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NaCl tolerance studies at seedling stage among different genotypes of *Helianthus annus* L.

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A greenhouse research was conducted at the research area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad to evaluate 20 accessions for the identification of salt tolerant genotypes of sunflower (Helianthus *annuus* L.) as well as their characteristics. The experiment was conducted in completely randomized design with three repeats. Salinity was developed with NaCl to achieve the final levels of 3, 6 and 9 dsm^{-1} salinity, whereas control contained tap water. After 60 days of planting, 10 seedlings of each accession from each treatment and replication were uprooted and data was recorded. Sunflower genotypes G-36, G-61, A-23, A-61 and A-185 performed better in both controlled and saline conditions. These genotypes showed better shoot and root growth and biomass by least concentration of Na^+ and higher concentration of Cl^- in leaf sap.

Key words: Tap water, NaCl, replication, leaf sap.

INTRODUCTION

Sunflower (*Helianthus annuus* L.) is the second most important oilseed crop after soybean worldwide (Paniego et al., 2002). Sunflower is high yielding and non-conventional oilseed crop. It had desirable traits that is high oil contents (40-47%), protein (23%), high linoleic acid, toxic free elements and contain vitamins A, D, E, K. Salinity in soil or water is one of the major stresses and especially in arid and semi arid regions, can severely limit crop production. Salinity impairs seed germination, reduces nodule formation, retards plant development and reduces crop yield. High levels of soil salinity negatively affect productivity of most field crops (Munns, 1993). Saline soils remarkably reduce oil production potential and oil yield of sunflower (Szabolcs, 1994).The plants that grow in saline soils have diverse ionic compositions and a range in concentrations of dissolved salts. These concentrations fluctuate because of changes in water source, drainage, evapotranspiration, and solute availability. About 7% of arable lands of the world are under salinity pressure (Jumsoon et al., 1996). Soil

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Table 1. Soil analysis.

Determination	Value
Electrical conductivity (E.C.)	1.23 (d Sm^{-1})
Saturation percentage (S.P)	25.70 (%)
Total soluble salt (TSS)	17.7 (me L^{-1})

Table 2. Water analysis.

Parameter	Value
EC	1.036 (me L^{-1})
Na^{+}	3.83 (me L^{-1})
$Ca^{+} + Mg^{++}$	6.53 (me L^{-1})
TSS	10.36 (me L^{-1})

salinity reduces water availability of plant roots via negative (low) osmosis potential, as well as decrease of germination dynamics of plant seeds by ionic toxicity of behavior and response of different accessions of sunflower to tolerate salt stress at seedling stage. The Na+ and Cl- (Munns et al., 1988).

The study was conducted to understand the genetic information so obtained will be useful in formulating criteria for salt stress tolerance and high yield. The objective was also the development of selection criteria through correlation and path analysis studies. The selected types could be used in hybridization programme aimed at breeding for sunflower yielding high under salt stress conditions. The availability of high yielding salt stress tolerant sunflower is perceived to attract farmer to use the land resources otherwise left fallow due to salt stress.

MATERIALS AND METHODS

The present study was carried out under the glass house of the department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The research material was comprised of 20 accessions of sunflower developed by the Oilseed Research Programme of the Department. These accessions (G-16, G-30, G-32, G-36, G-44, G-45, G-61, G-64, G-66, G-68, G-86, A-2, A-14, A-23, A-56, A-60, A-61, A-79, A-133 and A-185) were planted and evaluated for various traits in the salinity experiments.

Experimental layout

Experiment was conducted in a glass house with no control of humidity, temperature and light. The experiment was laid out following factorial complete randomized design in three replications. The sunflower seed were planted in iron trays. Each tray was filled with soil and sand in the ratio of 1:1. The seeds were sown at the depth of 1.5 cm by maintaining distance of 2.5 cm each for row to row and seed to seed.

