Evaluation of some Bread Wheat Genotypes under Saline Soil Conditions Using Tolerance Indices and Multivariate Analysis

Darwish, M. A. H. [1] ; W. M. Fares[2] and Eman M. A. Hussein[2]
[1] Wheat Research Department, Field Crops Research Institute, ARC, Egypt.
[2] Central Laboratory for Design & Statistical Analysis Research, ARC, Egypt.

ABSTRACT

The present investigation was conducted in a field experiments at Sakha Agricultural Research Station Farm to evaluate 24 bread wheat genotypes during the two growing seasons 2014/2015 and 2015/2016 under normal and salinity stress conditions. The experimental design used was a randomized complete block design with three replicates. Eleven stress tolerance indices (STI's) were calculated based on average grain yield under normal and stress conditions across the two seasons. Moreover, cluster analysis was performed to identify the similarity/dissimilarity among the tested genotypes for grain yield and salinity tolerance. Results showed large values of broad-sense heritability (h_b^2) coupled with high values of genetic advance as a percent of mean (GA%) at 5% selection intensity for number of spikes/m^2 and number of grains/spike in the adequate site. Concerning the salt stressed soil, the grain yield ratio, number of spikes/m^2 and grain yield recorded the highest values of h_b^2 and GA%. However, there were crucial differences among tested genotypes in respect to grain yield under non-stress and salt stress sites, which demonstrates high genetic diversity among them that enabled us to screen salt tolerant genotypes. Already, the tested wheat genotypes exhibited different responses for salinity stress tolerance indices (STI's). Perfect and positive correlation coefficients (r = 1) were found between three pairs of indices (STI and GMP), (SSPI and TOL) and (CV and SSI) where each one of the previous three pairs occupied one dot on the biplot graph indicating that the three indices are identical for ranking genotypes for salinity tolerance and they could be interchangeably used as a substitute for each other. Therefore, using these pairs of (STI's) together in the same study is considered a waste of time and effort. The cluster analysis classified the tested genotypes into five main groups (clusters) where each group contained the genotypes that showed similar yield potential and salinity tolerance. The fifth cluster contained two promising genotypes namely; lines 2 and 17 that were characterized by moderate grain yield in each of the normal and salt soils recording the lowest grain yield reduction. Also, they occupied the first and second ranks among the tolerant genotypes for salinity stress. Accordingly, results would give a good chance to achieve genotypic improvement of wheat through the hybridization among genotypes taken from different clusters.
Keywords: Wheat, Genotypes salinity tolerance indices, biplot graph, cluster analysis.

INTRODUCTION

Salinity is one of the major abiotic stresses that adversely affect crop productivity and quality, Chinnusamy *et al.* (2005). Adverse effects of salinity on plant growth may be due to osmotic stress and ion cytotoxicity. Soil salinity is a pioneer dilemma spread, especially in arid and semiarid areas. Egypt is one of the countries that suffer severe salinity problems, Al-Naggar *et al.* (2015 a,c). Salinization is mainly due to low precipitation (<25 mm annual rainfall), high temperature (during summer, temperature reaching from 35 to 45°C), high surface evaporation (1500-2400 m/year), poor drainage system with 98% of the cultivated land under irrigated, rising water table (less than one meter below the soil surface), and irrigating with low quality water up to salinity of 4.5 dS/m, El-Hendawy *et al.* (2005), which retarded the aimed sustainable crop production, especially in the north delta of Egypt.

Wheat (Triticum aestivum L.) is the first strategic cereal crop in Egypt. Increasing wheat production is a national target in Egypt to minimize the gap between wheat consumption and production. Wheat is moderately tolerant to salt with threshold without yield loss at 6 dS m-1 and with yield 50% loss at 13 dS m-1, Mass and Hoffmann (1977). Wheat genotypes show wide variation for salinity stress tolerance. Therefore, the breeding programs for high and stable yield potential and tolerance to biotic/abiotic stresses is a vital goal for the national plans of wheat development in Egypt. The reduction in production of soils affected by salinity is about 30% threatening the livelihoods of the poor farming and having a significant negative impact on the food production of Egypt as whole, El-Lakany *et al.* (1986). Salt tolerance can be defined as the ability of plants to survive and maintain their growth and produce relatively profitable yield under saline conditions.

Stress tolerance indices (STI's) were widely used as simple mathematical equations that quantify and compare the grain yields under stressed and non-stressed conditions to differentiate the tolerant/sensitive genotypes, Mitra (2001). There are various stress tolerance indices such as tolerance index (TOL), mean productivity "MP", Rosielle and Hamblin (1981). stress susceptibility index "SSI", Fischer and Maurer (1978). geometric mean productivity (GMP), stress tolerance index (STI's), Fernandez (1992). and others that have been employed to evaluate the comparative yield performance of promising wheat genotypes under both optimal and stressful (saline) conditions. Saad *et al.* (2014) on barely, Abd El-Mohsen *et al.* (2015), Singh *et al.* (2015) and Ali and El-Sadek (2016) on bread wheat, and Mohammadi *et al.* (2016) on durum wheat, found perfect or highly significant associations between some (STI's), indicating that these indices are identical for ranking genotypes for salt tolerance and they can be used as a substitute for each other.

Knowledge on heritability and genetic advance is a basic step to identify the characters amenable to genetic improvement through selection. It is worthy to emphasize that, without considering genetic advance; the heritability values (h2) would not be practically useful in breeding program depending on visual selection. A number of researches estimated the genetic parameters under the normal and stress environments. Al-Naggar *et al.* (2015 b,d) reported that the broad-sense heritability decreased as salinity increased more than 3000 ppm to 6000 and 9000 ppm NaCl, respectively.

Cluster analysis is a valuable biometrical tool aimed to quantify the degree of genetic divergence among tested genotypes based on their performance and their contributing characters. But it was found that the run of cluster analysis depending on (STI's) parameter is useful to differentiate

wheat genotypes for salt tolerance, Saad *et al.* (2014) Abd El-Mohsen *et al.* (2015) and Singh *et al.* (2015).

The main objectives of this research were to: 1- Evaluate the influence of salinity soil stress on grain yield and its components of wheat genotypes, 2- Identify the saline tolerant wheat genotypes based on tolerance indices (STI's) 3- Study the interrelationships and overlapping among (STI's) using Spearman's rank correlation and biplot graph method and 4- Classify the tested wheat genotypes using cluster analysis depending on the high yield and (STI's). The results may be helpful to plan appropriate selection strategies for improving both of grain yield and salt tolerance in wheat crop in Egypt.

MATERIALS AND METHODS

This study was conducted at the Experimental Farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt (31° 5' 12" North, 30° 56' 49" East) during tow success of seasons 2014/2015 and 2015/2016. Twenty-four bread wheat genotypes were used and grown on 28th November during the two growing seasons. The tested wheat genotypes contained 20 lines that were selected as promising lines from the local breeding program in addition with four cultivars used as cheeks). The name and pedigree of the studied genotypes are listed in Table 1.

Table 1. Name and pedigree of the studied wheat genotypes*.

Genotype	Pedigree/Cross Name
Line # 1	SAKHA 94 /6/ GIZA 158 /5/ CFN /CNO "S" // RON /3/ BB / NOR 67 /4/ TL /3/ FN / TH // NAR 59*2.
Line # 2	CAZO / KAUZ // KAUZ /4/ PJN / BOW // OPATA*2 /3/ CROC-1 / AE.SQUARROSA (224) // OPATA.
Line # 3	CAZO / KAUZ // KAUZ /4/ PJN / BOW // OPATA*2 /3/ CROC-1 / AE.SQUARROSA (224) // OPATA.
Line # 4	CAZO / KAUZ // KAUZ /3/ MILAN / KAUZ // CHIL / CHUM18.
Line # 5	CAZO / KAUZ // KAUZ /3/ MILAN / KAUZ // CHIL / CHUM18.
Line # 6	ATTILA*2 / PBW65 /4/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /3/ 2*KAUZ.
Line # 7	ATTILA*2 / PBW65 /4/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /3/ 2*KAUZ.
Line # 8	VEE / KOEL // 2* SKAUZ /3/ KAUZ // BOW / NKT.
Line # 9	VEE / KOEL // 2* SKAUZ /3/ KAUZ // BOW / NKT.
Line # 10	VEE / KOEL // 2* SKAUZ /3/ KAUZ // BOW / NKT.
Line # 11	VEE / KOEL // 2* SKAUZ /3/ KAUZ // BOW / NKT.
Line # 12	DVERD 2 / AE - SQUARROSA (214)// 2* BCN /5/ WEAVER /4/ NAC / TH.AC // 3* PVN /3/ MIRLO / BUC.
Line # 13	DVERD 2 / AE - SQUARROSA (214)// 2* BCN /5/ WEAVER /4/ NAC / TH.AC // 3* PVN /3/ MIRLO / BUC.
Line # 14	PFAU / MILAN /5/ WEAVER /4/ NAC / TH.AC // 3* PVN /3/ MIRLO / BUC.
Line # 15	PFAU / MILAN /5/ WEAVER /4/ NAC / TH.AC // 3* PVN /3/ MIRLO / BUC.
Line # 16	PFAU / MILAN /5/ WEAVER /4/ NAC / TH.AC // 3* PVN /3/ MIRLO / BUC.
Line # 17	OASIS / SKAUZ // 4* BCN /6/ CNDO / R143 // ENTE / MEXI 2 /3/ AEGILOPS .SQUARROSA (TAUS) /4/ WEVER /5/ 2*TAUZ.
Line # 18	CHEN / AEGILOPS SQUARROSA (TAUS) // BCN/3/2*KAUZ /4/ PJN / BOW // OPATA*2 /3/ CROC-1 / AE.SQUARROSA (224) // OPATA.
Line # 19	CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /3/ 2*KAUZ /4/GEN*2 // BUC / FLK /3/ BUCHIN.
Line # 20	GEN*2 // BUC / FLK /3/ BUCHIN /7/ BUC // 7C / ALD /5/ MAYA74 / ON // 1160.147 /3/ BB / GLL /4/ CHAH"S" /6/ MAYA / VUL // CMH74A.630 / 4*SX S.
Sids 12	BUC//7C/ALD/5/MAYA74/ON//II60.147/3/BB/GLL/4/CHAT"S"/6/MAYA/VUL//CMH74A.630/4*SX.
Misr 1	OASIS/SKAUZ//4*BCN/3/2*PASTOR.
Giza 171	SAKHA 93 / GEMMEIZA 9.
Misr 2	SKAUZ/BAV92.

