

RESPONSE OF WHEAT SPECIES TO THE CONTRASTING SALINE REGIMES

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Abstract

Salinity is a major production constraint for wheat. Therefore, an experiment was conducted to determine the interspecific variability among the species for salinity stress. Species have changed their relative ranking across the salinity regimes, thus show the relative tolerance of the species to the salinity stress. Correlations between the ploidy levels and morphological traits were significantly positive under saline conditions, showing values of morphological traits increased with number and types of genomes. Trait such as leaf yellowness was independent of ploidy level and may be used to discriminate and compare the species for salt tolerance. Phenotypic scoring of this trait further makes it appropriate to be used in breeder's large segregating populations. Thus lower values of leaf yellowness may be used to discriminate genotypes for salinity resistance.

Introduction

Salinity is major production constraint in crop species and wheat in particular (Ali *et al.*, 2007; Afzal *et al.*, 2008). Intensity of the problem in Pakistan may be indicated from the statistics that 33% (6.8mha) of the cultivated area in Pakistan is affected by the salinity stress (Anon., 2008). Furthermore on global basis salinity stress ranked second after the drought (Singh, 2004). Identification of suitable source of resistance is prerequisite for carrying out successful salinity tolerance breeding program. Therefore, plant breeders remain focused on screening cultivated germplasm to discriminate on the basis of salt tolerance as a first line strategy (Rauf, 2008). Resultantly large numbers of reports are available indicating some variation for salt tolerance in cultivated germplasm (El-Hendawy, 2005; Ali *et al.*, 2007; Mahmood, 2009). In addition, it is also important to discriminate wheat wild species for salt tolerance (Badridze *et al.*, 2009). Wild species contain greater genetic diversity and broad genetic base that help to adopt extreme environmental conditions (Rauf *et al.*, 2010). Therefore they are obvious candidate for screening and indentifying gene of interest in them (Sayed, 1985).

In addition to screen the source of salinity resistance, traits to form the basis of selection are also an important consideration for the salinity resistance breeding. Biochemical traits such as species ability to discriminate K⁺ over Na⁺ are gaining importance (Gorham *et al.*, 1997; Colmer *et al.*, 2006; Munns *et al.*, 2006). These traits may be useful to understand the mechanism of salinity tolerance in a specific genotype (Munns *et al.*, 2006). However, such types of traits are complex and costly to determine and hence cannot be applied to breeder's large segregating populations unless molecular markers of these traits may be developed (Gorham *et al.*, 1997). Alternatively morphological traits are useful because of their stability in a particular species and ease to determine (El-Hendawy, 2005).

Keeping the same in mind a study was conducted to determine the level of resistance in various cultivated and wild species belonging to various allopolyploidy levels. The study would help to formulate future salinity resistance breeding program.

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Materials and Methods

i. Plant material: Seed of various plant species (*T.monococum*, *T.turgidum*, *T.uruta* and *T. sphaerococum*) were obtained from USA and grown to multiply and acclimatize. The seed of other two species (*T. aestivum* and *T. durum*) were obtained from local germplasm sources. Multiplied seed was further used to conduct the experiment.

There were six species and three ploidy levels (Diploid AA=14; tetraploid AABB=28; and hexaploid AABBDD=42), two species from a particular ploidy level. Accessions belonging to various species were randomly selected from germplasm collections. There were 42 accessions. Distribution of these accessions in various species was as follows:

Triticum monococum and *uruta* was represented by 3 accessions each; *turgidum* was represented by 4 accessions; *durum* was represented by 12 accessions; *sphaerococum* was represented by 5 accession and 15 accessions of *aestivum* from post green revolution period.

ii. Location and saline regimes: All accessions were sown at two locations (University College of Agriculture, Sargodha and University of Agriculture, Faisalabad) in large plastic bags, having 40 kg of soil (sand: silt: organic matter) in equal proportion under open environment. Seed sowing was done on October, 15 and 21 in Sargodha and Faisalabad respectively. Each bag comprised of 4 plants. Irrigating the bags with brackish water developed saline regime of 10dsm^{-1} while non-saline regime was irrigated with normal water. Electric conductivity of the soil was measured at each irrigation with brackish water. Sixteen irrigations were given to reach the salinity level of 10dsm^{-1} . Experiments were repeated twice.