Planting medium

Normal soil free from any salinity and sodicity hazards was collected from the research area of department of Plant Breeding and Genetics, University of Agriculture Faisalabad. The mixture of sand and soil was air dried, ground and passed through 2 mm sieve and analyzed for chemical characters (Table 1).

Treatments

Tap water was applied for irrigation for 15 days according to requirement. After germination, four salt (NaCl) levels of irrigation water were maintained: treatment 1 = normal water (tap water); treatment 2 = 3 dsm^{-1}; treatment 3 = 6 dsm^{-1}; Treatment 4 = 9 dsm^{-1}. Composition of tap water is given in Table 2.

Tissue sap analysis for ion uptake

Sample collections

The 10 randomly selected plants per replication and per treatment for each genotype were uprooted. Two lower leaves (form the basal node) and two upper leaves (from the top node) were collected, washed with tap water to remove the soil residues and then dipped instantly in distilled water for a short period of time. The samples were blotted dry with the help of a sheet of blotting paper, placed in polyethylene bags, marked with the spirit marker and stored in the deep freezer for tissue sap extraction.

Extraction of leaf sap

Frozen leaf samples were thawed, after washing with distilled water, the tissue sap was extracted by using metal rod .The tissue sap oozing out from the samples was collected in epindroph tubes and immediately stored back in the deep freezer.

Centrifugation of tissue sap

The epindroph tubes were taken out from the freezer and placed at the room temperature to thaw. Then the thawed tissue sap was centrifuged at the 6500 rpm for 5 min. The supernatant tissue sap samples from epindroph tubes were analyzed for chloride, sodium and potassium ions.

Determination of chloride ions

Chloride ions in the tissue sap was determined by chloride analyzer (Sherwood chloride analyzer 926).

Determination of sodium ions

The tissue sap was diluted as required with distilled water. Sodium ions were determined using Flame Photometer (Sherwood flame photometer 410).

Data recording

After 60 days of planting, ten seedlings of each accession from each treatment and replication were uprooted. Data were recorded from the experiment on following parameters viz. Germination percentage (G %), emergence index (EI), emergence rate index (ERI), chlorophyll content, root: shoot ratio, mortality (M %).

Table 3. Comparisons of mean square values of analysis of variance of different salt stress levels on different traits.

Character	Control (0 d sm^{-1})		Salt stress level 1 (3 d sm^{-1})		Salt stress level 2 (6 d sm^{-1})		Salt stress level 3 (9 d sm^{-1})	
	Genotype	Error	Genotype	Error	Genotype	Error	Genotype	Error
Shoot length	24.820**	1.323	40.789**	7.374	50.263**	10.248	21.455**	2.115
Root length	0.432**	0.007	0.892**	0.106	0.563**	0.061	0.361**	0.042
Na^+ content	34.856**	1.317	139.807**	0.950	285.863**	0.933	767.530**	1.517
Cl^- content	1317.631**	1.717	2608.351**	1.183	1752.754**	1.667	3275.074**	5.800
Chlorophyll	26.799**	1.937	27.316**	4.588	34.025**	2.897	37.409**	0.434
Mortality %	10.877**	0.283	33.010**	4.908	57.202**	5.343	190.789**	9.207
Root / shoot ratio	0.014**	0.005	0.001**	4×10^{-3}	0.001**	2.5×10^{-4}	0.001**	1.75×10^{-3}

*Significant, **highly significant; ^{NS}Non significant.

Table 4. Mean Squares from the analysis of variance for germination percentage (G%), emergence index (EI), emergence rate index (ERI) of different sunflower genotypes.

SOV	DF	G %	E.I.	E.R.I.
Genotype	19	245.263^{NS}	71.835*	0.005^{NS}
Error	40	140.000	30.773	0.004
Total	59			
C.V.		12.20%	6.65%	7.00%

LSD value of emergence index = 9.154.

RESULTS AND DISUCSSION

The experimental results were obtained, presented and discussed separately.

