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CORRELATION ANALYSIS BETWEEN MORPHOLOGICAL, PHYSIOLOGICAL AND YIELD TRAITS UNDER SALINITY STRESS CONDITION IN WHEAT (*TRITICUM AESTIVUM* L.) GENOTYPES

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ABSTRACT

Salinity is one of the key factors reducing the plant growth and productivity of major crops including wheat. However, identifying the multiple genetic parameters associated with salt tolerance during different growth stages is critical for the evaluation and enhancement of wheat genotypes. In this context, a field experiment in non-saline and saline soil was carried out for correlation analysis of 17 morphological, physiological and yield traits in 22 genotypes of wheat. The experiment was carried out at experimental field of NIA, Tandojam during 2018-2019 in a Randomized Complete Block Design (RCBD) with three replications and two treatments (non-saline soil and salinity level of 12 dS m^{-1}). The obtained mean squares showed significant differences among the tested genotypes for all the studied characters, reflecting that there are abundant genetic variations present in these wheat genetic resources for further utilization in wheat improvement programs. The correlation analysis demonstrated that a variety of characters, including spike length (non-saline $r = 0.59^{**}$; salinity $r = 0.37^{*}$), spikelets spike^{-1} (non-saline $r = 0.49^{**}$; salinity $r = 0.46^{**}$), grains spike^{-1} (non-saline $r = 0.49^{**}$; salinity $r = 0.43^{**}$), biological yield plot^{-1} (non-saline $r = 0.56^{**}$; salinity $r = 0.70^{**}$), harvest index (non-saline $r = 0.24^{*}$; salinity $r = 0.26^{*}$), relative water content (non-saline $r = 0.53^{**}$; salinity $r = 0.50^{**}$), seed index (non-saline $r = 0.29^{*}$; salinity $r = 0.52^{**}$) and K^+ (non-saline $r = 0.28^{*}$; salinity $r = 0.32^{**}$) showed positive and significant associations with grain yield plot^{-1} in non-saline and salinity stress conditions. The results suggest that these above-mentioned characters may be set as selection criteria in breeding study to improve wheat genotypes for high yielding under saline filed conditions.

Keywords: correlation, salinity, wheat, yield, yield components

INTRODUCTION

Bread wheat is an annual herb, belonging to the family poaceae, which is cultivated worldwide (Belderok *et al.,* 2000). According to an estimate, more than 60% of people in Pakistan are entirely dependent on wheat for their daily diet (Shah *et al.,* 2017). There are multiple uses of wheat; it is staple food of masses and major ingredient of animal feed. The wheat cultivation in the country was recorded on an area of 8740 thousand hectares during 2018-19, indicating 0.6 percent decrease in area under this crop over preceding year (GoP, 2019). Soil salinity is considered as one of most important abiotic stresses, which affects adversely on germination of seeds, plant growth and productivity (Sairam *et al.,* 2002). Decline in productivity of economic characters and even death of the crop plants is quite expected due to high extent of soil salinity (Garciadeblás *et al.,* 2003; Qados, 2011). Many crop plants have established mechanisms whether to eliminate salts from their tissues or to tolerate within the tissues (Kumar *et al.,* 2005; Carillo *et al.,* 2011). While some mechanisms have been developed in other crops, such as osmotic adjustment, K^+ retention and tissue tolerance process, but these are more difficult for bread wheat because of its large, complicated and hexaploid genome (Marcussen *et al.,* 2014; Wang and Xia, 2018). Nevertheless, the mechanisms underlying salinity tolerance in wheat, including leaf Na^+ exclusion mediated by high-affinity K^+ transporters and reactive oxygen species detoxification have been addressed (Munns and Gilliham, 2015). Correlation analysis is used as an effective tool to determine the relationship among different traits in genetic diverse population for enhancement of crop improvement process (Dhami *et al.,* 2018; Kandel *et al.,* 2018). In plant breeding, the correlations are very important because of its reflection in dependence degree between two or