iii. Measurement of plant traits: When required level of salinity was achieved, plants were harvested (60 days after sowing) for the measurement of various plant traits. Root weight or shoot weight were measured on weighing balance and expressed in grams (g). Lateral root number and yellow leaves were counted. Shoot length was determined by measuring the tiller with the highest length and total root length was determined by measuring the length of each and every root and its secondary branches.

iv. Experiment layout: Experiment was laid out in randomized complete block design with location and species as factor in two replications. Accessions performance was averaged within particular species. Coefficient of within specie variation was measured as the ratio of square root of genotypic variance to mean performance of species and expressed in percentages.

Results

Analyses of variance showed significant ($p \leq 0.05$) variation due to species and salinity level while magnitude of variation due to location \times species was very low as compared to the other factors i.e., species and salinity level. Therefore mean values are presented in Table 1 by averaging over locations. Repressing effects of salinity stress were observed on all traits except number of yellow leaves, which increased under salinity stress. Weight based traits i.e., shoot weight followed by root weight showed the highest repressing impact of salinity stress. However magnitude of increase was the highest in number of yellow leaves under salinity stress (Fig. 1).

Table 1. Mean values of morphological traits i.e., root weight = RW, LRN= lateral root number, SL= shoot length, SW= shoot weight, SN= shoot number, YL= yellow leaves, TRL= total root length.

Species	Ploidy level	RW (g)		LRN		SL(cm)		SW(g)		SN		YL		TRL(cm)	
		SL*	NS**	SL	NS	SL	NS	SL	NS	SL	NS	SL	NS	SL	NS
<i>Triticum monococcum</i>	AA=14	10.73	4.85	30.33	24.33	30.03	40.31	26.27	48.40	17.11	19.11	5.33	0.33	261.55	564.25
		137%	10%	20%	8%	11%	16%	33%	3%	26%	15%	21%	2%	17%	11%
<i>Triticum urvata</i>	AA=14	4.85	7.75	22.33	41.22	35.78	30.11	25.61	36.90	14.13	26.33	3.33	2.11	254.11	433
		40%	17%	17%	14%	11%	16%	35%	8%	23%	16%	19%	5%	21%	15%
<i>Triticum turgidum</i> var. <i>durum</i>	AABB=28	7.21	9.82	23.2	34.11	40.15	54.55	51	83.5	16.4	20.8	6.2	4.8	328.25	583.5
		17%	19%	23%	21%	19%	16%	27%	29%	18%	27%	32%	6%	26%	16%
<i>Triticum turgidum</i> var. <i>turgidum</i>	AABB=28	7.47	46.09	28.13	59.11	40.81	50.22	53.22	126.89	24.33	39.66	8.23	2.22	382.21	922.25
		27%	19%	31%	21%	19%	21%	33%	26%	26%	17%	32%	9%	28%	23%
<i>Triticum aestivum</i> var. <i>sphaerococum</i>	AABBDD=42	18.51	26.13	51.66	30.22	58.81	65.11	73.29	110.28	16.11	13.33	2.14	0.33	694.25	441.25
		31%	21%	26%	19%	26%	17%	35%	23%	18%	14%	13%	2%	31%	25%
<i>Triticum aestivum</i> var. <i>aestivum</i>	AABBDD=42	13.13	15.64	29.88	35.11	39.06	42.33	54.74	119.00	21.12	26	5.44	3.33	304.5	604.11
		27%	18%	23%	18%	37%	29%	38%	28%	39%	33%	41%	11%	21%	16%
LSD value	-	4.21	3.91	2.51	4.88	4.66	5.11	3.88	4.11	5.23	3.11	1.01	1.85	14.33	11.91

* SL= Salinity stress; **NS= Non-stress, †= Coefficient of variation within species %

Table 2. Correlation coefficient among the morphological traits and ploidy levels under non-saline (above diagonal) and saline conditions (below diagonal) where PL= ploidy level, RW= root weight, LRN= lateral root number, SL= shoot length, SW= shoot weight, SN= shoot number, YL= yellow leaves, TRL= total root length.