Analysis of variance under four treatments

Under salt stress condition level 2 (6 dS m^{-1}) and level 3 (9 dS m^{-1}), significant differences and marked variation among accessions for all the traits were detected under normal and all salt stress levels, furthermore, the genotypes behaved differently to the stress. The comparison of treatment expression of various plant traits under normal and salt stress level 3 (9 dS m^{-1}) conditions suggested that salt stress adversely affected for the characters (Table 3).

Germination percentage (G%)

The analysis of variance of germination percentage of sunflower population under the study (Table 3). Non significant differences existed among of genotypes of the sunflower.

Emergence index (EI)

The analysis of variance of sunflower genotypes for emergence index is shown in Table 4. The results indicate that sunflower genotypes had significant differences and ranged from 91.80 to 75.00 (Table 5). The maximum value 91.80 was observed in the genotype A-85 followed by the genotype A-14 (90.40) and genotype A-133 (89.13).

Emergence rate index (ERI)

Table 4 reveals that the differences for emergence rate index among genotypes were non-significant.

Effect of salt stress (NaCl) on shoot length (cm)

Table 6 indicates that the shoot length was decreased significantly with increasing salinity levels. Interaction of all the genotypes and treatments was found significant.

Table 6 shows that accession G-36 closely followed by G-66 and A-23 had maximum shoot length and accession A-60 followed by A-2 and G-30 had minimum shoot length under normal condition. Accession A-23 closely followed by G-36 and G-64 had maximum shoot length under salt stress level 1 (3 dsm^{-1}). Accessions G-36 closely followed by G-45 and G-44 had maximum shoot length under salt stress level 2 (6 dsm^{-1}). Accession G-86 closely followed by G-30 and A-14 had maximum shoot length under salt stress level 3 (9 dsm^{-1}). Ramoliya and Panday (2003); Mer et al. (2000) and Ramdiya and Panday (2003) also demonstrated that salinity in nutrient

Table 5. Statistical Mean values of emergence index among various genotype of sunflower.

Genotype	Mean
A-185	91.80 A
A-14	90.40 A B
A-133	89.13 ABC
G-61	88.47 ABCD
G-45	87.80 ABCD
A-79	87.00 ABCD
G-64	86.93 ABCD
G-32	84.93 ABCDE
A-2	84.53 ABCDE
A-60	84.40 ABCDE
A-61	84.40 ABCDE
A-56	82.40 ABCDE
G-68	80.80 BCDE
G-66	80.40 BCDE
G-86	79.27 CDE
G-16	78.52 CDE
G-44	77.87 DE
G-30	77.67 DE
G-36	77.50 DE
A-23	75.00 E

The lines sharing common letters do not differ significantly from each other at 5% probability level.

solution reduced the growth of black spot (*Diospyros digvna* Jacq).

Effect of salt stress (NaCl) on root length (cm)

Table 7 shows that accession A-133 closely followed by A-60 and A-185 had maximum root length under normal condition. Accession G-66 closely followed by A-2 and A-79 had maximum root length under salt stress level 1 (3 dsm^{-1}). Accessions G-36 closely followed by A-2 and A-23 had maximum root length under salt stress level 2 (6 dsm^{-1}). Accession G-44 closely followed by G-36 and A-185 had maximum root length under salt stress level 3 (9 dsm^{-1}). Qureshi et al. (1998), Hussain and Rehman (1995) and Ghumman (2000) also conducted experiments on sunflower and found that root length and relative root length decreased with increase in salinity.

Effect of salt stress (NaCl) on chlorophyll content

Table 8 shows that accession A-79 closely followed by G-68 and G-32 had maximum chlorophyll under normal condition. Accession G-86 closely followed by G-68 and A-23 had maximum chlorophyll under salt stress level 1 (3 dsm^{-1}). Accessions A-61 closely followed by A-185 and A-60 had maximum chlorophyll under salt stress level 2 (6 dsm^{-1}). Genotypes G-68 closely followed by A-185 and G-66 had maximum chlorophyll under salt stress level 3 (9dsm^{-1}).

