

## EVALUATION OF BREAD WHEAT GENOTYPES FOR SALINITY STRESS TOLERANCE BASED ON SEEDLING TRAITS

NAILA GANDAH<sup>1</sup>, ABDUL WAHID BALOCH<sup>1</sup>, M. UBAIDULLAH SHIRAZI<sup>2</sup>, TAUQEER AHMAD YASIR<sup>3</sup>, WAJID ALI JATOI<sup>1</sup>, MUHARAM ALI<sup>4</sup> AND M. NAWAZ KANDHRO<sup>5</sup>

<sup>1</sup>Department of Plant Breeding & Genetics; <sup>2</sup>Department of Biotechnology, Sindh Agriculture University, Tandojam, Pakistan; <sup>3</sup>College of Agriculture Bahauddin Zakariya University, Bahadur Sub-Campus Layyah-Pakistan

<sup>4</sup>Nuclear Institute of Agriculture, Tandojam, Pakistan.

<sup>5</sup>Department of Agronomy, Sindh Agriculture University, Tandojam, Pakistan

\*Corresponding author's email: [balochabdulwahid@yahoo.com](mailto:balochabdulwahid@yahoo.com)

### Abstract

The constant salinization of arable land is a warning to the world food security. Salinized soils spreading across the various countries of the world lead to a great loss of cultivated land. Bread wheat (*Triticum aestivum* L.) is one of most important crops worldwide but suffers from a considerable grain yield losses due to soil salinity. The current study was designed to evaluate bread wheat genotypes for salt tolerance based on seedling traits. In this context, a set of 22 bread wheat genotypes were assessed against salinity stresses at early seedling stage (12 and 16 dSm<sup>-1</sup>) along with control. The obtained mean squares indicated that genotypes, treatments and genotype x treatment interactions differed significantly for all seedling traits, suggesting that genetic resources exploited in the current study were worth to be used in future wheat breeding programs. Based on mean performance under salinity stress conditions, a group of seven wheat genotypes like TD-1, Kiran-95, Hamal, NIA-Sarang, AS-2002, LU-26s and NIA-AS-14 were identified as salinity tolerant; hence these genotypes may be used for further genetic analysis under salinity stress. With respect to cluster analysis based on early seedling performance, all genotypes were classified into four groups. The first group composed of seven wheat genotypes (NIA-Sarang, AS-2002, Kiran-95, LU-26s, NIA-AS-14, TD-1 and Hamal), indeed the genotypes of this group reflected a vigorous growth nevertheless recognized as tolerant against salinity stress, indicating that these bread wheat genotypes may provide useful genetic recombinations for salinity stress hence may be exploited for further breeding programs. However, second group was tagged as moderately tolerant while third and fourth group of genotypes were specified as sensitive and highly sensitive to salinity, respectively.

**Key words:** Bread wheat, Salinity, Genetic variation, Early seedling.

### Introduction

Bread wheat is cultivated almost in all parts of Pakistan under irrigated and rain fed systems, with 70 and 30% ratio, respectively (Muhammad & Mohammad, 2018); it contributes 9.6% to value addition in agriculture and 1.9% to national Gross Domestic Product (GoP, 2017). Modern wheat breeding emphasis on development of new high yielding varieties suited best to diversified agro-climatic conditions. It needs knowledge regarding genetic variability which is present in the available crop germplasm, inheritance pattern functioning for the yield and its related characters. It can be achieved by breeders through identification of superior germplasm and crossing them to each other by using various hybridization strategies to create new variability and wheat plants with elevated levels of genetic diversity and/or recombination (Ishaq *et al.*, 2018).

Continuous conversion of arable land into saline soils is a real threat to food security; and reportedly (Anon., 2010) more than 800 million ha of land are considered as salinity affected which accounts for about 6% of the total land area of the world and consequently around 20% present day agriculture is severely affected (Mickelbart *et al.*, 2015). The soils under salinity are spread across continents and annually more than 10 million ha of arable land is being affected by the salinity. In order to combat irrigation induced salinity, annually US\$ 27.3 billion are

spent (Qadir *et al.*, 2014). Due to salinity toxic Na<sup>+</sup> and Cl<sup>-</sup> ions are accumulated in plant tissues causing osmotic and ionic stress in plants. According to Food and Agriculture Organization (2015), wheat is the most cultivated crop worldwide and the annual grain production is about 736 million tons. However, this most important crop is challenged by soil salinity and significant quantity of grain is lost due to salinity every year. Although, several strategies are continuously formed for enhancement of wheat grain production in saline soils through development of effective drainage system and by development of salinity tolerant genotypes to overcome problems associated with low wheat production on saline soils. Hence, identification of wheat genotypes tolerant to salinity is prerequisite and such tolerant wheat varieties needs to be evolved that have proven adaptability under salinity conditions. The ultimate solution to cope-up with adverse effects of salinity is to evolve salt tolerant wheat varieties which could survive in soil fertility deficit-areas. Keeping in view the above facts, a set of 21 wheat genotypes along with check wheat varieties were assessed for salinity tolerance at early seedling stage.

### Materials and Methods

The present study was carried out to assess the genetic basis of salinity tolerance in bread wheat genotypes. In this regard, 22 (one check) wheat genotypes

of diverse origin as mentioned in Table 2 were evaluated for early seedling traits under salinity stress conditions in laboratory conditions in growth cabinets. The experiment was conducted in water culture using 1/4<sup>th</sup> strength of Hoagland nutrient solution as growing media in plastic bowls (Size: 8.4 x 4.5cm). The experiment was conducted at Plant Physiology Division, Nuclear Institute of Agriculture, Tandojam, having three treatments ( $T_1$  = Control;  $T_2$  =12 dSm<sup>-1</sup>;  $T_3$  =16 dSm<sup>-1</sup>) and three replications. Seeds were planted on molded plastic sieves placed in plastic bowls, containing sufficient nutrient solution. The bowls were placed in programmed controlled growth cabinets maintained at 25/20°C day/night temperatures and 12 hours photoperiod. The experiment was terminated after 10 days (240 hours). A total of eight early seedling traits were investigated such as germination (%), root length (cm), shoot length (cm), root fresh weight (g), shoot fresh weight (g), K<sup>+</sup>, Na<sup>+</sup> and K<sup>+</sup>/Na<sup>+</sup> ratio (Ansari & Flowers, 1986). The data obtained was subjected to statistical computer package (Statistix Ver. 8.1) for analysis of variance and LSD test, whereas cluster analysis (Ward's method) was carried out with the help of SPSS v.21 computer software.

