

**RESEARCH ARTICLE**

Genetic Variation for different Sodium and Potassium Contents in Tomato Leaves and Roots under Salinity Stress

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Abstract

High salt contents is one of the most pressing agricultural problem in the world. The growth and development of plants are hindered by salt stress, which ultimately reduce crop yields. Salt affects approximately 32 million hectares of agricultural region in the world. In this study, 20 tomato genotypes were evaluated against two different NaCl concentrations 6 and 12 dSm⁻¹ along with a control treatment. The research was conducted in the glasshouse of the Faculty of Agriculture, under completely randomized design (CRD) with three replications. The data of the following morphological characters like root length, shoot length, fresh root weight, fresh shoot weight, Na⁺ determination of roots, Na⁺ determination of leaves, K⁺ determination of roots and K⁺ determination of leaves. Through analysis of variance, genetic variation among different genotypes of tomato was calculated. Results of ANOVA showed that genotypes are significantly different from each other. Results from ANOVA illustrated that, significant differences were present among genotypes of tomato and treatments under study also gave significant results. The interaction between treatments and genotypes mostly remained non-significant. Traits like fresh root weight, fresh shoot weight and K⁺ determination of roots showed non-significant differences between treatment and genotype interaction. All characters under study exhibited significant and highly significant results for genotypes except K⁺ determination of roots. Similarly, treatments showed significant differences for all traits except K⁺ determination of roots. Under control condition, genotype CLN-2498A performed best for all traits and genotype Nadar performed poor for these parameters. Genotype PGRI-17902 was considered as best genotype for all traits under NaCl stress (6 dSm⁻¹) and genotype PGRI-19905 performed poor while under (12 dSm⁻¹) NaCl condition, PGRI-17260 appeared to be best genotype for all traits and Sundar behaved as poor genotype. Genotypes showing salt tolerance may be used in further breeding program for the development of salt tolerant tomato cultivars.

KEYWORDS

Salt stress, Tolerant, Tomato, Cultivars

1 | INTRODUCTION

Tomatoes acquire the position of an important and commercial commodity in the world in terms of acreage, production, yield, commercial use and consumption. After potatoes, lettuce and onions, tomato is considered as fourth most important fresh vegetable around the world, rich in carbohydrates, proteins, vitamins, minerals etc. Out of 397 million hectares around the world fall under the category of saline soils, 2.1% of cultivated dry lands and 19.5%

of irrigated lands are salt-affected (Rehman et al., 2023).

Salinity stress results in yield reduction due to decrease in photosynthetic rate, chlorophyll content, stomatal closure, total plant biomass and increase in oxidative stress (Zafar et al. 2022; Chattha et al. 2022). Ionic stress also induces by increase in NaCl concentration due to which toxic ions absorption increases such as Na⁺ and essential ions absorption

decreases like K^+ (Acosta-Motos et al. 2017; Chattha et al. 2024). Plants regulate their physiological and biochemical procedures under abiotic stresses (Chattha et al. 2019; Zafar et al. 2024). Throughout the life cycle of plant development, seed germination is the most delicate phase in stress conditions.

Tomato is a glycophyte plant and phyto-hormonal characteristic of this plant makes it suitable for adoption in high salinity conditions. Strong evaporation and less rainfall results in the assemblage of salt precipitates on upper layers of soil, which in turn retard seed germination and decline in crop yield (Zafar et al., 2022). Plant growth and production ultimately affected by increasing salt stress, due to which plants become unable to uptake nutrients from soil. Crop productivity and the EC of salt in the soil has been affected by soil salinity ranges from 0.6 - 3.2 dSm^{-1} (Arif et al. 2020). By the disruption in the water absorption of plants occur due to salinity results in hyperosmotic stress (Dabrowski-Tumanski et al. 2017). High salt levels (8–16 dSm^{-1}) limit root development while low moderate salinity (2-8 dSm^{-1}) can enhance the root growth, it completely depends upon the plant species or genotype ability to tolerate salt stress (Julkowska and Testerink, 2015). In agriculture, various techniques like crop management, plant breeding and genetic engineering have been developed to control the concentration of salts in rhizosphere and to improve the plant tolerance against saltiness (Wani et al. 2020).

In order to develop salt tolerant varieties, breeding programs have been dependent on complicated genetic study, physiological traits and inadequacy of efficient selection methods. Morphological, physiological, biochemical, and molecular divergence in plants results by ionic imbalance and changes in cellular water potential by soil salinization. Some appropriate natural stress reactions like K^+ transport, phospholipid modifications, stimulating reactive oxygen species unwanted enzymes, play a significant role in activation of plant tolerance on saline soils (Arif et al. 2020). The objectives of present study were (i) To devise selection criteria for salinity tolerance (ii) To select the salinity tolerant and non-tolerant genotypes.