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more traits. Correlation analysis shows the intensity of dependence (correlation) between studied traits. Correlations disclose the extent and direction of the linking between yield and its contributing traits. Correlation studies stretch a perfect depiction of traits association which is commonly happened due to gene linkage, pleiotrophic effects, physiological association in developmental and biochemical pathway (Chitralekha *et al.,* 2018). In wheat breeding, the breeders mostly elucidate the relationship between grain yield and other agronomic and morphological traits by using simple correlation (Kharel *et al.,* 2018). Chitralekha *et al.* (2018) reported that seed yield plant^{-1} exhibited highly significant and positive correlations with number of seeds spike^{-1}. Recently in Pakistan, various researchers (Baloch *et al.,* 2014; Sohail *et al.,* 2018; Rattar, 2019; Khan, 2020) found that traits like spike length, grains spike^{-1}, seed index, biological yield and harvest index disclosed positive and significant associations with grain yield. However, these all above studies were carried out in non-saline soil conditions. Therefore, the current study was designed to identify best characters which may be used to develop improved bread wheat genotypes for commercial cultivation in saline soils.

MATERIALS AND METHODS

This study was aimed to estimate correlation in non-saline and saline soil (12 dS m^{-1}) under natural field conditions. The salinity level of 12 dS m^{-1} was used since the threshold level of salinity for wheat crop is 6 dS m^{-1}, indicating that above this level of salinity would create stress for wheat crop. In this regard, twenty two wheat genotypes of diverse origin were used, such as NIA-Sundar, NIA-Sarang, NIA-AS-14, NIA-AS-9, NIA-AS-10, NIA-2B, Hamal, NIA-5B, Salt-6, SRN-87, SRN-11, CT-49, NRC-1236, Bathoor-08, Tatara, TJ-83, TD-1, Benazir, AS-2002, Sehar-2006, Kiran-95 and LU-26s for morpho-physiological and yield traits. The characters days to 75% heading and days to 75% maturity were observed visually in the field, while plant height (cm) tillers plant^{-1}, spike length (cm), spikelets spike^{-1}, grains spike^{-1}, grain yield plot^{-1} (kg) biomass plot^{-1} (kg), harvest index (%), seed index (1000-grain weight, g) were recorded after harvesting and flag leaf area (cm^{-2}) was measured when flag leaf was fully emerged. Relative water content and chlorophyll content were measured according to Bonnet *et al.* (2000) and Lichtenthaler (1987), respectively from fully fresh expanded leaves. K^+ and Na^+ contents were measured in the toluene extract (Ansari and Flowers, 1986). The wheat genotypes were sown in two sets (non-saline and saline soil) in a plot size of 20 × 15 meter. The randomized complete block designs having three replicates were used for non-saline and saline experiments. Recommended fertilizer dose was also applied i.e. nitrogen @ 120 kg ha^{-1} (in two splits) in the form of ammonium sulphate $(NH_4)_2\ SO_4$; phosphorus @ 90 kg ha^{-1} (full dose at the time of sowing) in the form of single superphosphate Ca $(H_2PO_4)_2$ and potassium @ 60 kg ha^{-1} (full dose) in the form of potassium sulphate (K_2SO_4). The analysis of variances and correlation coefficient was calculated with the help of computer package (Statistix Ver. 8.1).

RESULTS AND DISCUSSION

With respect to mean squares, the genotypes, treatments and genotypes x treatments interaction were significantly different ($P \leq 0.05$) for all the traits, such as days to 75% heading, days to 75% maturity, plant height, tillers plant^{-1}, spikelets spike^{-1}, grains spike^{-1}, spike length, grain yield plot^{-1}, biological yield plot^{-1}, harvest index, seed index, leaf area, relative water content, chlorophyll content, and K^+, Na^+ and K^+ Na^+ ratio (Table 1). The obtained results disclose that genotypes tend to possess genetic variation for different morpho-yield and physiological parameters; consequently, these bread wheat genotypes may be selected for further breeding experiments. Naggar *et al.* (2015) also reported combined analysis of variance across the four locations under different levels of salinity, which revealed that genotypes differed significantly for all studied traits at all locations and salinity levels.

In recent years, several breeders have been widely carried out correlation analysis in various field crops and unveiled the positive association of different yield contributing characters with seed yield, such as in rice (Hasan *et al.,* 2013; Baloch *et al.,* 2016), rapeseed (Banglian *et al.,* 2017; Solanki *et al.,* 2017; Rout *et al.,* 2018), sunflower (Gorgieva *et al.,* 2015; Baloch *et al.,* 2016), maize (Aman *et al.,* 2020), sorghum (Mengesha *et al.,* 2019), millet (Chavan *et al.,* 2019), barley (Hailu *et al.,* 2016) and oat (Surje and De, 2014). In the present study, the correlations result in non-saline soil (Table 2) showed that a number of characters established positively significant associations with grain yield plot^{-1}, such as days to 75% maturity (r= 0.25*), days to 75% heading (r= 0.53**), tillers plant^{-1} (r=