## Results and Discussion

Regarding mean squares of genotypes, treatments and genotypes x treatment interaction were significantly different ( $p \leq 0.05$ ) for all the traits, such as germination %, root length, shoot length, root fresh weight, shoot fresh weight, Na<sup>+</sup>, K<sup>+</sup> and Na<sup>+</sup>/K<sup>+</sup> ratio (Table 1). It refers that genotypes tended to possess genetic variability for various seedling and physiological parameters; hence these bread wheat genotypes may be preferred for further breeding experiments. Hussain *et al.*, (2105) reported that twenty-five genotypes were significantly different for root length, shoot length and root-shoot fresh weight at various NaCl levels, whereas six salinity treatments and interaction of genotype x salinity treatments were also significant. Similarly, Mahboob *et al.*, (2016) also observed significant differences among different bread wheat genotypes for some physiological traits including Na<sup>+</sup>, K<sup>+</sup> and Na<sup>+</sup>/K<sup>+</sup> ratio, while imposing genotypes at different levels of NaCl.

The results noticeably pointed-out that increasing level of NaCl caused adverse effects on fresh as well as dry biomass production. Nevertheless, there was substantial variability for salt tolerance among the assessed bread wheat genotypes. Salt sensitive genotypes showed larger decrease in plant biomass while comparing with salt tolerant genotypes. The variation in response of the tested genotypes could basically be associated with genetic constitution of varieties. It has been described that wheat genotypes possess higher plant biomass at early seedling stage thus showing improved salt tolerance at maturity (Ahmadi & Ardekani, 2006). Production of more vigorous seedlings is a key phase towards the life cycle of crop plants. Assessment of genotypes with regard to salinity tolerance at the seedling stage can save substantial time if done at maturity (Gurmani *et al.*, 2014).

Like previous studies, the current study also showed more adverse effect on germination and plant biomass as the level of salt increased. However, several varieties also performed outstandingly for germination and plant biomass under salt stress conditions (Tables 2-4). Under both salt stress (12 and 16 dSm<sup>-1</sup>) conditions, different genotypes expressed promising performance for germination and different early seedling traits, such as NIA-AS-14 (96.66 and 89.67%), NIA-Sarang (94.44 and 91.33%) and Kiran-95 (94.44 and 93.66%) for germination; TD-1 (11.84 and 11.05 cm), Hamal (11.08 and 10.65 cm) and NIA-AS-14 (11.00 and 10.65 cm) for root length; NIA-AS-14 (20.95 and 19.45 cm), TD-1 (20.73 and 18.25 cm) and Kiran-95 (20.89 and 19.42 cm) for shoot length; AS-2002 (0.84 and 0.68 g), Kiran-95 (0.96 and 0.75 g) and Benazir (0.84 and 0.64 g) for root fresh weight and wheat genotypes like Kiran-95 (2.01 and 1.57 g), AS-2002 (1.92 and 1.72 g) and TD-1 (1.33 and 0.97 g) for shoot fresh weight. The above-mentioned genotypes maintained higher plant biomass and showed minimum growth reduction when exposed to 12 dSm<sup>-1</sup> and 16 dSm<sup>-1</sup>. All in all, the genotypes Kiran-95, TD-1, Hamal, NIA-AS-14 and AS-2002 displayed desirable performance under salinity stresses. The wheat genotypes showed differential response to salt stress might be due to their differential genetic potential for salt tolerance. It is a well-known fact that tolerance ability of genotype at adult stage is being reflected by the tolerance capacity of genotype at early seedling stage. A great success of this fact has been reported in maize, sorghum, wheat, soybean and cotton by Khan *et al.*, (2003a), Kausar *et al.*, (2012), Ali *et al.*, (2012), Kamal *et al.*, (2003) and Azhar & Ahmad, 2000, respectively. During early screening trial at seedling stage, Sheerazi *et al.*, (2018) identified four genotypes as tolerant at 16 dSm<sup>-1</sup> salinity and narrated that better tolerance of those genotypes might be due to higher shoot and root dry weights. Naz *et al.*, (2015) also reported that growth parameters, including shoot and root length, shoot and root fresh weight, shoot and root dry weight of wheat genotypes reduced with applied NaCl in solution culture at different levels as compared to their respective controls, yet the higher level of salinity was found to be as more damaging and resulted in higher growth reductions against low level of salinity. Under salt stress, variation in different varieties has also been reported for other crops, such as maize (Carpici *et al.*, 2010; Hoque *et al.*, 2015; Billah *et al.*, 2017), sunflower (Shahbaz *et al.*, 2011; Achakzai *et al.*, 2015), barley (Mahmood, 2011; Abd El-Wahed *et al.*, 2015), sorghum (Kausar *et al.*, 2012), mungbean (Rahman *et al.*, 2016), rice (Sheikh & Wani, 2014; Mouhamad *et al.*, 2017), chickpea (Shanko *et al.*, 2017), cowpea (Lima *et al.*, 2017), berseem clover (Daneshnia & Chaichi, 2018), cotton (Soares *et al.*, 2018), millet (Caruso *et al.*, 2018), lentil (Foti *et al.*, 2018) and sugarcane (Granja *et al.*, 2018).