2 MATERIAL AND METHOD

Research Material

The experiment was conducted in the screen house of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. Twenty tomato genotypes were examined against control, 6 and 12 $dSm^{-1}NaCl$ levels. The experiment was performed into two factor factorials under Completely Randomized Design (CRD) against three $NaCl$ levels viz. T1 (normal), T2 (6 $dSm^{-1}NaCl$) and T3 (12 $dSm^{-1}NaCl$) with three replications. First, tomato seeds

were sown to establish the nursery during crop season 2021 for the time period of 3 weeks. After 21 days, healthy plants of uniform size were transplanted from nursery into the plastic cups (width: 45 cm, height: 11 cm) that were already placed in the screen house, filled with approximately 800g of sand/cup for each replication. Three plants of each genotype were transplanted from nursery into the cups having one plant/cup. Tomato genotypes were arranged randomly by using lottery method.

Treatments

$NaCl$ was applied in three treatment levels i.e., 0, 6 and 12 dSm^{-1} after 1 week of transplanting from the nursery to avoid severe transplant shock. For the application of $NaCl$ and to provide proper nutrients to tomato genotypes, Hoagland's solution was prepared (Arnon & Hoagland, 1938). After 7 weeks, seedlings were harvested from the plastic cups and data of the following morphological and biochemical traits was recorded.

Determination of Na^+ and K^+ ions

Na^+ and K^+ ions concentration in roots and leaves of tomato genotypes were determined by using an instrument called flame photometer. For sample digestion 0.25 g of plant dry sample was measured with the help of portable digital balance, then sample was placed into 50 ml conical flask, nitric acid and perchloric acid was added in 3:1, with the help of a pipette, 4ml solution was taken and added into the flask and covered with aluminum foil then left for overnight. Next day material was heated on hotplate at 200-250° C temperature until volume reached to 1 ml. After cooling, 50 ml of distilled water was added and the solution was filtered with filter paper and poured into the plastic bottle. All the laboratory work was done in the fume hood.

Morphological and Biochemical Traits

Data of the following morphological and biochemical traits was recorded at seedling stage.

Root Length (cm)

At first root and shoot part of the plants was detached with the help of scissor. Then using scale, length of three plant roots per genotype was measured.

Shoot Length (cm)

For measuring shoot length shoot part of the plants was detached with the help of scissor and length was obtained from the base to the tip of the shoot and averaged.

Fresh Root Weight (g)

Plants were mildly pulled out from sand and cleaned with tap water for cleansing of sand particles. After detaching roots, digital balance (JL-180) was used for measuring root fresh weight in grams.

Fresh Shoot Weight (g)

Plants were mildly pulled out from sand and cleaned with tap water for cleansing of sand particles. After detaching shoots digital balance (JL-180) was employed for computing fresh shoot weight in grams.

K⁺ and Na⁺ Determination (ppm)

Na⁺ and K⁺ concentration of roots and leaves was figured out by using Flame Photometer.

Statistical Analyses

Analysis of variance (ANOVA) (Steel et al. 1997) was performed to investigate the variation among the genotypes for these traits and moreover, principal component analysis (Pearson, 1901) was used to identify tolerant and non-tolerant tomato genotypes.

3 RESULTS

Shoot Length (cm)

Table 1 showed the results of analysis of variance for shoot length from all the genotypes of tomato. According to the results, treatments showed highly significant results. Interaction between treatments and genotypes appeared to be highly significant. Similarly, genotypes gave highly significant differences from each other. Pairwise comparisons also shown in Table 2. Results of genotypes along with their mean values had been shown under all three treatments. Genotypes H-24, CLN-2498A and PGRI-19900 gave maximum values (49.530, 45.953, 31.750 respectively) under treatment 1 with no salinity stress. Genotypes Nadir, Target-T-66, CLN-2001A and PGRI-17260 showed minimum values (16.000, 19.000, 19.333 and 20.000 respectively). Under treatment 2 with (6 dSm⁻¹) salinity level, genotypes Picdeneato, Target-T-66, PGRI-19905 and CLN-2001A gave maximum values (67.733, 48.767, 46.143 and 36.553), while PGRI-19908, PGRI-17256 and Nadir showed minimum values (13.167, 15.580, 15.833) respectively. Under third treatment with (12 dSm⁻¹) salinity stress, maximum values showed by the genotypes PGRI-17902, PGRI-17263 and Aut-318 (22.000, 21.000 and 20.667 respectively) whereas minimum values given by the genotypes Sundar, H-24 and Nadir (12.000, 13.667, 14.000).