0.63**), spike length (r= 0.59**), spikelets spike^{-1} (r=0.49**), grains spike^{-1} (r=0.40**), seed index (r=0.29*), biological yield plot^{-1} (r=0.56**), harvest index (r=0.24*), relative water content (r=0.53**) and K^{+} (r=0.28*). These characters may be preferred in selection program to introduce high yielding varieties. Mentioning the correlation findings at phenotypic and genotypic levels, Parihar *et al.* (2018) reported that seed yield disclosed its significant and positive associations with number of spikelets plant^{-1}, effective tillers plant^{-1} and 1000-seed weight. Singh *et al.* (2017) described that grain yield plant^{-1} shared positive significant correlations with different yield enhancing characters.

The obtained correlation results under salinity stress conditions (Table 3) displayed that a number of traits also made significantly positive associations with grain yield plot^{-1}, such as spike length (r=0.37**), spikelets spike^{-1} (r=0.46**), grains spike^{-1} (r=0.43**), seed index (r=0.52**), biological yield plot^{-1} (r=0.70**), harvest index (r=0.26**), leaf area (r=0.45**), relative water content (r=0.50**) and K^{+} (r=0.32**). These all yield attributing traits displayed positive correlations with grain yield plot^{-1}, signifying the value of these traits towards contribution in yield of salinity affected wheat field. Due to these positive correlations of different parameters with yield, referring the importance of such traits as criteria for evolving high yielding wheat cultivars for saline soils. Results are in consonance with those of Ahmad *et al.* (2013), where spike length, spikelets spike^{-1}, grains spike^{-1} and seed index disclosed positive and significant associations with grain yield plant^{-1} under NaCl stress. Recently, Gadallah *et al.* (2017) also observed a significantly positive association of grain yield with K^{+} and K^{+}/Na^{+} ratio under salinity stress in wheat crop. More recently, Waseer (2018) witnessed that traits namely peduncle length, spike length and biological yield plot^{-1} showed positive and significant associations with grain yield under moderate salinity. These kinds of results were also reported by Goudarzi and Pakniyat (2008) and Chamekh *et al.* (2017). The current study also exhibited significant ($P<0.05$) and positive correlations among various traits under salinity stress conditions, such days to 75% heading with plant height; (r=0.64**), plant height with grains spike^{-1} (r=0.35**), tillers plant^{-1} with spikelets spike^{-1} (r=0.32**), relative water content (r=0.34*) and harvest index (r=0.38**), spike length with spikelets spike^{-1} (r=0.34**), grains spike^{-1} with biological yield plot^{-1} (r=0.37**) and relative water content (r=0.26*), spikelets spike^{-1} with grains spike^{-1} (r=0.30*), grains spike^{-1} with seed index (r=0.47**), seed index with biological yield plot^{-1} (r=0.31*), biological yield plot^{-1} with leaf area (r=0.47**), relative water content with K^{+} (r=0.29*) and leaf area with K^{+} (r=0.24*). Overall, an intensive selection for these growth, yield and physiological traits will ultimately improve seed yield in wheat under salinity stress conditions. Dashti *et al.* (2012) observed significantly negative associations between K^{+}/Na^{+} ratio and Na^{+} concentration, while K^{+}/Na^{+} ratio was significantly and positively interrelated with K^{+}. Asgari *et al.* (2012) also reported similar associations under salinity, including tillers plant^{-1} with spikelets spike^{-1}, grains spike^{-1}, K^{+} and K^{+}/Na^{+} ratio, spike length with spikelets spike^{-1}, K^{+} with K^{+}/Na^{+} ratio and seed index with tillers plant^{-1}, spike length and spikelets spike^{-1}.