**Table 1. Mean squares for different seedling and physiological traits of bread wheat genotypes under normal and salinity stresses at early seedling stage.**

Source of variance	D.F.	Germination (%)	Root length	Shoot length	Root fresh weight	Shoot dry weight	K <sup>+</sup>	Na <sup>+</sup>	K <sup>+</sup> /Na <sup>+</sup> ratio
Replications	2	0.33	1.47	8.11	0.002	0.00074	0.0205	0.0226	0.368
Genotypes (G)	21	1.12**	12.82**	115.51**	0.27**	0.04**	0.6687**	0.9588**	7.718**
Treatments (T)	2	22.79**	259.75**	746.85**	2.28**	0.24**	29.112**	22.9075**	286.11**
G x T interaction	42	0.07**	3.19**	6.77**	0.05**	0.04**	0.2915**	0.1036**	1.399**
Error	130	0.009	0.67	2.15	0.004	0.0002	0.0111	0.0209	0.089

\*\* Represents significant level at 1% of probability

**Table 2. Mean performance of germination (%) and root length (cm) under normal and salinity stresses at early seedling stage.**

Genotypes	Germination (%)			Root length (cm)		
	Control	12dSm <sup>-1</sup>	16dSm <sup>-1</sup>	Control	12dSm <sup>-1</sup>	16dSm <sup>-1</sup>
NIA-AS-14	97.66	96.66	89.67	12.08	11.00	10.65
NIA-AS-9	98.89	91.11	82.67	11.23	8.90	7.17
NIA-AS-10	95.55	92.22	85.33	13.93	8.75	4.52
NIA-2B	97.77	90.11	88.67	9.92	9.57	6.15
NIA-5B	100.00	87.66	72.22	10.42	9.49	6.88
SALT-6	98.67	90.00	85.33	9.73	7.46	5.37
SRN-87	94.44	91.11	75.59	10.98	9.96	8.65
SRN-11	97.77	89.11	89.66	13.60	8.18	7.57
CT-49	100.00	86.67	63.67	11.84	9.41	8.68
NRC-1236	96.66	92.44	92.99	11.33	8.41	6.73
NIA-Sundar	100.00	87.33	71.00	10.78	9.62	8.05
NIA-Sarang	97.33	94.44	91.33	13.07	10.77	9.16
Kiran-95	98.89	94.44	93.66	13.04	11.41	9.95
TD-1	92.22	90.89	83.33	12.88	11.84	11.05
Benazir	94.44	90.44	83.65	9.52	6.11	5.17
Hamal	93.11	87.33	60.89	12.73	11.08	10.65
AS-2002	98.89	93.33	90.77	11.13	9.53	8.94
Sehar-2006	93.33	85.55	65.55	10.39	7.78	6.88
Bathoor-08	85.33	58.89	55.00	8.86	6.69	6.56
Tatara	100.00	87.33	92.22	11.53	9.17	6.80
TJ-83	87.33	77.78	68.00	11.17	8.48	4.44
LU-26s(check)	96.43	93.33	93.33	10.93	10.64	10.61
Average	96.12	85.40	80.51	11.41	9.08	7.47
Range	85.33-100.00	58.89-96.66	22.78-93.66	8.86-13.93	6.11-11.00	4.44-10.61
LSD at 5% (G)		5.13			0.76	
LSD at 5% (T)		1.89			0.28	
LSD at 5% (G xT)		8.88			1.33	

Based on ion selectivity, the screening of wheat genotypes against salinity stress is an important physiological trait and it may help to provide salt tolerant wheat genotypes for cultivation under salinity stress conditions (Khan *et al.*, 2017). The variations for salt tolerance within population may be due to variability in selective uptake of Na<sup>+</sup> ions or restricted moving of such ions to the active parts of the leaves for photosynthesis (Aurangzeb *et al.*, 2013). There was lower accumulation of sodium (Na<sup>+</sup>) found in a group of wheat genotypes under salinity stresses. The minimum accumulation of Na<sup>+</sup> at 12 and 16dSm<sup>-1</sup> was expressed by Hamal (0.46 and 0.59), TD-1 (0.68 and 1.02), Kiran-95 (0.72 and 1.77), NIA-Sarang (0.85 and 1.77) and LU-26s (0.66 and 1.32) (Table 5), registering that these genotypes tended to possess a variety of resistant genes against salinity stress.

Such tolerance against salinity by above genotypes may be due to inherent capacity and the presence of more tolerant genes to confer salinity stress resistance. The better growth of these genetic materials than sensitive ones may be attributed to reduced Na<sup>+</sup> accumulation and possibly mobilization of the defense mechanisms, including antioxidative enzymes such as catalase, superoxide dismutase and ascorbate peroxidase, which might have suppressed the Na<sup>+</sup> transport to further tissues (Gupta & Huang, 2014). Our results are in agreement with Khan *et al.*, (2017) who demonstrated that wheat genotypes (WSP-1 and LU-26s) accumulated less quantity of Na<sup>+</sup>. Naz *et al.*, (2015) also reported that SARC-I, Sehar-2006 and Shafaq-2006 were found tolerant to salinity because of better growth, lower NaCl relative toxicities and lower leaf Na<sup>+</sup>.

