

ASSESSMENT OF SOME NEWLY DEVELOPED WHEAT LINES (*TRITICUM AESTIVUM* L.) UNDER NATURAL SALINE FIELD ENVIRONMENTS

MUHAMMAD UBAIDULLAH SHIRAZI*, MUHAMMAD ALI KHAN,
MUHAMMAD ATHAR KHAN, ASMA AND AISHA SHEREEN

Plant Physiology Division, NIA, Tandojam

*Corresponding author's email: shirazi050465@yahoo.com

Abstract

To evaluate salt tolerance in some newly developed genotypes of wheat (*Triticum aestivum* L.), field trials were conducted under natural saline field for two consecutive years i.e. Rabi 2018-19 and 2019-20 at Nuclear Institute of Agriculture (NIA), Tandojam. Wheat genotypes were collected from NIFA, Peshawar (20 genotypes), NIAB Faisalabad (1) and ARI Tandojam (1), along with local salt tolerant check i.e. Kiran-95. The soil at control site was non-saline ($EC = <4$ dS/m) while EC_e of saline site ranged from slightly saline (4-8 dS/m) to very highly saline ($EC_e >16$ dS/m). However the genotypes were evaluated on selected uniform patches of medium to high saline i.e. 9-12 dS/m. The genotypes were evaluated on the basis of growth and yield performance. The data illustrated a significant ($R^2 @ 0.5$) reduction in grain yield due to soil salinity. The combine results based on two years growth performance showed that genotype NRL-1683 was tolerant followed by NRL-1677, NRL-1646, NRL-1651, NRL-1685 and NRL-1687. On the contrary poor performance were exhibited by genotypes NRL-1625, NRL-1624, NRL-1680, NRL-1681 and ASYT-1CT-161287, thus categorized as sensitive to high salinity stress. Better performance of tolerant genotypes might be due to less decrease in K^+/Na^+ ratio and less reduction in chlorophyll (SPAD index), in consequence to lower decrease of leaf area.

Key words: Wheat genotypes, Salt tolerance, K^+/Na^+ ratio and SPAD index.

Introduction

Soil salinity is a serious concern for economical production of agricultural crops. Increasing salinity in the growing medium of plants disturbs plants ionic homeostasis and creates hyperosmotic environments. It delays/ decrease seed germination due to low osmotic potential as seeds fail to absorb water under the presence of toxic ions (Na^+ and Cl^-) present in the rooting medium (Hasan *et al.*, 2015). In sensitive plants there is also a change in individual development, prohibition in growth and differentiation of tissues and organs, the growing period shortens, root volume and length is reduce. The leaf becomes dark in color, reduction in leaf area and creates a weak stem that cannot support the weight of shoots and roots (Jiang *et al.*, 2006). In contrast to this, the tolerant plants have a high capacity to resist salt stress through biosynthesis and accumulation of compatible solutes both organic (proline, glycine betain, sugars) and inorganic (potassium). This empowers the plants for water absorption and turgor maintenance by increasing overall osmotic potential. It has been well documented that a high K^+/Na^+ ratio in cytosol is pre-requisite for normal functioning of the plant cell. The regulation of expression and activity of K^+ and Na^+ transporters and H^+ pumps creates a driving force for transport, which affirms a high K^+ concentration and low Na^+ concentration in the cytosol. By achieving ionic balance among the cytoplasm, vacuole and extracellular environment, plant maintains a comparatively high K^+ cytoplasmic concentration; thereby maintain the activity of various enzymes (Yu *et al.*, 2012).

Genetically there exist naturally salt tolerance in field crop; however the degree of salt tolerance varies among the plant species and varieties within the species. Wheat is generally classed as moderately salt tolerant (Munns *et al.*, 2006). According to Turki *et al.*, (2012), large scale

screening of available/ newly developed germplasm of wheat, might be the most promising strategy for improving wheat production. The relative salt tolerance of different wheat varieties of Pakistan was investigated by many workers on the basis of yield, physiological and biochemical responses under saline environment (Khan *et al.*, 2006, Khan, 2009). Recent advance to develop new salt tolerant plants either through traditional breeding or transgenic methods have made a good progress. In Pakistan better adaptability have been observed in number of wheat genotypes and promising cultivars have been released through this bidirectional breeding approaches. However it has been suggested that long term experiments are necessary to detect genotypic differences in growth and their yield potential by exposing plants to salinity for several months under natural saline environments (Kingsbury & Epstein, 1984; Francois *et al.*, 1986; Fortmeier & Schubert, 1995; Munns *et al.*, 1995). It is also suggested that most of the screening experiments carried out under controlled environments were not exposed to those conditions that prevail in natural environment of salt-affected soil, such as spatial and temporal heterogeneity of soil chemical and physical properties, high diurnal temperatures, low humidity and presence of drought stress (Munns & James, 2003). Hence evaluation of wheat genotypes under natural saline environments is a vital estimation approach, since the plants are screened under practical and natural soil environments such as soil heterogeneity, drought stress, and fluctuations of air temperature at the same time with salinity stress (Dadshani *et al.*, 2019). Therefore in the present investigations some newly developed wheat genotypes were evaluated under natural saline field conditions on the basis of yield and yield contributing characters along with some physiological features to avoid such reservation.

Materials and Methods

Testing materials: Wheat lines were collected from different research organizations, i.e. twenty genotypes (20) collected from Nuclear Institute of Food and Agriculture (NIFA), Peshawar, one each from Nuclear Institute of Agriculture & Biology (NIAB) Faisalabad and Agriculture Research Institute (ARI) Tandojam. One high yielding wheat variety PK-15 from NIFA and one local salt tolerant check i.e. Kiran-95 (NIA, Tandojam) was included in the study (Table 1).

Table 1. List of wheat genotypes tested in the present screening trial.