Table 1. Mean squares of various traits of bread wheat genotypes grown in non-saline and salinity stress conditions

Source of variance	**Replication D.F. (2)**	**Genotypes (G) D.F. (21)**	**Treatments (T) D.F. (1)**	**G x T interaction D.F. (21)**	**Error D.F. (82)**
Days to 75% heading	0.11	14.83**	1781.16**	5.84**	1.65
Days to 75% maturity	3.47	13.82**	3229.66**	11.51**	1.70
Plant height	26.8	325.2**	14247.4**	32.2	23.2
Tillers plant^{-1}	0.656	18.043**	119.603**	0.391^{ns}	0.652
Spike length	1.1204	6.4196**	68.4254**	1.3863*	0.5564
Spikelets spike^{-1}	0.387	17.301**	612.43**	1.081^{ns}	0.926
Grains spike^{-1}	5.20	471.59**	4956.18**	12.08^{ns}	6.45
Grain yield plot^{-1}	0.00023	0.17128**	3.17478**	0.00357^{ns}	0.00449
Biological yield plot^{-1}	0.00692	0.12351**	4.76178**	0.03918**	0.00833
Harvest index	0.96	127.07**	1464.24**	5.80**	1.98
Seed index	23.10	80.14**	2796.45**	4.80^{ns}	6.20
Leaf area	0.271	49.420**	904.909**	4.429**	1.198
Relative water content	123.8	233.1**	51280.2**	249.2**	68.8
Chlorophyll	0.53	198.46**	3382.85**	6.08^{ns}	5.55
K^{+}	0.0977	0.4424**	22.5724**	0.1106**	0.0538
Na^{+}	0.00963	0.16203**	2.98841**	0.02383*	0.00847
K^{+}/Na^{+} ratio	0.111	7.526**	167.818**	0.562*	0.364

**,* represent significant at 1 and 5% of probability level, respectively, while ns shows non-significant

Table 2. Correlation coefficient (r) between morphological, physiological and yield traits of bread wheat genotypes in non-saline conditions

Traits	DM	DH	PH	TP	SL	SPS	GS	GYP	SI	BP	HI	CHL	RWC	LA	N
DH	-0.21^{ns}	-													
PH	-0.20^{ns}	-0.11^{ns}	-												
TP	0.15^{ns}	0.41**	0.04^{ns}	-											
SL	0.12^{ns}	0.32*	-0.12^{ns}	0.42**	-										
SPS	0.18^{ns}	0.51**	-0.19^{ns}	0.31*	0.31*	-									
GS	0..09^{ns}	0.34**	0.10^{ns}	0.26*	0.49**	0.33**	-								
GYP	0.25*	0.53**	0.06^{ns}	0.63**	0.59**	0.49**	0.40**	-							
SI	0.20^{ns}	0.26*	-0.67**	0.09^{ns}	0.35**	0.30*	0.18^{ns}	0.29*	-						
BYP	0.19^{ns}	0.16^{ns}	0.29*	0.41**	0.37**	0.17^{ns}	0.12^{ns}	0.56**	0.01^{ns}	-					
HI	0.6^{ns}	0.27*	-0.33**	0.13^{ns}	0.32*	0.20^{ns}	0.25*	0.24*	0.32*	0.58**	-				
CHL	0.21^{ns}	0.17^{ns}	-0.28*	0.33**	0.33**	0.31*	0.16^{ns}	0.17^{ns}	0.49**	0.04^{ns}	0.16^{ns}	-			
RWC	0.20^{ns}	0.45**	-0.05^{ns}	0.59**	0.42**	0.48**	0.53**	0.53**	0.35**	0.30*	0.23*	0.48**	-		
LA	0.21^{ns}	-0.02^{ns}	0.36**	0.15^{ns}	0.32*	0.12	0.11^{ns}	0.16^{ns}	0.35**	0.12^{ns}	0.01^{ns}	0.17^{ns}	0.16^{ns}	-	
N	-0.07^{ns}	0.15^{ns}	-0.24*	0.02^{ns}	-0.03^{ns}	-0.05^{ns}	-0.01^{ns}	0.01^{ns}	0.16^{ns}	0.14^{ns}	0.20^{ns}	0.01^{ns}	-0.04^{ns}	0.18^{ns}	-
K	0.40**	0.40**	-0.35**	0.20^{ns}	0.28*	0.48**	0.12^{ns}	0.28*	0.28*	0.04^{ns}	0.15^{ns}	0.20^{ns}	0.21^{ns}	0.21^{ns}	0.09^{ns}
KNR	0.22^{ns}	0.01^{ns}	0.06^{ns}	0.06^{ns}	0.20^{ns}	0.27*	0.11^{ns}	0.13^{ns}	-0.03^{ns}	0.15^{ns}	-0.10^{ns}	0.12^{ns}	0.13^{ns}	0.34**	0.82**