Effect of salt stress (NaCl) on sodium concentration (mol m^{-3}) in extracted leaf sap

Table 9 shows that accession A-23 closely followed by A-14 and A-61 had maximum Na+ content under normal condition. Accession A-56 closely followed by A-133 and A-61 had maximum Na^+ content under salt stress level 1 (3 dsm^{-1}). Genotype A-133 closely followed by A-56 and A-60 had maximum Na^+ content under salt stress level 2 (6 dsm^{-1}). The line A-133 closely followed by A-56 and A-60 had maximum Na^+ content under salt stress level 3 (9 dsm^{-1}). Nawaz et al. (2002) in sunflower also reported that the increase in sodium contents in leaves with increasing salinity was attributed to the increased amount of sodium ion in rooting medium, passive Na^+ diffusion through damaged membranes, decreased efficiency of exclusion mechanism.

Effect of salt stress (NaCl) on potassium concentration (mol m^{-3}) in extracted leaf sap of sunflower genotypes

Table 7 shows that accession A-60 closely followed by G-68 and G-32 had maximum K^+ content under normal condition. Accession G-32 closely followed by G-44 and G-45 had maximum K^+ content under salt stress level 1 (3 dsm^{-1}). The line A-56 closely followed by G-61 and G-44 had maximum K^+ content under salt stress level 2 (6 dsm^{-1}). Accession G-68 closely followed by G-66 and A-56 had maximum K^+ content under salt stress level 3 (9 dsm^{-1}). Decrease in K^+ concentration with increasing salinity was also reported a significant reduction of potassium in sorghum with increasing salinity. There is a debate that K^+ influx could be used as an index to salinity tolerance Shainberg and Levy (1992).

Effect of salt stress (NaCl) on chloride concentration (mol m^{-3}) in extracted leaf sap

Table 10 shows that genotype G-30 closely followed by G-185 and G-68 had maximum Cl^- content under normal condition. Accession G-68 closely followed by A-2 and A-56 had maximum Cl^- content under salt stress level 1 (3 d Sm^{-1}). The line G-32 closely followed by G-36 and A-61 had maximum Cl^- content content under salt stress level 2 (6 d Sm^{-1}). Accession A-185 closely followed by G-36 and G-61 had maximum Cl^- content under salt stress level 3 (9 dsm^{-1}).

Table 6. Statistical comparison of varietal means for shoot length for various salt stress levels.

Genotype	Normal (0 dsm^{-1})	Salt stress Level 1 (3 dsm^{-1})	Salt stress Level 2 (6 dsm^{-1})	Salt stress Level 3 (9 dsm^{-1})
G-16	43.44De	39.19a-f	30.97d-g	24.52ef
G-30	40.78Gh	40.70a-e	34.57b-e	29.81ab
G-32	43.54De	37.68b-f	30.23d-g	27.60b-d
G-36	51.14A	42.76ab	42.21a	26.77c-e
G-44	43.16d-f	41.46a-c	37.85a-c	26.97c-e
G-45	45.86C	41.65a-c	38.66ab	24.22ef
G-61	44.30Cd	41.34a-c	32.24c-g	27.40b-d
G-64	46.22C	42.11a-c	35.89b-d	24.89d-f
G-66	48.87B	33.95fg	31.85c-g	24.54ef
G-68	44.32Cd	35.52d-g	28.93e-g	23.15fg
G-86	44.40Cd	41.82a-c	36.46b-d	30.34a
A-2	40.29Gh	30.82g	28.37e-g	21.00gh
A-14	43.22d-f	39.29a-f	34.37b-e	27.87a-c
A-23	46.41C	43.45a	33.28b-f	23.02fg
A-56	43.44De	40.89a-d	30.94d-g	26.48c-e
A-60	39.57H	31.76g	26.18g	20.14h
A-61	41.81e-g	36.98c-f	30.32d-g	26.81c-e
A-79	43.64De	35.90d-g	29.11e-g	26.27c-e
A-133	40.84Gh	35.53e-g	27.54fg	22.75fg
A-185	41.23f-h	37.74b-f	31.54d-g	24.47ef

Means sharing common letters do not differ significantly at 5% probability level using LSD. LSD for genotypes under Normal condition =1.898; LSD for genotypes at salt stress level 1 (3 dsm^{-1}) = 4.589; LSD for genotypes at salt stress level 2 (6 dsm^{-1}) = 5.283; LSD for genotypes at salt

Table 7. Statistical comparison of varietal means for root length for various salt stress levels.