S #	Genotypes	Source
1.	NRL-1621	NIFA, Peshawar
2.	NRL-1624	NIFA, Peshawar
3.	NRL-1625	NIFA, Peshawar
4.	NRL-1643	NIFA, Peshawar
5.	NRL-1646	NIFA, Peshawar
6.	NRL-1651	NIFA, Peshawar
7.	NRL-1664	NIFA, Peshawar
8.	NRL-1666	NIFA, Peshawar
9.	NRL-1677	NIFA, Peshawar
10.	NRL-1679	NIFA, Peshawar
11.	NRL-1680	NIFA, Peshawar
12.	NRL-1681	NIFA, Peshawar
13.	NRL-1683	NIFA, Peshawar
14.	NRL-1685	NIFA, Peshawar
15.	NRL-1687	NIFA, Peshawar
16.	PK-15 (Pakhtunkhawa)	NIFA, Peshawar
17.	ASYT-CT-161074	NIFA, Peshawar
18.	ASYT-CT-161082	NIFA, Peshawar
19.	ASYT-CT-161085	NIFA, Peshawar
20.	ASYT-1CT-161106	NIFA, Peshawar
21.	ASYT-1CT-161287	NIFA, Peshawar
22.	V-158	NIAB- Faisalabad
23.	V-11006	ARI-Tandojam
24.	Kiran-95	NIA,Tandojam

Experimental details: Studies were conducted for two successive years i.e. Rabi 2018-19 and Rabi 2019-20. On the basis of visual observations, two suitable sites (saline and non-saline) were selected at NIA, experimental farm, Tandojam. Root zone salinity of both sites, was evaluated on the basis of soil electrical conductivity (EC_e), collected at 0-30 cm depth. At non-saline site values for electrical conductivity (EC_e) were < 4.0 dSm⁻¹, ranged between (1.06 to 3.34 dSm⁻¹). The selected saline patch was medium to highly saline (EC_e = 8-12 and 12-16 dSm⁻¹), neutral in reaction (pH = 6.5-7.5), dominated with sodium chloride (NaCl) salts. To maintain the uniformity of soil salinity, sowing was done on small sub-plots of 2.0 m² size. Four rows of 2.0 meter length at 30 cm, spacing were planted in each sub plot. The experiment was laid out according to randomized complete block design (RCBD), with three replicates. To observe the growth performance three plants from each replicate of both treatments (i.e. non saline and saline) were selected. Yield related traits i.e. Plant height, number of productive tillers, spike length, number of

spiklets/ spike, number of grains on main spike, grain weight / spike, grain and biological yield / plot were recorded at the time of crop maturity. Wheat genotypes were categorized according to Gill *et al.*, (2004). Physiological parameters i.e. leaf area, SPAD chlorophyll, relative water contents (RWC) recorded after 50% flowering. To study the ionic relations, inorganic solutes i.e. Na⁺, K⁺ and Ca⁺² contents in plant leaf samples (next to flag leaf) were also determined, using flamphotometer (jenway, Model PFP-7). Analysis of variance (ANOVA) and correlations studies among different growth parameters were performed (Steel *et al.*, 1997), using Statistix-08 computer package.

Results and Discussions

Growth performances: Effects of salinity were significant in all of the studied growth parameters i.e. plant height, productive tillers, spike length, spiklets/ spike, grain /spike, number of grains/ spike, gain weight/ spike, biological yield, grain yield and harvest index except seed index (Table 2). Seed germination was delayed in some genotypes however, the germination improved instantaneously later by irrigating the soil after 10-12 days of sowing (data not shown). The growth responses of various wheat genotypes to salinity and genotype x environmental interaction were also significant in case of all the growth parameters. Minimum and maximum values under non saline and saline plots and relative decrease in growth parameters (Plant height, productive tillers, spike length, spiklets/ spike, grain /spike, number of grains/ spike, gain weight/ spike) are presented in table 2. Average plant height was 95 and 80 cm under non saline and saline environments, respectively, ranged from 80 to 103 cm under non-saline and 70.0 to 92 cm under saline conditions and the average reduction of only 15% (Table 3). Generally less reduction in plant height under medium to high salinity patches was also observed in our previous studies (Khan *et al.*, 2014, Shirazi *et al.*, 2018). Among the individual genotypes the reduction in genotype NRL-1621 and NRL-1624 was almost nil i.e. 2 and 4%, respectively. The other genotypes also having slight decrease in plant height (<10%) were NRL-1643, NRL-1646 and NRL-1651. Comparatively higher reductions were observed in NRL-1666, NRL-1680 and PK-15 (24% reduction). Tillering capacity of wheat genotypes was also reduced under salinity. It ranged from 5.2 to 6.2 cm under non-saline and 4.4 to 5.9 cm under saline conditions with average values of 5.6 and 5.1, respectively. Average reduction in productive tillers was only 9%. Minimum or no decrease was observed in genotypes NRL-1680 (0.1%) and NRL-1643 (1.1%). In contrast to this the relative decrease in genotypes NRL-1677 and NRL -1651 was high i.e. 24 and 25%, respectively. Decreased uptake of essential nutrients and available water due to presence of excessive salts in growth medium may cause restricted plant height (Desoky & Merwad, 2015) and less number of productive tillers (Khan *et al.*, 2014). Reduction in spike length and spiklets/ spike was also less i.e. only 9 and 10% relative decrease, respectively. The only genotype which had higher reduction under salinity was PK-15 i.e. 25% reduction both for spike length and spiklets/ spike) (Table 4). Lower values for spike length and spiklets also reflected on

