-Eur. J. Agric. Environ. Sci.* 8: 230-232.

Hussain SS, Rasheed M, Ahmed ZA, Jilani G (2023). Characterizing maize genotypes for salt tolerance using morphological and ionic traits at seedling stage. *Int. Lett. Natu. Sci.* 86: 1-24. doi: https://doi.org/10.56431/p-03pzu8.

Jamil M, Ashraf M, Rehman S, Ahmad M, Rha ES (2012). Salinity induced changes in cell membrane stability, protein, and RNA contents. *Afr. J. Biotechnol.* 11(24): 6476-6483.

Jattan M, Kumari N, Rani B, Phogat DS, Kumari S, Ravika, Chawla R (2023). Conventional breeding and advance approaches to mitigate drought and salt stress in crop plants. In: Salinity and Drought Tolerance in Plants: Physiol. Pers. pp. 121-135. Singapore: Springer Nature Singapore.

Katerji N, Van-Hoorn JW, Hamdy A, Mastrorilli M (2000). Salt tolerance classification of crops according to soil salinity and to water stress day index. *Agric. Water Manag. 43*(1): 99-109.

Mazhar T, Ali Q, Malik MSRA (2020). Effects of salt and drought stress on growth traits of *Zea mays* seedlings. *Life Sci. J.* 17(7): 48-54.

Mustafa HSB, Ahsan M, Aslam M, Ali Q, Bibi T, Mehmood T (2013). Genetic variability and traits association in maize (*Zea mays* L.) accessions under drought stress. *J. Agric. Res*. 51(3): 231-238.

Noiur AM, Weibel DE, Tood GW (1978). Evaluation of root characteristics in grain sorghum. *Agron. J.* 70:217-218.

Pessarakli M, Kopec DM (2009). Screening various ryegrass cultivars for salt stress tolerance. *J. Food Agric. Environ. 7*(3): 4.

Quintero JM, Fournier JM, Benlloch M (2007). Na+ accumulation in shoot is related to water transport in K+-starved sunflower plants but not in plants with a normal K+ status. *J. Plant Physiol.* 164: 60-67. https://doi.org/10.1016/j. jplph.2005.10.010.

Raza MA, Saeed A, Munir H, Ziaf K, Shakeel A, Saeed N, Rehman F (2017). Screening of tomato genotypes for salinity tolerance based on early growth attributes and leaf inorganic osmolytes. *Arch. Agron. Soil Sci.* 63(4): 501-512.

Ren S, Tan J, Zhou S, Sun H, Li H, Li W, Li N, Wu J, Ren X, Ci J (2025). Germplasm selection and comprehensive evaluation of maize inbred lines at germination and seedling stage for saline–alkali tolerance. *Agronomy* 15(3): 626. https://doi.org/10.3390/agronomy15030626.

Richards LA (1954). Diagnosis and improvement of saline and alkaline soils. United States Department of Agriculture Handbook # 60. Washington D.C.

Sairam RK (1994). Effects of homobrassinolide application on plant metabolism and grain yield under irrigated and moisture-stress conditions of two wheat varieties. *Plant Growth Reg.* 14: 173-181.

Steel RGD, Torrie JH, Dicky DA (1997). Principles and Procedures of Statistics: A Biometrical Approach, 3rd ed. McGraw Hill Book Co., New York.

Willenborg CJ, Wildeman JC, Miller AK, Rossnage BG, Shirtliffe SJ (2005). Oat germination characteristics differ among genotypes, seed sizes and osmotic potentials. *Crop Sci.* 45: 2023-2029.

Zahra N, Raza ZA, Mahmood S (2020). Effect of salinity stress on various growth and physiological attributes of two contrasting maize genotypes. *Braz. Arch. Biol. Tech.* 63. https://doi.org/10.1590/1678-4324-2020200072.