Table 1: Analysis of Variance for Shoot Length

Source	Treatment	Genotypes	Treatment* Genotypes	Error Genotypes
DF	2	19	38	120
Shoot Length	1349.25**	256.04**	282.73**	47.88
Root length	2023.42**	276.81**	191.49**	33.25
Fresh Root Weight	9.426**	0.531**	0.178 ^{NS}	0.169
Fresh Shoot Weight	34.949**	2.437**	1.087 ^{NS}	0.973
Root Na ⁺	5.56×10 ⁸ **	2.99×10 ⁷ **	2.61×10 ⁷ **	8.50×10 ⁶
Leaves Na ⁺	2.05×10 ⁹ **	6.37×10 ⁶ **	1.16×10 ⁷ **	1.79×10 ⁶
roots K ⁺	5.07×10 ⁶ ^{NS}	1.55×10 ⁷ ^{NS}	1.60×10 ⁷ ^{NS}	1.51×10 ⁷
leaves K ⁺	2.01×10 ⁷ **	2.74×10 ⁶ **	5.34×10 ⁶ **	9.12×10 ⁵

N.S. = At probability value > 0.05, ** = At probability value < 0.01, * = At probability value >0.01 or < 0.05

Table 2: Tukey's HSD All-Pairwise Comparisons Test of Shoot Length under controlled and salinity stressed conditions

Genotypes	T1 (0 dSm ⁻¹)	T2 (6 dSm ⁻¹)	T3 (12 dSm ⁻¹)	Mean
H-24	49.530 ab	17.333 fg	13.667 fg	26.843 ABC
CLN-2498A	45.953 a-e	21.667 fg	20.000 fg	29.207 AB
PGRI-19900	31.750 b-g	29.333 b-g	20.667 fg	27.250 AB
PGRI-17902	22.860 d-g	26.667 b-g	22.000 fg	23.842 BC
Galia	25.470 c-g	22.183 fg	16.000 fg	21.218 BC
PGRI-19908	23.080 d-g	13.167 fg	16.667 fg	17.638 BC
BGH-24	21.233 fg	19.470 fg	14.333 fg	18.346 BC
PGRI-17884	27.433 b-g	18.963 fg	17.333 fg	21.243 BC
PGRI-19905	21.107 fg	46.143 a-d	16.000 fg	27.750 AB
Picdeneato	22.683 d-g	67.733 a	20.333 fg	36.917 A
Target-T-66	19.000 fg	48.767 a-c	16.000 fg	27.922 AB
PGRI-17256	22.500 d-g	15.580 fg	17.000 fg	18.360 BC
PGRI-17260	20.000 fg	17.027 fg	16.667 fg	17.898 BC
PGRI-17263	22.500 d-g	18.290 fg	21.000 fg	20.597 BC
CLN-2001A	19.333 fg	36.553 b-f	14.333 fg	23.407 BC
Aut-318	25.167 c-g	22.240 fg	20.667 fg	22.691 BC
PGRI-17255	23.833 d-g	18.963 fg	18.333 fg	20.377 BC
Sundar	22.333 e-g	17.867 fg	12.000 g	17.400 BC
Peelo	21.333 fg	17.367 fg	16.000 fg	18.233 BC
Nadir	16.000 fg	15.833 fg	14.000 fg	15.278 C
Mean	25.155 A	25.557 A	17.150 B	

Tukey's value for Treatment= 2.999; Tukey's value for Genotype= 11.817; Tukey's value for Treatment*Genotype= 23.648

Root Length (cm)

Table 1 showed the results of analysis of variance for root length and the significance level of all genotypes. Table indicated the significance level of treatments. All treatments indicated to be highly significant. The relation between treatment and genotype also gave highly significant results. Genotypes showed highly significant results and appeared to be distinctive from each other.

In Table 3 all pairwise comparisons shown under three treatment levels. Genotypes along their mean values had been illustrated. According to the data in Table, under treatment 1 genotype H-24 appeared to be at highest level giving the value 56.303 and lowest values (17.380, 18.807, 19.023) given by the

genotypes PGRI-17902, Galia and PGRI-17884 respectively. Table also indicated the significance level of genotypes under treatment 2 and 3. Genotypes CLN-2001A, Picdeneato and PGRI-19905 showed maximum values (56.580, 49.530, 48.683) under treatment 2 while genotype PGRI-19908 and PGRI-17884 gave minimum values (13.067, 18.123). Under 3rd treatment highest values (23.000, 22.000) given by the genotypes CLN-2001A and H-24, similarly PGRI-19908, Picdeneato showed lowest values (13.667 and 14.333).

Table 3: Tukey's HSD all-pairwise comparisons test of root length under controlled and salinity stress conditions

