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SALINITY TOLERANCE ASSESSMENT IN WHEAT GENOTYPES UNDER HYDROPONIC CONDITIONS

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Abstract

This study aimed to evaluate the performance of 24 wheat genotypes using a hydroponic system under 100 mM,140 mM and 200 mM NaCl treatments. Among the genotypes tested MH-21 and SARC-4 exhibited notable salt tolerance, displaying minimal reductions in growth and maintaining high SPAD values. Conversely, Lasani 2008 and AARI-11 demonstrated sensitivity, showing significant decreases in growth parameters. Furthermore, the measurement of MSI and RWC indicated that the salt-tolerant genotypes maintained better cellular membrane stability and water retention capacity up to 21% and 41% under high salinity stress compared to the salt-sensitive genotypes. Ionic analysis revealed that the salt-tolerant genotypes MH-21 and SARC-4 exhibited efficient ion regulation, with lower Na^+ accumulation up to 86% and 85% and higher K^+ retention up to 62 % and 58% at higher salinity level compared to the salt-sensitive genotypes Lasani 2008 and AARI-11. This suggested that ion homeostasis and selective ion uptake mechanisms play a critical role in salt tolerance in wheat. MH-21 and SARC-4 were ranked as salt tolerant genotypes in Principle Component Analysis based on Salt Tolerance Index$_{TDM}$ and Salt Tolerance Index$_{K^+/Na^+}$.

Key words: Salt resistant genotypes; Abiotic stress; Genetic diversity; Genotypic evaluation; Vegetative parameters; Crop adaptation; Ion homeostasis

Introduction

Wheat is an integral part of global agriculture and plays a vital role in food production and nutritional security. As the global population rises and food demand intensifies, ensuring stable wheat yields has become increasingly important. However, wheat production faces multiple challenges, including climate change, water scarcity, soil degradation, and biotic stresses such as pests and diseases (Yanagi, 2024; Asseng *et al.*, 2015). Water scarcity and soil degradation further exacerbate these challenges impacting crop yields and sustainability (Lal, 2020; Raimondo *et al*., 2021). Additionally, pests and diseases such as rust pathogens and insect pests pose substantial threats to wheat productivity (Ding *et al.*, 2021). Market fluctuations and trade policies can also influence food availability and access affecting global food security (Barlow *et al.*, 2020).

Salinity stress is a significant abiotic factor that poses a major challenge to agricultural productivity particularly in arid and semi-arid regions (Munns & Tester, 2008; Smith *et al.*, 2009; Mukhopadhyay *et al.*, 2021). It negatively affects various aspects of wheat growth and development. High salt concentrations disrupt the osmotic balance leading to reduced water availability for plants which impairs cell expansion, reduced leaf area and stunted plant growth (Hailu and Mehari, 2021; He *et al.*, 2021). Additionally, salinity stress disrupts the photosynthetic process and hampers the carbon assimilation process leading to decreased biomass production and yield losses (Munns & Gilliham, 2015; Zahra *et al.*, 2022; Chauhan *et al.*, 2023). Moreover, salinity-induced ion imbalances particularly excessive accumulation of sodium (Na^+) ions interferes with nutrient uptake and cause nutrient deficiencies further compromising plant health and productivity (Wang *et al.*, 2018; Balasubramaniam *et al.*, 2023).

To address the challenges posed by salinity stress in wheat production sustainable management strategies are imperative. Breeding and selection of salt-tolerant wheat varieties coupled with molecular approaches offer promising avenues for developing cultivars with enhanced salinity tolerance (Munns *et al.*, 2020). Additionally, the application of exogenous osmo-protectants, soil amendments and biofertilizers has shown potential in alleviating the detrimental effects of salinity on wheat growth and yield (Ashraf & Foolad, 2007).

This study hypothesizes that certain wheat genotypes possess intrinsic physiological and biochemical mechanisms that confer enhanced tolerance to salinity stress, allowing them to maintain growth and cellular stability under high salinity conditions. By evaluating these genotypes in a controlled hydroponic system, it is possible to identify and characterize the salt-tolerant genotypes, which can then be utilized in breeding programs to develop more resilient wheat varieties.

Identifying salt-tolerant wheat varieties was essential for several reasons. Firstly, salt-tolerant varieties could withstand and adapt to saline soil conditions enabling them to maintain growth and productivity under high salt levels. By cultivating salt-tolerant varieties farmers could minimize yield losses and ensure stable wheat production in salinity-affected areas.

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Secondly, the identification of salt-tolerant wheat varieties contributed to resource conservation and sustainable agricultural practices. Salt-tolerant varieties had the ability to efficiently utilize water and nutrients in saline soils reducing the need for excessive irrigation and fertilizer application. This not only conserved precious resources but also minimized the environmental impact associated with irrigation and fertilizer runoff.

Furthermore, salt-tolerant wheat varieties enhanced the resilience and livelihoods of farmers in regions prone to salinity. By providing farmers with improved varieties that could withstand salinity stress they were empowered to continue wheat cultivation, maintain their incomes, and sustain their agricultural communities.

Material and Methods

Location of experiment and genotype gathering: The experimental site for this study was located at SARC, Institute of Soil and Environmental Sciences, University of Agriculture Faisalabad (31.25 ^{0}N, 73.09 ^{0}E) from Mid Oct-December 2021. The site was chosen based on its suitability for conducting research and its representative characteristics of the target environment. The collection of wheat genotypes involved the selection of twenty-four genotypes that were diverse in their genetic backgrounds to know for their potential salinity tolerance or sensitivity. The genotypes were obtained from reputable sources to identify Salt-Tolerant Wheat genotypes as seed banks of Ayub Agriculture Research Institute, Soil Salinity Research Institute, Pindi Bhattian and Saline Agriculture Research Center, UAF. Care was taken to ensure the purity and authenticity of the genotypes throughout the experimental process. Proper documentation and labeling were maintained to track and identify each genotype accurately during the screening process.

Experimental setup and treatment plan: The experimental setup consisted of a controlled environment with hydroponic systems to evaluate the response of the twenty-four wheat genotypes to salinity stress. For wheat nursery planting sand was first washed in 0.05 N hydrochloric acid (HCl) then the acid was removed by washing with tap water. Sand that has been acid-washed was then placed to iron trays after being cleaned with distilled water. In these trays, healthy seeds from 24 different wheat genotypes were planted on 20th October. While growing wheat genotype seedlings, distilled water was used for irrigation. The genotypes were randomly allocated to different treatment groups representing four salinity levels. The treatments included a control group without any salt application as well as three salinity treatments 100 mM NaCl, 140 mM NaCl and 200 mM NaCl were selected to represent moderate to high salinity stress conditions commonly used in wheat salinity tolerance studies. At two leaf stage healthy seedling of all the twenty-four wheat genotypes on 29th October was transplanted into polystyrene sheets with foam plugs over half-strength Hoagland's solution (Hoagland and Arnon, 1950) in tubs with pH adjusted daily at 6.0 ± 0.5 using 1 N H_2SO_4 or NaOH. Three replications of each genotype were placed in each tub arranged in a completely randomized design. The salinity levels were applied after seven days of wheat transplantation in hydroponics by adding NaCl salt in three increments starting from 5th November. The solution was continuously aerated for 8 hrs by using an aeration pump. Each genotype was replicated three times to ensure the reliability of the results and to account for any potential variability. To maintain solution quality and ionic stability, the nutrient solution in each tub was renewed every fifteen days to prevent ion accumulation or nutrient depletion. During this process, the respective NaCl concentrations were re-established after each renewal to maintain consistent salinity levels. The genotypes were grown under controlled environmental conditions with adequate lighting, temperature and humidity throughout the experimental period. Compared to soil-based screening, the hydroponic system offers enhanced control over nutrient availability and salinity levels, enabling precise and uniform stress application. This allows for more accurate differentiation of genotypic responses to salinity under standardized conditions.

Harvesting: This experimental design allowed for the comprehensive evaluation of the genotypes' performance under varying levels of salinity stress and provided insights into their salt tolerance or sensitivity. Harvesting of the wheat plants was carried out after forty days of transplanting on 08th December. The plants were carefully uprooted from the tubs ensuring minimum damage to the roots and shoots. Following harvesting, the plants were separated into above-ground biomass (shoot) and below-ground biomass (root).

Measurement of growth traits: To determine growth-related traits, measurements such as shoot length and root length were recorded using a ruler. Fresh shoot and root weights were determined by weighing the harvested plant parts immediately after collection. To obtain dry shoot and root weights, the plant samples were dried in an oven at 65^{o}C until a constant weight was achieved.

Measurement of physiological traits: Physiological traits related to salinity stress response were also assessed. After one month on November 28th the SPAD value, an indicator of chlorophyll content and photosynthetic activity was measured using a hand-held SPAD-502 meter from leaf tip to its base and averaged (Saqib *et al*., 2012). For measuring the membrane stability index (MSI) fully expanded young leaves were collected from each replication and thoroughly washed with distilled water. The fresh mass of the leaves was measured. Subsequently, 0.2g of fresh leaves were weighed and placed in test tubes containing 10 ml of distilled water. The test tubes were then immersed in a water bath at 40°C for 30 minutes, after which the electrical conductivity (EC) of the samples was measured and recorded as C1. Following this, the test tubes were put into a water bath at 95°C for 10 minutes, and the EC of the samples was measured again and recorded as C2. The membrane stability index (MSI) was then computed using this method (Sairam *et al.*, 2002).

$$MSI = \left(1 - \frac{C1}{C2}\right) \times 100$$

To minimize environmental variation, all samples were processed in a temperature-controlled laboratory, and measurements were taken immediately to prevent post-harvest physiological changes.

For measuring the Relative Water Content (RWC) fully expanded leaves were collected from each replication and washed thoroughly with distilled water. The fresh weight (FW) of the leaves was measured. The leaves were then immersed in distilled water for 4 hours and maintained in test tubes. After the 4-hour period, the leaves were removed from the water, and their weight was measured again, recording it as the turgid weight (TW). Subsequently, the leaves were dried in an oven for three days to obtain the dry weight (DW). The relative water content was calculated using the method described by (Weatherly, 1951).

$$RWC\ (\%) = [(FW-DW) / (TW-DW)] \times 100$$

Measurement of ionic concentration and K^+/Na^+ in plant tissue: Plant samples were oven-dried at 65°C until reaching a constant weight. The dried samples were ground and 200 mg of the resulting material was digested using a di-acid mixture of HNO_3 and $HClO_4$ in a 2:1 ratio on a hot plate until complete combustion of organic matter and the production of a clear solution. After digestion, the samples were diluted with double-distilled water to a final volume of 50 ml. Subsequently, the concentrations of Na^+ and K^+ ions in the digested samples were determined using a flame photometer (PFP7-Jenway, UK).

Salt tolerance index: The salt tolerance index of genotypes was calculated based on the total dry matter (TDM) production and K^+/Na^+ ratio using the following formulas (Fernandez,1992).

$$STI_{TDM} = (TDM_{control} \times TDM_{stressed\ plant}) / (Average\ TDM_{control})^2$$

$$STI_{K+/Na+} = (K^+/Na^+_{control} \times K^+/Na^+_{stressed\ plant}) / (Average\ K^+/Na^+_{control})^2$$

Statistical Analysis

Treatments of the trial were applied according to the Completely Randomized Design (CRD). Statistic 8.1 software was used for analysis and comparison of data. The data collected was analyzed using ANOVA, followed by least significant difference test at a 95% significance level.

Results

Effect of salinity on SPAD value of different wheat genotypes: The results of the study revealed significant variations in the SPAD values of different wheat genotypes under varying salinity treatments. As shown (Table 1) the SPAD values of all genotypes decreased consistently with increasing NaCl concentration. Among the tested genotypes, MH-21 and SARC-4 exhibited the highest SPAD values at all salinity levels indicating their superior tolerance to salt stress (SPAD values: 41.10±0.36, 39.00±0.42, 30.47±0.23, 25.23±0.20 and 40.23±0.22, 37.43±0.73, 29.90±0.23, 24.47±0.30 for control, 100mM NaCl, 140mM NaCl and 200mM NaCl treatments respectively). On the other hand, AARI-11 and Lasani-08 displayed the lowest SPAD values suggesting their susceptibility to salinity stress (SPAD values: 30.53±0.67 and 30.07±0.30 for control and 26.00±0.44 and 27.83±0.61 for 100mM NaCl treatments respectively). Furthermore, the mean SPAD values across all genotypes showed a clear decreasing trend with increasing salinity levels (mean SPAD values: 35.26 A, 31.55 B, 25.49 C and 20.63 D for control, 100mM NaCl, 140mM NaCl and 200mM NaCl treatments respectively).