*Source: Wheat Res. Depr., FCRI, ARC, Egypt.

In each season, the aimed entries were evaluated in two experimental sites represent two different site conditions namely normal (N) and saline soils (S) using flood method of irrigation. The recommended cultural practices for wheat cultivation in old land in Egypt were applied at the proper time. Before soil preparation some physical and chemical analyses of each experimental site were performed where two composite surface and subsurface soil samples at 0-30 cm and 30-60 cm depth were collected during the two studied seasons in laboratory. The meteorological data were recorded for the two winter growing seasons from Sakha meteorological station (Table 2). Details of soil properties belong to each research site for the two seasons are given in Table 3.

There were manifested declines in the temperature throughout the second season compared with the first one.

Table 2. Mechanical and chemical soil analyses of normal and salt-affected soils during two growing seasons.

Location	Sample depth	Soil structure	PH	EC dsm^{-1}	Anion mEq/l				Cation mEq/l			
					CO3$^-$	HCO3$^-$	CL$^-$	SO4$^-$	Ca^{++}	Mg^{++}	Na$^+$	K$^+$
						2014/015						
Normal	0 - 30	Clay	8.61	2.33	-	2.5	10	43.32	10.6	6.1	12.38	0.29
soil	30 - 60	Clay	8.7	2.1	-	2.25	12.5	48.69	6.6	4.9	8	0.33
Saline	0 - 30	Clay	8.9	11.4	-	3	70	101.98	87.1	56.9	78.15	1.58
soil	30 - 60	Clay	8.7	10.1	-	3	120	95.59	70.35	59.25	57.5	1.49
						2015/016						
Normal	0 - 30	Clay	8.06	2.01	_	3	8.11	9.11	5.6	3.91	10.34	0.31
soil	30 - 60	Clay	7.90	1.5	_	2.5	4.8	7.16	3.23	2.33	8.42	0.29
Saline	0 - 30	Clay	8.8	10.31	_	4	34.56	45.6	24.9	16.9	44.23	0.45
soil	30 - 60	Clay	8.7	8.65	_	3	25.9	42.6	12.1	10.2	40.59	0.33

Table 3. Metrological data during two growing seasons.

Month	Temperature				RH* %		Rainfall (mm)	
	2014/015		2015/016		2014/015	2015/016	2015/015	2015/016
	Max.	Min.	Max.	Min.				
Nov.	21.46	11.46	22.50	11.30	78.00	72.80	3.50	17.40
Dec.	21.19	10.10	15.60	7.36	76.40	76.40	5.70	15.00
Jan.	22.03	10.50	15.80	5.61	70.10	74.50	7.04	5.11
Feb.	20.45	9.30	22.20	9.61	75.50	65.50	5.50	-
March.	23.93	12.84	21.30	14.62	71.10	67.80	18.00	4.50
April.	28.60	15.30	27.00	18.60	91.30	65.00	5.60	-
May.	32.50	21.50	26.90	20.90	88.00	85.00	-	-
Means.	32.50	22.50	26.90	21.90	88.00	85.00	-	-

RT: Relative Humidity

A randomized complete block design with three replications was used for each soil conditions. The plot area (3.6 m2) consisted of six rows, 3 m long and 20 cm apart. Grains were manually drilled in the rows at the rate of 300 seeds m-2.

The studied characteristics were: Number of days to heading (DH) and to maturity (DM), grain filling period (GFP) in days, grain filling rate (GFR) in g m^{-2} days^{-1}, plant height (PH, cm), number of spikes/m^2 (SM), number of kernels per spike (KS), 1000-kernel weight (KW, g) and grain yield (GY, ard./fad.).

Statistical analysis

All data were subjected to individual and combined analysis of variance of randomized complete block design across the two cultivated sites (normal and salt) for each season, Steel *et al*. (1997). As a routine statistical step, Levene test (1960) was run prior to the combined analysis to confirm the homogeneity of individual error terms. Least significant of difference (LSD) test was used to detect the significant differences among the proper items at 0.05 probability level.

Based on the combined analysis of each cultivated site across the two seasons, the genotypic (GCV%) and phenotypic (PCV%) variances their corresponding genotypic and phenotypic coefficient of variations and) were estimated using the proper mean square expectations according to the method suggested by Johnson *et al*. (1955). Broad-sense heritability (hb2) and genetic advance (GA %) in terms of percentage of mean (with 5 % selection intensity) were estimated according to Allard (1999).

For each genotype, ten stress tolerance indices were calculated based on average grain yield under normal (Yn) and stressed (Ys) sites across the two seasons. The names, equations and references of the stress tolerance indices are shown in Table 4. In addition, the authors supposed the use of coefficient of variation (CVI) as a novel measure of stress tolerance index (STI).

The genotypes which possess high values of mean productivity (MP), harmonic mean (HM), geometric mean productivity (GMP), stress tolerance index (STI), yield index (YI), yield stability index (YSI) and modified stress tolerance index (MSTI) or low values of Tolerance Index (TOL), stress susceptibility percentage index (SSPI), stress susceptibility index (SSI) and coefficient of variation (CVI) are considered to be more tolerant to soil salinity stress.

Table 4. The name, equation and reference of 11 salinity tolerance indices.

No.	Index name	Formula	Reference
	% Reduction	$(Y_n-Y_s)\times 100/Y_n$	
	The high values of the following indices indicated salinity stress tolerance		
1	Mean Productivity (MP)	$(Y_n+Y_s)/2$	(Rosielle and Hamblin, 1981)
2	Harmonic Mean (HM)	$(2\times Y_n\times Y_s)/(Y_n+Y_s)$	(Jafari *et al*., 2009)
3	Geometric Mean Productivity (GMP)	$(Y_n\times Y_s)^{0.5}$	(Fernandez, 1992)
4	Stress Tolerance Index (STI)	$(Y_n\times Y_s)/(\overline{Y}_n)^2$	(Fernandez, 1992)
5	Yield Index (YI)	$Y_s/\overline{Y}_s$	(Gavuzzi *et al*., 1997)
6	Yield Stability Index (YSI)	Y_s/Y_p	(Bouslama and Schapaugh,1984)
7	Modified Stress Tolerance Index (MSTI)	$(YI)^2\times STI$	(Farshadfar and Sutka, 2002)
	The low values of the following indices indicated salinity stress tolerance		
8	Tolerance Index (TOL)	Y_n-Y_s	(Rosielle and Hamblin, 1981)
9	Stress Susceptibility Percentage Index (SSPI)	$Tol\times 100/(2\overline{Y}_n)$	(Moosavi *et al*., 2008)
10	Stress Susceptibility Index (SSI)	$[1-(Y_s/Y_n)]/[1-(\overline{Y}_s/\overline{Y}_n)]$	(Fisher and Maurer, 1978)
11	Coefficient of variation (CVI)	SD/Mean of Y_n and Y_s	Authors

- Y_n and Y_s indicate to average grain yield of each genotype under normal and stress conditions, respectively.

- $\overline{Y}_n$ and $\overline{Y}_s$ indicates to average grain yield overall genotypes under normal and stress conditions, respectively.

To give an overall picture about the interrelationships and overlapping among the eleven stress tolerance indices, Spearman's rank correlation coefficients between all pairs of these eleven (STI's) were calculated. Principal component (PC) analysis was also run for grouping the similar/dissimilar stress tolerance indices. For better visualization, the first two principal components (PC1 and PC2) were graphically plotted against each other using biplot graph, Yan and Rajacan (2002).

To differentiate the tested genotypes for grain yield and salinity stress tolerance, the model of agglomerate hierarchical cluster analysis was worked out using the average grain yield and the eleven stress tolerance indices. A dendrogram was constructed based on Euclidean distance procedure. Genotypes were clustered using un-weighted pair group method using arithmetic average as outlined by Kovach (1995).

RESULTS AND DISCUSSION

The results of Levene test (1960) proved the homogeneity of separate error variances for all studied character that permits to apply combined analysis across the two sites in each growing season.