Genotypes	T1 (0 dSm ⁻¹)	T2 (6 dSm ⁻¹)	T3 (12 dSm ⁻¹)	Mean
H-24	56.303 a	33.000 b-d	22.000 c-f	37.101 A
CLN-2498A	33.363 b-d	17.333 c-f	17.000 c-f	22.566 CDE
PGRI-19900	20.470 c-f	24.667 c-f	20.000 c-f	21.712 CDE
PGRI-17902	17.380 c-f	23.667 c-f	19.000 c-f	20.016 CDE
Galia	18.807 c-f	22.773 c-f	16.667 d-f	19.416 CDE
PGRI-19908	19.557 c-f	13.067 ef	13.667 d-f	15.430 E
BGH-24	20.197 c-f	32.853 b-d	14.667 d-f	22.572 CDE
PGRI-17884	19.023 c-f	18.123 c-f	15.333 d-f	17.493 DE
PGRI-19905	20.963 c-f	48.683 ab	14.667 d-f	28.104 ABC
Picdeneato	20.650 c-f	49.530 ab	14.333 d-f	28.171 ABC
Target-T-66	22.333 c-f	36.493 bc	19.333 c-f	26.053 BCD
PGRI-17256	20.333 c-f	22.687 c-f	14.667 d-f	19.229 CDE
PGRI-17260	22.000 c-f	30.723 b-e	19.333 c-f	24.019 BCDE
PGRI-17263	22.167 c-f	24.380 c-f	18.000 c-f	21.516 CDE
CLN-2001A	21.667 c-f	56.580 a	23.000 c-f	33.749 AB
Aut-318	21.333 c-f	22.550 c-f	15.667 d-f	19.850 CDE
PGRI-17255	24.500 c-f	26.587 c-f	17.000 c-f	22.696 CDE
Sundar	19.500 c-f	20.573 c-f	10.000 f	16.691 DE
Peelo	27.333 c-f	17.857 c-f	15.667 d-f	20.286 CDE
Nadir	22.667 c-f	20.233 c-f	11.667 ef	18.189 DE
Mean	23.527 B	28.118 A	16.583 C	

Tukey's value for Treatment = 2.499; Tukey's value for Genotype = 9.847; Tukey's value for Treatment*Genotype = 19.707

Fresh Root Weight (g)

Table 1 of analysis of variance cleared that treatments were highly significant to each other. All twenty genotypes showed highly significant differences under treatments. Interaction between genotypes and treatments was non-significant for this trait.

According to Table 4 the pairwise comparison results of all genotypes, under no salinity stress, highest value (2.087) given by the genotype Galia and lowest value (0.963) showed by Nadir. Under 6 dSm⁻¹NaCl level, maximum value (1.653) shown by the genotype H-24. On contrast, genotypes PGRI-19905, PGRI-17256 and Peelo stood at least values (0.577, 0.607, 0.707) respectively. Under (12 dSm⁻¹) NaCl stress level, genotype PGRI-17263 showed maximum value 1.403 while Sundar and Nadir gave minimum values (0.253, 0.367).

Table 4: Tukey's HSD all-pairwise comparisons test of fresh root weight under controlled and salinity stress conditions

Genotypes	T1 (0 dSm ⁻¹)	T2 (6 dSm ⁻¹)	T3 (12 dSm ⁻¹)	Mean
H-24	1.593	1.653	0.77	1.339 ABC
CLN-2498A	1.86	1.033	0.843	1.246 ABC
PGRI-19900	1.24	1.373	0.643	1.086 ABC
PGRI-17902	1.703	1.587	1.193	1.494 A
Galia	2.087	1.617	0.677	1.46 A
PGRI-19908	1.617	1.003	0.713	1.111 ABC
BGH-24	1.223	1.127	0.397	0.916 ABC
PGRI-17884	1.907	0.983	0.823	1.238 ABC
PGRI-19905	1.413	0.577	0.42	0.803 ABC
Picdeneato	1.42	1.077	0.927	1.141 ABC
Target-T-66	1.3	1.59	0.59	1.16 ABC
PGRI-17256	1.397	0.607	0.827	0.943 ABC
PGRI-17260	1.733	1.28	1.243	1.419 AB
PGRI-17263	1.787	1.087	1.403	1.426 AB
CLN-2001A	1.593	0.847	0.753	1.064 ABC
Aut-318	1.613	1.303	1.107	1.341 ABC
PGRI-17255	1.793	1.21	0.693	1.232 ABC
Sundar	1.013	0.913	0.253	0.727 BC
Peelo	1.673	0.707	0.453	0.944 ABC
Nadir	0.963	0.74	0.367	0.69 C
Mean	1.547 A	1.116 B	0.755 C	

Tukey's value for Treatment = 0.178; Tukey's value for Genotype = 0.701; Tukey's value for Treatment*Genotype = 1.403

Mean values of all genotypes indicated minimum and maximum values. Genotype PGRI-17902 appeared to be the best genotype among all genotypes for the trait. Mean value of this genotype was 1.494 and gave significant difference with genotypes Nadir and Sundar. Similarly, genotype PGRI-17902 showed non-significant differences with all other genotypes.

Fresh Shoot Weight (g)

Table 1 represented analysis of variance indicated highly significant differences of all treatments i.e. control, 6 and 12 dsm⁻¹ level. All the genotypes of tomato also indicated highly significant differences regardless of treatment. On the other hand, it was clear from the table that the interaction between genotype and treatment appeared to be non-significant.