**Table 3. Mean performance shoot length (cm) and root fresh weight (g) under normal and salinity stresses at early seedling stage.**

Genotypes	Shoot length (cm)			Root fresh weight (g)		
	Control	12 dSm <sup>-1</sup>	16 dSm <sup>-1</sup>	Control	12 dSm <sup>-1</sup>	16 dSm <sup>-1</sup>
NIA-AS-14	21.74	20.95	19.45	0.72	0.68	0.48
NIA-AS-9	22.43	17.12	15.37	0.66	0.48	0.41
NIA-AS-10	22.43	19.95	16.54	0.77	0.79	0.47
NIA-2B	22.80	17.32	12.62	0.86	0.77	0.65
NIA-5B	23.88	18.57	16.23	0.73	0.71	0.51
SALT-6	15.52	12.17	8.68	0.43	0.33	0.21
SRN-87	22.52	20.89	19.42	0.78	0.59	0.53
SRN-11	21.22	19.23	14.23	0.82	0.72	0.32
CT-49	22.30	18.16	15.43	0.61	0.41	0.18
NRC-1236	22.33	17.62	15.00	0.84	0.49	0.39
NIA-Sundar	19.30	15.69	13.28	0.43	0.31	0.18
NIA-Sarang	19.87	18.81	16.86	1.14	0.78	0.42
Kiran-95	19.37	17.81	14.86	1.26	0.96	0.75
TD-1	23.12	20.73	18.25	0.83	0.64	0.52
Benazir	14.01	14.91	13.61	1.00	0.89	0.64
Hamal	18.32	16.96	15.00	1.13	0.50	0.46
AS-2002	19.14	17.63	16.93	1.01	0.84	0.68
Sehar-2006	20.50	17.62	14.13	0.72	0.47	0.38
Bathoor-08	18.11	14.04	14.73	1.58	0.61	0.42
Tatara	16.08	5.48	3.92	0.98	0.54	0.29
TJ-83	18.32	14.81	11.13	1.11	0.82	0.55
LU-26s (check)	23.35	18.96	16.41	0.75	0.48	0.41
Average	20.05	15.99	13.38	0.87	0.63	0.45
Range	14.01-23.88	5.48-20.89	3.92-18.25	0.43-1.58	0.31-0.96	0.18-0.75
LSD at 5% (G)		1.36			0.06	
LSD at 5% (T)		0.51			0.02	
LSD at 5% (G xT)		2.39			0.10	

**Table 4. Mean performance shoot fresh weight (g) and K<sup>+</sup> under normal and salinity stresses at early seedling stage.**

Genotypes	Shoot fresh weight (g)			K <sup>+</sup>		
	Control	12 dSm <sup>-1</sup>	16 dSm <sup>-1</sup>	Control	12 dSm <sup>-1</sup>	16 dSm <sup>-1</sup>
NIA-AS-14	2.08	1.14	0.90	3.38	3.15	2.26
NIA-AS-9	1.92	1.04	0.88	2.68	2.13	1.74
NIA-AS-10	2.51	1.79	1.26	2.93	2.25	1.87
NIA-2B	2.00	1.01	0.69	2.96	1.95	1.77
NIA-5B	1.85	0.91	0.78	3.15	2.45	1.94
SALT-6	1.35	0.82	0.35	3.23	2.27	1.16
SRN-87	1.98	1.33	0.97	3.26	2.31	1.76
SRN-11	2.03	1.42	0.95	3.18	2.10	1.95
CT-49	1.88	1.06	0.78	3.25	2.45	2.17
NRC-1236	1.90	1.10	0.98	2.85	2.20	1.84
NIA-Sundar	1.79	0.71	0.85	3.74	2.70	2.16
NIA-Sarang	2.39	1.40	0.76	3.07	2.38	1.63
Kiran-95	3.27	2.01	1.57	3.66	3.31	2.64
TD-1	1.91	1.30	0.94	3.52	3.32	2.74
Benazir	2.51	1.72	1.23	3.27	2.69	2.31
Hamal	1.38	0.85	0.62	3.37	2.84	2.68
AS-2002	2.92	1.92	1.72	3.40	2.76	2.27
Sehar-2006	2.01	1.15	0.94	3.10	2.21	1.84
Bathoor-08	1.56	0.91	0.82	2.93	2.36	1.80
Tatara	2.26	1.18	0.54	2.87	2.07	1.68
TJ-83	1.85	1.03	0.92	2.85	2.20	1.48
LU-26s(check)	2.08	1.35	0.99	3.13	2.78	2.23
Average	2.06	1.23	0.93	3.17	2.49	2.00
Range	1.35-3.27	0.71-2.01	0.35-1.72	2.68-3.74	1.95-3.32	1.16-2.74
LSD at 5% (G)		0.09			0.13	
LSD at 5% (T)		0.03			0.04	
LSD at 5% (G xT)		0.16			0.23	

**Table 5. Mean values of Na<sup>+</sup> and K<sup>+</sup>/Na<sup>+</sup> ratio under normal and salinity stresses at early seedling stage.**

Genotypes	Na <sup>+</sup>			K <sup>+</sup> /Na <sup>+</sup> ratio		
	Control	12 dSm <sup>-1</sup>	16 dSm <sup>-1</sup>	Control	12 dSm <sup>-1</sup>	16 dSm <sup>-1</sup>
NIA-AS-14	0.61	1.50	1.72	7.29	4.62	1.70
NIA-AS-9	0.68	1.50	2.12	3.97	1.42	0.82
NIA-AS-10	0.47	0.69	1.33	4.83	1.50	1.10
NIA-2B	0.67	1.48	1.78	4.45	1.32	1.00
NIA-5B	0.76	1.23	2.05	4.18	1.98	0.98
SALT-6	0.77	1.23	2.74	4.24	1.84	0.42
SRN-87	0.70	1.30	1.58	4.67	1.78	1.17
SRN-11	0.80	1.50	1.60	3.99	1.42	1.22
CT-49	0.66	1.00	1.88	4.94	2.47	1.16
NRC-1236	0.72	1.63	2.13	3.99	1.36	0.87
NIA-Sundar	0.74	0.95	1.80	5.05	2.87	1.21
NIA-Sarang	0.75	0.85	1.77	4.29	2.83	0.54
Kiran-95	0.72	0.72	1.77	5.12	4.63	1.50
TD-1	0.50	0.68	1.02	7.08	4.92	2.71
Benazir	0.47	1.55	1.84	7.06	1.74	1.26
Hamal	0.77	0.46	0.59	7.38	4.17	1.52
AS-2002	0.75	0.85	1.91	7.70	3.91	1.19
Sehar-2006	0.64	1.78	2.16	4.84	1.24	0.84
Bathoor-08	0.62	1.04	2.42	4.78	2.28	0.75
Tatara	0.54	1.00	2.10	5.30	2.07	0.80
TJ-83	0.46	0.68	1.76	3.73	1.20	0.49
LU-26s(check)	0.51	0.66	1.32	6.20	4.23	1.70
Average	0.63	1.16	1.96	5.23	2.54	1.13
Range	0.46-0.80	0.66-1.84	1.02-3.01	3.73-7.70	1.20-4.92	0.42-1.70
LSD at 5% (G)		0.09			0.27	
LSD at 5% (T)		0.03			0.10	
LSD at 5% (G x T)		0.17			0.48	