Analysis of variance:

The experimental sites were chosen to represent the agricultural environments of wheat production areas in North Delta. Rajaram *et al*. (1996) concluded that simultaneous evaluation of the germplasm under both near optimum conditions (to identify genotypes with high yield potential) and stress conditions (to activate the alleles of saline soil tolerance) is important to breed for selecting higher yielding and salinity tolerant genotypes. Moreover, the experiments have been repeated across two seasons to give greater reliability of the results.

Mean squares of the studied characters across the two salinity soil conditions for each one of the two seasons are presented in Table 5. The effect of salinity source of variation was significant or highly significant for all characters, except for 1000 kernels weight in the first season. The current conclusions are supported by Al-Naggar *et al*. (2015 a,c). As well as, there were significant or highly significant differences among the tested wheat genotypes for all studied characters for the tow growing seasons.

Interactions between genotypes and soil salinity were significant and highly significant for all characters as illustrated in Table 5. The significance of the interaction is a result of the different abilities of the cultivars to adjust their characters to the environment, suggesting the importance of genotype assessment under different environments to identify the best ones for a particular environment. Previous studies have been indicated that most earliness and yield and yield component characteristics were significantly affected by salinity soil, genotypes, and the interaction between genotypes and salinity stress. In general, these results are in harmony with those reported by El-Hendawy *et al*. (2005, 2009 and 2011), Asadi *et al*. (2012), Al-Ashkar and El-Kafafi (2014), Al-Naggar *et al*. (2015 a,b), Hassan *et al*. (2015), Ragab and Taha (2015), and Gadallah *et al*. (2017).

Table 5. Mean squares (MS) of the studied characteristics under normal and saline soils in each season 2014/2015 and 2015/2016.

S.O.V.	df	Seasons	DH	DM	GFP	GFR	PH	SM	KS	KW	GY
Salinity (S)	1	2014/2015	1827.5 **	4301.7 **	521.3 **	4332.3 **	23002.7 **	2579305 **	8137.7 **	2.1	9961.4 **
		2015/2016	1190.2 **	2236.5 **	163.6 **	1134.1 **	13953.5 **	2286956 **	5337.5 **	121.9*	4316.6 **
Rep./Salinity	4	2014/2015	89.9	128.5	20.7	8.1	38.9	1080.9	12.4	4.1	11.5
		2015/2016	2.7	12.6	7.5	23	55.4	15600.5	38.8	6.4	38.07
Genotypes (G)	23	2014/2015	52.9 **	44.4 **	18.9 *	12.2 *	98.4 *	8535 **	75.9 **	42.2**	19.79 **
		2015/2016	26.5 **	54.5 **	66.3 **	26.1 **	191.3 *	1533 **	57.01 **	48.4 **	28.8 **
G x S	23	2014/2015	9.1 **	22.8 **	17.8 *	11.1 **	76.3 **	12681 **	145.01 **	32.4 **	16.38 **
		2015/2016	11.6 **	17.3 **	37.3 *	11.3 **	48.2 **	11985 **	61.9 **	29.9 **	11.49 *
Error	92	2014/2015	5.5	6.4	7.4	3.9	28.6	1774	27.8	9.5	5.03
		2015/2016	4.6	6.7	12.3	4.9	21.6	4585	28.08	21.1	6.85

*, **: Significant at 0.05 and 0.01 levels of probability, respectively.

Means performance:

Highly significant differences were found among the 24 wheat genotypes for the nine studied characters, during the two growing seasons 2014/2015 and 2015/2016 under both normal and saline soil conditions as shown in Table 6.

Results in Table 6 show the average, maximum, minimum, range values and coefficient of variation (CV%) of the studied characteristics under the two saline soil conditions in the two seasons. The means of all genotypes decreased significantly under the saline soil for all characters in the two seasons, except for 1000-kernel weight (KW) in the first season.

The maximum and minimum values of the studied characters tended to decrease under saline soil conditions in the two seasons, except for minimum values of DM and GFP in the 2nd season; and maximum values of KW in the 2nd season. The ranges between the maximum and minimum values of all characters decreased under the saline soil conditions, except for KW in the two seasons; GY in the 1st season; and DH and SM in 2nd season as shown in Table 6.

The means of all genotypes in the second season were higher than those obtained in the first season under normal and saline soil conditions for all studied characteristics, except for KS and KW under the two soil conditions, and for each of GFR and GY under normal soil conditions.

As combined values across the two soil conditions, the average, maximum, minimum and range values of most characters increased in the second season compared to the first one, except for the average values of GFR, KS, KW and GY, the maximum values of DH, KS and KW, the minimum values of GFR, GFP, KS, KW and GY, and the range between the maximum and minimum values of DH, KS and KW.

On the other hand, the most coefficients of variation (CV%) were located at the statistically acceptable range according to each studied character which supports the validity of the obtained results.

The results exhibited significant differences among the tested genotypes for all studied characters under each soil condition. This provides an evidence for the possibility to carry out a sufficient selection program on the basis of these characters using the tested genotypes.

Concerning the earliness character, it is clear that lines No. 1, 14 and 15 were among the earliest heading genotypes over the two soil conditions in the 1st season while lines no. 10 and 18 were the earliest in the 2nd season. However, line No. 19 and Misr 2 headed later across the two cultivated sites in the 1st season while lines No. Lines No. 6 and 7 were the latest ones in the 2nd season. There were differences between the results of the two seasons which may be attributed to the environmental effects. Regarding days to maturity, results showed that lines No. 13 and lines No 14 were early matured than the others while line no. 16, Giza 171 and Misr 2 were the

latest in maturity across the two soil conditions in the two growing seasons.

Under the two cultivated areas and combined across the two seasons, Line No. 2 was among the genotypes showing the longest grain filling period (GFP) while Line no. 13 was among the shortest GFP genotypes. On the other hand, the highest grain filling ratio (GFR) was observed by lines no. 10, 12 and 16 across the two soil conditions in the 1st season while lines no. 5, 17 and 18 showed the slowest GFR. In the 2nd season, lines no. 3, 7 and 14 had the longest GFR while lines no. 10, 12 and Sids 12 had the shortest GFR. In general, overall the three earliness characters (DH, DM and GFP), the wheat plants tended to mature early under the stress conditions. The current results are in agreement with those reported by Gadallah *et al.* (2017) who found that number of days to heading was decreased with the increasing of salinity levels. But, Al-Naggar *et al*, (2015 b,d) reported that there was lateness in maturity and heading due to the increase of salt stress to 9000 ppm NaCl in average 15 and 11 days, respectively. This conflict in the results may be due to the use of different tested genotypes, use of over dose of salt stress (9000 ppm NaCl), and their experiment were conducted in pots unlike the current field trial. The considerable variability among the tested genotypes for early characters provides a good chance to develop early cultivars of wheat crop.

With respect to plant height, line no.6, Giza 171 and Misr 2 were among the genotypes of tallest plants across the two soil conditions combined across the two growing seasons. The shortest plants were obtained by lines no. 8 and 10 in the 1st season under the two soil conditions while in the 2nd season, lines no. 11, 12 and 13 recorded the minimum plant height. As an overview of these results, it is clear that the wheat plants were dwarfed under the stress (salinity) conditions.

Table (6) also elucidates the yield components behavior under adequate and stress (salinity) conditions in the two growing seasons. These characters were dramatically influenced by the effects of salinity and growing season.

Table 6. Mean values of the studied characteristics for 24 wheat genotypes under normal (N) and salinity (S) conditions and their combined analysis in 2014 / 2015 and 2015 /2016 seasons.