Pairwise comparisons of genotypes shown in Table 5. According to the data, genotype CLN-2498A and PGRI-17884 showed maximum values 5.117, 4.58 respectively for fresh shoot weight under control conditions while, genotype Nadir and Target-T-66 represented least values 2.067, 2.45. Under concentration of 6 dSm⁻¹NaCl level, maximum value was shown by PGRI-17902 with 4.313. Genotypes PGRI-17256 and Nadir showed minimum values 1.497, 1.777 respectively. Under 12 dSm⁻¹NaCl level, genotype PGRI-17263 gave highest value 3.563, similarly genotype PGRI-19905 showed lowest value 0.947 among all genotypes.

Table 5: Tukey's HSD all-pairwise comparisons test of fresh shoot weight under controlled and salinity stress conditions

Genotypes	T1 (0 dSm ⁻¹)	T2 (6 dSm ⁻¹)	T3 (12 dSm ⁻¹)	Mean
H-24	4.127	3.02	1.813	2.987 ABC
CLN-2498A	5.117	3.053	2.503	3.558 AB
PGRI-19900	3.55	3.677	2.047	3.091 ABC
PGRI-17902	4.097	4.313	3.21	3.873 A
Galia	4.193	3.017	1.763	2.991 ABC
PGRI-19908	3.343	2.697	2.083	2.708 ABC
BGH-24	3.903	2.16	1.3	2.454 ABC
PGRI-17884	4.58	2.61	2.04	3.077 ABC
PGRI-19905	4.007	2.01	0.947	2.321 ABC
Picdeneato	3.763	3.34	2.767	3.29 ABC
Target-T-66	2.45	3.49	1.76	2.567 ABC
PGRI-17256	2.957	1.497	2.183	2.212 ABC
PGRI-17260	3.133	2.483	3.087	2.901 ABC
PGRI-17263	3.637	2.063	3.563	3.088 ABC
CLN-2001A	3.137	1.873	1.723	2.244 ABC
Aut-318	3.533	2.707	2.707	2.982 ABC
PGRI-17255	3.633	2.37	2.503	2.836 ABC
Sundar	3.16	2.07	1.013	2.081 BC
Peelo	3.71	1.787	1.713	2.403 ABC
Nadir	2.067	1.777	1.417	1.753 C
Mean	3.605 A	2.601 B	2.107 C	

Tukey's value for Treatment = 0.428; Tukey's value for Genotype = 1.685; Tukey's value for Treatment*Genotype = 3.371

According to the mean value of fresh shoot weight, genotypes H-24, Galia and Aut-318 gave same results with values 2.987, 2.991 and 2.982 respectively. Mean value table indicated the maximum value 3.873 shown by the genotype PGRI-17902. Genotypes Nadar and Sundar appeared to be least performing having values 1.753, 2.081.

Na⁺ Determination of Roots

The results of analysis of variance for the parameter Na⁺ determination of roots of different genotypes of tomatoes illustrated in the Table 1. It was clear from the interpretation that genotypes showed highly significant variation from one another. On the other hand the interaction between genotype and treatments indicated to be highly significant as well. Similarly, highly significant distinction could be seen for NaCl levels.

In Table 6, pairwise comparison had been given that illustrated the values of different genotypes. From the table it was clear that genotype PGRI-17260, PGRI-17256 and Sundar gave maximum values (11128, 9901, 8963) under no salinity stress. Minimum values (4644, 5643, 5860) were shown by the genotypes PGRI-19905, H-24 and Picdeneato respectively. At 6 dSm⁻¹NaCl level, highest values (16994, 15485, 15036) were showed by the genotypes PGRI-17255, PGRI-17902 and PGRI-19908 and lowest values given by the genotypes Nadir (9111), Galia (9136) and PGRI-17884 (9278) respectively at the same level of stress. Genotypes BGH-24 and PGRI-17255 both stood at

highest level by giving maximum values (25448, 20750) at level of 12 dSm⁻¹NaCl stress. Similarly, genotypes Galia and PGRI-17902 gave least values 7543, 7922. From the table the maximum mean value for this trait was shown by genotype BGH-24 (15035) while, minimum mean value was recorded by the genotype Galia showing the value of (8089). On comparison genotype BGH-24 was non-significant from all other genotypes except Galia, Target-T-66, Nadir, H-24 and PGRI-19900.

Table 6: Tukey's HSD all-pairwise comparisons test of Na⁺ determination of roots under controlled and salinity stress conditions