Genotype	Normal (0 dsm^{-1})	Salt stress Level 1 (3 dsm^{-1})	Salt stress Level 2 (6 dsm^{-1})	Salt stress Level 3 (9 dsm^{-1})
G-16	6.730J	6.540c-e	6.349c-f	5.93b-d
G-30	6.730j	6.650c-e	6.117ef	5.47f-h
G-32	7.097g-i	5.533f	6.553b-e	5.20h
G-36	7.357De	7.117a-c	7.717a	6.25ab
G-44	7.130gh	6.233de	6.473b-f	6.54a
G-45	7.407d	7.147a-c	6.067f	5.92b-d
G-61	7.283d-f	6.850b-d	6.207d-f	5.90b-d
G-64	7.117g-i	6.623c-e	6.097ef	5.66d-g
G-66	7.080g-i	7.690a	6.260d-f	5.45f-h
G-68	6.973I	7.160a-c	6.273d-f	5.44f-h
G-86	7.187f-h	6.790c-e	6.343c-f	5.89b-e
A-2	6.593Jk	7.630a	7.513a	5.51e-h
A-14	7.217e-g	6.210e	6.570b-e	5.50f-h
A-23	7.620C	7.417ab	6.870b	5.78c-f
A-56	6.497K	6.250de	6.443b-f	5.57d-h
A-60	7.797ab	6.597c-e	6.773bc	5.29gh

Table 7. Contd.

A-61	7.227e-g	6.917bc	6.327c-f	5.45f-h
A-79	7.053Hi	7.537a	6.580b-e	5.42f-h
A-133	7.883A	6.530c-e	6.627b-d	5.33gh
A-185	7.703Bc	7.080a-c	6.797bc	6.07bc

Means sharing common letters do not differ significantly at 5% probability level using LSD. LSD for genotypes under Normal condition =0.138; LSD for genotypes at salt stress level 1 (3 dsm^{-1}) = 0.537; LSD for genotypes at salt stress level 2 (6 dsm^{-1}) = 0.408; LSD for genotypes at salt stress level 3 (9 dsm^{-1}) = 0.338.

Table 8. Statistical comparison of varietal means for chlorophyll for various salt stress levels.

Genotype	Normal (0 dsm^{-1})	Salt stress Level 1 (3 dsm^{-1})	Salt stress Level 2 (6 dsm^{-1})	Salt stress Level 3 (9 dsm^{-1})
G-16	31.73e-g	31.39e-g	35.79de	30.81l
G-30	35.44a-c	28.24g	33.06ef	36.07hi
G-32	36.14ab	30.24fg	34.65de	35.18ij
G-36	24.96i	34.19c-f	40.38ab	34.63j
G-44	31.22f-h	33.38def	35.35de	36.42gh
G-45	29.02h	32.84ef	41.28ab	37.48fg
G-61	34.77a-d	35.03b-e	40.69ab	37.52fg
G-64	29.66gh	37.57a-d	35.85de	36.18hi
G-66	32.76d-f	35.32b-e	41.91ab	39.59c
G-68	37.02a	39.11ab	39.57bc	46.46a
G-86	31.10f-h	40.58a	36.41d	39.44cd
A-2	31.74e-g	37.29a-d	35.36de	38.26d-f
A-14	34.13b-e	37.11a-d	36.93cd	36.42gh
A-23	35.56a-c	37.86a-c	35.72de	37.91ef
A-56	32.02e-g	33.96c-f	37.47cd	38.76c-e
A-60	33.37c-f	34.28c-f	42.21ab	38.98c-e
A-61	31.45f-h	34.57c-e	42.95a	32.86k
A-79	37.15a	37.81a-c	37.02cd	38.84c-e
A-133	32.62d-f	33.88c-f	31.75f	34.81j
A-185	35.14a-d	34.71c-e	42.90a	44.50b