Genotype	Days to heading						Days to maturity						Grain filling period (days)					
	2014 / 2015			2015 / 2016			2014 / 2015			2015 / 2016			2014 / 2015			2015 / 2016		
	N	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.
Line 1	91.7	85.7	88.7	96.0	92.3	94.2	145.3	134.7	140.0	151.0	142.7	146.8	53.7	49.0	51.3	55.0	50.3	52.7
Line 2	94.7	86.3	90.5	94.7	88.0	91.3	150.0	136.0	143.0	152.3	143.7	148.0	55.3	49.7	52.5	57.7	55.7	56.7
Line 3	98.7	89.0	93.8	101.7	89.0	95.3	151.0	136.3	143.7	155.3	145.0	150.2	52.3	47.3	49.8	53.7	56.0	54.8
Line 4	99.0	88.3	93.7	96.7	92.7	94.7	152.0	136.7	144.3	153.3	141.3	147.3	53.0	48.3	50.7	56.7	48.7	52.7
Line 5	97.0	90.0	93.5	97.3	90.3	93.8	148.3	136.0	142.2	147.3	140.0	143.7	51.3	46.0	48.7	50.0	49.7	49.8
Line 6	96.3	86.7	91.5	101.3	96.0	98.7	143.0	137.7	140.3	156.3	144.5	150.4	46.7	51.0	48.8	55.0	48.5	51.8
Line 7	104.0	93.3	98.7	101.0	93.3	97.2	155.7	139.3	147.5	147.7	139.7	143.7	51.7	46.0	48.8	46.7	46.3	46.5
Line 8	99.0	92.7	95.8	96.3	92.0	94.2	145.0	138.0	141.5	154.7	145.7	150.2	46.0	45.3	45.7	58.3	53.7	56.0
Line 9	95.7	88.3	92.0	96.0	93.7	94.8	146.3	138.0	142.2	153.0	142.3	147.7	50.7	49.7	50.2	57.0	48.7	52.8
Line 10	99.0	90.3	94.7	93.7	88.0	90.8	151.0	136.3	143.7	154.0	143.0	148.5	52.0	46.0	49.0	60.3	55.0	57.7
Line 11	95.3	89.7	92.5	101.3	93.7	97.5	144.3	136.3	140.3	150.7	144.0	147.3	49.0	46.7	47.8	49.3	50.3	49.8
Line 12	95.0	90.3	92.7	94.3	90.0	92.2	144.7	135.3	140.0	150.0	146.0	148.0	49.7	45.0	47.3	55.7	56.0	55.8
Line 13	94.3	91.3	92.8	97.0	90.0	93.5	144.7	135.3	140.0	145.3	139.3	142.3	50.3	44.0	47.2	48.3	49.3	48.8
Line 14	91.7	85.3	88.5	99.7	89.7	94.7	144.0	137.7	140.8	139.3	140.7	140.0	52.3	52.3	52.3	39.7	51.0	45.3
Line 15	93.7	84.3	89.0	94.0	91.0	92.5	146.3	135.7	141.0	151.3	142.7	147.0	52.7	51.3	52.0	57.3	51.7	54.5
Line16	97.7	94.3	96.0	98.3	91.0	94.7	155.0	139.7	147.3	155.3	148.0	151.7	57.3	45.3	51.3	57.0	57.0	57.0
Line 17	94.7	87.7	91.2	98.0	90.3	94.2	140.7	137.0	138.8	153.0	144.7	148.8	46.0	49.3	47.7	55.0	54.3	54.7
Line 18	94.3	89.7	92.0	92.3	86.0	89.2	146.3	136.3	141.3	147.3	142.0	144.7	52.0	46.7	49.3	55.0	56.0	55.5
Line 19	103.7	94.0	98.8	96.0	90.3	93.2	155.7	140.3	148.0	152.0	143.3	147.7	52.0	46.3	49.2	56.0	53.0	54.5
Line 20	99.7	95.3	97.5	92.3	93.0	92.7	150.3	139.7	145.0	154.7	141.0	147.8	50.7	44.3	47.5	62.3	48.0	55.2
Sids 12	93.0	87.7	90.3	94.0	92.7	93.3	143.7	135.7	139.7	147.0	142.0	144.5	50.7	48.0	49.3	53.0	49.3	51.2
Misr 1	95.0	91.3	93.2	96.7	91.3	94.0	144.0	138.3	141.2	149.0	148.0	148.5	49.0	47.0	48.0	52.3	56.7	54.5
Giza 171	98.3	87.7	93.0	98.3	91.3	94.8	152.0	135.7	143.8	156.0	147.3	151.7	53.7	48.0	50.8	57.7	56.0	56.8
Misr 2	102.0	93.0	97.5	99.3	92.7	96.0	154.3	139.3	146.8	156.7	146.7	151.7	52.3	46.3	49.3	57.3	54.0	55.7
Mean	96.81	89.68	93.2	96.93	91.18	94.1	148.1	137.1	142.6	151.4	143.5	147.4	51.26	47.46	49.4	54.43	52.3	53.4
Max	104.0	95.3	98.8	101.7	96.0	98.7	155.7	140.3	148.0	156.7	148.0	151.7	57.3	52.3	52.5	62.3	57.0	57.7
Min	91.7	84.3	88.5	92.3	86.0	89.2	140.7	134.7	138.8	139.3	139.3	140.0	46.0	44.0	45.7	39.7	46.3	45.3
Range	12.3	11.0	10.3	9.3	10.0	9.5	15.0	5.7	9.2	17.3	8.7	11.7	11.3	8.3	6.8	22.7	10.7	12.3
CV%	2.51			2.28			1.77			1.76			6.21			6.58		
LSD 0.05 G	3.75	3.94	2.62	3.7	3.3	2.64	5.21	2.7	2.9	4.4	5.38	2.97	5.68	4.29	2.42	8.04	5.5	4.29
LSD 0.05 S	**			**			**			**			**			**		
LSD 0.05 S × G	3.79			3.48			4.1			4.2			3.42			6.06		

* and** : Significant and highly significant at 0.01 probability level.

- Underlined cells indicate the lowest values while bold and underlined cells indicate the highest values.

In the 1st season, lines no. 11, 16 and Misr2 produced the maximum number of spikes/m2 (SM) while line no. 20 gave the minimum SM under the optimal conditions. Under the saline soils, the highest SM was obtained by lines no. 7, 18 and Sids12 while the lowest SM was obtained by lines no. 4, 10 and 12.

In the 2nd season, under the normal conditions, it is obvious that lines no. 4, 8 and Misr1 produced the highest SM while the lowest SM belonged to line no. 1, Sids12 and Giza171. Under the saline soil, lines 5 and 6 gave the maximum (SM) while lines no. 12, 13 and 20 gave the minimum (SM).

Results showed that the two sets of genotypes (lines no.3, 14 and Sids12) and (lines no.4, 17 and Misr1) produced the profuse number of kernels/spike (KS) under normal and saline soils in the 1st season, respectively, while the two sets of genotypes (lines no. 4, 7 and 15) and (lines no. 9, 12 and Sids12) had the lowest KS, respectively. In the 2nd season, the two sets of genotypes (lines no. 11, 17 and Misr1) and (lines no. 1, 6 and 8) gave the maximum KS under normal and saline soils, respectively while the two sets of genotypes (lines no. 12, 15 and Giza171) and (lines no. 3, 14 and Misr2) had the lowest KS, respectively. Gadallah *et al.* (2017) mentioned that there were significant variations with all agronomical and physiological character, as influenced by salinity levels, cultivars and the interaction between them, except number of grains/spike which was not affected by the interaction. They also showed that the wheat cultivars responded differently either within the same, or among, the salinity levels for all studied character except number of grains/spike but in general, all studied agronomical character were decreased with the increasing of salinity levels.

With regard to the weight of 1000 kernels (KW), Giza171 gave the heaviest weight under optimal and stressed soils in the 1st season while lines no. 6 and 19 had the lightest weight (KW) under normal and saline soils, respectively. In the 2nd season and across the two soil conditions, the heaviest kernel weight (KW) was obtained by lines no. 12, lines no lines no 13 and 20 while the lightest weight was gained by lines no. 6 and lines no 10.

Since the aim of this research is to identify the high yielding and salinity tolerant genotypes, it would be better to focus the discussion on the genotypes that gave the profuse grain yield in the two (normal and saline) soils. Results revealed that lines no. 5 and 18 out-yielded the profuse grain yield over the two soil conditions in the 1st season, while line no. 12 had the least grain yield. In the 2nd season and across the two soil conditions, the highest grain yield values were obtained by line no. 3 and Misr2, while Sids12 gave the lowest grain yield values. The aforementioned results showed that there are some tested lines that have already surpassed the check cultivars for most studied characteristics, indicating their magnitude as promising genotypes that may be used in breeding programs of wheat crop. The current results are similar to the findings obtained by Al-Ashkar and El-Kafafi (2014), Al-Naggar *et al.* (2015 b,d), Hassan *et al.* (2015), and Ragab and Taha (2016).

Genetic parameters

Estimates of phenotypic (PCV%) and genotypic (GCV%) coefficients of variation, broad sense heritability (hb2), and genetic advance as a percent of the mean (GA %) for the studied characters under the two sites (normal and salt) are presented in Table 7.

In general, the values of (PCV%) were slightly higher than their corresponding values of (GCV%) for all studied character, indicating that the variations among tested genotypes were mostly attributed to genetic makeup rather than environmental effects at the two sites.

Cont. Table 6.