number of grains/ spike and grain weight/ spike as well. The reduction in number of grains/ spike and grain weight/ spike in PK-15 were also higher showing approximately 30 and 40% reduction, respectively. Conversely the genotype NRL-1664 had lower decrease in number of grains/ spike (1.4%) and grain wt/ spike (6.8%). Relative reduction in genotype NRL-1687 was also low i.e. (5.8%). Mean reduction in number of grains/ spike and grain wt/ spike were (15.7%) and (21.6%), respectively. The ultimate goal of study was to increase of crops growth and maintain higher yield under adverse conditions. The effect of salinity was more prominent in case of biological and grain yield, where > 50% reduction was recorded in seven genotypes for biological yield and for grain yield in eight genotypes. The negative impact salinity on biological yield and grain yield among the tested genotypes indicates the tolerance variability of wheat genotypes at high (12-16dS/m) salt stress. According to Ahmed *et al.*, (2011), total dry biomass and grain yield are the good selection criteria under salinity stress. Among the tested genotypes the genotype NRL-1687 exhibited maximum biological and grain yield under salinity i.e. 3.1 and 0.91 kg/ plot (2m²), respectively. The other genotypes also having higher values for biological and grain yield were NRL-1677, NRL-1683 and NRL-1685. Poor performances were observed by genotypes, NRL-1624, NRL-1625, NRL-1664, NRL-1681, PK-15 and ASY-CT-161074 in case of biological and grain yield. Francoise *et al.*, (1994) reported that the reduction in grain yield could be the result of poor tiller formation due to ionic toxicity and osmotic stress created by the excessive salts. Further the shortened duration of spikelet differentiation and grain filling period may cause decrease in grain yield under salinity. To expose the magnitude and direction of the relationship between various yield contributing traits and grain yield, correlation studies were performed (Table 5). A strong association of grain yield was found with plant height (0.75), grain weight/ spike (0.82) and biological yield ((0.89), spike length (0.68), spikelets/ spike (0.72), number of grains/ spike (0.69) and grain weight/ spike (0.82). Biological yield was also highly significant and positively related with plant height (0.83), spike length (0.68), spikelets/ spike (0.72), number of grains/ spike (0.65) and grain weight/ spike (0.72). The relations of grain weight/ spike were also found positive and highly

significant with spike length (0.75), spikelets/ spike (0.80) and number of grains/ spike (0.81). Positive correlation among the studied traits suggested that these traits are link with salinity tolerance and could be used to evaluate wheat genotypes for salinity tolerance. On the other hand very weak relations were observed for harvest index with all the studied parameters except grain yield (0.58).

The tested genotypes were categorized according to Gill *et al.*, (2004). On the basis of growth performances the genotype NRL-1683 was classed as tolerant followed by, NRL-46 NRL-1651, NRL-1685 and NRL-1687. Poor performance were displayed by genotypes NRL-1624, NRL-1625, NRL-1680, NRL-1681 and ASYT-1CT-161287 thus categorized as sensitive (S) to high salinity stress.

Physiological features: Wheat genotypes were also evaluated for physiological features i.e Leaf area, SPAD chlorophyll values, relative water contents (RWC) and ionic contents (Na⁺, K⁺ and Ca²⁺), after 50% flowering (Table 6). The data illustrated that leaf area was significant and positively related to RWC (0.53), Ca (0.67) and K/Na ratio (0.70). There was significant negative relation of leaf area with leaf Na⁺ contents (-0.80). Negative relations of leaf area with Na⁺ contents indicate that higher contents of Na⁺ ions may have decreased the availability of water in plant which resulted in less cell expansion thus there is decrease in leaf area (Wang *et al.*, 2001, Shrivastava and Kumar, 2015). There was an average of 51 % decrease in leaf area of wheat genotypes. Irrespective of tolerance or sensitivity nine of the tested genotypes had < 50% decrease in leaf area i.e. NRL-1683, NRL-1621, NRL-1643, Kiran-95, ASYT-CT-161082, ASYT-CT-161085, NRL-1624, NRL-1681 and ASYT-CT-161087 (former four are tolerant or medium tolerant while later five are medium sensitive or sensitive). It is reported that presence of salts inside the plant affects cell expansion of young leaves, causing a decrease in leaf area (Munns & Tester, 2008). Comparatively higher reduction was observed in NRL-1680, NRL-1679 and V-158 i.e. 72.0%, 70.9% and 71.2%, respectively. Poor capability of these genotypes for nutrient and water absorption may have led to reduction in leaf area. The correlations of leaf area with biological yield and grain yield were highly significant and positive i.e. 0.81 and 0.76, respectively.

Table 2. Minimum and Maximum values and relative reduction, Mean square of Treatment, genotype and interaction of genotypes with treatment for different growth parameters.

Parameters	Control		12 dS/m		R. Dec (%)		Treatment (T)	Genotypes (G)	Interaction (T x G)
	Min	Max	Min	Max	Min	Max	DF=1	DF=23	DF=23
Plant height (cm)	79.9	103	70.2	91.7	2.10	24.3	7304**	2753 **	1310 **
Productive Tillers	5	6.2	4.4	5.9	0.1	25.2	6.661**	0.404 NS	33815 NS
Spike length (cm)	10.5	13.4	8.9	11.1	0.0	24.7	36.55**	2.142*	1.032*
Spiklet/ spike	17.2	21.5	15.7	18.8	0.8	25.0	147.72**	4.17**	2.35**
No. of Grain / spike	46.0	68.0	40.0	59.0	1.4	30.5	2968 **	167.8**	52.44**
Grain weight/ spike (g)	1.9	3.1	1.5	2.6	5.0	40.5	11.55 **	0.35 **	0.166**
Biological yield/ plot (Kg/ 2m ²)	3.3	5.1	1.8	3.4	15.2	60.4	141.87**	0.59 NS	0.45 NS
Grain yield/ plot (Kg/ 2m ²)	0.9	1.5	0.4	0.9	20.2	72.2	2.012**	0.118*	0.1056**
Harvest Index	0.2	0.7	0.3	0.3	2.4	63.6	0.0438 NS	0.0131 NS	0.0164NS
Seed Index	40.0	54	33.1	48.8	0.4	26.7	547.05**	72.24**	28.95**

** = Significant @ 0.01, * = Significant @ 0.05 and NS = Non-significant

Table 3. Growth performance of wheat genotypes under non-saline and saline environment.