Traits	PL	RW (g)	LRN	SL(cm)	SW(g)	SN	YL	TRL(cm)
PL	1.00	0.42 ^{NS}	0.00 ^{NS}	0.68*	0.85**	-0.15 ^{NS}	0.16 ^{NS}	0.06 ^{NS}
RW (g)	0.72**	1.00	0.77**	0.47*	0.78**	0.60	-0.10 ^{NS}	0.73**
LRN	0.60**	0.93**	1.00	-0.07 ^{NS}	0.42*	0.92	0.26 ^{NS}	0.75**
SL(cm)	0.74**	0.70**	0.83**	1.00	0.64**	-0.33	-0.05 ^{NS}	0.10 ^{NS}
SW(g)	0.93**	0.69**	0.70**	0.88**	1.00	0.31 ^{NS}	0.19 ^{NS}	0.57**
SN	0.35 ^{NS}	0.01 ^{NS}	-0.07 ^{NS}	-0.05 ^{NS}	0.31 ^{NS}	1.00	0.30 ^{NS}	0.83**
YL	-0.11 ^{NS}	-0.49**	-0.56**	-0.46*	-0.09 ^{NS}	0.77**	1.00	0.22 ^{NS}
TRL(cm)	0.65**	0.77**	0.92**	0.97**	0.83**	-0.04	-0.46*	1.00