Effect of salinity on shoot length (cm) of different wheat genotypes: The results presented (Table 2) demonstrate significant variations in shoot length among the tested genotypes under different salinity treatments. Among the wheat genotypes MH-21 exhibited the highest shoot length across all salinity levels indicating its enhanced tolerance to salt stress. The shoot lengths for MH-21 were as follows: 77.67±0.33 cm (control), 67.67±0.33 cm (100mM NaCl), 58.00±1.16 cm (140mM NaCl) and 44.67±0.33 cm (200mM NaCl). SARC-4 also displayed noteworthy shoot lengths, showcasing its relatively high tolerance to salinity stress. The shoot lengths for SARC-4 were as follows: 76.33±0.33 cm (control), 65.67±0.33 cm (100mM NaCl), 56.33±0.33 cm (140mM NaCl) and 42.33±0.33 (200mM NaCl). Conversely, AARI-11 demonstrated lower shoot lengths compared to other genotypes indicating its susceptibility to salinity stress. The shoot lengths for AARI-11 were as follows: 54.00±0.58 cm (control), 42.33±0.33 cm (100mM NaCl), 34.00±0.58 cm (140mM NaCl) and 24.33±0.33 cm (200mM NaCl). Lasani-08 also exhibited relatively lower shoot lengths suggesting its reduced tolerance to salinity stress. The shoot lengths for Lasani-08 were as follows: 56.00±1.00 cm (control), 44.67±0.88 cm (100mM NaCl), 35.67±0.33 cm (140mM NaCl) and 26.33±0.33 cm (200mM NaCl). The mean shoot length across all genotypes exhibited a consistent decrease with increasing salinity levels (mean shoot length: 64.014 A, 53.611 B, 45.319 C and 33.528 D for control, 100mM NaCl, 140mM NaCl and 200mM NaCl treatments respectively). These results indicated the contrasting responses of wheat genotypes to salinity stress with MH-21 and SARC-4 showing higher shoot lengths and AARI-11 and Lasani-08 displaying lower shoot lengths under saline conditions.

Effect of salinity on fresh shoot weight (g) of different wheat genotypes: The results revealed significant variations in fresh shoot weight across the tested genotypes and salinity levels (Table 3). Generally, as salinity increased there was a noticeable reduction in fresh shoot weight among most of the wheat genotypes. However, some genotypes displayed unique responses to salinity stress. Among the genotypes, MH-21 exhibited remarkable salt tolerance as indicated by its consistently higher fresh shoot weight compared to other genotypes across all salinity levels (20.733 a). It maintained superior growth even under high salinity conditions (7.77±0.15 200mM NaCl). Similarly, SARC-4 also showed significant salt tolerance exhibiting a relatively higher fresh

shoot weight at elevated salinity levels (22.67±0.33 100mM NaCl and 13.30±0.15 140mM NaCl) (19.025 b). Conversely, Lasani and AARI-11 were identified as salt-sensitive genotypes displaying decreased fresh shoot weight with increasing salinity. Lasani, in particular, showed a considerably lower fresh shoot weight compared to other genotypes across all salinity levels (7.892 o). AARI-11 also exhibited sensitivity to salinity stress, with a notable decrease in fresh shoot weight (6.292 p).

These findings highlighted the importance of understanding the salt tolerance mechanisms in wheat genotypes and highlight the potential for developing salt-tolerant varieties to ensure sustainable crop production in saline environments. Further investigation and analysis are necessary to elucidate the genetic and physiological factors contributing to the observed salt tolerance or sensitivity in these wheat genotypes paving the way for targeted breeding efforts to enhance salt tolerance in wheat crops (20.529 A, 13.889 B, 8.108 C, 4.55 D).

Effect of salinity on dry shoot weight (g) of different wheat genotypes: The current study investigated the effect of salinity on the dry shoot weight of various wheat genotypes. The results showed significant variations in dry shoot weight among the tested genotypes under different salinity levels (Table 4). Overall, an increase in salinity led to a reduction in dry shoot weight in most of the genotypes indicating a negative impact of salinity stress on wheat growth. However, certain genotypes exhibited different responses to salinity stress. Among the genotypes, MH-21 displayed remarkable salt tolerance as evidenced by its consistently higher dry shoot weight compared to other genotypes across all salinity levels (2.9958 a). It maintained superior growth even under high salinity conditions (1.24±.02 200mM NaCl). Similarly, SARC-4 also demonstrated notable salt tolerance with a relatively higher dry shoot weight at elevated salinity levels (3.00±0.05 100mM NaCl and 2.13±0.01 140mM NaCl) (2.8325 b).

On the other hand, Lasani and AARI-11 were identified as salt-sensitive genotypes showing decreased dry shoot weight with increasing salinity. Lasani exhibited a significantly lower dry shoot weight compared to other genotypes across all salinity levels (1.2058 o). AARI-11 also displayed sensitivity to salinity stress with a notable decrease in dry shoot weight (1.1317 p). These findings highlight the importance of understanding the mechanisms underlying salt tolerance in wheat genotypes and emphasize the need for developing salt-tolerant varieties to ensure sustainable crop production in saline environments. Further investigations are required to elucidate the genetic and physiological factors contributing to the observed salt tolerance or sensitivity in these wheat genotypes facilitating targeted breeding efforts to enhance salt tolerance in wheat crops (2.9381 A, 2.1786 B, 1.5535 C, 0.65 D).

Table 1. SPAD value of different wheat genotypes in different levels of NaCl.

Genotypes	Control	100 mM NaCl	140 mM NaCl	200 mM NaCl	Mean
Akbar-1	35.73 ± 0.33 F-H	30.87 ± 0.32 Q-S	24.97 ± 0.33 e-g	20.37 ± 0.29 n-r	27.98 E-G
Pasban-90	33.33 ± 0.58 L-0	29.20 ± 0.58 V-Y	24.93 ± 0.35 e-g	20.17 ± 0.37 p-r	26.90 IJ
Fsd-08	37.23 ± 0.20 DE	35.20 ± 0.82 F-I	27.53 ± 0.32 a-c	24.33 ± 0.30 f-h	31.07 C
Subhani-21	35.07 ± 0.35 G-J	29.13 ± 0.61 W-Y	23.63 ± 0.26 h-j	19.37 ± 0.29 r-t	26.8 IJ
AS-2002	32.13 ± 0.71 OP	30.40 ± 0.59 S-V	24.30 ± 0.25 f-h	18.80 ± 0.40 st	26.40 J
SH-2002	37.20 ± 0.21 DE	33.83 ± 0.64 J-M	27.50 ± 0.17 a-c	24.40 ± 0.25 f-h	30.73 C
Dilkash-20	36.23 ± 0.38 E-G	32.80 ± 0.78 M-P	25.20 ± 0.47 d-f	20.03 ± 0.44 q-s	28.56 DE
Galaxy-13	35.30 ± 0.29 F-I	30.27 ± 0.35 S-X	25.97 ± 0.43 de	21.43 ± 0.29 l-o	28.24 EF
Lasani-08	30.07 ± 0.30 S-X	27.83 ± 0.61 Z-b	22.90 ± 0.23 i-k	16.60 ± 0.20 u	24.35 L
AARI-11	30.53 ± 0.67 R-T	26.00 ± 0.44 de	22.60 ± 0.42 j-l	16.43 ± 0.19 u	23.89 L
Anaj-17	35.47 ± 0.29 F-I	32.47 ± 0.30 N-P	26.37 ± 0.26 cd	21.53 ± 0.32 l-n	28.95 D
Ujala-16	37.93 ± 0.61 CD	35.77 ± 0.58 F-H	27.30 ± 0.26 bc	21.87 ± 0.20 k-m	30.71 C
Millat-11	34.60 ± 0.67 H-K	32.50 ± 0.56 N-P	25.00 ± 0.26 e-g	19.70 ± 0.26 q-s	27.95 E-G
Punjab-11	35.50 ± 0.70 F-I	30.33 ± 0.58 S-W	24.27 ± 0.54 f-h	18.80 ± 0.32 st	27.22 HI
MH-21	41.10 ± 0.36 A	39.00 ± 0.42 BC	30.47 ± 0.23 S-U	25.23 ± 0.20 d-f	33.95 A
Shafaq-06	33.83 ± 0.55 J-M	29.87 ± 0.37 S-X	24.93 ± 0.09 e-g	20.00 ± 0.26 q-s	27.15 HI
Sis-32	36.33 ± 0.64 EF	32.10 ± 0.66 O-Q	23.87 ± 0.38 g-i	19.17 ± 0.32 r-t	27.86 FG
SARC-1	33.80 ± 0.44 K-M	29.13 ± 0.26 W-Y	25.10 ± 0.31 e-g	20.27 ± 0.34 o-r	27.07 HI
SARC-2	35.10 ± 0.63 F-I	33.50 ± 0.23 K-N	23.60 ± 0.32 h-j	18.43 ± 0.29 t	27.65 F-H
SARC-3	34.33 ± 0.78 I-L	29.43 ± 0.29 T-Y	25.03 ± 0.27 e-g	20.83 ± 0.23 m-q	27.40 G-I
SARC-4	40.23 ± 0.22 AB	37.43 ± 0.73 DE	29.90 ± 0.23 S-X	24.47 ± 0.30 f-h	33.00 B
SARC-5	39.87 ± 0.67 AB	32.33 ± 0.75 N-P	29.03 ± 0.35 X-Z	23.47 ± 0.38 h-j	31.17 C
SARC-7	33.47 ± 0.63 K-N	29.27 ± 0.78 U-Y	24.30 ± 0.26 f-h	21.30 ± 0.38 m-p	27.08 HI
SARC-8	31.77 ± 0.72 P-R	28.57 ± 0.38 Y-a	22.97 ± 0.29 i-k	18.20 ± 0.40 t	25.37 K
Mean	**35.26 A**	**31.55 B**	**25.49 C**	**20.63 D**	

LSD*: Genotype = 0.61, Treatment = 0.25, Genotype × Treatment = 1.23

All the values are average of three replicates ± SE and interaction effect. Means with capital lettering shows the LSD pairwise comparison for treatments and wheat genotypes at $p<0.05$. *Critical value for pairwise comparison in least significance difference test.

Table 2. Shoot length (cm) of different wheat genotypes in different levels of NaCl.