Genotypes	Plant height (cm)			Productive tillers			Spike length (cm)			Spiklets/spike			Grains / spike			Grain weight (g) / spike		
	Cont	Saline	R. D	Cont	Saline	R. D	Cont	Saline	R. D	Cont	Saline	R. D	Cont	Saline	R. D	Cont	Saline	R. D
	NRL-1621	84.3	81.1	3.8	5.4	4.8	11.3	11.3	10.0	11.7	17.7	15.9	9.9	50	46.5	6.3	2.4	1.9
NRL-1624	83.7	82.0	2.1	5.9	5.3	9.5	11.2	11.1	1.3	17.4	17.3	0.8	56	40.9	27.0	2.4	1.9	22.5
NRL-1625	92.9	77.8	16.3	5.6	5.0	10.9	12.3	11.1	9.8	19.5	15.9	18.7	58	40.6	30.5	2.9	1.9	34.4
NRL-1643	87.8	81.4	7.3	5.4	5.3	1.1	12.0	11.0	8.1	20.2	17.3	14.2	66	52.2	21.2	3.0	2.3	23.3
NRL-1646	90.6	83.8	7.5	5.7	4.8	14.7	10.9	10.1	7.5	18.5	18.0	2.7	57	49.6	12.6	2.5	2.2	12.1
NRL-1651	89.0	82.5	7.3	6.2	4.8	23.4	10.8	10.8	0.0	18.1	16.4	9.1	52	45.4	11.9	2.7	2.1	21.8
NRL-1664	98.9	80.3	18.8	5.4	5.1	5.6	10.7	9.9	8.1	17.2	16.7	3.3	46	45.4	1.4	2.2	2.0	6.8
NRL-1666	97.6	73.9	24.2	5.2	5.1	2.3	11.0	10.6	3.8	20.4	18.1	11.3	63	55.7	11.9	3.1	2.2	29.1
NRL-1677	91.8	78.8	14.3	5.9	4.4	25.2	11.6	10.6	9.3	19.4	18.8	3.0	64	57.1	10.4	2.9	2.4	16.1
NRL-1679	92.7	75.7	18.4	5.7	5.1	10.7	10.9	10.4	4.6	17.8	15.7	11.6	52	43.1	17.5	2.4	1.8	23.9
NRL-1680	96.7	73.2	24.3	5.2	5.2	0.10	12.4	10.4	15.5	20.9	18.7	10.5	68	58.9	13.4	2.8	2.0	29.5
NRL-1681	79.9	70.2	12.1	5.8	5.7	1.9	11.0	10.3	6.1	18.7	16.6	11.3	49	41.9	13.8	1.9	1.5	23.6
NRL-1683	103.4	91.7	11.3	6.0	5.9	1.7	11.4	10.3	10.2	19.2	18.4	4.2	59	50.9	14.2	2.8	2.6	5.0
NRL-1685	97.0	85.3	12.1	5.7	5.3	7.7	10.9	10.2	6.2	19.6	16.9	13.6	57	47.3	16.3	2.4	2.1	12.0
NRL-1687	101.4	84.2	16.9	5.8	5.0	13.1	11.5	10.2	11.4	20.3	16.9	16.4	59	52.0	11.2	2.4	2.2	5.8
Kiran -95	98.1	80.5	17.9	5.7	5.1	9.8	11.6	10.1	12.9	19.1	16.0	16.1	59	49.0	16.8	2.6	2.1	17.6
PK-15	101.1	77.2	23.7	5.3	4.5	15.6	13.4	10.1	24.7	21.5	16.1	25.0	68	47.6	30.1	3.1	1.8	40.5
ASYT-CT-161074	92.7	79.2	14.5	5.0	4.9	2.0	12.7	9.9	21.9	18.7	16.0	14.4	56	45.0	19.8	3.0	2.2	27.8
ASYT-CT-161082	96.3	79.1	17.9	5.6	5.4	2.5	10.8	9.8	9.2	18.2	15.9	12.8	56	40.0	28.3	2.6	1.8	30.8
ASYT-CT-161085	99.7	81.9	17.8	5.8	5.7	1.7	11.2	9.7	13.6	19.4	17.3	10.4	55	47.6	14.0	2.6	1.8	28.8
ASYT-1CT-161106	99.9	79.8	20.1	5.5	5.2	5.0	11.4	9.7	14.7	18.6	16.8	9.9	51	43.8	14.1	2.4	2.0	19.2
ASYT-1CT-161287	98.4	84.4	14.2	5.6	5.0	9.9	10.5	9.6	9.2	18.3	17.0	7.1	54	49.8	7.2	2.3	1.7	23.9
V-158	100.1	85.8	14.3	5.2	5.1	1.6	11.9	9.4	21.0	19.6	17.3	11.7	64	48.5	23.9	2.5	1.8	27.6
V-11006	96.8	79.0	18.4	5.4	4.5	16.3	10.8	8.9	17.7	19.4	17.6	9.4	68	54.6	19.8	2.9	2.0	30.3
Mean	94.6	80.4	15.0	5.6	5.1	8.9	11.3	10.3	8.9	19.0	17.0	10.5	57	48.4	15.7	2.6	2.0	21.6

R. D. = Relative decrease

Table 3. (Cont'd.).