Genotypes	T1 (0 dSm ⁻¹)	T2 (6 dSm ⁻¹)	T3 (12 dSm ⁻¹)	Mean
H-24	5643 ef	14437 b-f	8175 c-f	9418 B
CLN-2498A	8241 c-f	14197 b-f	9340 c-f	10593 AB
PGRI-19900	8169 c-f	11227 b-f	9114 c-f	9503 B
PGRI-17902	8602 c-f	15485 b-e	7922 c-f	10670 AB
Galia	7588 d-f	9136 c-f	7543 d-f	8089 B
PGRI-19908	6834 ef	15036 b-e	14226 b-f	12032 AB
BGH-24	8385 c-f	11272 b-f	25448 a	15035 A
PGRI-17884	8241 c-f	9278 c-f	11394 b-f	9638 B
PGRI-19905	4644 f	10454 c-f	13403 b-f	9500 B
Picdeneato	5860 ef	11919 b-f	14526 b-f	10768 AB
Target-T-66	6004 ef	10151 c-f	10569 c-f	8908 B
PGRI-17256	9901 c-f	12089 b-f	11821 b-f	11270 AB
PGRI-17260	11128 b-f	10562 c-f	12865 b-f	11518 AB
PGRI-17263	6942 ef	13405 b-f	13653 b-f	11333 AB
CLN-2001A	7232 d-f	14698 b-e	13004 b-f	11645 AB
Aut-318	6818 ef	14825 b-e	11408 b-f	11017 AB
PGRI-17255	6509 ef	16994 a-d	20750 ab	14751 A
Sundar	8963 c-f	12945 b-f	15470 b-e	12459 AB
Peelo	7086 d-f	13509 b-f	17817 a-c	12804 AB
Nadir	7159 d-f	9111 c-f	11128 b-f	9132 B
Mean	7497 B	12536 A	12979 A	

Tukey's value for Treatment = 1263.1; Tukey's value for Genotype = 4977.5; Tukey's value for Treatment*Genotype = 9961.3

Na⁺ Determination of Leaves

The results of analysis of variance for the parameter Na⁺ determination of leaves of different genotypes of tomatoes illustrated in the Table 1. It was clear from the interpretation that genotypes showed highly significant variation from one another. On the other hand, the interaction between genotype and treatments indicated to be highly significant as well. Similarly, highly significant distinction could be seen for salinity levels.

In Table 7, pairwise comparison had been given that illustrated the values of different genotypes. From the table it was clear that genotypes PGRI-17256, PGRI-17260 and CLN-2001A represented maximum values 3767, 3550, 3406 respectively under at (0 dSm⁻¹) NaCl level. Minimum values (952, 1024, 1097) were shown by the genotypes H-24, PGRI-19900 and Galia. Under treatment 2 (6 dSm⁻¹), highest value (13220) was given by the genotype H-24 and least value (6942) showed by

Peelo. Maximum values (18663, 16443, 15385) were given by the genotypes PGRI-17255, Sundar and PGRI-19908 at (12 dSm⁻¹) salinity level while minimum values (8674, 9684, 10839) given by the genotypes CLN-2498A, PGRI-19900 and PGRI-17256 respectively. From this table, the maximum mean value for this trait was shown by the genotype PGRI-19905 (10038) and minimum value was recorded by the genotype PGRI-17902 (7255). This genotype showed significant differences from genotypes PGRI-17902, PGRI-19900, PGRI-17256 and CLN-2498A.

Table 7: Tukey's HSD all-pairwise comparisons test of Na⁺ determination of leaves under controlled and salinity stress conditions

Genotypes	T1 (0 dSm ⁻¹)	T2 (6 dSm ⁻¹)	T3 (12 dSm ⁻¹)	Mean
H-24	952 q	13220 b-i	12932 b-j	9035 AB
CLN-2498A	2107 q	11705 c-l	8674 i-m	7495 B
PGRI-19900	1024 q	11416 c-m	9684 f-m	7375 B
PGRI-17902	1313 q	8891 h-m	11561 c-l	7255 B
Galia	1097 q	12434 b-k	13353 b-h	8961 AB
PGRI-19908	952 q	11112 c-m	15385 a-c	9150 AB
BGH-24	2540 pq	8385 j-m	14542 a-e	8489 AB
PGRI-17884	1241 q	8818 h-m	14231 a-f	8097 AB
PGRI-19905	2049 q	12680 b-k	15385 a-c	10038 A
Picdeneato	2973 pq	9396 g-m	13155 b-i	8508 AB
Target-T-66	2756 pq	8746 i-m	12860 b-k	8121 AB
PGRI-17256	3767 n-q	7808 l-o	10839 c-m	7471 B
PGRI-17260	3550 o-q	12585 b-k	11918 b-l	9351 AB
PGRI-17263	2756 pq	10695 d-m	13172 b-i	8874 AB
CLN-2001A	3406 o-q	11142 c-m	11200 c-m	8583 AB
Aut-318	1120 q	9107 g-m	14038 b-f	8088 AB
PGRI-17255	1385 q	8313 k-n	18663 a	9454 AB
Sundar	3262 o-q	10334 e-m	16443 ab	10013 A
Peelo	1024 q	6942 m-p	15097 a-d	7688 B
Nadir	1313 q	11633 c-l	13549 b-g	8832 AB
Mean	2029 C	10268 B	13334 A	

Tukey's value for Treatment = 579.73; Tukey's value for Genotype = 2284.6; Tukey's value for Treatment*Genotype = 4572.0

K⁺ Determination of Roots

Table 1 showed the results of analysis of variance for K⁺ determination of roots and the significance level of all genotypes. Table indicated the significance level of treatments. All treatments indicated to be non-significant. The relation between treatment and genotype gave non-significant results. Genotypes also showed non-significant results and were similar to each other.