Genotypes	Control	100 mM NaCl	140 mM NaCl	200 mM NaCl	Mean
Akbar-1	57.00 ± 0.58 M-Q	48.67 ± 0.88 X-a	41.67 ± 0.33 f-h	31.67 ± 0.88 q-t	44.75 MN
Pasban-90	58.33 ± 0.33 K-N	50.00 ± 1.53 W-Y	44.67 ± 0.33 c-e	32.67 ± 0.33 p-s	46.42 k
Fsd-08	62.67 ± 1.45 HI	55.33 ± 1.33 P-S	47.00 ± 1.16 a-c	36.67 ± 0.33 l-n	50.42 I
Subhani-21	56.33 ± 0.33 N-R	47.33 ± 1.20 Z-b	39.67 ± 0.33 h-k	30.67 ± 0.67 r-u	43.50 OP
AS-2002	59.00 ± 0.58 J-M	51.33 ± 1.45 U-W	37.33 ± 0.33 k-m	33.00 ± 0.58 p-r	45.17 LM
SH-2002	68.33 ± 1.45 D-F	55.67 ± 0.33 O-S	45.33 ± 0.33 b-d	34.67 ± 0.88 n-p	51.00 HI
Dilkash-20	60.33 ± 0.88 I-L	51.33 ± 0.88 U-W	42.33 ± 0.67 e-g	30.33 ± 0.33 s-u	46.08 KL
Galaxy-13	57.33 ± 0.33 M-P	46.67 ± 0.33 a-c	38.00 ± 0.00 j-m	28.67 ± 0.33 u-w	42.67 P
Lasani-08	56.00 ± 1.00 N-S	44.67 ± 0.88 c-e	35.67 ± 0.33 m-o	26.33 ± 0.33 wx	40.67 Q
AARI-11	54.00 ± 0.58 R-T	42.33 ± 0.33 e-g	34.00 ± 0.58 o-q	24.33 ± 0.33 x	38.67 R
Anaj-17	60.67 ± 0.33 H-K	55.00 ± 1.00 P-T	50.67 ± 0.67 V-X	41.00 ± 0.58 f-i	51.83 GH
Ujala-16	58.00 ± 0.58 L-O	45.33 ± 0.33 b-d	42.33 ± 1.20 e-g	28.33 ± 0.33 u-w	43.50 OP
Millat-11	72.00 ± 1.00 BC	60.33 ± 1.45 I-L	56.67 ± 1.45 M-Q	41.67 ± 0.33 f-h	57.67 C
Punjab-11	66.33 ± 1.20 FG	56.33 ± 1.45 N-R	49.67 ± 0.33 W-Z	38.67 ± 0.33 i-l	52.75 FG
MH-21	77.67 ± 0.33 A	67.67 ± 0.33 E-G	58.00 ± 1.16 L-O	44.67 ± 0.33 c-e	62.00 A
Shafaq-06	68.33 ± 1.67 D-F	57.33 ± 0.33 M-P	51.33 ± 0.33 U-W	38.67 ± 0.33 i-l	53.92 EF
Sis-32	72.67 ± 0.67 B	60.33 ± 1.45 I-L	43.33 ± 0.33 d-f	29.00 ± 0.58 uv	51.33 HI
SARC-1	69.67 ± 0.88 C-E	52.67 ± 1.20 T-V	48.00 ± 1.16 Y-a	30.33 ± 0.33 s-u	50.17 I
SARC-2	70.33 ± 1.45 B-D	58.33 ± 0.88 K-N	53.67 ± 1.45 S-U	39.33 ± 0.33 h-k	55.42 D
SARC-3	72.00 ± 0.58 BC	61.67 ± 1.45 HI	47.00 ± 1.16 a-c	36.67 ± 0.33 l-n	54.33 DE
SARC-4	76.33 ± 0.33 A	65.67 ± 0.33 G	56.33 ± 0.33 N-R	42.33 ± 0.33 e-g	60.17 B
SARC-5	59.00 ± 2.08 J-M	48.33 ± 0.33 X-a	40.33 ± 0.33 g-j	27.33 ± 0.33 vw	43.75 N-P
SARC-7	61.00 ± 0.58 H-J	49.67 ± 0.33 W-Z	38.33 ± 0.33 j-l	28.33 ± 0.33 u-w	44.33 M-O
SARC-8	63.00 ± 1.53 H	54.67 ± 1.45 Q-T	46.33 ± 0.33 a-c	29.33 ± 0.33 t-v	48.33 J
Mean	**64.014 A**	**53.611 B**	**45.319 C**	**33.528 D**	

LSD*: Genotype = 1.16, Treatment = 0.47, Genotype × Treatment = 2.33

All the values are average of three replicates ± SE and interaction effect. Means with capital lettering shows the LSD pairwise comparison for treatments and wheat genotypes at $p<0.05$. *Critical value for pairwise comparison in least significance difference test.

Table 3. Fresh shoot weight (g) of different wheat genotypes in different levels of NaCl

Genotypes	Control	100 mM NaCl	140 mM NaCl	200 mM NaCl	Mean
Akbar-1	20.00 ± 0.58 IJ	11.50 ± 0.29 VW	8.83 ± 0.17 bc	3.57 ± 0.07 rs	10.96 H
Pasban-90	16.67 ± 0.33 MN	10.57 ± 0.30 XY	7.53 ± 0.15 e-g	4.10 ± 0.10 o-r	9.72 LM
Fsd-08	31.00 ± 0.58 C	22.00 ± 0.58 GH	6.60 ± 0.10 hi	3.93 ± 0.07 p-r	15.88 C
Subhani-21	20.00 ± 0.58 IJ	10.50 ± 0.29 XY	6.10 ± 0.10 ij	4.83 ± 0.09 m-o	10.35 IJ
AS-2002	25.67 ± 0.67 E	19.33 ± 0.33 JK	9.87 ± 0.13 Y-a	6.13 ± 0.13 ij	15.25 D
SH-2002	20.03 ± 0.15 IJ	18.67 ± 0.33 K	9.27 ± 0.27 Z-b	4.60 ± 0.10 m-p	13.14 F
Dilkash-20	21.33 ± 0.33 H	20.33 ± 0.33 I	11.93 ± 0.07 UV	4.93 ± 0.07 l-n	14.63 E
Galaxy-13	29.00 ± 0.58 D	13.33 ± 0.33 T	9.20 ± 0.20 ab	5.63 ± 0.13 j-l	14.29 E
Lasani-08	14.33 ± 0.33 RS	8.60 ± 0.21 b-d	5.63 ± 0.13 j-l	3.00 ± 0.06 s	7.89 O
AARI-11	13.33 ± 0.33 T	6.27 ± 0.15 ij	3.93 ± 0.07 p-r	1.63 ± 0.03 t	6.29 P
Anaj-17	18.67 ± 0.33 K	15.33 ± 0.33 PQ	11.27 ± 0.15 V-X	5.90 ± 0.06 ij	12.79 F
Ujala-16	18.67 ± 0.33 K	10.50 ± 0.29 XY	5.77 ± 0.15 jk	4.50 ± 0.12 m-q	9.86 KL
Millat-11	15.67 ± 0.33 OP	11.67 ± 0.33 U-W	6.10 ± 0.10 ij	4.23 ± 0.12 n-r	9.42 MN
Punjab-11	15.67 ± 0.33 OP	12.33 ± 0.33 U	8.17 ± 0.17 c-e	5.10 ± 0.10 k-m	10.32 J
MH-21	35.00 ± 0.58 A	25.33 ± 0.33 E	14.83 ± 0.17 QR	7.77 ± 0.15 e-g	20.73 A
Shafaq-06	17.67 ± 0.33 L	12.33 ± 0.33 U	7.93 ± 0.07 d-f	4.97 ± 0.03 l-n	10.73 HI
Sis-32	17.33 ± 0.33 LM	13.67 ± 0.33 ST	5.77 ± 0.15 jk	4.00 ± 0.00 p-r	10.19 JK
SARC-1	16.33 ± 0.33 NO	10.93 ± 0.07 WX	7.93 ± 0.07 d-f	4.10 ± 0.10 o-r	9.83 KL
SARC-2	23.00 ± 0.58 F	13.67 ± 0.33 ST	5.83 ± 0.09 i-j	3.73 ± 0.09 q-s	11.56 G
SARC-3	16.33 ± 0.33 NO	10.00 ± 0.00 YZ	7.27 ± 0.15 f-h	4.10 ± 0.10 o-r	9.42 MN
SARC-4	34.00 ± 0.58 B	22.67 ± 0.33 FG	13.30 ± 0.15 T	6.13 ± 0.09 ij	19.02 B
SARC-5	15.67 ± 0.33 OP	9.90 ± 0.10 Y-a	7.07 ± 0.12 gh	4.33 ± 0.09 m-r	9.24 N
SARC-7	18.67 ± 0.33 K	10.57 ± 0.30 XY	6.27 ± 0.15 ij	4.13 ± 0.09 o-r	9.91 KL
SARC-8	18.67 ± 0.33 K	13.33 ± 0.33 T	8.20 ± 0.20 c-e	3.83 ± 0.09 p-r	11.01 H
Mean	**20.529 A**	**13.889 B**	**8.108 C**	**4.55 D**	

LSD*: Genotype = 0.39, Treatment = 0.15, Genotype × Treatment = 0.78

All the values are average of three replicates ± SE and interaction effect. Means with capital lettering shows the LSD pairwise comparison for treatments and wheat genotypes at $p<0.05$. *Critical value for pairwise comparison in least significance difference test.

Table 4. Dry shoot weight (g) of different wheat genotypes in different levels of NaCl

Genotypes	Control	100 mM NaCl	140 mM NaCl	200 mM NaCl	Mean
Akbar-1	2.42 ± 0.04 MN	2.05 ± 0.01 V-X	1.66 ± 0.02 de	0.45 ± 0.01 uv	1.65 IJ
Pasban-90	2.34 ± 0.02 O	2.01 ± 0.01 WX	1.60 ± 0.02 ef	0.53 ± 0.01 r-t	1.62 I-K
Fsd-08	4.80 ± 0.03 C	2.97 ± 0.01 I	1.59 ± 0.03 ef	0.53 ± 0.01 r-t	2.48 C
Subhani-21	2.48 ± 0.01 LM	2.03 ± 0.01 WX	1.54 ± 0.01 f-h	0.59 ± 0.01 q-s	1.66 I
AS-2002	3.91 ± 0.01 E	2.47 ± 0.06 LM	1.51 ± 0.03 g-i	0.97 ± 0.02 o	2.22 D
SH-2002	2.72 ± 0.02 J	2.37 ± 0.01 NO	1.74 ± 0.02 bc	0.60 ± 0.01 qr	1.86 F
Dilkash-20	3.41 ± 0.02 F	2.99 ± 0.01 HI	1.89 ± 0.01 z	0.63 ± 0.01 q	2.23 D
Galaxy-13	4.12 ± 0.09 D	2.07 ± 0.01 U-W	1.66 ± 0.02 de	0.97 ± 0.01 o	2.20 D
Lasani-08	1.98 ± 0.02 XY	1.32 ± 0.02 l	1.03 ± 0.01 o	0.49 ± 0.01 tu	1.21 O
AARI-11	1.81 ± 0.04 ab	1.36 ± 0.04 Kl	0.97 ± 0.01 o	0.38 ± 0.01 v	1.13 p
Anaj-17	2.98 ± 0.02 HI	2.21 ± 0.01 P-S	1.86 ± 0.05 za	1.01 ± 0.01 o	2.02 E
Ujala-16	2.44 ± 0.03 MN	2.01 ± 0.03 WX	1.04 ± 0.03 o	0.52 ± 0.01 s-u	1.50 MN
Millat-11	2.38 ± 0.02 NO	2.07 ± 0.01U-W	1.46 ± 0.03 h-j	0.52 ± 0.01 s-u	1.61 JK
Punjab-11	2.52 ± 0.01 L	2.14 ± 0.03 S-U	1.74 ± 0.04 bc	0.73 ± 0.01 p	1.78 G
MH-21	5.45 ± 0.07 A	3.09 ± 0.05 G	2.21 ± 0.02 P-S	1.24 ± 0.02 m	2.99 A
Shafaq-06	2.54 ± 0.03 L	2.13 ± 0.05 PQ	1.57 ± 0.01 fg	0.59 ± 0.00 q-s	1.73 H
Sis-32	2.63 ± 0.01 K	2.17 ± 0.01 Q-T	1.13 ± 0.02 n	0.50 ± 0.01 tu	1.61 K
SARC-1	2.16 ± 0.01 R-T	1.93 ± 0.01 YZ	1.46 ± 0.03 ij	0.59 ± 0.00 q-s	1.53 LM
SARC-2	3.05 ± 0.02 GH	2.06 ± 0.01 VW	1.19 ± 0.01 mn	0.51 ± 0.01 tu	1.70 H
SARC-3	2.26 ± 0.02 P	1.88 ± 0.02 Za	1.61 ± 0.04 ef	0.53 ± 0.01 r-t	1.57 Ll
SARC-4	5.02 ± 0.09 B	3.00 ± 0.05 HI	2.13 ± 0.01 T-V	1.19 ± 0.01 mn	2.83 B
SARC-5	2.18 ± 0.01 Q-T	1.71 ± 0.03 cd	1.51 ± 0.03 g-i	0.53 ± 0.01 r-t	1.48 N
SARC-7	2.21 ± 0.01 P-S	1.91 ± 0.04 z	1.39 ± 0.03 jk	0.49 ± 0.01 tu	1.49 MN
SARC-8	2.70 ± 0.02 JK	2.23 ± 0.05 P-R	1.78 ± 0.03 bc	0.50 ± 0.01 tu	1.80 G
Mean	**2.9381 A**	**2.1786 B**	**1.5535 C**	**0.65 D**	

LSD*: Genotype = 0.03, Treatment = 0.01, Genotype × Treatment = 0.07

All the values are average of three replicates ± SE and interaction effect. Means with capital lettering shows the LSD pairwise comparison for treatments and wheat genotypes at $p<0.05$. *Critical value for pairwise comparison in least significance difference test.