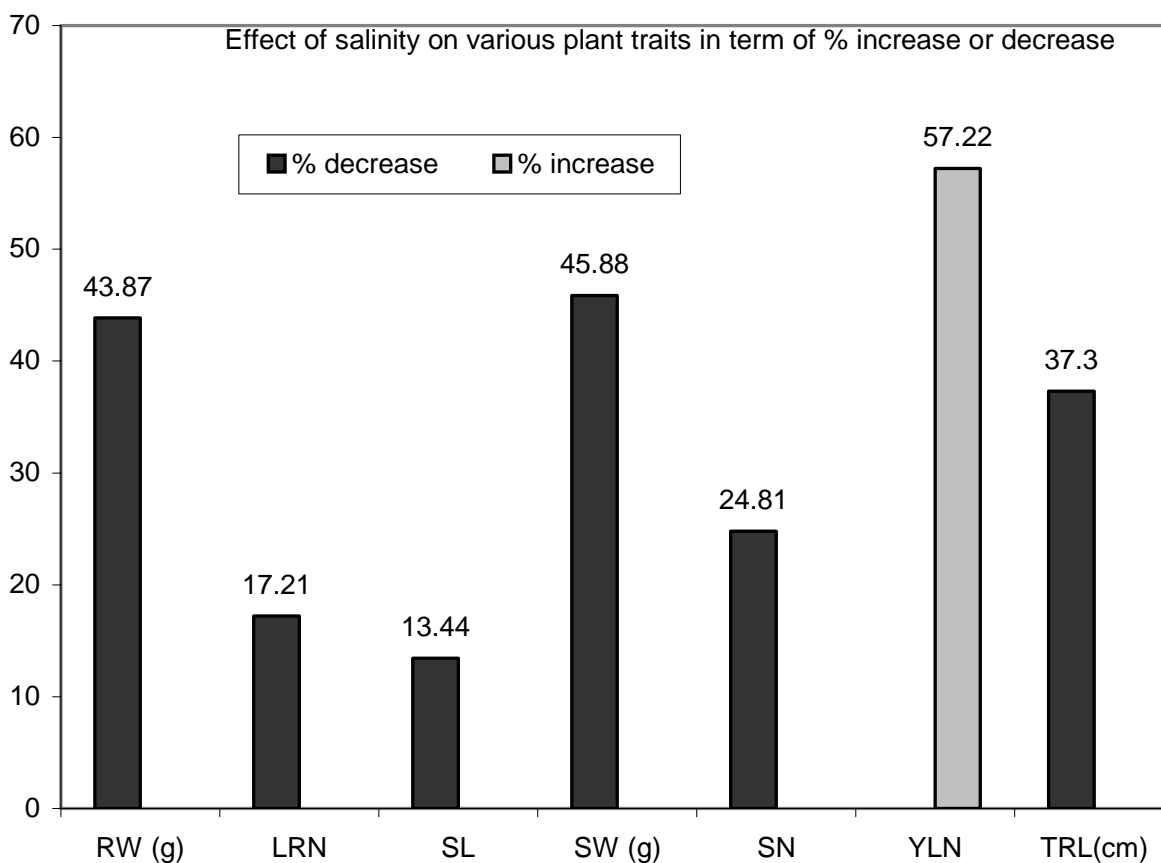


Fig. 1. Percent increase or decrease in traits values i.e., root weight (RW), lateral root number (LRN), shoot length (SL), shoot weight (SW), shoot number (SN), yellow leaves number (YLN) and total root length (TRL) over species after exposing them to the salinity stress.

Salinity showed repressing effect on root weight in all species except *T. mononcocum* (Fig. 2) in which root weight increased under salinity stress. Despite this increase *T. sphaerococum* (Fig. 3) showed the highest root weight under salinity stress. In addition this species also showed the highest lateral root number; shoot length, shoot weight and total root length under saline stress while *T. turgidum* (Fig. 2) showed the highest root weight, lateral root number, shoot number, shoot weight and lateral root length under non-saline stress and number of shoots under saline condition (Table 1). Suppressing effect of salinity was not observed for shoot number in case of *Triticum sphaerocoocum*. *Triticum turgidum* showed the highest number of yellow leaves under saline conditions while species durum showed the highest under non-saline conditions (Table 1).

Coefficient of within species variations (percentages) are also presented in the Table 1. Generally species showed higher magnitude of variations under salinity stress in comparison to non-stress regime which indicated species differential response to salinity stress. Among the species, *Triticum urata* showed the highest variation for root weight while *Triticum turgidum* showed the highest variation for lateral root number under salinity stress (Table 1). On the other hand, *Triticum aestivum* showed the highest variation for shoot based traits such as shoot length, shoot weight, shoot number and leave yellowness. This variation may have arisen due to breeder selection for above ground plant traits under diverse environmental conditions. *Triticum sphaerococum* showed the highest variation for total root length (Table 1).

Polyploidy was significantly related with the species performance for all traits in the study except number of yellow leaves and shoot number under saline condition (Table 2).