Genotypes	Biological Yield (Kg)			Grain yield (Kg)			Seed Index (g)			Harvest Index		
	Cont	Saline	R. D	Cont	Saline	R. D	Cont	Saline	R. D	Cont	Saline	R. D
NRL-1621	4.62	2.4	48.9	1.21	0.68	43.7	49.3	41.11	16.7	0.31	0.27	12.9
NRL-1624	3.83	1.9	50.3	1.09	0.49	54.7	45.9	42.44	7.6	0.31	0.28	9.7
NRL-1625	4.52	1.8	60.4	1.44	0.40	72.2	49.4	46.75	5.4	0.33	0.22	32.7
NRL-1643	4.68	3.4	28.1	1.42	0.70	50.4	46.4	43.82	5.5	0.30	0.21	30.8
NRL-1646	4.82	2.7	43.9	1.03	0.77	25.2	44.2	43.99	0.4	0.31	0.31	0.0
NRL-1651	3.75	2.5	33.5	1.17	0.67	42.5	51.2	46.14	9.8	0.31	0.29	6.4
NRL-1664	4.88	2.0	59.7	1.32	0.54	59.2	46.6	43.62	6.4	0.28	0.28	-2.4
NRL-1666	3.33	2.8	15.2	1.18	0.63	47.0	53.0	40.41	23.7	0.39	0.25	35.6
NRL-1677	4.53	3.0	34.6	1.43	0.84	41.3	45.9	41.38	9.8	0.33	0.30	9.1
NRL-1679	4.55	2.5	45.6	1.20	0.65	45.7	46.5	43.15	7.2	0.27	0.27	0.0
NRL-1680	4.67	2.1	55.7	1.34	0.59	56.3	45.2	33.12	26.7	0.32	0.30	6.3
NRL-1681	4.33	2.2	49.0	1.15	0.61	47.1	42.1	34.90	17.0	0.29	0.27	6.9
NRL-1683	4.67	3.0	36.8	1.37	0.86	37.3	52.1	46.83	10.1	0.30	0.29	3.3
NRL-1685	5.00	2.7	45.3	1.30	0.83	36.2	44.2	43.42	1.9	0.29	0.26	10.3
NRL-1687	5.03	3.1	38.1	1.14	0.91	20.2	42.9	42.25	1.6	0.30	0.23	23.3
ASYT-CT-161074	4.87	2.5	49.1	1.50	0.72	52.1	54.0	48.82	9.6	0.33	0.31	6.1
ASYT-CT-161082	4.80	2.9	38.9	1.16	0.82	29.2	45.6	44.35	2.7	0.32	0.25	21.9
ASYT-CT-161085	5.08	2.6	49.8	0.97	0.68	30.5	46.9	38.83	17.2	0.28	0.20	28.6
ASYT-1CT-161106	4.75	2.9	39.5	1.18	0.83	29.7	50.0	45.22	9.6	0.37	0.26	29.7
ASYT-1CT-161287	4.58	3.1	33.5	0.88	0.64	27.6	43.1	34.52	19.9	0.22	0.20	9.1
V-158	4.50	2.7	39.3	1.10	0.75	32.1	40.0	37.52	6.1	0.66	0.24	63.6
V-11006	4.62	2.3	50.2	1.36	0.78	42.5	44.4	37.47	15.6	0.36	0.30	16.7
Kiran-95	4.17	2.7	34.6	1.19	0.74	38.0	43.8	43.14	1.4	0.42	0.26	38.1
PK-15	5.05	2.4	52.1	1.26	0.52	58.8	43.8	39.15	10.6	0.25	0.25	0.0
Mean	4.57	2.58	43.5	1.22	0.69	43.4	46.5	40.90	12.0	0.27	0.26	3.7

R. D. = Relative decrease (%)

Table 4. Correlations (Pearson) studies for growth and physiological attributes of tested wheat genotypes.

	PH	PT	SL	SPLT	GNPS	GWPS	BY	GY	SI	HI	LA	SPAD	RWC	Na	K	Ca
PT	0.47NS															
SL	0.58*	0.33 NS														
SPLT	0.71**	0.37NS	0.71**													
GNPS	0.61**	0.21NS	0.62**	0.89**												
GWPS	0.73**	0.34NS	0.75**	0.80**	0.81**											
BY	0.83**	0.55*	0.68**	0.72**	0.65**	0.72**										
GY	0.75**	0.49*	0.68**	0.72**	0.69**	0.82**	0.89**									
SI	0.50*	0.32 NS	0.49 NS	0.25 NS	0.16 NS	0.66**	0.46 NS	0.58*								
HI	0.43NS	0.09 NS	0.39 NS	0.43 NS	0.46 NS	0.43 NS	0.34 NS	0.42 NS	0.21 NS							
LA	0.74**	0.53*	0.59*	0.68**	0.56*	0.61**	0.81**	0.76**	0.41 NS	0.43 NS						
SPAD	-0.50*	-0.50*	-0.54*	-0.44 NS	-0.39 NS	-0.52*	-0.61**	-0.65**	-0.41 NS	-0.28 NS	-0.53*					
RWC	0.44*	0.12 NS	0.48 NS	0.51*	0.46 NS	0.46 NS	0.47 NS	0.43 NS	0.26 NS	0.28 NS	0.51*	-0.26 NS				
Na	-0.74**	-0.58*	-0.66**	-0.66**	-0.61**	-0.67**	-0.87**	-0.85**	-0.45 NS	-0.46 NS	-0.79**	0.64**	-0.43 NS			
K	0.38NS	0.31 NS	0.18 NS	0.19 NS	0.06 NS	0.29 NS	0.29 NS	0.25 NS	0.41 NS	-0.05 NS	0.17 NS	-0.25 NS	0.19 NS	-0.16 NS		
Ca	0.47NS	0.34 NS	0.59*	0.44 NS	0.29 NS	0.41 NS	0.58*	0.49 NS	0.38 NS	0.32 NS	0.67**	-0.54*	0.50*	-0.57*	0.24 NS	
K/Na	0.72**	0.60**	0.65**	0.60*	0.53*	0.67**	0.85**	0.82**	0.54*	0.38 NS	0.70**	-0.63**	0.45 NS	-0.91**	0.45 NS	0.49 NS