Table 5. Root length (cm) of different wheat genotypes in different levels of NaCl

Genotypes	Control	100 mM NaCl	140 mM NaCl	200 mM NaCl	Mean
Akbar-1	39.33 ± 0.88 HI	34.33 ± 0.88 P-R	29.00 ± 0.58 YZ	18.67 ± 0.33 h-j	30.33 EF
Pasban-90	37.33 ± 0.33 K-N	31.33 ± 0.88 VW	25.00 ± 0.58 b	17.33 ± 0.33 jk	27.75 KL
Fsd-08	37.67 ± 0.33 J-M	32.00 ± 0.58 T-W	27.33 ± 0.33 a	19.50 ± 0.29 gh	29.13 H-J
Subhani-21	38.67 ± 0.88 H-K	33.00 ± 0.58 R-U	28.00 ± 0.58 Y-a	19.67 ± 0.33 gh	29.83 F-H
AS-2002	44.00 ± 0.58 BC	34.67 ± 0.33 O-Q	31.00 ± 0.58 W	22.00 ± 0.58 de	32.92 D
SH-2002	43.00 ± 0.58 CD	38.67 ± 0.67 H-K	33.00 ± 0.58 R-U	21.67 ± 0.33 ef	34.08 C
Dilkash-20	43.67 ± 0.67 BC	37.00 ± 0.58 L-N	30.67 ± 0.33 WX	19.17 ± 0.44 g-i	32.63 D
Galaxy-13	38.67 ± 0.88 H-K	31.17 ± 0.60 VW	24.33 ± 0.33 bc	14.67 ± 0.33 lm	27.21 LM
Lasani-08	37.00 ± 0.58 L-N	31.67 ± 0.33 U-W	24.00 ± 0.58 bc	10.83 ± 0.17 p	25.88 N
AARI-11	36.00 ± 0.58 NO	31.00 ± 0.58 W	22.00 ± 0.58 de	8.17 ± 0.17 q	24.29 O
Anaj-17	38.33 ± 0.88 I-L	34.33 ± 0.88 P-R	29.33 ± 0.33 XY	19.33 ± 0.33 gh	30.33 EF
Ujala-16	39.33 ± 0.88 HI	33.67 ± 0.88 P-S	28.00 ± 0.58 Y-a	14.33 ± 0.33 l-m	28.83 IJ
Millat-11	43.33 ± 0.88 C	37.00 ± 0.58 L-N	30.67 ± 0.33 WX	20.33 ± 0.33 fg	32.83 D
Punjab-11	39.33 ± 0.88 HI	35.00 ± 0.58 OP	28.00 ± 0.58 Y-a	20.17 ± 0.44 f-h	30.63 EF
MH-21	46.67 ± 0.33 A	43.00 ± 0.58 CD	39.00 ± 0.58 H-J	23.33 ± 0.33 cd	38.00 A
Shafaq-06	39.67 ± 0.88 G-I	32.67 ± 0.67 SV	29.00 ± 0.58YZ	18.67 ± 0.33 h-j	30.00 FG
Sis-32	39.00 ± 0.58 H-J	31.83 ± 0.17 T-W	27.00 ± 0.58 a	15.83 ± 0.44 kl	28.42 JK
SARC-1	41.00 ± 0.58 E-G	36.67 ± 0.88 MN	25.00 ± 0.58 b	13.67 ± 0.33 mn	29.08 H-J
SARC-2	41.67 ± 0.88 DE	33.33 ± 0.88 Q-T	27.00 ± 0.58 a	15.33 ± 0.33 l	29.33 G-I
SARC-3	41.33 ± 0.88 EF	37.33 ± 0.67 K-N	28.00 ± 0.58 Y-a	17.67 ± 0.33 ij	31.08 E
SARC-4	45.00 ± 1.16 B	41.00 ± 0.58 E-G	37.67 ± 0.33 J-M	22.17 ± 0.44 de	36.46 B
SARC-5	37.33 ± 0.33 K-N	31.33 ± 0.33 VW	23.83 ± 0.44 bc	11.50 ± 0.29 op	26.00 N
SARC-7	40.00 ± 0.58 F-H	33.00 ± 0.58 R-U	27.50 ± 0.29 Za	13.50 ± 0.29 mn	28.50 JK
SARC-8	37.67 ± 0.88 J-M	31.17 ± 0.73 VW	25.00 ± 0.58 b	12.83 ± 0.17 no	26.67 MN
Mean	**40.208 A**	**34.424 B**	**28.306 C**	**17.097 D**	

LSD*: Genotype = 0.81, Treatment = 0.33, Genotype × Treatment = 1.63

All the values are average of three replicates ± SE and interaction effect. Means with capital lettering shows the LSD pairwise comparison for treatments and wheat genotypes at $p<0.05$. *Critical value for pairwise comparison in least significance difference test.

Effect of salinity on root length (cm) of different wheat genotypes: The present study investigated the impact of salinity on the root length of different wheat genotypes. The results revealed significant variations in root length among the tested genotypes under different salinity levels (Table 5). Generally, an increase in salinity resulted in a reduction in root length across most genotypes indicating the detrimental effect of salinity stress on root development. However, certain genotypes displayed different responses to salinity stress. MH-21 exhibited exceptional salt tolerance as evidenced by its consistently longer root length compared to other genotypes across all salinity levels (38.00 a). It displayed superior root growth even under high salinity conditions (23.33±0.33 200mM NaCl) suggesting its strong adaptability to saline environments. Similarly, SARC-4 demonstrated notable salt tolerance with a relatively longer root length observed at elevated salinity levels (41.00±0.58 100mM NaCl and 37.67±0.33 140mM NaCl) (36.46 b). On the other hand, Lasani and AARI-11 were identified as salt-sensitive genotypes displaying significantly shorter root lengths under all salinity conditions. Lasani exhibited the shortest root length compared to other genotypes across all salinity levels (25.88 n). AARI-11 also showed sensitivity to salinity stress with a significantly reduced root length (24.29 o).

Effect of salinity on fresh root weight (g) of different wheat genotypes: The results indicated that salinity had a significant impact on the fresh root weight of the tested genotypes (Table 6). Overall, increasing salinity levels led to a decrease in fresh root weight across most genotypes highlighting the negative effect of salinity stress on root development. However, some genotypes exhibited variations in their response to salinity stress. Among the genotypes, MH-21 displayed the highest salt tolerance as evidenced by its consistently higher fresh root weight compared to other genotypes across all salinity levels (7.925 g) (a). It exhibited remarkable root growth even under high salinity conditions (13.33±0.33 mM NaCl) indicating its adaptability to saline environments. SARC-4 also showed notable salt tolerance with a relatively higher fresh root weight observed at elevated salinity levels (11.50±0.29 mM NaCl) (6.967 b). On the other hand, Lasani and AARI-11 were identified as salt-sensitive genotypes exhibiting significantly lower fresh root weights under all salinity conditions. Lasani displayed the lowest fresh root weight compared to other genotypes across all salinity levels (3.675 g) (p). AARI-11 also showed sensitivity to salinity stress with a significantly reduced fresh root weight (2.979 g) (q).

Effect of salinity on dry root weight (g) of different wheat genotypes: The analysis of variance revealed a significant effect of salinity on the dry root weight of wheat genotypes (p<0.05). As the NaCl concentration increased, the dry root weight generally decreased for most genotypes (Table 7). Notably, MH-21 exhibited the highest dry root weight across all salinity treatments indicating its potential as a salt-tolerant genotype. In contrast, AARI-11 displayed the lowest dry root weight suggesting its vulnerability to salinity stress.

Effect of salinity on membrane stability index of different wheat genotypes: The analysis of variance revealed a significant effect of salinity on the MSI of wheat genotypes (p<0.05). As the NaCl concentration increased, the MSI generally decreased for most genotypes indicating increased membrane damage (Table 8). The highest mean MSI value was observed in genotype MH-21 across all salinity treatments (36.408a) indicating superior membrane stability and potential salt tolerance. Conversely, genotype AARI-11 exhibited the lowest mean MSI value (26.075o) suggesting its susceptibility to salinity-induced membrane damage.

These findings provide valuable insights into the response of wheat genotypes to salinity stress and highlight the genetic variation in membrane stability among different varieties. The significant differences observed in MSI values emphasize the importance of selecting and breeding wheat genotypes with enhanced membrane integrity to mitigate the negative effects of salinity stress. Further investigations into the underlying mechanisms of membrane stability and its association with salt tolerance will contribute to the development of salt-tolerant wheat cultivars ultimately improving crop productivity in saline environments.

Effect of salinity on relative water content of different wheat genotypes: The relative water content (RWC) of different wheat genotypes was significantly influenced by salinity levels. As the NaCl concentration increased there was a consistent reduction in RWC values indicating a decrease in water retention capacity as shown (Table 9). Among the genotypes, MH-21 exhibited the highest mean RWC value (64.533 a) indicating its superior ability to maintain water content under saline conditions. On the other hand, genotype AARI-11 had the lowest mean RWC value (52.607 m) suggesting its reduced ability to retain water in the presence of high salt concentrations. The significant differences observed in RWC values highlight the potential of certain genotypes such as MH-21 in maintaining higher water content and potentially possessing greater salt tolerance.

Effect of salinity on sodium concentration (mg g^{-1} DW) of different wheat genotypes: The effect of salinity on the sodium **concentration** of different wheat genotypes was investigated. As the NaCl concentration increased there was a general increase in sodium levels among the wheat genotypes (Table 10). The mean sodium values for each salinity treatment were 8.628 D for the control, 33.14 C for 100mM NaCl, 40.579 B for 140mM NaCl and 52.615 A for 200mM NaCl. Among the wheat genotypes, Lasani-08 and AARI-11 exhibited the highest sodium concentration with mean values of 39.525a and 39.392a respectively. On the other hand, MH-21 had the lowest sodium **concentration** with a mean value of 27.325 m, indicating its relatively better ability to regulate sodium accumulation under salinity stress. Genotypes with lower sodium **concentration** such as MH-21 may possess mechanisms for efficient sodium exclusion or compartmentalization contributing to their potential salt tolerance.