Genotype	Grain filling rate (g/m⁻¹/day⁻¹)						Plant height (cm)						No. of spikes/m²					
	2014 / 2015			2015 / 2016			2014 / 2015			2015 / 2016			2014 / 2015			2015 / 2016		
	N	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.
Line 1	22.8	8.4	15.6	16.1	9.7	12.9	116.7	78.3	97.5	125.0	93.3	109.2	400.0	166.6	283.3	435.6	291.1	363.3
Line 2	17.4	11.1	14.2	15.2	14.1	14.6	115.0	83.3	99.2	111.7	98.3	105.0	352.2	188.4	270.3	478.9	267.8	373.3
Line 3	20.3	7.6	14.0	21.4	15.5	18.5	115.0	83.3	99.2	110.0	96.7	103.3	442.2	144.6	293.4	568.9	326.7	447.8
Line 4	20.4	7.6	14.0	15.3	12.7	14.0	105.0	85.0	95.0	113.3	91.7	102.5	503.3	113.7	308.5	695.6	292.2	493.9
Line 5	22.9	12.8	17.9	19.2	14.1	16.7	120.0	85.0	102.5	121.7	96.7	109.2	345.6	238.2	291.9	526.7	438.9	482.8
Line 6	21.9	10.4	16.1	15.4	13.9	14.6	115.0	95.0	105.0	116.7	102.5	109.6	516.7	228.6	372.7	543.3	411.7	477.5
Line 7	20.2	13.2	16.7	20.8	14.8	17.8	108.3	93.3	100.8	110.0	88.3	99.2	477.8	274.3	376.0	625.6	347.8	486.7
Line 8	21.9	8.7	15.3	15.3	12.4	13.9	106.7	76.7	91.7	106.7	90.0	98.3	408.9	166.8	287.8	651.1	260.0	455.6
Line 9	21.5	8.5	15.0	16.0	9.6	12.8	115.0	88.3	101.7	120.0	96.7	108.3	472.2	192.7	332.5	520.0	371.1	445.6
Line 10	20.5	7.4	13.9	14.5	9.8	12.2	101.7	80.0	90.8	105.0	86.7	95.8	458.5	139.4	298.9	542.2	307.8	425.0
Line 11	21.7	8.7	15.2	18.1	9.4	13.8	100.0	86.7	93.3	106.7	81.7	94.2	533.3	149.5	341.4	575.6	305.6	440.6
Line 12	17.5	6.3	11.9	15.6	9.0	12.3	105.0	86.7	95.8	101.7	86.7	94.2	437.8	122.1	279.9	537.8	251.1	394.4
Line 13	19.0	11.4	15.2	19.9	14.3	17.1	106.7	81.7	94.2	101.7	86.7	94.2	380.0	225.1	302.5	595.6	231.1	413.3
Line 14	19.7	8.9	14.3	25.7	12.3	19.0	110.0	81.7	95.8	111.7	83.3	97.5	531.1	159.4	345.2	494.4	285.6	390.0
Line 15	21.1	8.6	14.9	17.1	10.7	13.9	106.7	86.7	96.7	108.3	91.7	100.0	491.1	175.4	333.3	574.4	250.0	412.2
Line16	16.2	10.0	13.1	18.0	12.8	15.4	105.0	85.0	95.0	106.7	88.3	97.5	565.6	161.6	363.6	552.2	302.2	427.2
Line 17	24.1	11.6	17.9	16.0	14.8	15.4	111.7	86.7	99.2	110.0	95.0	102.5	416.7	194.1	305.4	474.4	342.2	408.3
Line 18	21.9	12.3	17.1	18.7	11.3	15.0	108.3	81.7	95.0	120.0	88.3	104.2	493.3	252.2	372.8	637.8	322.2	480.0
Line 19	21.1	9.3	15.2	19.1	12.7	15.9	111.7	78.3	95.0	113.3	93.3	103.3	411.1	196.4	303.8	525.6	342.2	433.9
Line 20	17.7	11.9	14.8	16.4	9.2	12.8	110.0	91.7	100.8	113.3	90.0	101.7	297.8	192.1	244.9	500.0	170.0	335.0
Sids 12	21.3	10.7	16.0	14.9	7.6	11.2	108.3	90.0	99.2	106.7	88.3	97.5	402.2	270.3	336.3	456.7	173.7	315.2
Misr 1	24.0	9.5	16.7	21.1	12.4	16.8	111.7	90.0	100.8	108.3	93.3	100.8	513.3	150.6	332.0	642.2	245.6	443.9
Giza 171	18.8	10.1	14.5	16.3	11.4	13.9	118.3	88.3	103.3	116.7	105.0	110.8	437.8	143.8	290.8	451.1	243.3	347.2
Misr 2	22.5	8.5	15.5	18.2	14.9	16.6	125.0	86.7	105.8	123.3	103.3	113.3	577.8	196.6	387.2	602.2	378.9	490.6
Mean	20.7	9.7	15.2	17.7	12.1	14.9	110.7	85.4	98.1	112.0	92.3	102.2	452.8	185.1	318.9	550.3	298.3	424.3
Max	24.1	13.2	17.9	25.7	15.5	19.0	125.0	95.0	105.8	125.0	105.0	113.3	577.8	274.3	387.2	695.6	438.9	493.9
Min	16.2	6.3	11.9	14.5	7.6	11.2	100.0	76.7	90.8	101.7	81.7	94.2	297.8	113.7	244.9	435.6	170.0	315.2
Range	7.9	6.9	5.9	11.3	6.9	7.8	25.0	18.3	15.0	23.3	23.3	19.2	280.0	160.6	142.3	260.0	268.9	178.7
CV%		13			14.92			5.5			4.6			13.2			16.0	
LSD 0.05 G	4.76	2.88	4.4	5.2	3.37	5.3	8.39	9.2	601	8.97	6	5.3	82.42	52.9	48.3	121.2	100.5	77.7
LSD 0.05 S		**			**			**			**			**			**	
LSD 0.05 SxG		6.2			7.5			8.7			7.5			68.3			109.8	

* and** : Significant and highly significant at 0.01 probability level.

- Underlined cells indicate the lowest values while bold and underlined cells indicate the highest values.

Cont. Table 6.

Genotype	No. of kernels per spike						1000-kernel weight						Grain yield					
	2014 / 2015			2015 / 2016			2014 / 2015			2015 / 2016			2014 / 2015			2015 / 2016		
	N	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.
Line 1	57.0	41.2	49.1	50.1	43.9	47.0	44.6	45.7	45.1	39.2	37.4	38.3	34.2	11.5	22.9	24.6	12.7	18.6
Line 2	66.0	44.0	55.0	57.4	41.5	49.4	43.5	49.0	46.3	41.5	40.2	40.8	27.0	15.3	21.1	24.3	19.2	21.8
Line 3	70.2	40.7	55.5	50.8	36.8	43.8	46.4	45.7	46.0	36.0	48.7	42.4	29.8	10.1	19.9	32.0	18.8	25.4
Line 4	42.1	52.4	47.3	48.9	43.3	46.1	49.9	45.6	47.7	38.8	39.0	38.9	30.1	10.2	20.2	24.3	15.8	20.0
Line 5	52.1	45.7	48.9	51.6	38.8	45.2	44.4	42.0	43.2	38.7	38.9	38.8	32.9	16.5	24.7	26.9	16.9	21.9
Line 6	60.3	38.7	49.5	58.0	43.9	50.9	35.9	44.7	40.3	36.7	33.3	35.0	28.4	14.8	21.6	23.7	16.6	20.2
Line 7	46.1	40.2	43.2	44.6	37.9	41.3	42.1	43.2	42.7	38.7	39.7	39.2	29.2	16.9	23.1	26.4	16.2	21.3
Line 8	55.2	42.0	48.6	50.8	43.7	47.3	39.9	42.2	41.1	39.4	35.5	37.5	28.0	11.0	19.5	24.9	17.2	21.0
Line 9	58.3	37.3	47.8	51.7	42.1	46.9	42.6	44.0	43.3	36.6	38.1	37.3	30.5	11.9	21.2	25.4	12.5	18.9
Line 10	60.9	43.3	52.1	57.2	42.9	50.1	39.8	43.3	41.6	37.4	35.4	36.4	29.8	9.5	19.7	24.5	13.6	19.0
Line 11	58.8	42.0	50.4	58.3	38.4	48.3	41.2	49.0	45.1	41.1	28.2	34.6	29.6	11.2	20.4	24.7	11.3	18.0
Line 12	58.1	37.6	47.9	43.8	41.9	42.9	47.9	41.2	44.6	42.6	45.7	44.2	24.3	7.9	16.1	24.3	13.1	18.7
Line 13	56.3	47.7	52.0	47.4	38.3	42.8	41.5	40.6	41.1	48.1	42.6	45.3	26.7	14.1	20.4	26.6	16.9	21.8
Line 14	68.4	43.9	56.2	48.7	36.7	42.7	42.5	47.8	45.2	40.7	38.8	39.8	28.9	12.6	20.7	28.6	14.0	21.3
Line 15	48.0	44.3	46.2	41.4	39.0	40.2	41.9	43.5	42.7	39.4	39.4	39.4	31.2	12.3	21.7	27.4	14.5	20.9
Line16	58.9	48.4	53.7	57.2	41.6	49.4	43.8	42.7	43.3	41.2	37.5	39.4	25.9	12.7	19.3	28.7	17.8	23.2
Line 17	52.4	49.1	50.7	59.1	39.7	49.4	42.4	44.8	43.6	41.4	35.4	38.4	31.0	16.0	23.5	24.6	19.4	22.0
Line 18	53.5	43.4	48.5	49.3	39.4	44.3	42.0	44.3	43.2	42.0	38.7	40.3	31.8	16.2	24.0	28.8	15.8	22.3
Line 19	61.3	47.8	54.6	54.8	37.4	46.1	45.6	32.8	39.2	45.4	40.8	43.1	30.6	12.1	21.4	29.8	16.7	23.3
Line 20	62.1	39.1	50.6	57.7	39.4	48.5	43.0	44.3	43.7	45.7	43.2	44.5	25.1	14.7	19.9	28.6	12.5	20.5
Sids 12	75.0	38.2	56.6	51.0	39.0	45.0	45.6	44.3	45.0	40.0	38.2	39.1	30.1	14.6	22.3	22.0	10.2	16.1
Misr 1	60.3	48.9	54.6	61.0	40.4	50.7	48.6	45.3	46.9	45.6	40.2	42.9	32.0	12.5	22.2	30.7	17.6	24.2
Giza171	55.6	42.3	49.0	44.6	43.3	43.9	51.5	50.2	50.9	41.2	41.8	41.5	28.3	13.7	21.0	26.3	15.7	21.0
Misr 2	66.0	44.1	55.1	56.8	30.9	43.9	42.4	38.7	40.5	39.9	36.4	38.1	33.0	11.0	22.0	29.3	19.7	24.5
Mean	58.5	43.4	50.9	52.2	40.0	46.1	43.7	44.0	43.8	40.7	38.9	39.8	29.5	12.9	21.2	26.6	15.6	21.1
Max	75.0	52.4	56.6	61.0	43.9	50.9	51.5	50.2	50.9	48.1	48.7	45.3	33.0	16.9	24.7	32.0	19.7	25.4
Min	42.1	37.3	43.2	41.4	30.9	40.2	35.9	32.8	39.2	36.0	28.2	34.6	24.3	7.9	16.1	22.0	10.2	16.1
Range	32.9	15.1	13.5	19.6	12.9	10.7	15.6	17.4	11.6	12.1	20.4	10.7	8.7	9.1	8.6	10.0	9.5	9.3
CV%		10.4			11.5			7.0			8.6			10.6			12.4	
LSD 0.05 G	10.23	6.1	6.1	10.4	5.3	6.1	5.43	4.7	3.5	5.21	6.0	3.9	3.64	3.7	2.6	4.59	4.0	3.0
LSD 0.05 S.		**			**			NS			*			**			**	
LSD 0.05 SxG		8.6			8.6			5.0			5.5			3.6			4.2	

* and** : Significant and highly significant at 0.01 probability level.