PH = Plant height, PT = Productive tillers, SL = Spike length, SPLT = Spiklets/spike, GN/SP = Number of grains/spike, GW/SP = Grain weight/spike, BY = Biological yield, GY = Grain yield, SI = Seed Index, HI = Harvest Index, LA = Leaf area, SPAD = Spade Chlorophyll Index, RWC = Relative water contents,

** = Significant @ 0.01, * = Significant @ 0.05 and NS = Non-significant

The ability to maintain water contents in tissues at optimal levels is an important strategy to dilute the internal salt concentration of tissues (Khan *et al.*, 2020). Plants under salinity faces difficulty in absorbing water from the area of low water potential (more negative), which effect on cell expansion, cell division, stomatal opening, abscisic acid (ABA) accumulation etc. (Hsiao and Xu, 2000). Comparatively less decrease in relative water contents (RWC) was recorded in all the tested wheat genotypes (Table 6). The average RWC values were 93% and 86%, under non-saline and saline condition, respectively with average reduction of only 7.4%. It is reported that there are two components responsible for water relations of a plant i.e. water potential and hydraulic conductivity (Negrao *et al.*, 2017). Maximum decrease in relative water contents (RWC) was observed in Kiran-95 (27%) followed by ASYT-CT-161074(21%). On the other hand the genotypes NRL-1646, NRL-1651, NRL-1685, NRL-1621, NRL-1643 and NRL-1666 had maintained their RWC quite successfully (former three are tolerant and later three are medium tolerant). Positive relations of RWC with Ca (0.50) and K/Na ratio (0.45) and negative with Na⁺ contents (-0.43) were observed in the present investigations.

The measurement of chlorophyll fluorescence is usually adopted to explain genetic variation in crop performance (Araus *et al.*, 1998). SPAD index technique was used for the estimation of chlorophyll contents in wheat. It is the ratio between leaf thickness (as determined by the transmission of light in the IR range) and leaf greenness (as determined by the transmission of light in the red light range (Negrao *et al.*, 2017). The data for SPAD index illustrated an increasing trend under salinity. Maximum increase in SPAD index values, was observed in NRL-1666 (i.e. 22%) followed by V-11006 (19%). Increased values of SPAD chlorophyll under saline environment indicate high salinity stress in these two genotypes due to presence of Na ions which may have resulted concentrated deposition of green pigment. Khatkar and Kuhad (2000) also observed increases in total chlorophyll per leaf area to incremental increases in salinities in wheat at flowering stage. Moderate salinity stress enhances the biosynthesis of total chlorophyll and cretonoids contents in order to preserve proper functioning of photosynthesis system (shah *et al.*, 2017). Intense deposition of chlorophyll may also be due to reduced leaf area, as salinity results thicker leaves due to higher number of cells per unit area with reduce cell size (Bizhani & Salehi, 2014, Gomez- Bellot *et al.*, 2015). In the present studies significantly negative correlation (-0.53) between leaf area and SPAD index values were observed. As it is reported that under salinity stress, leaf expansion is associated with changes in leaf anatomy (smaller and thicker leaves), resulting in higher chloroplast density per unit leaf area (Munns and Tester, 2008). Almost all the tolerant genotypes showed slight increase in SPAD index (-1.6 to 6.4%) except NRL-1646, illustrated elevated increase in SPAD index i.e. 15%. Hasan *et al.*, (2016) also reported increased SPAD values over control, under moderate salinity level, among different wheat genotypes. The increment was more in salt sensitive wheat genotypes compared to that in salt-tolerant genotypes. Correlation of SPAD index with biological yield and grain yield were also significantly negative i.e. -0.87 and -0.85, respectively, while significantly positive (0.64) with Na⁺ contents.

Table 6. Physiological features of tested wheat genotypes grown under non saline and saline field conditions.