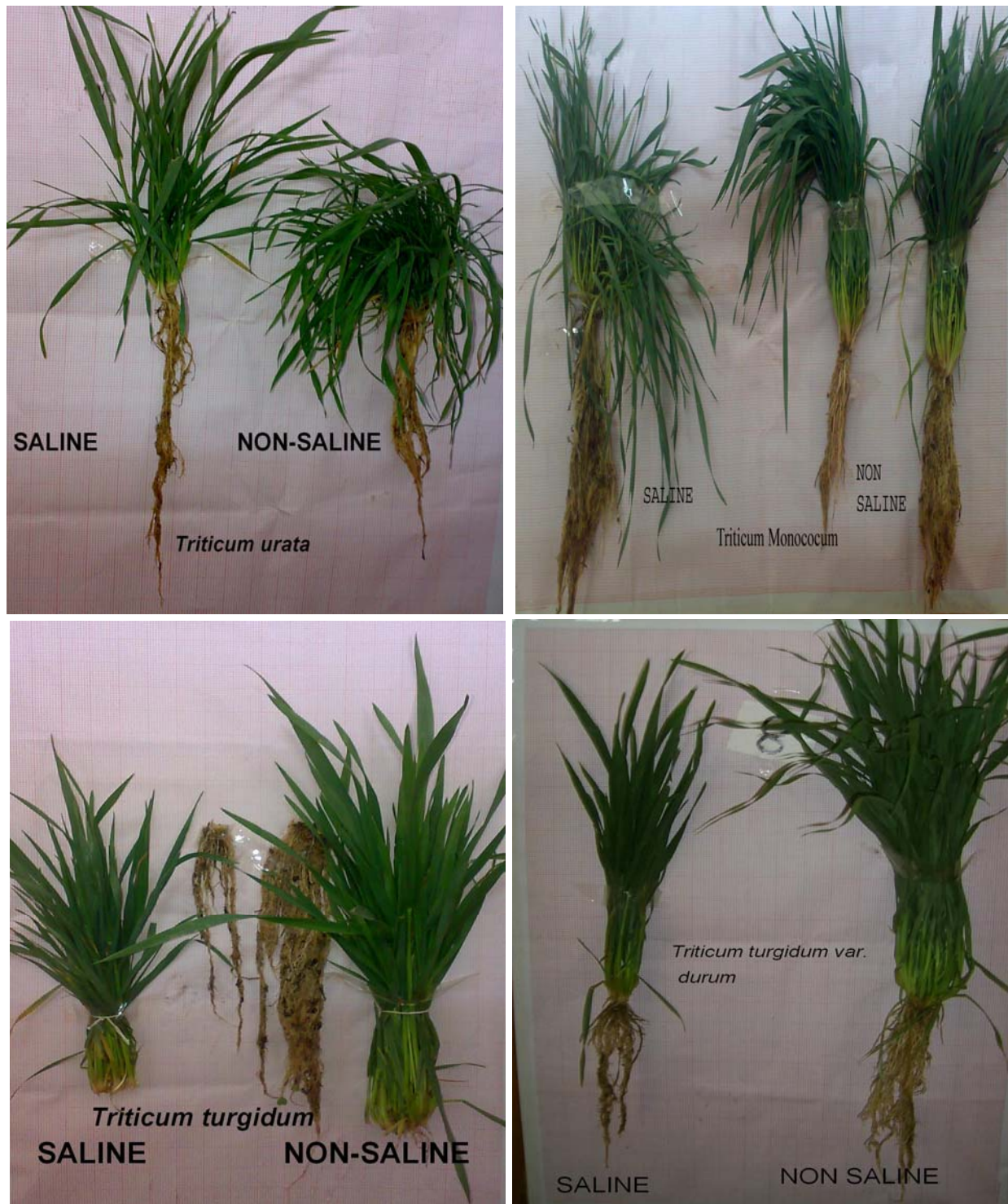


Fig. 2. Comparison of various species for morphological traits under saline and non saline regimes.

Discussions

Species changed their relative ranking across the salinity regimes, thus show the relative tolerance of the species to the salinity stress (Colmer *et al.*, 2006; Badridze *et al.*, 2009). Among the species, *T. sphaerococum* showed the highest mean performance for most of the traits under saline conditions. On the other hand *T. turgidum* showed the highest mean performance for most of the traits under normal conditions. Introgression from both species may provide some useful genes to enhance the productivity of cultivated wheat under both conditions.