In Table 8, all pairwise comparisons shown under all three treatment levels. Genotypes along their mean values had been illustrated. According to the data in table, genotypes Target-T-66, Galia and PGRI-17260 showed highest values (5706, 5276, 4703) under control condition, as well as minimum values shown by the genotypes Aut-318, BGH-24 and Peelo by giving the values (2592, 2624, 2839) respectively.

Table 8: Tukey's HSD all-pairwise comparisons test of K⁺ determination of roots under controlled and salinity stress conditions

Genotypes	T1 (0 dSm ⁻¹)	T2 (6 dSm ⁻¹)	T3 (12 dSm ⁻¹)	Mean
H-24	3627	6565	1613	3935.0
CLN-2498A	3627	5419	2683	3909.6
PGRI-19900	3341	4910	2929	3726.3
PGRI-17902	3556	3065	1995	2871.7
Galia	5276	1446	2273	2998.3
PGRI-19908	3341	3596	2159	3031.6
BGH-24	2624	4846	18088	8519.3
PGRI-17884	3197	1466	2195	2286.3
PGRI-19905	3087	1014	2280	2126.9
Picdeneato	3484	4078	2658	3406.3
Target-T-66	5706	2954	2996	3885.3
PGRI-17256	4487	6585	3270	4780.7
PGRI-17260	4703	3311	4193	4068.9
PGRI-17263	2910	5379	5204	4497.9
CLN-2001A	3341	5916	4487	4581.4
Aut-318	2592	5105	2717	3471.6
PGRI-17255	3484	5057	3835	4125.1
Sundar	3412	5801	2072	3762.0
Peelo	2839	4190	3482	3503.6
Nadir	3125	2285	3627	3012.5
Mean	3587.9	4149.3	3737.8	

Tukey's value for Treatment = 1681.2; Tukey's value for Genotype = 6625.2; Tukey's value for Treatment*Genotype = 13259

Under the application of (6 dSm⁻¹) NaCl stress, highest values were recorded by the genotypes PGRI-17256 (6585), H-24 (6565) and CLN-2001A (5916) while, lowest values were recorded by the genotypes PGRI-19905 (1014), Galia (1446) and PGRI-17884 (1466) respectively at the same level of stress. Under treatment 3 (12 dSm⁻¹), genotype BGH-24 found to be at highest level by giving the maximum value (18088) from all genotypes and genotype H-24 showed minimum value (1613). Overall mean values pointed towards the maximum and minimum values under all treatments such as genotype BGH-24 gave the maximum mean value (8519.3). On a similar level genotype PGRI-19905 gave the minimum mean value (2126.9).

K⁺ Determination of Leaves

Table 1 showed the results of analysis of variance for K⁺ determination of leaves and the significance level of all genotypes. Table indicated the significance level of treatments. All treatments indicated to be highly significant. The relation between treatment and genotype also gave highly significant results. Genotypes gave highly significant results and they were distinctive from each other. In Table 9, all pairwise comparisons shown under all three treatment levels. Genotypes along their mean values had been illustrated. According to the data in table, genotypes PGRI-17884, Galia and PGRI-17260 showed highest values (10007, 9649, 9505)

under no salinity stress, as well as minimum values shown by the genotypes PGRI-17263, PGRI-19905 and CLN-2001A by giving the values (7068, 7842, 8000) respectively. Under the application of (6 dSm⁻¹) NaCl stress, highest values were recorded by the genotypes PGRI-19908 (10921), CLN-2001A (10784) and Picdeneato (10652) while, lowest values were recorded by the genotypes PGRI-19905 (6122), PGRI-19900 (6566) and PGRI-17884 (6781) respectively at the same level of stress. Under treatment 3 (12 dSm⁻¹), genotype PGRI-17263 found to be at highest level by giving the maximum value (11488) from all genotypes and genotype Picdeneato showed minimum value (5231). Overall mean values pointed towards the maximum and minimum values under all treatments such as genotype PGRI-19908 gave the maximum mean value (9738.2). On a similar level genotype PGRI-17884 gave the minimum mean value (7354.8).