It is also thought that appropriate source of K<sup>+</sup> is the key factor to reduce the toxic effects of Na<sup>+</sup> (Khan *et al.*, 2017). Therefore, the K<sup>+</sup> in different wheat genotypes affected differentially by salinity stress due to their different genetic makeup. Nevertheless, salt tolerant genotypes like, TD-1 (3.32 and 2.74), Kiran-95 (3.31 and 2.64), NIA-AS-14 (3.15 and 2.26), Hamal (2.84 and 2.68) and AS-2002 (2.76 and 2.27) maintained higher uptake of K<sup>+</sup> at both salinity levels (Table 4). Gurmani *et al.*, (2014) observed that beyond the stress of salinity, some wheat genotypes including N-13, Shorawaki, Kharchia-65 N-7 and N-9 sustained larger uptake of K<sup>+</sup> at all salinity levels. Considering the physiological mechanisms of salt tolerance, such as identification of genotypes with narrow Na<sup>+</sup> uptake or with maximum uptake of K<sup>+</sup> over Na<sup>+</sup> have been seen to help in selection of salt tolerance (Flowers, 2004). The trait K<sup>+</sup>/Na<sup>+</sup> ratio, is considered the main selection criteria of salt tolerance in plant. It has been well known that there is positive correlation between increase soil salinity and increase concentration of Na<sup>+</sup> and decrease K<sup>+</sup> in wheat genotypes, which results in low extent of K<sup>+</sup>/Na<sup>+</sup> ratio (Aurangzeb *et al.*, 2013). Present study indicates that those genotypes, which showed higher K<sup>+</sup> content, ultimately reflect higher concentration of K<sup>+</sup>/Na<sup>+</sup> ratio. The genotypes TD-1 (4.92 and 2.71),

NIA-AS-14 (4.62 and 1.70), Kiran-95 (4.63 and 1.50), LU-26s (4.23 and 1.70) and Hamal (4.17 and 1.52) also showed higher concentration of K<sup>+</sup>/Na<sup>+</sup> ratio (Table 5). Gurmani *et al.*, (2014) referred that salinity tolerance by plants includes the ability of plant to exclude Na<sup>+</sup> and the capacity to accumulate K<sup>+</sup> in leaf tissue, while K<sup>+</sup>/Na<sup>+</sup> ratio declines with increasing salt concentration.

This study also identified a group of bread wheat genotypes, whose performance under salinity was poor; hence proved susceptible to salinity stresses. The adverse effects of salinity stress on plant growth with respect to biomass production have been already reported (Ma *et al.*, 2013). The increase in osmotic potential leads in dehydration and ionic imbalance in tissue, which cause reduction in cell division and cell elongation and may be the major reason for low root and shoot production, subsequently inhibit wheat plant growth at considerable level (Zhu, 2001; Munns, 2005; Huang *et al.*, 2006). A drastic performance under salinity treatments (12 and 16 dSm<sup>-1</sup>) was revealed by Bathoor-08 (58.89 and 55.00%), Sehar-2006 (85.55 and 65.55%) and TJ-83 (87.33 and 68.00%) for germination; Benazir (6.11 and 5.17 cm), Bathoor (6.69 and 6.56 cm) and Salt-6 (7.46 and 5.37 cm) for root length; Tatara (5.48 and 3.92 cm), Salt-6 (12.17 and 8.68 cm) and TJ-83 (14.81 and 11.13 cm) for shoot

length; NIA-Sundar (0.31 and 0.18 g), Salt-6 (0.33 and 0.21 g) and CT-49 (0.41 and 0.18 g) for root fresh weight; NIA-Sundar (0.71 and 0.85 g), Salt-6 (0.82 and 0.35 g) and Bathoor (0.91 and 0.82 g) for shoot fresh weight; Sehar-2006 (1.78 and 2.16), NRC-1236 (1.63 and 2.13) and NIA-AS-9 (1.50 and 2.12) for  $\text{Na}^+$ ; NIA-2B (1.95 and 1.77), Tatar (2.07 and 1.68) and SRN-11 (2.10 and 1.95) for  $\text{K}^+$ ; TJ-83 (1.20 and 0.80), Sehar-2006 (1.24 and 0.84), NRC-1236 (1.36 and 0.87) and NIA-2B (1.32 and 1.00) for  $\text{Na}^+/\text{K}^+$  ratio (Tables 2-5). The reduction in growth in plants subjected to NaCl stress, which is, however, linked with reduced photosynthetic pigments and such decrease in chlorophyll contents due to salinity stress has been observed in different crops, including wheat, canola and maize (Raza *et al.*, 2006; Ali *et al.*, 2007). Though, above mentioned genotypes expressed poor performance under salinity stress conditions; nevertheless, these genotypes may also be exploited in various breeding programs, while crossing with tolerant genotypes, inheritance pattern of different genes may be known, identification of quantitative trait loci, gene mapping and gene linkage.