Note: **,* represents significant level at 1 and 5% of probability levels, respectively, while ns show non-significant
DH= Days to 75% heading; DM= Days to 75% maturity; PH= Plant height; TP= Tillers plant^{-1}; SL= Spike length; SPS= Spikelets spike^{-1}; GS= Grains spike^{-1}; GYP= Grain yield plot^{-1}; SI= Seed index; BP= Biological yield plot^{-1}; HI= Harvest index; CHL=Chlorophyll; RWC= Relative water content; LA= Leaf area; N= N^+; K= K^+; KNR= K^+/N^+ ratio

Table 3. Correlation coefficient (r) between morphological, physiological and yield traits of bread wheat genotypes under salinity stress conditions

Traits	DM	DH	PH	TP	SL	SPS	GS	GYP	SI	BP	HI	CHL	RWC	LA	N	K
DH	-0.17^{ns}	-														
PH	0.16^{ns}	0.64**	-													
TP	0.22^{ns}	-0.39**	-0.41**	-												
SL	-0.06^{ns}	-0.44**	-0.45**	0.20^{ns}	-											
SPS	-0.09^{ns}	-0.42**	-0.25*	0.32*	0.34**	-										
GS	0.09^{ns}	-0.44**	0.35**	0.06^{ns}	0.55**	0.30*	-									
GYP	-0.04^{ns}	-0.36**	-0.33**	0.24^{ns}	0.37**	0.46**	0.43**	-								
SI	0.03^{ns}	-0.51**	-0.32*	0.31*	0.16^{ns}	0.14^{ns}	0.47**	0.52**	-							
BYP	-0.16^{ns}	-0.05^{ns}	-0.09^{ns}	-0.08^{ns}	0.24*	0.30*	0.37**	0.70**	0.31*	-						
HI	0.18^{ns}	-0.41**	-0.29*	0.38**	0.15^{ns}	0.11^{ns}	0.13^{ns}	0.26*	0.26*	-0.41**	-					
CHL	0.08^{ns}	-0.28*	-0.24*	0.18^{ns}	0.13^{ns}	0.07^{ns}	0.07^{ns}	0.17^{ns}	0.03^{ns}	0.00^{ns}	0.23^{ns}	-				
RWC	0.02^{ns}	-0.50**	-0.40**	0.34**	0.32*	0.21^{ns}	0.26*	0.50**	0.51**	0.20^{ns}	0.23^{ns}	0.13^{ns}	-			
LA	0.08^{ns}	-0.28*	-0.06^{ns}	0.20^{ns}	0.22^{ns}	-0.36**	0.23^{ns}	0.45**	0.47**	0.47**	0.03^{ns}	0.13^{ns}	0.23^{ns}	-		
N	0.01^{ns}	0.20^{ns}	0.01^{ns}	0.01^{ns}	0.01^{ns}	0.02^{ns}	-0.04^{ns}	0.10^{ns}	0.01^{ns}	0.21^{ns}	0.17^{ns}	-0.11^{ns}	0.17^{ns}	0.17^{ns}	-	
K	0.02^{ns}	-0.46**	-0.32*	0.25*	0.23^{ns}	0.30*	0.34**	0.32*	-0.29*	0.16^{ns}	0.23^{ns}	0.04^{ns}	0.29*	0.24*	0.09^{ns}	-
KNR	-0.04^{ns}	-0.35**	-0.22^{ns}	0.07^{ns}	0.09^{ns}	0.07^{ns}	0.15^{ns}	-0.01^{ns}	0.07^{ns}	-0.14^{ns}	0.21^{ns}	0.06^{ns}	-0.04^{ns}	-0.11^{ns}	-0.91**	0.23^{ns}

CONCLUSION

Correlation results in non-saline and saline soil exhibited that a number of traits made positively significant interrelationships with grain yield plot^{-1}, such as spike length, spikelets spike^{-1}, grains spike^{-1}, seed index, biological yield plot^{-1}, relative water content and K^+. Hence, these traits may be used as selection criteria to develop high yielding wheat genotypes for non-saline and salinity stress conditions.

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AUTHOR'S CONTRIBUTION

N. Gandahi: Conducted the experiments and wrote the manuscript

A. W. Baloch: Design the experiment and corrected the final version of manuscript

S. A. Sarki: Helped in revision

M. M. Lund: Helped in revision

M. N. Kandhro: Technical evaluation of manuscript

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