Means sharing common letters do not differ significantly at 5% probability level using LSD. LSD for genotypes under Normal condition= 2.297; LSD for genotypes at salt stress level 1 (3 dsm^{-1})= 3.535; LSD for genotypes at salt stress level 2 (6 dsm^{-1}) = 2.440; LSD for genotypes at salt stress level 3 (9 dsm^{-1})= 1.087.

Table 9. Statistical comparison of varietal means for na^{+} concentration (mol m^{-3}) for various salt stress levels.

Genotype	Normal (0 dsm^{-1})	Salt stress Level 1 (3 dsm^{-1})	Salt stress Level 2 (6 dsm^{-1})	Salt stress Level 3 (9 dsm^{-1})
G-16	17.67e-g	23.00j	55.00e	72.00g
G-30	16.00G	31.00fg	50.00gh	62.67j
G-32	19.00c-f	40.00c	44.67i	49.67k
G-36	17.33e-g	24.33ij	51.67fg	71.33g
G-44	17.00Fg	29.00h	38.67k	43.33l
G-45	12.67h	36.00de	69.00b	68.33h
G-61	16.00g	23.00j	50.00gh	73.33fg
G-64	20.00b-d	25.33i	52.00f	65.00i
G-66	19.00c-f	38.67c	59.67c	73.33fg

Table 9. Contd.

G-68	17.00fg	29.67gh	45.33i	90.00c
G-86	16.00g	26.00i	60.67c	91.00c
A-2	17.00fg	36.67d	59.00c	83.00d
A-14	21.33b	34.33e	51.00fg	77.00e
A-23	30.33a	35.00de	49.00h	75.00ef
A-56	19.00c-f	46.33a	70.00b	100.00a
A-60	18.00d-g	31.67f	69.67b	95.00b
A-61	20.67bc	41.67b	59.00c	65.33i
A-79	17.00fg	31.00fg	41.00j	51.67k
A-133	19.33b-e	43.00b	72.33a	101.30a
A-185	19.00c-f	31.00fg	57.00d	73.00fg

Means sharing common letters do not differ significantly at 5% probability level using LSD. LSD for genotypes under normal condition = 1.894; LSD for genotypes at salt stress level 1 (3 dsm^{-1}) = 1.608; LSD for genotypes at salt stress level 2 (6 dsm^{-1})=1.594; LSD for genotypes at salt stress level 3 (9 dsm^{-1})= 2.032.

Table 10. Statistical comparison of varietal means for cl^- concentration (mol m^{-3}) for various salt stress levels.

Genotype	Normal (0 dsm^{-1})	Salt stress Level 1 (3 dsm^{-1})	Salt stress Level 2 (6 dsm^{-1})	Salt stress Level 3 (9 dsm^{-1})
G-16	46.00j	80.67k	152.30f	128.00hi
G-30	98.00a	71.00m	136.30h	126.70i
G-32	61.00g	41.00q	169.70a	173.70c
G-36	78.67e	71.33m	166.00b	181.70b
G-44	66.00f	67.67no	76.67o	82.67l
G-45	82.67d	74.00l	150.00f	83.00l
G-61	78.33e	117.00f	126.30k	175.00c
G-64	47.00j	87.33j	141.70g	152.30e
G-66	39.00l	119.00e	150.30f	155.70e
G-68	86.00c	145.70a	135.00h	165.00d
G-86	33.00m	123.70d	128.70j	147.30f
A-2	38.00l	137.70b	152.00f	131.00h
A-14	42.00k	56.67p	100.30n	144.70fg
A-23	57.00h	73.33l	132.00i	147.00f
A-56	39.67l	134.00c	158.00d	93.67k
A-60	54.67i	66.00o	152.30f	124.70i
A-61	55.00hi	68.33n	160.30c	141.00g
A-79	32.33m	101.00g	114.70l	111.30j
A-133	34.00m	91.00i	103.00m	91.67k
A-185	88.67b	93.67h	154.70e	196.00a