Table 9: Tukey's HSD all-pairwise comparisons test of K⁺ determination of leaves under controlled and salinity stress conditions

Genotypes	T1 (0 dSm ⁻¹)	T2 (6)	T3 (12 dSm ⁻¹)	Mean
H-24	8143 b-h	8843 a-g	7355 e-h	8113.6 ABC
CLN-2498A	8789 a-g	9290 a-g	7498 d-h	8525.7 ABC
PGRI-19900	9434 a-f	6566 f-h	8645 a-g	8215.1 ABC
PGRI-17902	8430 a-h	7857 b-h	8932 a-g	8406.2 ABC
Galia	9649 a-f	7992 b-h	6693 f-h	8111.4 ABC
PGRI-19908	8860 a-g	10921 ab	9434 a-f	9738.2 A
BGH-24	9004 a-g	8789 a-g	6803 e-h	8198.3 ABC
PGRI-17884	10007 a-e	6781 e-h	5276 h	7354.8 C
PGRI-19905	7842 b-h	6122 gh	9290 a-g	7751.5 BC
Picdeneato	8789 a-g	10652 a-d	5231 h	8224.1 ABC
Target-T-66	8430 a-h	9362 a-g	6710 f-h	8167.3 ABC
PGRI-17256	8287 a-h	8573 a-g	7211 e-h	8023.9 BC
PGRI-17260	9505 a-f	7216 e-h	7873 b-h	8198.1 ABC
PGRI-17263	7068 e-h	9290 a-g	11488 a	9282.0 AB
CLN-2001A	8000 b-h	10784 a-c	7570 c-h	8784.7 ABC
Aut-318	9118 a-g	8789 a-g	6835 e-h	8247.1 ABC
PGRI-17255	8072 b-h	8860 a-g	7590 c-h	8174.1 ABC
Sundar	8000 b-h	8358 a-h	6142 gh	7500.0 C
Peelo	8143 b-h	8932 a-g	7068 e-h	8047.8 BC
Nadir	8645 a-g	9075 a-g	8934 a-g	8884.7 ABC
Mean	8610.7 A	8652.6 A	7628.9 B	

Tukey's value for Treatment = 413.86; Tukey's value for Genotype = 1630.9; Tukey's value for Treatment*Genotype = 3263.9

4 | DISCUSSION

Results from ANOVA illustrated that highly significant differences were present among all treatments for all morphological and biochemical traits except K⁺ determination of roots. Genotypes also showed highly significant variations for all traits except K⁺ determination of roots and Na⁺/K⁺ ratio of roots and showed dissimilarities from each other. The interaction between treatments and genotypes mostly appeared to be non-significant for all traits except plant length, shoot

length, root length, fresh root/shoot weight ratio, Na⁺ determination of roots and leaves, K⁺ determination of leaves and Na⁺/K⁺ ratio of leaves respectively. Plant height significantly reduced by increasing NaCl stress levels (Sassine et al. 2020).

Results indicated that root length was significantly reduced by increasing salt stress (Tahir et al. 2018). Tomato shoots became more sensitive than roots due to salinity stress so, roots and shoots elongation could be used for selection of tolerant genotypes against saltiness.

Most common physiological impact of NaCl stress, strength of NaCl salinity, exposure period, climatic conditions and plant genetic variations regarding salinity damages in many glycophytes is the reduction in plant growth and biomass production (Gharbi et al. 2016). A significant reduction showed by all genotypes of tomato in shoot length as NaCl concentration increased (Sivakumar et al. 2020). Different NaCl concentrations were applied to classified sensitive and tolerant tomato germplasms based on parameters like fresh root weight, and dry root weight. The significant reduction in shoot fresh weight but not dry weight mainly due to the adverse effect of NaCl salinity on water relation of plants rather than merely on leaf photosynthesis. Both parameters were decreased linearly with an increase in the external NaCl concentration. Fresh root and shoot weight, dry root and shoot weight were decreased by increasing stress level (Alzahib et al. 2021). Roots are the first organ subjected to the soil or medium salinity, and root allocations of more photo assimilates are a general plant response to salinity (Ahmadi and Souri, 2018).

Moreover, salinity also caused the nutrient imbalance, overproduction of ROS, and inhibition of enzymatic activities, which significantly affected the cellular components and biological membranes and caused a decrease in biomass production. As salinity stress increased, Na⁺ concentration in roots and leaves significantly increased but K⁺ concentration in roots and leaves decreased ultimately and these results were explained by (Benazzouk et al. 2018). Under stress conditions, genotypes PGRI-17902 and PGRI-17260 showed positive results for maximum traits so these genotypes could be used as salt tolerant genotypes for future breeding programs under highly stressed conditions. Genotypes Nadir, Peelo and Sundar showed negative relations for all traits under stress conditions so they were considered as salt susceptible genotypes and would not recommend for breeding purpose. Under control conditions, genotype CLN-2498A considered as best genotype for all parameters by showing positive relation with all traits and genotype Nadir considered as poor genotype for all traits. To identified salt tolerant genotypes a selection criterion should be devised that best explained the behavioral retort of genotypes over multiple saline conditions.

Conclusion

Under control condition, genotype CLN-2498A performed best for all traits and genotype Nadar performed poor for these parameters. Genotype PGRI-17902 was considered as best genotype for all traits under NaCl stress (6 dSm⁻¹) and genotype PGRI-19905 performed poor while under (12 dSm⁻¹) NaCl condition, PGRI-17260 appeared to be best genotype for all traits and Sundar behaved as poor genotype.

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