In order to separate the superior bread wheat genotypes with respect to salinity stress, the average performance of genotypes for all the studied characters under both salinity stresses ( $12\text{dSm}^{-1}$  and  $16\text{dSm}^{-1}$ )

were averaged and used for grouping the superior and inferior bread wheat genotypes through cluster analysis. The averaged data of each character were used for hierarchical cluster analysis using ward method and Euclidean distance. With respect to cluster analysis based on early seedling performance, all genotypes classified into three major and one minor group (Fig. 1). The first group composed of seven wheat genotypes (NIA-Sarang, AS-2002, Kiran-95, LU-26s, NIA-AS-14, TD-1 and Hamal), infact the genotypes of this group revealed a vigorous growth nevertheless recognized as tolerant against salinity stress. The second cluster collected eight genotypes, such as NIA-2B, SRN-11, NRC-1236, NIA-AS-9, Benazir, NIA-AS-10, Salt-6 and Tatar; however considered as moderately tolerant since a moderate decline was observed in growth due to salinity stress. The third group also consisted of six wheat genotypes, including NIA-5B, NIA-Sundar, SRN-87, CT-49, Sehar-2006 and TJ-83, it was observed on the basis of seedling traits that these genotypes showed their poorer growth; therefore, regarded a group of sensitive wheat genotypes. Moreover, the fourth group only consisted of one genotype (Bathoor-08), which was regarded as highly sensitive against salinity.

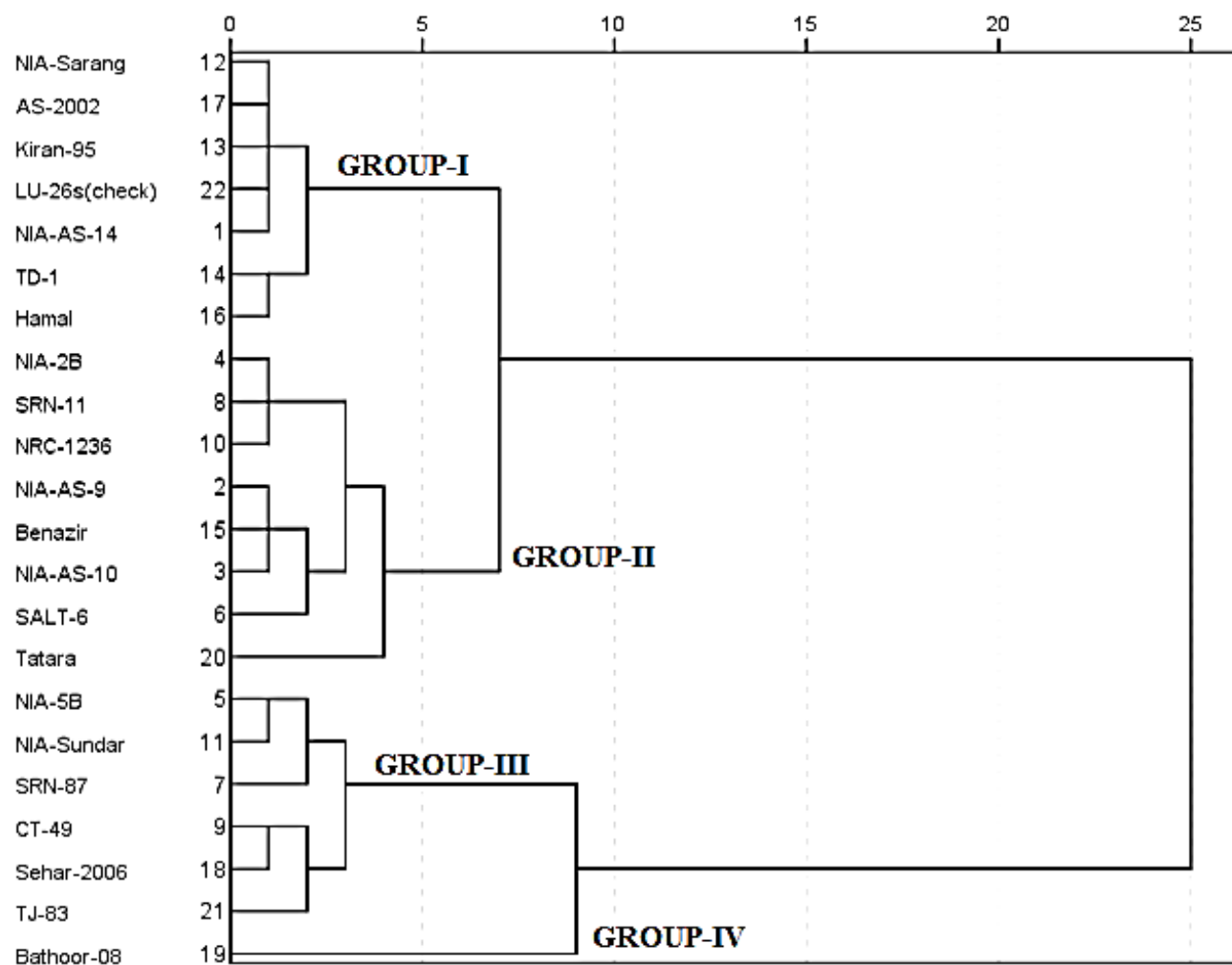


Fig. 1. Cluster analysis of 22 bread wheat genotypes on the basis of early seedling traits.

## Conclusions

It is concluded that on the basis of mean performance under salinity stress conditions, a group of seven wheat genotypes like TD-1, Kiran-95, Hamal, NIA-Sarang, AS-2002, LU-26s and NIA-AS-14 were isolated as tolerant against salinity; therefore these genotypes may be used for further genetic analysis under salinity stress.

## Acknowledgments

The authors acknowledge the Vice Chancellor, SAU, Tandojam and Director, NIA, Tandojam for providing the required funds and laboratory facilities to complete this work.