Geno types	LA (cm ²)		SPAD		RWC (%)		Na (%)		K (%)		Ca(%)		K/Na ratio								
	Cont	Saline	R. D (%)	Saline	R. I/D (%)	Cont	Saline	R. I/D (fold)	Cont	Saline	R. I/D (%)	Cont	Saline	R. I/D (%)	Cont	Saline					
NRL-1621	27.5	25.8	6.3	47.9	56.3	17.5	90.5	93.9	3.7	0.28	1.27	4.5	0.57	0.79	39.3	0.38	0.39	-2.6	2.01	0.62	69.0
NRL-1624	25.1	16.9	32.5	49.9	49.0	-1.7	91.8	87.3	-4.9	0.35	1.27	3.7	0.86	0.86	-0.3	0.31	0.37	-20	2.50	0.68	72.9
NRL-1625	32.7	13.1	59.8	50.5	54.5	7.9	94.7	87.5	-7.6	0.32	1.26	3.9	0.59	0.54	-8.7	0.34	0.33	1.0	1.84	0.43	76.6
NRL-1643	24.3	21.9	10.2	45.8	50.1	9.4	87.2	92.1	5.6	0.34	1.58	4.6	0.82	0.78	-4.7	0.40	0.31	21.8	2.39	0.49	79.4
NRL-1646	41.4	15.4	62.8	48.1	55.5	15.4	93.2	93.4	0.2	0.41	1.01	2.5	0.66	0.68	3.1	0.41	0.34	15.9	1.59	0.67	57.9
NRL-1651	37.8	12.9	65.8	49.9	49.2	-1.6	93.5	93.6	0.1	0.35	1.14	3.3	0.85	0.67	-21.1	0.35	0.35	-1.9	2.45	0.59	76.0
NRL-1664	39.9	12.3	69.1	48.9	54.3	11.2	93.1	92.4	-0.7	0.43	1.49	3.5	0.80	0.76	-4.5	0.42	0.32	23.8	1.87	0.51	72.7
NRL-1666	43.0	20.2	53.1	47.8	58.6	22.5	93.5	95.2	1.9	0.58	1.56	2.7	0.87	0.76	-13.2	0.39	0.31	19.3	1.50	0.48	67.7
NRL-1677	31.3	11.7	62.5	47.6	52.3	9.7	94.5	93.3	-1.2	0.36	1.37	3.8	0.72	0.82	14.8	0.38	0.32	16.1	2.01	0.60	70.1
NRL-1679	39.0	11.3	70.9	49.0	51.8	5.9	89.8	75.9	-15.5	0.35	1.04	2.9	0.87	0.75	-13.8	0.31	0.33	-5.2	2.45	0.72	70.6
NRL-1680	40.5	11.1	72.6	48.5	52.0	7.4	96.6	88.5	-8.4	0.38	1.04	2.8	0.68	0.55	-19.1	0.40	0.32	21.0	1.80	0.53	70.6
NRL-1681	41.2	21.8	47.1	47.6	51.8	8.7	96.7	77.0	-20.4	0.35	1.15	3.3	0.65	0.53	-17.8	0.42	0.31	24.2	1.87	0.47	75.1
NRL-1683	30.9	21.3	31.0	49.0	52.2	6.4	94.1	84.0	-10.8	0.41	1.25	3.0	0.71	0.77	8.0	0.34	0.31	9.4	1.73	0.61	64.4
NRL-1685	42.4	18.6	56.3	47.2	49.6	5.2	89.4	91.3	2.2	0.46	1.21	2.6	0.80	0.74	-8.2	0.39	0.31	19.2	1.75	0.61	65.2
NRL-1687	42.9	24.5	42.9	51.3	53.0	3.3	92.9	89.1	-4.1	0.42	1.40	3.3	0.89	0.83	-5.7	0.40	0.29	28.5	2.11	0.59	71.8
ASYT-CT-161074	29.9	13.4	55.2	49.5	56.3	13.8	92.2	72.5	-21.4	0.33	1.47	4.5	0.87	0.67	-23.2	0.35	0.29	18.3	2.66	0.46	82.9
ASYT-CT-161082	32.2	19.5	39.3	44.6	51.1	14.4	93.4	88.5	-5.2	0.40	1.20	3.0	0.82	0.74	-10.0	0.43	0.37	13.6	2.06	0.61	70.1
ASYT-CT-161085	27.2	16.4	39.6	51.4	54.1	5.3	92.2	80.7	-12.5	0.45	1.16	2.6	0.91	0.78	-13.8	0.34	0.30	14.2	2.02	0.67	66.8
ASYT-ICT-161106	42.2	20.5	51.4	51.7	53.2	2.8	99.0	78.0	-21.2	0.37	1.23	3.4	0.96	0.58	-40.0	0.40	0.27	31.1	2.62	0.47	82.2
ASYT-ICT-161287	28.7	17.5	39.1	50.5	57.1	12.9	91.3	84.6	-7.4	0.36	0.97	2.7	0.86	0.48	-43.5	0.36	0.28	20.9	2.39	0.50	79.1
V-158	41.5	12.0	71.2	51.0	51.2	0.3	92.9	76.0	-18.1	0.39	1.55	3.9	0.54	0.79	45.9	0.40	0.21	46.7	1.38	0.51	63.0
V-11006	43.4	16.3	62.5	48.2	57.4	19.2	94.9	90.0	-5.2	0.31	1.00	3.2	0.53	0.57	7.2	0.32	0.21	33.7	1.72	0.57	66.7
Kiran -95	22.9	15.8	30.9	47.7	50.6	6.2	92.0	66.9	-27.3	0.26	0.93	3.5	0.82	0.66	-19.3	0.29	0.30	-3.3	3.10	0.71	77.0
PK-15	43.1	17.1	60.3	50.5	51.3	1.5	94.4	95.1	0.8	0.41	1.32	3.2	0.67	0.55	-17.0	0.39	0.29	25.8	1.63	0.42	74.3
Mean	35.4	16.2	51.4	48.9	53.0	8.5	93.1	86.1	-7.4	0.4	1.2	3.4	0.80	0.70	0.9	0.37	0.31	15.5	2.02	0.56	72.4

LA = Leaf area, SPAD = Chlorophyll index, RWC = Relative water contents, Na = Sodium, K = Potassium, R D = Relative decrease, R I/D = Relative increase or decrease

Table 5. Categorization of different growth parameters according to Gill *et al.*, (2007).

Genotypes	PH	PT	SL	SPLT	GN/SP	GW/SP	BY	GY	SI	HI	Class
NRL-1621	II	II	II	III	II	II	II	II	II	II	MT
NRL-1624	II	II	I	II	III	II	III	III	II	II	S
NRL-1625	II	II	I	III	III	II	III	III	I	III	S
NRL-1643	II	II	I	II	II	I	I	II	II	III	MT
NRL-1646	II	II	II	I	II	II	II	II	II	I	T
NRL-1651	II	II	I	II	II	II	II	II	I	I	T
NRL-1664	II	II	II	II	II	II	III	III	I	II	MS
NRL-1666	III	II	II	I	I	II	II	II	II	II	MT
NRL-1677	II	III	II	I	I	I	I	I	II	I	MT
NRL-1679	III	II	II	III	II	II	II	II	II	II	MS
NRL-1680	III	II	II	I	I	II	III	II	III	I	S
NRL-1681	III	I	II	II	III	III	II	II	III	II	S
NRL-1683	I	I	II	I	II	I	I	I	I	II	T
NRL-1685	I	II	II	II	II	II	II	I	II	II	T
NRL-1687	II	II	II	II	II	II	I	I	II	II	T
ASYT-CT-161074	II	II	II	III	II	II	II	II	I	I	MT
ASYT-CT-161082	II	II	II	III	III	II	II	I	II	II	MS
ASYT-CT-161085	II	I	III	II	II	II	II	II	II	III	MS
ASYT-1CT-161106	II	II	III	II	II	II	II	I	I	II	MT
ASYT-1CT-161287	II	II	III	II	II	III	I	II	III	III	S
158	I	II	III	II	II	II	II	II	II	II	MT
V-11006	II	III	III	II	I	II	II	II	II	I	MS
Kiran-95	II	II	II	III	II	II	II	II	II	II	MT
PK-15 (Pakhtunkhawa)	II	III	II	II	II	II	II	III	II	II	MS