Means sharing common letters do not differ significantly at 5% probability level using LSD. LSD for genotypes under Normal condition= 2.162; LSD for genotypes at Salt Stress Level 1 (3 dsm^{-1})= 1.795; LSD for genotypes at Salt Stress Level 2 (6 dsm^{-1}) = 2.131; LSD for genotypes at Salt Stress Level 3 (9 dsm^{-1})= 3.974

Effect of salt stress (NaCl) on mortality % in sunflower genotypes

Table 11 shows that accession A-185 followed by A-66 and A-79 had minimum mortality % under normal condition. The genotype G -14 followed by G-61 and G-45 had minimum mortality % under salt stress level 1 (3 dsm^{-1}). The line G-44 followed by A-79 and G-16 had minimum mortality % under salt stress level 2 (6 dsm^{-1}). Accession G-30 followed by A-79 and G-68 had minimum

Table 11. Statistical comparison of varietal means for mortality (%) for various salt stress levels.

Genotype	Normal (0 dsm^{-1})	Salt stress Level 1 (3 dsm^{-1})	Salt stress Level 2 (6 dsm^{-1})	Salt stress Level 3 (9 dsm^{-1})
G-16	0.00c	7.41bc	14.81d	36.70de
G-30	3.33b	6.33bc	20.00c	16.67l
G-32	6.67a	13.33a	23.33a-c	50.00A
G-36	0.00c	10.37ab	21.48bc	36.30de
G-44	0.00c	6.67bc	10.00e	40.00cd
G-45	3.33b	3.33c	23.33a-c	36.67de
G-61	0.00c	3.33c	23.33a-c	30.00fg
G-64	0.00c	6.67bc	23.33a-c	33.33ef
G-66	0.00c	13.33a	26.67a	33.33ef
G-68	3.33b	13.33a	23.33a-c	26.67gh
G-86	0.00c	6.70bc	24.81ab	42.59bc
A-2	0.00c	3.33c	26.67a	26.67gh
A-14	0.00c	3.33c	20.00c	40.00cd
A-23	0.00c	7.04bc	21.48bc	28.89fg
A-56	0.00c	10.00ab	20.00c	33.33ef
A-60	0.00c	10.00ab	20.00c	26.67gh
A-61	0.00c	10.00ab	20.00c	36.67de
A-79	0.00c	6.67bc	13.33de	23.33H
A-133	3.33b	10.00ab	20.00c	46.67ab
A-185	0.00c	10.00ab	26.67a	33.33ef

Means sharing common letters do not differ significantly at 5% probability level using LSD. LSD for genotypes under Normal condition= 0.878; LSD for genotypes at salt stress level 1 (3 dsm^{-1}) = 3.656; LSD for genotypes at salt stress level 2 (6 dsm^{-1}) = 3955; LSD for genotypes at salt stress Level 3 (9 dsm^{-1})= 5.007.

mortality % under salt stress level 3 (9 dsm^{-1}). Several researchers have also documented that higher concentration of salt in the rooting medium cause mortality of many plant species (Donahave et al., 1983).

Conclusion

The research concluded that the accession G-86 closely followed by G-30 and A-14 had maximum shoot length under salt stress level 3 (9 dsm^{-1}) whereas genotype G-44 closely followed by G-36 and A-185 had maximum root length under salt stress level 3 (9 dsm^{-1}). Genotypes G-68 closely followed by A-185 and G-66 had maximum chlorophyll under salt stress level 3 (9 dsm^{-1}) whereas line G-30 followed by A-79 and G-68 had minimum mortality % under salt stress level 3 (9 dsm^{-1}).

Conflict of interest

The authors have not declared any conflict of interest.

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