Table 6. Fresh Root weight (g) of different wheat genotypes in different levels of NaCl

Genotypes	Control	100 mM NaCl	140 mM NaCl	200 mM NaCl	Mean
Akbar-1	7.83 ± 0.17 HI	6.77 ± 0.15 LM	4.17 ± 0.09 c-e	1.53 ± 0.03 p-s	5.08 FG
Pasban-90	7.60 ± 0.15 IJ	4.73 ± 0.12 Y-b	3.18 ± 0.09 i-k	1.73 ± 0.03 o-q	4.31 MN
Fsd-08	8.10 ± 0.10 GH	6.10 ± 0.10 O-Q	3.93 ± 0.07 d-g	1.67 ± 0.03 p-r	4.95 GH
Subhani-21	8.83 ± 0.17 F	6.30 ± 0.15 NO	3.63 ± 0.09 gh	1.87 ± 0.03 m-p	5.16 F
AS-2002	10.87 ± 0.13 C	7.03 ± 0.09 KL	4.83 ± 0.09 X-Z	2.03 ± 0.03 m-o	6.19 C
SH-2002	9.83 ± 0.17 D	7.37 ± 0.19 JK	5.87 ± 0.09 QR	2.20 ± 0.06 m	6.32 C
Dilkash-20	10.60 ± 0.31 C	6.17 ± 0.17 O-Q	5.20 ± 0.12 U-W	1.77 ± 0.03 n-q	5.93 D
Galaxy-13	7.37 ± 0.19 JK	4.80 ± 0.12 X-a	3.33 ± 0.09 h-j	1.63 ± 0.03 p-r	4.28 MN
Lasani-08	6.17 ± 0.17 O-Q	4.47 ± 0.09 a-c	2.90 ± 0.06 kl	1.17 ± 0.03 tu	3.67 P
AARI-11	5.47 ± 0.12 TU	3.37 ± 0.09 hi	2.10 ± 0.06 mn	0.98 ± 0.02 u	2.98 Q
Anaj-17	8.20 ± 0.12 G	5.50 ± 0.15 S-U	6.23 ± 0.12 N-P	1.77 ± 0.03 n-q	5.43 E
Ujala-16	7.73 ± 0.12 I	5.83 ± 0.07 Q-S	4.03 ± 0.09 d-f	1.47 ± 0.03 q-t	4.77 IJ
Millat-11	8.20 ± 0.20 G	5.93 ± 0.15 P-R	4.23 ± 0.15 cd	1.83 ± 0.03 n-p	5.05 FG
Punjab-11	8.20 ± 0.12 G	5.10 ± 0.12 V-X	3.87 ± 0.09 e-g	1.73 ± 0.03 o-q	4.73 IJ
MH-21	13.33 ± 0.33 A	9.27 ± 0.15 E	5.93 ± 0.07P-R	3.17 ± 0.09 i-k	7.93 A
Shafaq-06	8.13 ± 0.19 GH	4.67 ± 0.09 Z-b	3.73 ± 0.09 fg	1.63 ± 0.03 p-r	4.54 KL
Sis-32	9.23 ± 0.23 E	5.87 ± 0.09 QR	3.00 ± 0.00 j-l	1.33 ± 0.03 r-t	4.86 HI
SARC-1	8.13 ± 0.19 GH	6.27 ± 0.15 N-P	2.97 ± 0.03 kl	1.33 ± 0.03 r-t	4.68 JK
SARC-2	9.80 ± 0.12 D	5.23 ± 0.15 UV	3.10 ± 0.06 i-l	1.73 ± 0.03 o-q	4.97 GH
SARC-3	7.73 ± 0.12 I	4.87 ± 0.09 W-Z	3.93 ± 0.09 d-g	1.23 ± 0.03 s-u	4.44 LM
SARC-4	11.50 ± 0.29 B	7.70 ± 0.21 IJ	5.87 ± 0.07 QR	2.80 ± 0.06 l	6.97 B
SARC-5	6.70 ± 0.12 LM	5.07 ± 0.12 V-Y	2.93 ± 0.07 kl	1.27 ± 0.03 s-u	3.99 O
SARC-7	7.20 ± 0.20 K	5.73 ± 0.15 R-T	4.43 ± 0.09 bc	1.33 ± 0.03 r-t	4.68 JK
SARC-8	6.57 ± 0.18 MN	5.00 ± 0.06 V-Z	3.97 ± 0.03 d-g	1.33 ± 0.03 r-t	4.22 N
Mean	**8.4722 A**	**5.7972 B**	**4.0574 C**	**1.6896 D**	

LSD*: Genotype = 0.17, Treatment = 0.06, Genotype × Treatment = 0.34

All the values are average of three replicates ± SE and interaction effect. Means with capital lettering shows the LSD pairwise comparison for treatments and wheat genotypes at $p<0.05$. *Critical value for pairwise comparison in least significance difference test.

Table 7. Dry Root weight (g) of different wheat genotypes in different levels of NaCl

Genotypes	Control	100 mM NaCl	140 mM NaCl	200 mM NaCl	Mean
Akbar-1	0.53 ± 0.01 M	0.27 ± 0.00 Y	0.18 ± 0.00 f-h	0.12 ± 0.00 m-o	0.28 H
Pasban-90	0.49 ± 0.01 OP	0.24 ± 0.00 ab	0.17 ± 0.00 h	0.11 ± 0.00 no	0.25 K-M
Fsd-08	0.60 ± 0.01 HI	0.27 ± 0.00 Y	0.16 ± 0.00 i	0.12 ± 0.00 l-n	0.29 G
Subhani-21	0.61 ± 0.01 GH	0.29 ± 0.00 U-W	0.13 ± 0.00 j-l	0.12 ± 0.00 l-n	0.29 G
AS-2002	0.79 ± 0.01 C	0.30 ± 0.00 T	0.19 ± 0.00 e-g	0.13 ± 0.00 j-l	0.35 C
SH-2002	0.65 ± 0.01 EF	0.29 ± 0.01 T-V	0.20 ± 0.01 ef	0.15 ± 0.01 ij	0.32 D
Dilkash-20	0.67 ± 0.28 D	0.25 ± 0.01 Za	0.20 ± 0.01 ef	0.12 ± 0.01m-o	0.31 E
Galaxy-13	0.54 ± 0.01 LM	0.21 ± 0.00 cd	0.13 ± 0.00 l-n	0.10 ± 0.00 o-q	0.25 M
Lasani-08	0.38 ± 0.01 R	0.20 ± 0.01 de	0.12 ± 0.01 l-n	0.08 ± 0.01 s	0.19 O
AARI-11	0.35 ± 0.01 S	0.18 ± 0.00 f-h	0.11 ± 0.00 op	0.05 ± 0.00 t	0.17 P
Anaj-17	0.66 ± 0.01 E	0.23 ± 0.00 bc	0.19 ± 0.00 ef	0.12 ± 0.00 l-n	0.30 F
Ujala-16	0.49 ± 0.01 OP	0.24 ± 0.01 ab	0.18 ± 0.01 gh	0.12 ± 0.01 l-n	0.26 KL
Millat-11	0.64 ± 0.01 F	0.26 ± 0.01YZ	0.19 ± 0.01 e-h	0.13 ± 0.01 l-n	0.30 EF
Punjab-11	0.50 ± 0.01 NO	0.24 ± 0.00 ab	0.18 ± 0.00 f-h	0.11 ± 0.00 no	0.26 JK
MH-21	0.87 ± 0.01 A	0.64 ± 0.00 EF	0.44 ± 0.00 Q	0.30 ± 0.00 TU	0.56 A
Shafaq-06	0.55 ± 0.01 L	0.22 ± 0.01 c	0.13 ± 0.01 k-m	0.09 ± 0.01 p-s	0.25 M
Sis-32	0.58 ± 0.01 JK	0.24 ± 0.01 ab	0.13 ± 0.01 l-n	0.08 ± 0.01 rs	0.26 KL
SARC-1	0.59 ± 0.01 IJ	0.27 ± 0.01 XY	0.13 ± 0.01 l-n	0.09 ± 0.01 q-s	0.27 HI
SARC-2	0.62 ± 0.01 G	0.24 ± 0.00 a	0.14 ± 0.00 j-l	0.09 ± 0.00 rs	0.27 HI
SARC-3	0.57 ± 0.01 K	0.27 ± 0.00 Y	0.14 ± 0.00 j-l	0.09 ± 0.00 p-s	0.27 IJ
SARC-4	0.81 ± 0.01 B	0.62 ± 0.01 G	0.37 ± 0.01 RS	0.28 ± 0.01 V-X	0.52 B
SARC-5	0.44 ± 0.01 Q	0.26 ± 0.01 YZ	0.12 ± 0.01 l-n	0.08 ± 0.01 rs	0.23 N
SARC-7	0.48 ± 0.01 P	0.27 ± 0.00 W-Y	0.14 ± 0.00 i-k	0.09 ± 0.00 p-s	0.25 M
SARC-8	0.51 ± 0.01 N	0.26 ± 0.01 YZ	0.14 ± 0.01 j-l	0.10 ± 0.01 p-r	0.25 LM
Mean	**0.5804 A**	**0.2815 B**	**0.1746 C**	**0.1207 D**	

LSD*: Genotype = 7.54, Treatment =3.07, Genotype × Treatment = 0.01

All the values are average of three replicates ± SE and interaction effect. Means with capital lettering shows the LSD pairwise comparison for treatments and wheat genotypes at $p<0.05$. *Critical value for pairwise comparison in least significance difference test.

Table 8. Membrane stability index of different wheat genotypes in different levels of NaCl.

Genotypes	Control	100 mM NaCl	140 mM NaCl	200 mM NaCl	Mean
Akbar-1	51.73 ± 1.13 K	33.83 ± 0.92 U-W	21.73 ± 0.56 mn	9.50 ± 0.23 s-u	29.20 LM
Pasban-90	53.60 ± 0.64 H-K	34.73 ± 0.75 S-W	22.67 ± 0.50 k-m	10.50 ± 0.17 q-u	30.38 JK
Fsd-08	53.03 ± 1.38 JK	34.17 ± 0.82 U-W	24.93 ± 0.34 f-j	10.33 ± 0.26 q-u	30.62 I-K
Subhani-21	49.13 ± 0.80 L	33.30 ± 0.93 V-X	23.70 ± 0.67 i-m	9.83 ± 0.26 r-u	28.99 M
AS-2002	54.27 ± 1.26 F-J	34.70 ± 0.99 S-W	24.90 ± 0.46 f-j	11.03 ± 0.29 q-t	31.23 G-K
SH-2002	54.03 ± 1.16 G-J	33.97 ± 0.94 U-W	22.50 ± 0.59 lm	10.60 ± 0.31 q-u	30.27 K
Dilkash-20	54.50 ± 0.63 E-J	34.63 ± 0.87 S-W	25.57 ± 0.72 d-i	10.20 ± 0.21 q-u	31.23 G-K
Galaxy-13	55.53 ± 1.53 C-H	35.00 ± 1.00 S-V	25.40 ± 0.36 e-i	9.33 ± 0.13 tu	31.32 F-J
Lasani-08	48.30 ± 0.84 LM	32.90 ± 0.86 WX	20.13 ± 0.38 no	8.57 ± 0.20 uv	27.48 N
AARI-11	47.07 ± 1.24 M	31.47 ± 0.88 XY	18.83 ± 0.52 o	6.93 ± 0.15 v	26.07 O
Anaj-17	54.43 ± 0.52 E-J	34.70 ± 0.93 S-W	24.57 ± 0.58 g-k	9.73 ± 0.27 r-u	30.86 H-K
Ujala-16	55.90 ± 0.86 C-G	35.17 ± 0.95 S-V	24.63 ± 0.48 g-k	10.57 ± 0.29 q-u	31.57 F-I
Millat-11	55.40 ± 1.54 C-I	35.60 ± 0.79 R-U	26.17 ± 0.35 c-h	11.33 ± 0.30 q-t	32.13 E-G
Punjab-11	52.87 ± 1.47 JK	33.27 ± 0.33 V-X	23.27 ± 0.46 j-m	11.43 ± 0.29 q-s	30.21 KL
MH-21	60.77 ± 0.80 A	41.57 ± 1.10 N	29.77 ± 0.47 YZ	13.53 ± 0.38 p	36.41 A
Shafaq-06	53.43 ± 1.11 I-K	34.33 ± 0.52 T-W	24.33 ± 0.64 h-l	9.60 ± 0.26 r-u	30.43 JK
Sis-32	56.37 ± 1.52 B-E	36.23 ± 0.32 R-T	27.57 ± 0.66 a-d	10.47 ± 0.22 q-u	32.66 DE
SARC-1	57.23 ± 1.61 B-D	37.43 ± 0.73 P-R	28.37 ± 0.49 Z-b	11.50 ± 0.23 p-s	33.63 B-D
SARC-2	57.43 ± 0.68 BC	38.47 ± 0.75 O-Q	27.73 ± 0.69 Z-c	11.63 ± 0.32 p-r	33.82 BC
SARC-3	58.00 ± 0.85 B	38.50 ± 0.78 OP	26.40 ± 0.60 b-g	10.57 ± 0.29 q-u	33.37 CD
SARC-4	58.07 ± 1.12 B	39.87 ± 0.76 NO	28.50 ± 0.50 Za	11.97 ± 0.24 pq	34.60 B
SARC-5	55.63 ± 1.51 C-H	35.03 ± 1.00 S-V	27.53 ± 0.61 a-d	10.97 ± 0.29 q-t	32.29 EF
SARC-7	56.23 ± 1.24 B-F	36.43 ± 0.81 Q-S	27.03 ± 0.63 a-e	11.20 ± 0.17 q-t	32.73 DE
SARC-8	55.33 ± 1.03 D-I	35.43 ± 0.39 R-U	26.70 ± 0.26 a-f	9.70 ± 0.15 r-u	31.79 E-H
Mean	**54.512 A**	**35.447 B**	**25.122 C**	**10.46 D**	

LSD*: Genotype = 1.01, Treatment = 0.41, Genotype × Treatment = 2.03

All the values are average of three replicates ± SE and interaction effect. Means with capital lettering shows the LSD pairwise comparison for treatments and wheat genotypes at $p<0.05$. *Critical value for pairwise comparison in least significance difference test.