## References

- Abd El-Wahed, M.H., A.E. Sabagh, H.H. Mohammed, A. Ueda, H. Saneoka and C. Barutçular. 2015. Evaluation of barley productivity and water use efficiency under saline water irrigation in arid region. *Int. J. Agri. Crop Sci.*, 48(8): 765-773.
- Achakzai, A.K.K., M. Rahman, M. Yaqoob, A.M. Sarangzai, M.Y.K. Barozai and M. Din. 2015. Stem and leaf response of sunflower hybrids to salt stress. *Pak. J. Bot.*, 47(6): 2063-2067.0
- Ahmadi, S.H. and J.N. Ardekani. 2006. The effect of water salinity on growth and physiological stages of eight Canola (*Brassica napus*) cultivars. *Irrig. Sci.*, 25: 11-20.
- Ali, Q., M. Ashraf and H.R. Athar. 2007. Exogenously applied proline at different growth stages enhances growth of two maize cultivars grown under water deficit conditions. *Pak. J. Bot.*, 39: 1133-1144.
- Ali, Z., A. Salam, F.M. Azhar, I.A. Khan, A.A. Khan, S. Bahadur, T. Mahmood, A. Ahmad and R. Trethowan. 2012. The response of genetically distinct bread wheat genotypes to salinity stress. *Plant Breed.*, 131: 707-715.
- Anonymous. 2010. FAO land and plant nutrition management service. [www.fao.org](http://www.fao.org) [last accessed 10 December 2010].
- Ansari, R. and T.J. Flowers. 1986. Leaf to leaf distribution of ions in some monocotyledonous plants grown under saline conditions. In: Prospects for Biosaline Research (Eds.): Ahmed, R. and A. San Pietro. University of Karachi.
- Aurangzeb, R., S.D. Ahmad, S.M. Sabir, S.I. Awan, A.H. Shah, S.R. Abbas, S. Shafique, F. Khan and A. Chaudhary. 2013. Potential antioxidant activities improve salt tolerance in ten varieties of wheat (*Triticum aestivum* L.). *Amer. J. Plant Sci.*, 4: 69-76.
- Azhar, F.M. and R. Ahmad. 2000. Variation and heritability of salinity tolerance in upland cotton at early stage of plant development. *Pak. J. Bio. Sci.*, 3: 1991-1993.
- Billah, M., M.A. Latif, N. Hossain and M.S. Uddin. 2017. Evaluation and selection of salt tolerant hybrid maize under hydroponics culture. *Res. Crops*, 18(3): 481-489.
- Carpici, E.B., N. Celik, G. Bayram and B.B. Asik. 2010. The effects of salt stress on the growth, biochemical parameter and mineral element content of some maize (*Zea mays* L.) cultivars. *Afr. J. Biotech.*, 9: 6937-6942.
- Caruso, C., C. Maucieri, A. Berruti, M. Borin and A.C. Barbera. Responses of different *Panicum miliaceum* L. genotypes to saline and water stress in a marginal Mediterranean environment. *Agron.*, 8(8): 1-16.
- Daneshnia, F. and M.R. Chaichi. 2018. Field treatment effects on seed germination and early growth traits of berseem clover under salinity stress conditions. *Curr. Invest. Agri. Curr. Res.*, 2(1): 1-14.
- FAO. 2015. FAO Cereal Supply and Demand Brief. <http://www.fao.org/worldfoodsituation/csdb/en/> [last accessed 05 January 2016].
- Flowers, T.J. 2004. Improving crop salt tolerance. *J. Exp. Bot.*, 55: 307-319.
- Foti, C., E.M. Khah and O.I. Pavi. 2018. Germination profiling of lentil genotypes subjected to salinity stress. *Plant Biol.*, 1: 1-7.
- Gomez, K.A. and A.A. Gomez. 1984. Statistical procedures for agricultural research. John Wiley & Sons Inc. 2nd (ed.) New York U.S.A.
- Granja, M.M.C., M.J.L. Medeiros, M.M.A. Silva, T.R. Camara, L. Willadino and C. Ulisses. 2018. Response to in vitro salt stress in sugarcane is conditioned by concentration and condition of exposure to NaCl. *Acta Biol. Colomb.*, 23(1): 30-38.
- Gupta, B. and B. Huang. 2014. Mechanism of salinity tolerance in plants for physiological, biochemical and molecular characterization. *Int. J. Genom.*, 130: 2129-2141.
- Gurmani, A.R., S.U. Khan, F. Mabood, Z. Ahmed, S.J. Butt, J. Din, A. Mujeeb-Kazi and D. Smith. 2014. Screening and selection of synthetic hexaploid wheat germplasm for salinity tolerance based on physiological and biochemical characters. *Int. J. Agri. Biol.*, 16: 681-690.
- Hoque, M.M.I., Z. Jun and W. Guoying. 2015. Evaluation of salinity tolerance in maize (*Zea mays* L.) genotypes at seedling stage. *J. Bio. Sci. Biotechnol.*, 4(1): 39-49.
- Huang, Y., G.P. Zhang, F.B. Wu, J. Chen and Y. Xiao. 2006. Interaction of salinity and cadmium stresses on antioxidant enzymes, sodium, and cadmium accumulation in four barley genotypes. *J. Plant Nutr.*, 29: 2215-2225.
- Hussain, B., A.S. Khan and Z. Ali. 2015. Genetic variation in wheat germplasm for salinity tolerance at seedling stage: improved statistical inference. *Turk. J. Agri. For.*, 39: 182-192.
- Ishaq, M., G. Ahmad, K. Afridi, M. Ali, T.U. Khan, I.A. Shah, B. Ahmad, N. Ahmad, I. Ahmad, A. Saleem and M. Miraj. 2018. Combining ability and inheritance studies for morphological and yield contributing attributes through line  $\times$  tester mating design in wheat (*Triticum aestivum* L.). *Pure & App. Biol.*, 7(1): 160-168.
- Kamal, A., M.S. Qureshi, M.Y. Ashraf and M. Hussain. 2003. Salinity induced changes in some growth and physiochemical aspects of two soybean [*Glycine max* (L.) Merr.] genotypes. *Pak. J. Bot.*, 35: 93-97.
- Kausar, A., M.Y. Ashraf, I. Ali, M. Niaz and Q. Abbass. 2012. Evaluation of sorghum varieties/lines for salt tolerance using physiological indices as screening tool. *Pak. J. Bot.*, 44(1): 47-52.
- Khan, A.A., S.A. Rao and T.M. McNilly. 2003a. Assessment of salinity tolerance based upon seedling root growth response functions in maize (*Zea mays* L.). *Euphytica*, 131: 81-89.
- Khan, A.S., M.A. Asad and Z. Ali. 2003b. Assessment of genetic variability for NaCl tolerance in wheat. *Pak. J. Agri. Sci.*, 40: 33-36.
- Khan, M.A., M.U. Shirazi, A. Shereen, S.M. Mujtaba, M.A. Khan, S. Mumtaz and W. Mahboob. 2017. Identification of some wheat (*Triticum aestivum* L.) lines for salt tolerance on the basis of growth and physiological characters. *Pak. J. Bot.*, 49(2): 397-403.
- Lima, Y.B., F.V. Silva, M.F. Neto, E.P. Paiva and H.R. Gheyi. 2017. Accumulation of salts in the soil and growth of cowpea under salinity and phosphorus fertilization. *Revista Ciência Agronômica*, 48(5): 765-773.
- Ma, L.J., C.M. Yu, X.M. Li, Y.Y. Li, L.L. Wang, C.Y. Ma, S.Y. Tao and N. Bu. 2013. Pretreatment with NaCl induces tolerance of rice seedlings to subsequent Cd or Cd<sup>+</sup> NaCl stresses. *Biol. Plant*, 57: 567-570.