PH = Plant height, PT = Productive tillers, SL = Spike length, SPLT = Spiklets/spike, GN/SP = Number of grains/spike, GW/SP = Grain weight/spike, BY = Biological yield, GY = Grain yield, SI = Seed index and HI = Harvest Index
T = Tolerant, MT= Medium tolerant, MS = Medium sensitive and S = Sensitive

Accumulation of inorganic ions in plants plays a major role for osmotic adjustment to high salinities (Yang *et al.*, 2009). Plant samples (leaves) analyzed for inorganic ions (Na^+ , K^+ and Ca^{+2}) showed increased accumulation of Na^+ and decreased K^+ and Ca^{+2} accumulation under salinity. The relative increase in Na^+ contents under salinity was almost 2-4 folds. There was minimum accumulation of Na^+ in salt tolerant check (Kiran-95) under salinity followed by ASYT-CT-161087 and V-11006 i.e. 0.93, 0.97 and 1.0%, respectively. Comparatively high Na^+ accumulation was recorded in genotypes NRL-1643 (1.58%), NRL-1666 (1.52%), NRL-1664 (1.49%) and ASYT-CT-161074 (1.47%). High accumulation of Na^+ ions indicates poor salt control by these genotypes in the transportation route. According to Munns (2002) leaf blade is the main site of Na^+ toxicity where Na^+ accumulates through transpiration stream, rather than in the roots. Further the entry of Na^+ ions into the plants may also accelerated due to nonselective cation channels present in the root plasma membrane (Amtmann & Sanders, 1999). Numerous studies confirmed that Na^+ toxicity is not only due to toxic effects of Na^+ in the cytosol, but K^+ homeostasis is also disrupted possibly due to the ability of Na^+ competing for K^+ binding sites (Bartels & Ramanjulu, 2005, Jing *et al.*, 2021). Under saline conditions maintaining ion homeostasis can be particularly challenging for plants, as the accumulation of toxic ions (i.e. Na^+) can perturb the plant's selective ability to control accumulation for other ions (Negrao *et*

al., 2017). Therefore reducing Na^+ in the shoot, while maintaining K^+ homeostasis, is a key component of salinity tolerance in many cereals and other crops. The retention of high K^+ is also essential for maintenance of electrical potential across membrane, turgor, energy transfer and photosynthesis (Khan *et al.*, 2021). In the present studies potassium contents in wheat genotypes were observed optimal under non saline environments however under salinity, it decreased in all wheat genotypes except NRL-1621, NRL-1646, NRL-1683 and V-158, where bit increase was recorded. Under non saline environment K^+ contents ranged between 0.53-0.96 percent while under saline environments it varied between 0.48 to 0.86%. Maximum decrease in K^+ contents was observed in genotype ASY-CT161287 i.e. 43.5%. Potassium contents in genotype NRL-1624 remained constant under both environments. The correlations of K^+ were negative and non-significant with Na (-0.16) while significantly negative with Ca (-0.57). K^+ relations were positive but non-significant with biological yield and grain yield i.e. 0.29 and 0.25, respectively. On the other hand, relations of Na^+ were significantly negative with K^+/Na^+ ratio (-0.91). Shabala and Cuin, (2008) suggested that K^+/Na^+ ratio is proportionally much greater affected by changes in the Na^+ concentration than changes in the K^+ concentration, therefore it is common to express Na^+/K^+ ratio to determine the salinity tolerance of a plant. Positive response of K^+/Na^+ ratio resulted in higher biological yield and grain yield as is evident from

strongly positive relations of K^+/Na^+ ratio with biological yield (0.85) and grain yield (0.82) (Table 6). It is reported that the ratio of K^+/Na^+ is mainly associated with salt tolerance in plant (Gorham *et al.*, 1990, Dvorak *et al.*, 1994, Chen *et al.*, 2007). In the present studies relative decrease in K^+/Na^+ ratio was bit less in three tolerant genotypes i.e. NRL-1683(64%), NRL-1646(58%) and NRL-1685(65%). On the other hand all the sensitive genotypes had higher decrease in K^+/Na^+ ratio i.e. > 70-79%. According to Grattan & Grieve (1999), sodium (Na^+) induced potassium (K^+) deficiency and impaired K^+/Na^+ selectivity are the major factors for reduced growth and yield under saline conditions. Calcium contents in plant samples also showed decreasing trend. Average decrease in Ca contents was 16%. Maximum decrease was observed in genotype V-158 (47%) followed by V-11006 (34) and ASYT-1CT-161106 (32%). High accumulation of Ca was positively responded to biological yield and grain yield, showing significantly positive correlation i.e. $r @ (0.05) = 0.58$ for biological yield and (0.50) for grain yield. Calcium accumulation also responded positively with potassium showing significantly positive relations i.e. (0.56).

Conclusion

Keeping in view the results related to growth and physiological features, it can be concluded that better performance of tolerant genotypes (NRL-1683, NRL-1646 and NRL-1685) under medium to high salinities (9-12dS/m), might be due to less decrease in K^+/Na^+ ratio, chlorophyll (SPAD index), leaf area and improved accumulation of Ca in plant tissues..

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