Table 9. Relative water content of different wheat genotypes in different levels of NaCl.

Genotypes	Control	100 mM NaCl	140 mM NaCl	200 mM NaCl	Mean
Akbar-1	81.11 ± 0.52 JK	62.75 ± 0.62 T-W	52.74 ± 0.33 f-i	23.86 ± 0.43 s	55.12 JK
Pasban-90	82.66 ± 0.55 F-I	62.97 ± 0.52 S-W	52.21 ± 0.52 g-i	24.33 ± 0.33 s	55.54 IJ
Fsd-08	84.97 ± 0.46 CD	63.25 ± 0.80 S-U	53.95 ± 0.48 d-f	26.75 ± 0.45 o-q	57.23 FG
Subhani-21	80.77 ± 0.19 KL	62.19 ± 1.00 U-X	53.24 ± 0.58 e-g	24.09 ± 0.21 s	55.07 JK
AS-2002	83.11 ± 0.23 F-H	63.86 ± 0.52 Q-T	52.18 ± 0.14 g-i	24.07 ± 0.36 s	55.80 I
SH-2002	82.19 ± 0.59 H-J	64.84 ± 0.61 PQ	54.11 ± 0.50 c-e	25.94 ± 0.49 pq	56.77 F-H
Dilkash-20	83.02 ± 0.52 F-H	65.03 ± 0.52 PQ	54.94 ± 0.41 b-d	26.61 ± 0.59 o-q	57.40 EF
Galaxy-13	80.58 ± 0.67 KL	61.89 ± 0.57 V-X	51.83 ± 0.29 h-j	24.51 ± 0.48 rs	54.70 K
Lasani-08	79.72 ± 0.50 L	61.03 ± 0.48 XY	51.49 ± 0.50 ij	22.35 ± 0.19 t	53.65 L
AARI-11	79.68 ± 0.35 L	60.32 ± 0.30 Y	50.57 ± 0.33 j	19.85 ± 0.27 u	52.61 M
Anaj-17	82.53 ± 0.73 F-I	63.15 ± 0.42 S-V	53.00 ± 0.11 e-h	24.29 ± 0.31 n-s	55.74 IJ
Ujala-16	81.50 ± 0.48 I-K	63.45 ± 0.81 R-U	55.36 ± 0.24 bc	27.38 ± 0.29 no	56.92 F-H
Millat-11	80.74 ± 0.55 KL	62.12 ± 0.40 U-X	56.10 ± 0.52 ab	27.24 ± 0.48 n-p	56.55 H
Punjab-11	84.55 ± 0.35 C-E	64.15 ± 0.54 Q-S	56.89 ± 0.55 Za	28.22 ± 0.17 mn	58.45 D
MH-21	88.53 ± 0.38 A	71.74 ± 0.60 M	61.70 ± 0.48 WX	36.15 ± 0.16 k	64.53 A
Shafaq-06	85.50 ± 0.35 BC	65.96 ± 0.52 P	52.93 ± 0.51 e-h	27.60 ± 0.74 no	57.99 DE
Sis-32	83.81 ± 0.57 D-F	67.37 ± 0.27 O	56.99 ± 0.51 Za	29.43 ± 0.30 m	59.39 C
SARC-1	84.57 ± 0.27 C-E	67.92 ± 0.56 O	57.31 ± 0.29 Za	28.98 ± 0.47 m	59.70 C
SARC-2	83.54 ± 0.68 E-G	65.20 ± 0.42 PQ	57.52 ± 0.35 Z	28.28 ± 0.79 mn	58.63 D
SARC-3	83.20 ± 0.50 F-H	64.22 ± 0.38 Q-S	52.77 ± 0.45 e-i	26.59 ± 0.48 o-q	56.69 GH
SARC-4	86.32 ± 0.32 B	69.96 ± 0.51 N	59.92 ± 0.10 Y	32.65 ± 0.67 l	62.21 B
SARC-5	83.83 ± 0.37 D-F	65.77 ± 0.57 P	53.87 ± 0.55 d-f	26.27 ± 0.43 o-q	57.44 EF
SARC-7	82.45 ± 0.37 G-J	62.97 ± 0.52 S-W	53.70 ± 0.82 d-f	24.36 ± 0.46 s	55.87 I
SARC-8	83.10 ± 0.35 F-H	64.75 ± 0.61 P-R	52.81 ± 0.39 e-i	25.75 ± 0.41 qr	56.60 GH
Mean	**82.999 A**	**64.453 B**	**54.506 C**	**26.48 D**	

LSD*: Genotype = 0.67, Treatment = 0.27, Genotype × Treatment = 1.35

All the values are average of three replicates ± SE and interaction effect. Means with capital lettering shows the LSD pairwise comparison for treatments and wheat genotypes at $p<0.05$. *Critical value for pairwise comparison in least significance difference test.

Table 10. Sodium concentration (mg g^{-1} DW) of different wheat genotypes in different levels of NaCl.

Genotypes	Control	100 mM NaCl	140 mM NaCl	200 mM NaCl	Mean
Akbar-1	8.50 ± 0.23 p-s	31.57 ± 0.64 ij	39.63 ± 0.47 U-W	53.10 ± 0.17 G-I	33.20 H
Pasban-90	9.83 ± 0.18 n-p	31.37 ± 0.24 j	41.00 ± 0.32 S-U	55.80 ± 0.55 B-D	34.50 EF
Fsd-08	7.97 ± 0.12 rs	29.23 ± 0.22 k	39.20 ± 0.17 V-X	52.70 ± 0.63 H-J	32.28 J
Subhani-21	10.03 ± 0.18 n	34.47 ± 0.64 c-e	42.07 ± 0.49 Q-S	54.70 ± 0.55 D-F	35.32 CD
AS-2002	8.43 ± 0.18 q-s	33.27 ± 0.50 e-h	41.67 ± 0.46 R-T	55.17 ± 0.61 C-E	34.63 D-F
SH-2002	9.90 ± 0.25 no	32.53 ± 0.49 g-j	40.07 ± 0.43 UV	53.67 ± 0.64 F-H	34.042 FG
Dilkash-20	7.50 ± 0.21 r-t	32.40 ± 0.82 g-j	42.13 ± 0.26 Q-S	52.17 ± 0.81 I-K	33.55 GH
Galaxy-13	8.20 ± 0.21 rs	33.77 ± 0.55 d-g	42.60 ± 0.49 QR	54.20 ± 0.65 E-G	34.69 D-F
Lasani-08	13.40 ± 0.29 m	38.53 ± 0.47 W-Y	46.07 ± 0.43 O	60.10 ± 0.40 A	39.53 A
AARI-11	13.00 ± 0.25 m	38.70 ± 0.53 V-X	45.93 ± 0.49 O	59.93 ± 0.30 A	39.39 A
Anaj-17	7.27 ± 0.20 r-t	34.73 ± 0.79 cd	42.73 ± 0.45 QR	54.03 ± 0.79 E-H	34.69 D-F
Ujala-16	7.63 ± 0.22 r-t	35.33 ± 0.79 a-c	42.53 ± 0.52 QR	56.10 ± 0.87 BC	35.40 C
Millat-11	9.67 ± 0.22 n-q	36.37 ± 0.52 Z-b	42.83 ± 0.18 QR	56.90 ± 1.30 B	36.44 B
Punjab-11	8.47 ± 0.23 p-s	36.40 ± 0.25 Z-b	43.23 ± 0.30 PQ	51.70 ± 0.61 JK	34.95 C-E
MH-21	5.60 ± 0.15 u	26.83 ± 0.70 L	34.33 ± 0.30 c-f	42.53 ± 0.61 QR	27.33 M
Shafaq-06	9.60 ± 0.26 n-q	36.50 ± 0.55 Za	40.60 ± 0.49 TU	52.70 ± 0.61 H-J	34.85 C-E
Sis-32	8.63 ± 0.15 o-r	32.80 ± 0.40 g-j	40.07 ± 0.73 UV	51.83 ± 0.90 I-K	33.33 H
SARC-1	8.50 ± 0.15 p-s	31.97 ± 0.79 h-j	38.77 ± 0.41 V-X	50.23 ± 0.47 L-N	32.37 IJ
SARC-2	7.37 ± 0.15 r-t	32.80 ± 0.68 g-i	38.03 ± 0.35 XY	49.27 ± 0.64 N	31.87 JK
SARC-3	7.73 ± 0.12 r-t	32.97 ± 0.87 f-h	41.47 ± 0.78 R-T	49.77 ± 0.84 MN	32.98 HI
SARC-4	6.57 ± 0.18 tu	28.53 ± 0.47 k	35.10 ± 0.42 b-d	44.30 ± 0.42 P	28.63 I
SARC-5	7.23 ± 0.18 st	31.47 ± 0.58 ij	38.67 ± 0.43 WX	51.27 ± 0.54 KL	32.16 J
SARC-7	8.47 ± 0.23 p-s	33.13 ± 0.82 e-h	37.90 ± 0.29 XY	49.47 ± 0.51 N	32.24 J
SARC-8	7.57 ± 0.12 r-t	29.70 ± 0.42 k	37.27 ± 0.41 YZ	51.13 ± 0.50 K-M	31.42 K
Mean	**8.628 D**	**33.14 C**	**40.579 B**	**52.615 A**	

LSD*: Genotype = 0.69, Treatment = 0.28, Genotype × Treatment = 1.39

All the values are average of three replicates ± SE and interaction effect. Means with capital lettering shows the LSD pairwise comparison for treatments and wheat genotypes at $p<0.05$. *Critical value for pairwise comparison in least significance difference test.

Table 11. Potassium concentration (mg g^{-1} DW) of different wheat genotypes in different levels of NaCl

Genotypes	Control	100 mM NaCl	140 mM NaCl	200 mM NaCl	Mean
Akbar-1	20.60 ± 0.32 I-K	15.00 ± 0.32 Z-c	13.57 ± 0.29 g-k	10.00 ± 0.26 tu	14.79 LM
Pasban-90	21.53 ± 0.55 F-H	18.63 ± 0.55 N-P	16.73 ± 0.29 U-W	13.03 ± 0.24 j-n	17.48 DE
Fsd-08	21.27 ± 0.44 HI	17.40 ± 0.44 Q-U	16.17 ± 0.18 V-Y	12.40 ± 0.26 m-o	16.81 FG
Subhani-21	21.87 ± 0.23 F-H	17.50 ± 0.23 Q-U	15.73 ± 0.39 X-Z	11.40 ± 0.26 p-r	16.63 GH
AS-2002	20.13 ± 0.35 KL	16.30 ± 0.35 V-X	14.87 ± 0.15 a-c	13.90 ± 0.32 e-i	16.30 HI
SH-2002	18.80 ± 0.38 NO	15.57 ± 0.38 X-b	13.80 ± 0.33 c-g	10.97 ± 0.18 rs	14.88 l
Dilkash-20	21.30 ± 0.21 HI	17.27 ± 0.21 S-U	15.83 ± 0.32 X-Z	12.20 ± 0.35 n-p	16.65 GH
Galaxy-13	19.77 ± 0.41 K-M	16.77 ± 0.41 U-W	15.73 ± 0.27 X-Z	11.17 ± 0.32 qr	15.86 JK
Lasani-08	19.10 ± 0.26 MN	12.60 ± 0.26 l-o	10.13 ± 0.15 su	7.32 ± 0.13 v	12.29 O
AARI-11	18.67 ± 0.27 N-P	11.43 ± 0.27 p-r	9.70 ± 0.23 u	6.63 ± 0.18 v	11.61 P
Anaj-17	24.30 ± 0.31 BC	16.80 ± 0.31 U-W	13.03 ± 0.24 j-n	10.07 ± 0.26 tu	16.05 IJ
Ujala-16	24.30 ± 0.42 BC	15.40 ± 0.42 Y-b	12.80 ± 0.21 k-n	9.67 ± 0.12 u	15.54 k
Millat-11	21.10 ± 0.31 H-J	14.00 ± 0.31 d-h	11.93 ± 0.30 o-q	9.43 ± 0.15 u	14.12 N
Punjab-11	20.13 ± 0.48 KL	14.83 ± 0.48 b-d	11.43 ± 0.20 p-r	9.93 ± 0.26 u	14.08 N
MH-21	25.80 ± 0.40 A	20.30 ± 0.40 JK	18.13 ± 0.23 O-R	16.10 ± 0.36 V-Y	20.08 A
Shafaq-06	22.23 ± 0.38 E-G	14.50 ± 0.38 c-f	10.80 ± 0.21 r-t	9.97 ± 0.24 tu	14.30 MN
Sis-32	21.67 ± 0.47 F-H	17.67 ± 0.47 Q-T	16.03 ± 0.45 W-Y	13.07 ± 0.27 i-m	17.11 EF
SARC-1	24.43 ± 0.33 B	18.23 ± 0.33 O-Q	15.73 ± 0.33 X-Z	13.47 ± 0.20 g-k	17.97 C
SARC-2	22.73 ± 0.52 DE	16.93 ± 0.52 T-V	16.77 ± 0.15 U-W	14.23 ± 0.26 c-g	17.67 CD
SARC-3	22.37 ± 0.24 EF	17.27 ± 0.24 S-U	14.83 ± 0.20 b-d	13.27 ± 0.27 h-l	16.93 FG
SARC-4	25.53 ± 0.38 A	19.40 ± 0.38 L-N	17.37 ± 0.32 R-U	14.77 ± 0.30 b-d	19.27 B
SARC-5	21.40 ± 0.32 G-I	17.83 ± 0.32 P-S	16.93 ± 0.38 T-V	13.87 ± 0.20 f-j	17.51 DE
SARC-7	23.50 ± 0.23 CD	18.00 ± 0.23 O-S	15.70 ± 0.36 X-a	13.47 ± 0.23 g-k	17.67 CD
SARC-8	22.23 ± 0.38 E-G	18.67 ± 0.38 N-P	15.83 ± 0.32 X-Z	14.73 ± 0.29 b-e	17.87 CD
Mean	**21.865 A**	**16.596 B**	**14.582 C**	**11.877 D**	