- Underlined cells indicate the lowest values while bold and underlined cells indicate the highest values.

In accordance, the selection among the studied genotypes would be effective to improve these characters. Meanwhile, moderate values of (PCV% and GCV%) were only observed under the saline site with grain filing ratio (9.09 and 7.08) and number of grains/spike (11.83 and 10.38), respectively. On the other hand, the characters of days to heading, days to maturity, grain filling period, plant height, and 1000 grain weight recorded low estimates of PCV and GCV in the two studied sites.

It is important to emphasize that, without considering genetic advance (GA), the heritability values (h2) would not be practically valuable in the selection that depends on phenotypic appearance. Johnson *et al* (1955) confirmed that heritability estimates in conjunction with genetic advance would give more reliable index of selection value.

In the present study, the broad-sense heritability percentages (hb2) ranged from 61 for grain filing ratio and grain yield to 86 for plant height under normal conditions, while it ranged from 38 for number of grains/spike to 72 for plant height under saline site conditions. The values of genetic advance (GA based on 5 % selection intensity) ranged from 3.90 for days to heading to 18.77 for number of spikes/m2 in normal site whereas it ranged from 1.54 for days to maturity to 25.85 for number of spikes/m2 in salt site.

Maximum percentages of broad sense heritability (hb2) coupled with their corresponding genetic advance (GA) values at 5% selection intensity were obtained by number of spikes/m2 (77 and 18.77) and number of grains/spike (73 and 14.71) in the adequate site, respectively. Regarding the salt site, the grain filing ratio (71 and 20.90), number of spikes/m2 (70 and 25.85) and grain yield (68 and 19.23) recorded the highest values of hb2 and GA, respectively. This result indicated the importance of the additive gene effects, so, the selection in early generations would be effective to develop these characters.

Although, plant height recorded the highest broad sense heritability percentages (86 and 72), but it accompanied with moderate genetic advance value (9.40 and 7.19 at 5% selection intensity) in adequate and salt conditions, respectively. Days to heading (75 and 3.90) and days to maturity (81and 4.10) exhibited high broad sense heritability (hb2) but they were coupled with low genetic advance values in the adequate site, respectively. The smallest values of heritability and genetic advance were recorded by grain filling period and the weight of 1000 grains. From the above results, it is obvious the limited scope for improvement of these character among the studied genotypes. The current conclusions are supported by Al-Naggar, *et al*. (2015 b,d), Hassan *et al*. (2015), Mohammadi (2016) who confirmed that plant breeders can safely make their selection when they take in consideration high values of heritability and genetic advance.

Table 7. Genetic parameters of grain yield and its related characters computed from 24 wheat genotypes evaluated under normal and salt sites across the two seasons.

Characteristics	Genetic parameters									
	Grand mean		PCV (%)		GCV (%)		h_b^2 (%)		EGA (5 %)	
	Normal	Salt	Normal	Salt	Normal	Salt	Normal	Salt	Normal	Salt
DH	96.87	90.43	2.50	2.14	2.17	1.72	75	65	3.90	2.85
DM	145.72	138.31	2.44	1.18	2.20	0.94	81	63	4.10	1.54
GFP	48.82	47.95	5.98	3.88	4.76	2.77	63	51	7.83	4.07
GFR	42.56	20.80	9.09	14.25	7.08	12.02	61	71	11.37	20.90
PH	111.35	88.87	5.27	4.85	4.90	4.11	86	72	9.40	7.19
NOS/m²	501.54	241.69	11.83	18.02	10.38	15.03	77	70	18.77	25.85
NOG/S	55.32	41.68	9.83	7.53	8.37	4.66	73	38	14.71	5.94
1000 GW	42.21	41.41	6.03	5.74	4.88	4.13	66	52	8.16	6.14
GY	28.04	14.24	6.77	13.79	5.31	11.34	61	68	8.59	19.23

PCV%: Phenotypic coefficient of variations.   GCV%: Genotypic coefficient of variations.   Salt tolerance indices

Results in Table (8) presented the mean grain yield of genotypes under adequate (Yn) and salinity stress (Ys) conditions as well as the estimates of salt tolerance indices and their respective ranks. Under non-stress condition. The grain yield varied from 24.28 ard/fed for G12 to 31.34 ard/fed for Misr 1, with an average of 28.04 ard/fed while mean grain yield of genotypes under salt stressed site ranged from 10.48 ard/fed for G12 to 17.69 ard/fed for G17, with an average of 14.25 ard/fed. Mean grain yield in salinity stress conditions was 49.19 % lower than its respective yield under normal conditions. There were crucial differences among studied genotypes in respect to grain yield under non-stress and salt stress sites which demonstrates high genetic diversity among them that enabled us to screen salt tolerant genotypes.

The grain yields of tested genotypes under both normal and salt stress sites were formulated to calculate different sensitivity and tolerance indices (Table 7). Genotypes with high values of mean productivity (MP), harmonic mean (HM), geometric mean productivity (GMP), stress tolerance index (STI), yield index (YI), yield stability index (YSI), and modified stress tolerance index (MSTI) could be selected as salinity tolerant genotypes. However, genotypes with low values of tolerance index (TOL), stress susceptibility percentage index (SSPI), stress susceptibility index (SSI), and coefficient of variation (CVI) would be more tolerant to salt stress.

Table 8. Estimates of salinity tolerance indices (STI's) and their respective ranks of 24 bread wheat genotypes based on grain yield under adequate and salt and sites across the two seasons and Corresponding ranks.

Gen.	Grain yield				Salinity tolerance indices (STI)																					
	Yn	ranks	Ys	ranks	MP¹	ranks	HM¹	ranks	GMP¹	ranks	STI¹	ranks	YI¹	ranks	YSI¹	ranks	MSTI¹	ranks	TOL²	ranks	SSPI²	ranks	SSI²	ranks	CVI²	ranks
											Calculated values															
1	29.42	7	12.08	21	20.75	16	17.13	19	18.85	18	0.45	18	0.85	21	0.41	24	0.33	19	17.34	24	30.92	24	1.2	24	59.08	24
2	25.65	23	17.26	2	21.46	9	20.64	5	21.04	8	0.56	8	1.21	1	0.83	1	0.67	1	8.39	1	14.97	1	0.67	1	27.66	1
3	30.89	3	14.42	13	22.66	6	19.66	8	21.11	7	0.57	7	1.01	13	0.47	17	0.58	11	16.47	23	29.38	23	1.08	17	51.41	17
4	27.21	15	12.99	18	20.1	19	17.58	18	18.8	19	0.45	19	0.91	18	0.48	15	0.37	18	14.22	13	25.36	13	1.06	15	50.04	15
5	29.9	6	16.71	3	23.3	1	21.43	2	22.35	1	0.64	1	1.17	3	0.56	6	0.87	2	13.19	9	23.53	9	0.9	6	40.03	6
6	26.05	21	15.7	6	20.87	15	19.59	10	20.22	12	0.52	12	1.1	6	0.6	3	0.63	8	10.35	3	18.46	3	0.81	3	35.07	3
7	27.83	11	16.55	4	22.19	8	20.75	4	21.46	6	0.59	6	1.16	4	0.59	4	0.79	4	11.29	5	20.13	5	0.82	4	35.96	4
8	26.44	20	14.08	14	20.26	17	18.37	15	19.29	16	0.47	16	0.99	14	0.53	9	0.46	14	12.37	7	22.05	7	0.95	9	43.16	9
9	27.96	10	12.2	20	20.08	20	16.98	20	18.46	20	0.43	20	0.86	20	0.44	20	0.32	20	15.76	17	28.11	17	1.15	20	55.52	20
10	27.12	17	11.56	22	19.34	21	16.21	22	17.7	22	0.4	22	0.81	22	0.43	22	0.26	22	15.57	16	27.77	16	1.17	22	56.92	22
11	27.15	16	11.25	23	19.2	23	15.91	23	17.48	23	0.39	23	0.79	23	0.41	23	0.24	23	15.9	21	28.35	21	1.19	23	58.55	23
12	24.28	24	10.48	24	17.38	24	14.64	24	15.95	24	0.32	24	0.74	24	0.43	21	0.18	24	13.81	12	24.62	12	1.16	21	56.18	21
13	26.68	19	15.53	7	21.1	12	19.63	9	20.35	11	0.53	11	1.09	7	0.58	5	0.63	9	11.16	4	19.9	4	0.85	5	37.39	5
14	28.72	9	13.26	17	20.99	13	18.14	16	19.52	15	0.48	15	0.93	17	0.46	18	0.42	17	15.46	15	27.57	15	1.09	18	52.08	18
15	29.27	8	13.4	16	21.33	10	18.38	14	19.8	14	0.5	14	0.94	16	0.46	19	0.44	15	15.88	20	28.31	20	1.1	19	52.62	19
16	27.29	13	15.24	9	21.26	11	19.56	11	20.39	10	0.53	10	1.07	9	0.56	7	0.61	10	12.05	6	21.48	6	0.9	7	40.06	7
17	27.81	12	17.69	1	22.75	5	21.63	1	22.18	2	0.63	2	1.24	1	0.64	2	0.97	1	10.12	2	18.05	2	0.74	2	31.46	2
18	30.3	4	16.01	5	23.16	4	20.95	3	22.03	3	0.62	3	1.12	5	0.53	10	0.78	5	14.29	14	25.49	14	0.96	10	43.64	10
19	30.21	5	14.43	12	22.32	7	19.53	12	20.88	9	0.55	9	1.01	12	0.48	14	0.57	12	15.79	18	28.16	18	1.06	14	50.02	14
20	26.86	18	13.59	15	20.22	18	18.05	17	19.1	17	0.46	17	0.95	15	0.51	11	0.42	16	13.27	10	23.66	10	1	11	46.39	11
21	26.04	22	12.4	19	19.22	22	16.8	21	17.97	21	0.41	21	0.87	19	0.48	16	0.31	21	13.65	11	24.34	11	1.07	16	50.21	16
22	31.34	1	15.06	10	23.2	3	20.34	7	21.73	5	0.6	5	1.06	10	0.48	13	0.67	7	16.28	22	29.04	22	1.06	13	49.63	13
23	27.28	14	14.67	11	20.97	14	19.08	13	20	13	0.51	13	1.03	11	0.54	8	0.54	13	12.62	8	22.5	8	0.94	8	42.53	8
24	31.14	2	15.34	8	23.24	2	20.55	6	21.86	4	0.61	4	1.08	8	0.49	12	0.7	6	15.8	19	28.18	19	1.03	12	48.07	12