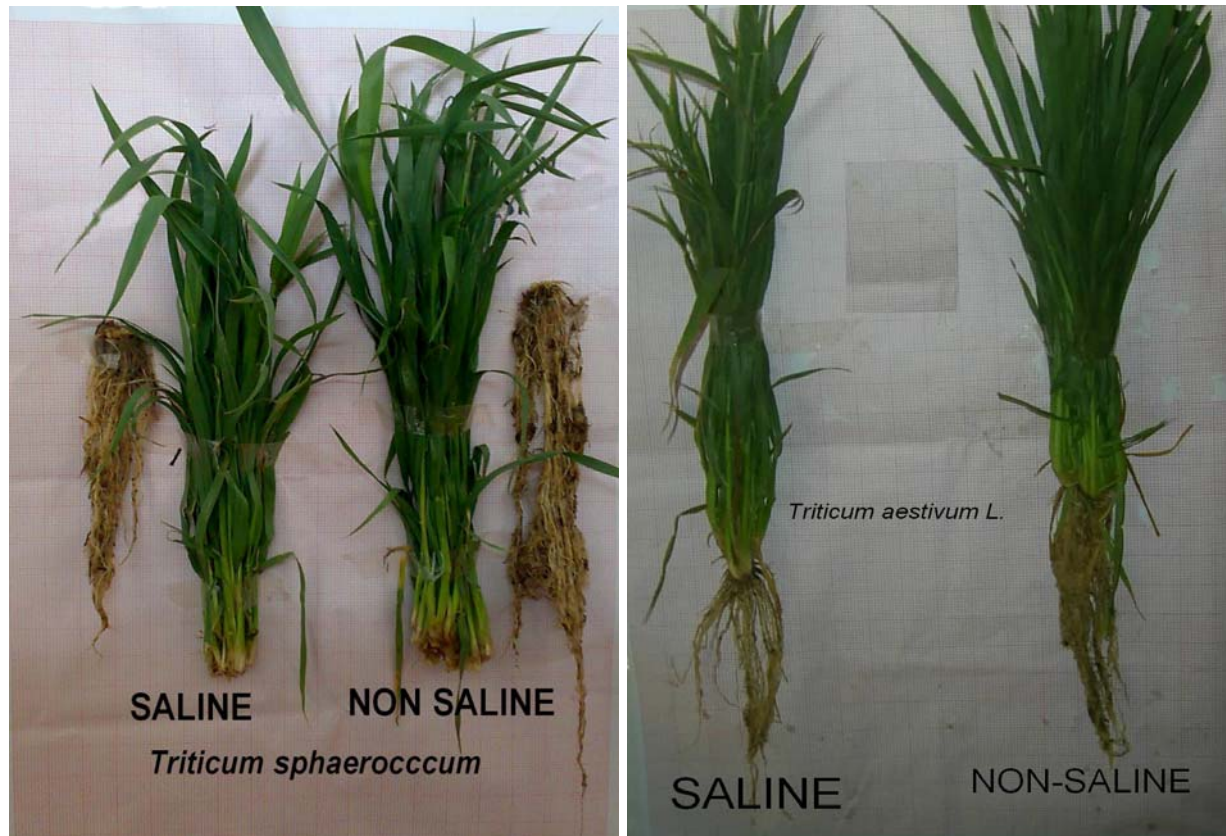


Fig. 3. Comparison of various species for morphological traits under saline and non saline regimes.

Despite this highest mean performance for most of traits and the lowest mean value for leaf yellowness by *Triticum sphaerococum*, *Triticum aestivum* showed the highest magnitude of variation for shoot based traits such as shoot length, weight, number and leaf yellowness. This variation was indicative of wheat breeding programs initiated to improve the above ground traits under diverse agro-environmental conditions. Rauf *et al.*, (2010) also concluded that cultivated wheat genetic diversity increased in the last era of 20th century due to breeder efforts. However, species *T. sphaerococum* showed the highest variation for root length and may be used to introgress this trait.

Correlations between the ploidy levels and morphological traits were significantly ($p \leq 0.05$) positive under saline conditions. Thus showing values of morphological traits increased with number and types of genomes. Positive impact of polyploidy has been discussed and reviewed by various scientists (Comai *et al.*, 2005). Higher performance may be due to locking of diverse genomes in a single species (Comai, 2005). Comai (2005) indicated that allopolyploidy was a mean of fixing heterosis due to addition of diverse genomes in single species. Therefore polyploidy was advantageous in species because of more vigor in comparison with diploid and tetraploid relatives and its ability to produce diverse gene product under stress environment (Comai, 2005).