LSD*: Genotype = 0.42, Treatment = 0.17, Genotype × Treatment = 0.85

All the values are average of three replicates ± SE and interaction effect. Means with capital lettering shows the LSD pairwise comparison for treatments and wheat genotypes at $p<0.05$. *Critical value for pairwise comparison in least significance difference test.

Table 12. Factor score showing the ranking of wheat genotypes based on total dry matter.

Factor scores: Principal Component Analysis			
Observation	**F1**	**F2**	**F3**
Akbar-1	-0.753	-0.117	0.194
Pasban-90	-0.834	0.008	0.118
Fsd-08	1.624	-0.952	-0.135
Subhani-21	-0.631	0.031	0.018
AS-2002	1.297	0.213	-0.322
SH-2002	-0.105	-0.130	0.126
Dilkash-20	0.855	-0.554	0.124
Galaxy-13	1.041	0.460	0.010
Lasani-08	-1.671	0.257	-0.094
AARI-11	-1.874	0.159	-0.104
Anaj-17	0.463	0.407	0.115
Ujala-16	-1.049	0.031	-0.263
Millat-11	-0.734	-0.034	0.023
Punjab-11	-0.419	0.128	0.118
MH-21	5.172	0.192	0.071
Shafaq-06	-0.624	-0.021	0.046
Sis-32	-0.844	-0.133	-0.255
SARC-1	-0.975	0.082	-0.018
SARC-2	-0.530	-0.139	-0.169
SARC-3	-0.904	0.022	0.137
SARC-4	4.212	0.177	-0.041
SARC-5	-1.157	0.106	0.090
SARC-7	-1.118	0.006	-0.008
SARC-8	-0.440	-0.199	0.219

Table 13. Factor score showing the ranking of wheat genotypes based on K^+/Na^+ ratio

Factor scores: Principal Component Analysis			
Observation	**F1**	**F2**	**F3**
Akbar-1	-0.777	-0.118	0.068
Pasban-90	-0.468	-0.162	0.015
Fsd-08	0.252	-0.238	0.050
Subhani-21	-0.840	-0.073	0.078
AS-2002	-0.484	0.180	-0.054
SH-2002	-1.333	0.013	0.007
Dilkash-20	0.203	-0.075	0.010
Galaxy-13	-0.591	-0.086	0.101
Lasani-08	-2.527	0.057	-0.050
AARI-11	-2.603	0.070	-0.022
Anaj-17	0.167	-0.266	-0.109
Ujala-16	-0.246	-0.181	0.027
Millat-11	-1.498	0.034	0.003
Punjab-11	-1.193	0.106	-0.152
MH-21	5.544	0.029	-0.131
Shafaq-06	-1.285	0.117	-0.119
Sis-32	-0.076	0.034	0.050
SARC-1	0.624	0.012	-0.016
SARC-2	1.033	0.295	0.237
SARC-3	0.346	0.164	-0.158
SARC-4	3.379	0.002	0.046
SARC-5	0.870	0.018	0.154
SARC-7	0.458	0.119	0.066
SARC-8	1.043	-0.049	-0.102

Effect of salinity on potassium content (mg g^{-1} DW) of different wheat genotypes: The result showed that as the NaCl concentration increased, there was a general decrease in potassium level among the wheat genotypes as shown (Table 11). The mean potassium values for each salinity treatment were 21.865 A for the control, 16.596 B for 100mM NaCl, 14.582 C for 140mM NaCl and 11.877 D for 200mM NaCl. Among the wheat genotypes MH-21 exhibited the highest potassium **concentration** with a mean value of 20.083 a. Conversely, Lasani-08 and AARI-11 had the lowest potassium **concentration** with mean values of 12.288 o and 11.608 p respectively.

Ranking of wheat genotypes according to factor score based on total dry matter: Based on the factor scores obtained from the principal component analysis (PCA), the ranking of wheat genotypes based on total dry matter revealed significant variations in performance (Table 12). MH-21 ranked first with a factor score of 5.172 followed by SARC-4 with a score of 4.212. Fsd-08 obtained the third position with a score of 1.624, indicating high total dry matter. Other genotypes such as AS-2002, Galaxy-13 and Dilkash-20 also performed well securing the fourth, fifth and sixth positions respectively. On the other hand, Lasani-08 and AARI-11 obtained the lowest ranking among the evaluated genotypes indicating lower total dry matter compared to the other genotypes. This ranking provides valuable information for breeders and researchers in selecting wheat genotypes with higher total dry matter for further breeding and cultivation ultimately contributing to improved wheat productivity.

Principal component analysis biplot of wheat genotypes based on total dry matter: The two axes F1 and F2 represented the first and second principal components which account for 96.46% and 2.84% of the variance in the data respectively (Fig. 1). This means that these two components capture most of the variability in the data. The arrows labeled TDM 100mM, TDM 140mM and TDM 200mM represented the effects of different salinity levels on TDM. The direction and length of these arrows indicate the magnitude and direction of the effect. Based on the biplot, genotypes like MH-21 and SARC-4 which are far from the origin might be more tolerant to increased salinity as they show distinct responses. The genotypes clustered near the origin are likely more sensitive as they show similar responses to salinity levels.

Ranking of wheat genotypes according to factor score based on K^+/Na^+ ratio: The ranking of wheat genotypes based on the $K^{+/}Na^+$ ratio was determined using Principal Component Analysis (PCA) factor scores (Table 13). The factor scores provide insights into the performance of each genotype in terms of their $K^{+/}Na^+$ ratio. In this analysis, the genotypes with higher factor scores are considered to have better K^+/Na^+ ratios indicating a more favorable balance of potassium to sodium. According to the results the wheat genotype MH-21 achieved the highest factor score of 5.544 indicating its superior performance in maintaining a desirable K^+/Na^+ ratio. This finding suggests that MH-21 possesses a higher potassium content compared to sodium which is beneficial for plant growth and overall productivity. Following MH-21, SARC-4 obtained the second-highest factor score of 3.379 further emphasizing its strong K^+/Na^+ ratio. The genotypes SARC-2, SARC-8 and SARC-5 also demonstrated favorable K^+/Na^+ ratios with factor scores of 1.033, 1.043 and 0.870 respectively. Conversely, genotypes such as Lasani-08 and AARI-11 displayed lower factor scores suggesting poorer performance in terms of the K^+/Na^+ ratio.

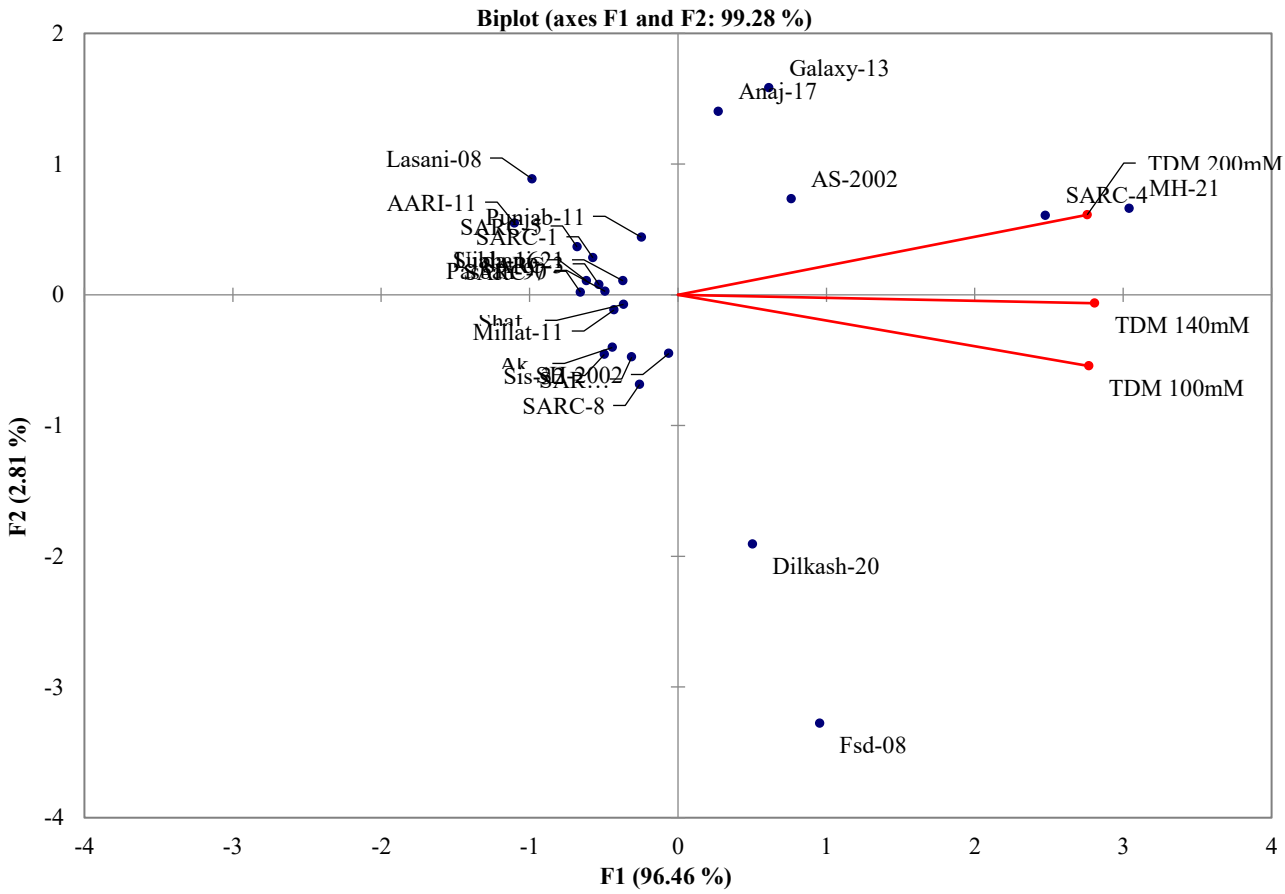

Fig. 1. Principal component analysis biplot of wheat genotypes based on total dry matter.