- Mahboob, W., M.A. Khan and M.U. Shirazi. 2016. Induction of salt tolerance in wheat (*Triticum aestivum* L.) seedlings through exogenous application of proline. *Pak. J. Bot.*, 48(3): 861-867.
- Mahmood, K. 2011. Salinity tolerance in barley (*Hordeum vulgare* L.): Effects of varying NaCl, K<sup>+</sup>/Na<sup>+</sup> and NaHCO<sub>3</sub> levels on cultivars differing in tolerance. *Pak. J. Bot.*, 43: 1651-1654.
- Mickelbart, M.V., P.M. Hasegawa and J. Bailey-Serres. 2015: Genetic mechanisms of abiotic stress tolerance that translate to crop yield stability. *Nat. Rev. Genet.*, 16: 237-251.
- Mouhamad, R.S., L.A. Mutlag, A.H. Atiyah, I.B. Razaq, M.A.A. Abdulhussein, M. Iqbal and A. Nazir. 2017. Salinity tolerance at seedling stage for rice genotypes: *In vitro* analysis. *Net. J. Agri. Sci.*, 5(4): 126-130.
- Muhammad, S. and F. Mohammad. 2018. Identifying stable bread wheat derived lines across environments through GGE biplot analysis. *Sarhad J. Agri.*, 34(1): 63-69.
- Munns, R. 2005. Genes and salt tolerance: bringing them together. *New Phytol.*, 167: 645-63.
- Naz, T., J. Akhtar, M.A. Haq and M. Shahid. 2015. Genetic variability in wheat genotypes for salt tolerance, growth and physiological responses. *Soil Environ.*, 34(2): 187-199.
- Qadir, M., E. Quillerou, V. Nangia, G. Murtaza, M. Singh, R.J. Thomas, P. Drechsel and A.D. Noble. 2014: Economics of salt-induced land degradation and restoration. *Nat. Resour. Forum*, 38: 282-295.
- Rahman, M.M., M.A. Ahsan, M.S.I. Sikdar, M. Shamsuzzoha and M.S. Islam. 2016. Evaluation of mungbean genotypes for salt tolerance at seedling stage and alleviation of saline stress by gypsum. *Fund. Appl. Agri.*, 1(1): 39-43.
- Raza, S.H., H.R. Athar and M. Ashraf. 2006. Influence of exogenously applied glycine betaine on the photosynthetic capacity of two differently adapted wheat cultivars under salt stress. *Pak. J. Bot.*, 38: 341-352.
- Shahbaz, M., M. Ashraf, N.A. Akram, A. Hanif, S. Hamid, S. Joham and R. Rehman. 2011. Salt-induced modulation in growth, photosynthetic capacity, proline content and ion accumulation in sunflower (*Helianthus annuus* L.). *Acta Physiologiae Plantarum*, 33: 1113-1122.
- Shanko, D., G. Jatani and A. Debela. 2017. Effects of salinity on chickpea (*Cicer arietinum* L.) landraces during germination stage. *J. Biochem. Mol. Biol.*, 3(2): 1-5.
- Sheikh, A. and M.R. Wani. 2014. Evaluation of the salinity tolerance of some rice (*Oryza sativa*) genotypes of Kashmir valley Subzar. *Int. J. Sci. Scient. Res. Develop.*, 2(5): 284-288.
- Shirazi, M.U. M.A. Khan, W. Mahboob, M.A. Khan, A. Shereen, S.M. Mujtaba and A. Asad. 2018. Inconsistency in salt tolerance of some wheat (*Triticum aestivum* L.) genotypes evaluated under various growing environments. *Pak. J. Bot.*, 50(2): 471-479.
- Soares, L.A.A., P.D. Fernandes, G.S. Lima, J.F. Suassuna, M.E.B. Brito and F.V. Sa. 2018. Growth and fiber quality of colored cotton under salinity management strategies. *Revista Brasileira de Engenharia Agrícola e Ambiental*, 22(5): 332-337.
- Zhu, J.K. 2001. Plant salt tolerance. *Trends Plant Sci.*, 2: 66-71.

(Received for publication 12 January 2019)