1- The highest value of this index indicates the more tolerant genotypes
2- The lowest value of this index indicates the more tolerant genotypes

It is noted that the two indices of GMP and STI gave similar ranks for salt tolerance where the three genotypes G5, G17, G18 were identified as salt tolerant genotypes. These genotypes had greater values of GMP and STI while G10, G11, and G12 were identified as susceptible genotypes, because of their low values for GMP and STI. In the same context, the two indices TOL and SSPI ranked the studied genotypes, for salt tolerance, in the same order. Using these

two indices, the genotypes G2, G17 and G6 were more tolerant for salinity stress while G1, G3 and G22 were more sensitive compared to the others. As well as, similar ranking pattern of tolerant/susceptible genotypes were obtained by the three indices of YSI, SSI and CVI. Accordingly, G2, G17 and G6 were preferred to be cultivated under the salinity conditions while G1, G10 and G12 were more susceptible for salinity.

The similarity among pairs or three indices in ranking genotypes for salt tolerance may be attributed to that these indices are function of each other as shown in Table (2). However, the three indices MP, HM and MSTI gave a different arrangement of genotypes for their tolerance to salinity. A similar trend of results was found by Asadi *et al.* (2012), Al-Ashkar and El-Kafafi (2014), Saad *et al.*, (2014), Al-Naggar *et al.* (2015 a,c), Hassan *et al.* (2015), Mohammadi (2016), Singh *et al.* (2015 b) and Ali and El-Sadek (2016).

On the other hand, yield index (YI) ranked the studied genotypes for salt tolerance exactly like the average grain yield under the stress (salt) conditions (Ys) which means that this index (YI) may be useless or unprofitable because it could not provide further information than the grain yield (Ys) itself.

The interrelationships and overlap among salinity tolerance indices

This part of this study aimed to explore the similarity/dissimilarity among the salinity tolerance indices that are closely related in ranking the tested wheat genotypes. To achieve this goal, Spearman rank correlation coefficients (r) among salinity tolerance indices as well as mean grain yield (under adequate and salt sites) were estimated and presented in Table (9). The rank correlation was used instead of Pearson coefficient of correlation because the salinity tolerance indices (estimates not measured values) cannot be assumed to be normally distributed. When perfect correlation coefficient (r =1) was obtained between two salinity tolerance indices, they would be considered identical indices. However, if the association between two salinity tolerance indices was very strong (highly significant but not perfect, 0.75 < r ≤1), these two indices would be as equivalent.

Table 9. Spearman's rank correlation coefficients among grain yield (under adequate and salt stressed sites), and their corresponding salt tolerance indices (STI's).

Indices	Y_n	Y_s	MP	H M	GMP	STI	YI	YSI	MSTI	TOL	SSPI	SSI	CV
Y_n	1												
Y_s	0.20	1											
MP	0.71**	0.80**	1										
H M	0.43*	0.96**	0.91**	1									
GMP	0.57**	0.90**	0.97**	0.98**	1								
STI	0.57**	0.90**	0.97**	0.98**	1**	1							
YI	0.20	1**	0.79**	0.96**	0.91**	0.91**	1						
YSI	-0.17	0.91**	0.50*	0.76**	0.66**	0.67**	0.91**	1					
MSTI	0.35	0.98**	0.88**	0.99**	0.96**	0.96**	0.98**	0.82**	1				
TOL	0.61**	-0.59**	-0.02	-0.37	-0.22	-0.23	-0.59**	-0.84**	-0.45*	1			
SSPI	0.61**	-0.59**	-0.02	-0.37	-0.22	-0.23	-0.59**	-0.84**	-0.45*	1**	1		
SSI	0.17	-0.91**	-0.50*	-0.76**	-0.67**	-0.67**	-0.91**	-1**	-0.82**	0.84**	0.84**	1	
CVI	0.17	-0.91**	-0.52**	-0.76**	-0.67**	-0.69**	-0.91**	-1**	-0.84**	0.83**	0.83**	1**	1

* and** : Significant and highly significant at 0.01 probability level, respectively

On the other hand, principal components (PC) analysis based on Spearman's rank correlation matrix, was performed. For best visualization, the loadings of the first two principal components were plotted against each other. The results are diagrammatically displayed as biplot graph of PC1 and PC2 in Figure (1). It is noted that the first two PC`s contributed by 99.5 % (88.1 and 11.4 % by PC1 and PC2, respectively) of the total variance structure, indicating that the biplot graph is characterized by a goodness of fit and successfully reflected the linear relations among stress tolerance indices.

The results showed that the yield under salt-stressed site (Ys) had a very weak association (r = 0.20) with the yield under optimal conditions (Yn), indicating that high potential yield under non-stressed conditions does not necessarily result in high yield under the stressed salinity conditions and *vice versa*. Therefore, indirect selection for a given trait based on the results of favorable conditions will not be enough or efficient.

Based on the rank correlation matrix (Table 9), it is observed that Yn was highly significant associated with each of MP, GMP, STI, TOL and SSPI, but with correlation coefficients of r < 0.75, while Ys was highly significant associated (r > 0.75) with all salinity tolerance indices, except TOL and SSPI. However, the grain yield under salt

stressed site (Ys) was perfectly associated (r = 1) with YI. These results indicated that the average grain yield under stress conditions (Ys) is the effective part in computing the most stress tolerance indices compared to (Yn). Graphically, Ys already was located close to the most stress tolerant indices whether with an acute angle (positive correlation) or (obtuse angle (negative correlation). Because the perfect association between Ys and YI, they occupied the same dot on the biplot graph.

Concerning the relationships among stress tolerance indices, the results appeared that there were significant (p ≤ 0.01) and positive associations between each pair of the indices MP, HM, GMP, STI, YI, YSI and MSTI. Therefore, their dots were closely located on the biplot graph with acute angles. Significant (p ≤ 0.01) and negative correlation coefficients (obtuse angles) were observed between YSI and each of TOL and SSPI. The two indices of SSI and CV were negatively and highly significant associated (obtuse angles) with all other indices, except TOL and SSPI which had positive and highly significant association (acute angles).

Perfect and positive correlation coefficient (r = 1) were found between three pairs of indices [(STI and GMP), (SSPI and TOL) and (CVI and SSI)] where each one of the previous pairs occupied one dot on the biplot graph. The associations between YSI and each of SSI and CVI were

exactly equaled (-1) (fell on the same line by angle = 180°), indicating that the three indices are identical for ranking genotypes and they could be interchangeably used as a substitute for each other. Therefore, using these identical pairs of STI's together in the same study is considered a waste of time and effort. These results are consistent with those reported by Saad *et al.* (2014), Abd El-Mohsen *et al.* (2015), Singh *et al.* (2015 b), Ali and El-Sadek (2016) and Mohammadi *et al.* (2016).
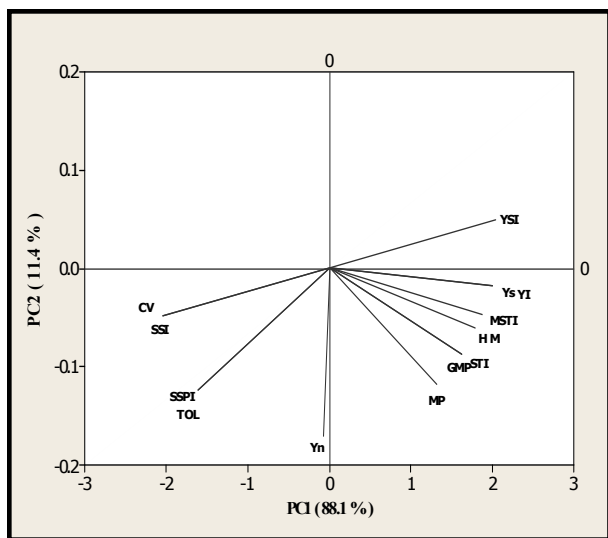

Fig. 1. Biplot graph of the first two principal component axes for 12 salt tolerance indices.