Ploidy levels showed the highest correlations with shoot weight (SW), thus showing specificity of the traits with the higher ploidy level. It may be concluded that higher value of this trait may be used to discriminate the genotypes for salinity tolerance in polyploid species. On the other hand traits such as leaf yellowness was independent of ploidy level, thus may be used to discriminate and compare the species for salt tolerance. Munns *et al.*, (2006) also mentioned that number of dead leaves was higher in sensitive genotypes and their number increased under salinity stress. Leaves yellowness is rapid approach to

evaluate the genotypes for their salinity tolerance and indicative of acceded accumulation of toxic elements such as Na^+ and Cl^- than genotype potential to compartmentize them in the vacuole (Munns *et al.*, 2006). Phenotypic scoring of this trait further makes it appropriate to be used in breeder's large segregating populations. Thus lower values of leaves yellowness may be used to discriminate genotypes for salinity resistance. Selection for lower values of this trait will simultaneously improve some other important traits such as root weight and lateral root number because of their negative relationship with this trait. Contrastingly, leaves yellowness was positively correlated with total number of shoots, an indicative of species overall responses toward the production of more shoots when leaves yellowness was high, a kind of recovery mechanism from salinity stress. Munns *et al.*, (2006) demonstrated that proportion of damaged leaves to the total number of leaves should be less than 20% in order to consider an effective recovery mechanism from salinity. Thus total number of leaves or shoots may not be a useful indicator of species performance under saline environment. On the other hand, percentage of damaged leaves to the total number of leaves may be better indicative of species resistance to the salinity stress. Among the species, *T. sphaerococum* showed the least percentage of damaged leaves (14%) or the highest percentage of undamaged leaves (87%).

References

- Afzal, I., S., Rauf, S.M.A. Basra and G. Murtaza. 2008. Halopriming improve vigor, metabolism of reserves and ionic contents in wheat seedling under salt stress. *Plant Soil Environ.*, 54: 382-388.
- Ali, Z., A. Salam, F.M. Azhar and I.A. Khan. 2007. Genotypic variation in salinity tolerance among spring and winter wheat (*Triticum aestivum* L.) accessions. *S. Afr. J. Bot.*, 73: 70-75.
- Anonymous. 2008. Ministry of Food, Agriculture and Livestock. Year Book 2008.
- Badridze, G., A Weidner, F. Asch and A. Borner. 2009. Variation in salt tolerance within a Georgian wheat germplasm collection. *Genet. Resour. Crop Ev.*, 56: 1125-1130.
- Colmer, T.D, T.J. Flowers and R. Munns. 2006. Use of wild relatives to improve salt tolerance in wheat. *J. Exp. Bot.*, 57: 1059-1078.
- Comai, L. 2005. The advantages and disadvantages of being polyploid. *Nature*, 6: 836-846.
- El-Hendaway S.E., Y. Hu, G.M. Yakout, A.M. Awad, S.E. Hafiz and U. Schmidhalter. 2005. Evaluating salt tolerance of wheat genotypes using the multiple parameters. *Europ. J. Agron.*, 22: 243-253.
- Gorham, J., J. Bridges, J. Dubcosky, J. Dvorak and P.A. Hollington. 1997. Genetic analysis and physiology of a trait for enhanced K^+ / Na^+ discrimination in wheat, *New Phytol.*, 137.
- Mahmood, A. 2009. A new rapid method for screening wheat germplasm at early stage of growth for salinity tolerance. *Pak. J. Bot.*, 41: 255-262.
- Munns, R., R.A. James and A. Lauchli. 2006. Approaches to increasing the salt tolerance of wheat and other cereals. *J. Exp. Bot.*, 57: 1025-1043.
- Rauf, S. 2008. Breeding sunflower for drought tolerance-Review. *Commun. Biometry Crop Sci.*, 3: 29-44.
- Rauf, S., A.A. Khan, A. Naveed and T. de Silva. 2010. Consequences of plant breeding on genetic diversity. *Int. J. Plant Breed.* (Accepted).
- Sayed, H.I. 1985. Diversity of Salt tolerance in a germplasm collection of wheat (*Triticum* spp.). *Theor. Appl. Genet.*, 69: 651-657.
- Singh, B.D. 2004. *Plant Breeding* 4th edition Kalyani Publishers, Banaras, India.