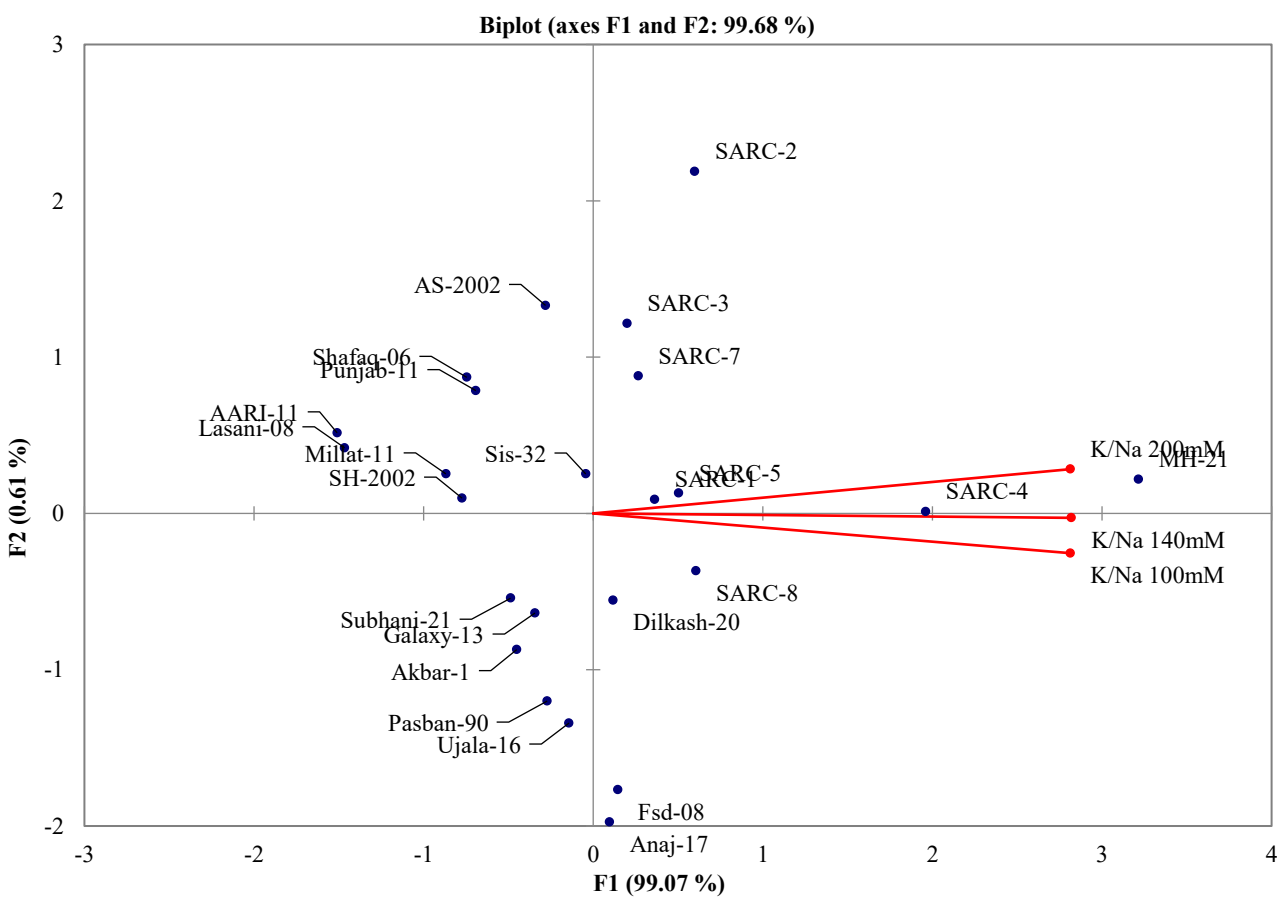

Fig. 2. Principal component analysis biplot of wheat genotypes based on K^+/Na^+ ratio.

Principal component analysis biplot of wheat genotypes based on K^+/Na^+ ratio: The biplot shows the relationship between different wheat genotypes and Potassium to sodium ratio on two principal axes F1 and F2, which account for 99.68% of the total variation in the data (Fig. 2). The biplot reveals three distinct clusters of data points, indicating different responses to salt stress among the wheat varieties. The first cluster consists of MH-21, SARC-4, SARC-2, SARC-3, SARC-7 etc which are located on the positive side of both axes. These varieties have high values of both F1 and F2 suggesting that they have high tolerance to salt stress and high potassium to sodium ratios. The second cluster includes SARC-8, Dilkash-20 etc which are located on the negative side of the F2 axis but positive on the F1 axis. These varieties have high values of F1 but low values of F2 indicating that they have moderate tolerance to salt stress and moderate potassium to sodium ratios. The third cluster comprises Lasani-08, AARI-11, AS-2002, Shafaq-06 etc which are located on the negative side of both axes. These varieties have low values of both F1 and F2 implying that they have low tolerance to salt stress and low potassium to sodium ratios. The vectors show the direction and magnitude of the variables contributing to the separation of the data points. The vector for K^+/Na^+ 200 mM has the longest length and the steepest angle indicating that it has the strongest influence on the variation in the data. The vector for K^+/Na^+ 100 mM has the shortest length and the smallest angle indicating that it has the weakest influence on the variation in the data. The vector for K^+/Na^+ 140 mM has a moderate length and angle indicating that it has a moderate influence on the variation in the data. The biplot suggests that the potassium to sodium ratio at 200 mM salt stress is the most important factor for discriminating the wheat varieties in terms of their salt tolerance.

Discussion

Salinity stress is known to disrupt photosynthetic processes and impair chlorophyll synthesis and stability in plants (Shah *et al.*, 2017). One of the key indicators of plant health and photosynthetic activity, the SPAD value showed a consistent decrease with increasing salinity levels indicating a decline in chlorophyll content and leaf greenness under salinity stress. Our findings are consistent with previous studies that have reported a decrease in SPAD values in various crop species under salinity stress (Barutcular *et al.*, 2016; Nounjan *et al.*, 2020). Salinity stress disrupts the balance between chlorophyll synthesis and degradation leading to chlorophyll breakdown and reduced photosynthetic capacity (Munns and Tester, 2008; Bilkis *et al.*, 2016). The decline in SPAD values observed in this study highlights the negative impact of salinity on leaf greenness and photosynthetic efficiency which can ultimately affect plant growth and productivity.

Furthermore, salinity stress significantly affected the growth parameters of wheat genotypes. The growth parameters of plants including shoot/root length, shoot /root fresh weight, dry shoot /root weight were considerably reduced with increasing salinity levels indicating the detrimental effect of salinity on biomass accumulation. Similar findings were reported in their investigations on wheat under salinity stress (Ashraf and Harris, 2013; Aycan *et al.*, 2021). The results demonstrated a significant reduction in all measured growth parameters under salinity stress conditions, indicating the inhibitory effect of high salt concentrations on plant growth. This stunted growth could be attributed to the inhibition of cell expansion and division caused by salt-induced osmotic stress (Munns & Tester, 2008). Our results are consistent with the findings of previous studies on wheat subjected to salinity stress (Nassar *et al.*, 2020; Saddiq *et al.*, 2021). The decrease in shoot and root lengths observed in this study reflects the restricted elongation and growth of plant organs under salinity stress. Similar findings have been reported in previous studies on various crop species subjected to salinity stress (Robin *et al.*, 2016; Din *et al.*, 2019). Salinity stress disrupts the balance between photosynthesis and respiration leading to reduced carbon assimilation and altered metabolic processes (Analin *et al.*, 2020; EL Sabagh *et al.*, 2021; Lal *et al.*, 2021).

Moreover, salinity stress influenced the physiological and biochemical aspects of wheat genotypes. The MSI and RWC important indicators of membrane integrity and water status respectively showed a decreasing trend with increasing salinity levels. This decline suggests that salinity stress leads to cellular membrane damage and reduced water retention capacity resulting in dehydration and impaired cellular functions (Singh *et al.*, 2020). Our results are in line with the studies conducted on various plant species under salinity stress (Ramani *et al.*, 2023). These findings are consistent with previous studies that have reported the detrimental effects of salinity on plant water relations and the resulting decrease in RWC (Chaurasia *et al.*, 2022; Muhammad *et al.*, 2023).

Strategies such as marker-assisted selection and genetic engineering can be employed to introgress genes responsible for membrane stability from salt-tolerant genotypes into susceptible ones (Snehi *et al.*, 2023). The higher RWC may be attributed to the efficient water uptake and transport systems as well as the activation of osmotic adjustment mechanisms (Mansour, 2023). The superior water retention capacity can contribute to the enhanced salt tolerance and better adaptation to saline environments. Strategies such as the identification and introgression of genes involved in osmotic adjustment and water conservation can be employed to enhance the salt tolerance and water retention capacity of wheat genotypes (Hossain *et al.*, 2021; Yadav *et al.*, 2022).

Ionic concentrations of Na^+ and K^+ were also measured to assess their influence on salinity tolerance. Our findings revealed that salinity stress caused a significant increase in Na^+ concentration and a decrease in K^+ concentration in both shoot and root tissues. This disrupted Na^+/K^+ homeostasis can lead to ion toxicity, osmotic imbalance and disturbances in nutrient uptake and transport (Hussain *et al.*, 2021; Saddiq *et al.*, 2021). Similar results have been reported in previous studies investigating the effects of salinity on wheat (Gul *et al.*, 2019; Tao *et al.*, 2021).

The accumulation of Na^+ and the subsequent increase in Na^+ percentage in wheat plants under salinity stress is a common response to osmotic stress. Excessive Na^+ uptake and its subsequent translocation to shoots can disrupt various physiological processes including photosynthesis and nutrient uptake leading to reduced plant growth and productivity (Okon, 2019). Conversely, the decrease in K^+ levels and the reduction in K^+ percentage observed in wheat genotypes under salinity stress can negatively affect plant growth and development. K^+ plays a vital role in various physiological processes, including enzyme activation, osmoregulation and maintenance of cell turgor (Wang *et al.*, 2013; Johnson *et al.*, 2022). The lower K^+ percentage in wheat plants under salinity stress may impair these processes and limit plant performance. Among the tested genotypes, MH-21 and SARC-4 consistently maintained higher MSI, RWC, and K^+/Na^+ ratios, suggesting that their superior performance under salinity is likely due to an integrated mechanism involving both ion exclusion and osmotic adjustment. Specifically, MH-21 exhibited the highest K^+ percentage, indicating a strong capacity for K^+ retention and selective ion transport. These traits point to efficient ion homeostasis mechanisms that limit Na^+ accumulation and sustain physiological processes under stress.

In this study, PCA was applied to evaluate wheat genotypes based on two important parameters total dry matter (TDM) and potassium to sodium ratio (K^+/Na^+ ratio). The results obtained from PCA provide valuable insights into the variability among genotypes and their potential implications for wheat productivity. The findings of this study align with previous research that highlights the importance of TDM and ion balance in determining wheat productivity (Abdehpour & Ehsanzadeh, 2019; Chaurasia *et al.*, 2022). The ability to identify genotypes with higher TDM and favorable K^+/Na^+ ratios through PCA can aid breeders in selecting superior genotypes for further breeding programs.

Conclusion

Salinity stress is a critical agricultural challenge, particularly in arid and semi-arid regions, as it reduces soil fertility, impairs water uptake and severely hampers crop growth and yields, ultimately threatening food production and food security in these vulnerable areas. This hydroponic screening study of twenty-four wheat genotypes during salinity stress revealed that MH-21 and SARC-4 as salt-tolerant genotypes while Lasani 2008 and AARI-11 are salt-sensitive genotypes. The salt-tolerant genotypes demonstrated higher SPAD values, better growth parameters (fresh shoot and root weight, dry shoot and root weight, shoot length and root length), enhanced membrane stability (MSI) and higher relative water content (RWC) under salinity stress. They also displayed better regulation of Na^+ and K^+ ionic concentrations. These findings provide important insights for wheat breeding programs aiming to enhance salt tolerance. However, to translate these results into practical applications, further research is necessary. Future work should focus on validating the performance of promising genotypes under field conditions, mapping quantitative trait loci (QTL), and conducting genome-wide association studies (GWAS) to identify markers linked to key tolerance traits. Moreover, integrating physiological data with molecular approaches, such as transcriptomics and marker-assisted selection, will be essential for developing resilient wheat cultivars suited to saline environments.

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