Cluster analysis

The genetic diversity among the tested genotypes is the key to get reliable and sustainable production of crops. The cluster analysis hierarchical classified genotypes into clusters which exhibit high homogeneity within a cluster and high heterogeneity between clusters. Within a group, genotypes show minimum variance and genetic distance, while between-groups, genotypes are dissimilar with maximum genetic distance.

In the present work, the similarity levels of the 24 wheat genotypes were estimated based on Yn, Ys and salinity tolerant indices. The genotypes were classified into five main groups (clusters) where each group contained the genotypes that showed similar yield potential and salinity tolerance. The clustering pattern of these genotypes is tabulated in Table 10 and diagrammatically displayed as dendrogram graph in Figure 2. Results showed that the main clusters are also divided into sub clusters except the 4th cluster which consisted of only one genotype (G12).

The first cluster included 9 genotypes (lines; 1, 4, 9, 10, 11, 14, 15, 20 and Sids 12) that had medium grain yield ranging from 26.86 to 29.42 ard/fed in the optimum soil and from 11.25 to 13.59 ard/fed in salt stressed soil with an average of 54.82 % as grain yield reduction and therefore they were sensitive to salinity (ranked between 14 and 24 for salt tolerance).

Six genotypes (lines; 3, 5, 18, 19, Misr 1 and Misr 2) were found among the second cluster that had the highest grain yields recording an average of 30.63 ard/fed in the adequate cultivated soil and 15.33 ard/fed in the salt soil. Unfortunately, these genotypes were sensitive to salinity making them less useful. Their grain yields were reduced by an average of 49.96 % when they cultivated under the salt stressed soil. They occupied the ranks between 4 and 15 for salt tolerance.

Table 10. Summary of hierarchical cluster analysis represents the classification of tested wheat genotypes based on grain yield and salt tolerance indices.

Cluster no.	Similarity level	Genotypes	Gain yield		Grain yield reduction %	Salt tolerance rank	Grain yield category	Salt tolerance degree
			Normal	Stress				
1	85.07	1	29.42	12.08	58.93	23	Moderate	Sensitive
		9	27.96	12.20	56.38	20		
		10	27.12	11.56	57.40	22		
		11	27.15	11.25	58.56	24		
		Sids 12	26.04	12.40	52.40	19		
		4	27.21	12.99	52.27	16		
		20	26.86	13.59	49.40	14		
		14	28.72	13.26	53.83	17		
		15	29.27	13.40	54.24	18		
		Mean	27.75	12.53	54.82			
2	87.80	3	30.89	14.42	53.32	15	High	Sensitive
		Misr 1	31.34	15.06	51.95	12		
		19	30.21	14.43	52.26	13		
		18	30.30	16.01	47.16	8		
		Misr 2	31.14	15.34	50.74	10		
		5	29.90	16.71	44.12	4		
		Mean	30.63	15.33	49.96			
3	88.26	6	26.05	15.70	39.74	5	Moderate	Moderate
		13	26.68	15.53	41.82	6		
		16	27.29	15.24	44.15	7		
		7	27.83	16.55	40.55	3		
		8	26.44	14.08	46.77	11		
		Giza 171	27.28	14.67	46.24	9		
		Mean	26.93	15.30	43.20			
4	82.38	12	24.28	10.48	56.86	21	Low	Sensitive
5	81.12	2	25.65	17.26	32.72	2	Moderate	Tolerant
		17	27.81	17.69	36.39	1		
		Mean	26.73	17.48	34.62			

The third cluster consisted of the genotypes (lines; 6, 7, 8, 13, 16 and Giza 171) that gave medium values of grain yield and acceptable degree of salt tolerance. These genotypes produced an average of 26.93 ard/fed under the non-stress conditions and 15.30 ard/fed under the stress conditions recording 43.20 % as grain yield reduction. They took place between the two ranks 3 and 11 in terms of tolerance to salinity stress.

The fourth croup contained one genotype (line 12) which was poorly performed considering each of grain yield and salt tolerance. It recorded the lowest value of grain yield (24.28 ard/fed in the adequate cultivated field and 10.48 ard/fed in the saline field reflecting grain yield reduction of 56.86 %. Accordingly, it is the worst item among the studied genotypes, recording the rank 21 for salt tolerance.

The two promising genotypes line 2 and line 17 formed the fifth cluster. They were characterized by medium grain yield (an average of 26.73 ard/fed in normal soil and 17.48 ard/fed in the salt stressed site recording the lowest grain yield reduction (34.62 %). They occupied the first and second ranks among the tolerant genotypes for salinity stress.

In the light of previous results that exhibited the presence of considerable genetic diversity among the tested genotypes for grain yield and salt tolerance, it gave a good chance to achieve sufficient scope for genotypic improvement of wheat through the hybridization among genotypes taken from divergent clusters (Saad *et al.* 2014, Abd El-Mohsen *et al.* 2015 and Singh *et al.* 2015 b).
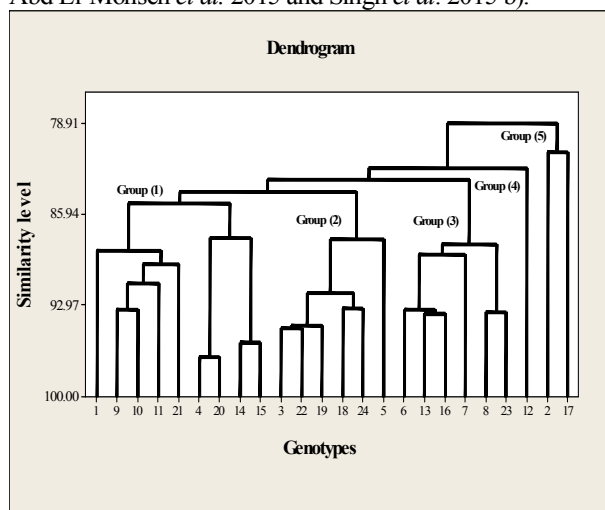

Fig. 2. Dendrogram showing the similarity among 24 wheat genotypes based on grain yield and salt tolerance indices

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تقييم بعض التراكيب الوراثية من قمح الخبز تحت ظروف ملوحة التربة باستخدام مؤشرات التحمل وتحليل المتغيرات المتعددة

محمد عبد الكريم حسن درويش[1] ، وليد محمد فارس[2] و إيمان محمود احمد حسين[2]

[1] قسم بحوث القمح ــ معهد بحوث المحاصيل الحقلية ـ مركز البحوث الزراعية.

[2] المعمل المركزي لبحوث التصميم والتحليل الإحصائيــ مركز البحوث الزراعية.

أجري هذا البحث بمحطة البحوث الزراعية بسخا خلال موسمي الزراعة 2015/2014 و 2016/2015 لتقييم 24 تركيب وراثي من قمح الخبز وذلك في موقعين منفصلين أحدهما تحت الظروف العادية و والآخر تحت ظروف الاجهاد الملحي والموقعين بمحطة بحوث سخا. وتم تنفيذ التجربة في تصميم القطاعات الكاملة العشوائية في ثلاث مكررات. تم إستخدام متوسط محصول الحبوب الناتج من التجربتين (الظروف العادية وظروف الاجهاد الملحي) فى تقدير 11 دليل لتحمل الاجهاد. كذلك تم إستخدام التحليل العنقودى فى تحديد مدى التقارب والتباعد بين التراكيب الوراثية المختبرة وذلك باستخدام محصول الحبوب ومدى القدرة على تحمل الاجهاد. أشارت النتائج إلى أن أعلى القيم من كفاءة التوريث العامة مصحوبة بأعلى قيم للتحسن الوراثي المتوقع قد تم الحصول عليها لصفات عدد السنابل/م2 وعدد حبوب/السنبلة وذلك تحت الظروف العادية بينما اعطت صفات عدد السنابل/م2 ومحصول الحبوب أعلى القيم تحت ظروف الاجهاد الملحى. أظهرت الدراسة إختلاف الآداء المحصولى للتراكيب الوراثية المختبرة تحت الظروف العادية وتحت ظروف الاجهاد الملحى حيث اعطت قيم متباينة لأدلة تحمل الاجهاد مما يشير إلى وجود تنوع وراثى فيما بينها مما يتيح إمكانية الإنتخاب بين هذه التراكيب الوراثية لكل من صفتى المحصول العالى وتحمل الإجهاد الملحى. أوضحت نتائج تحليل كل من معامل الارتباط وطريقة المكونات الأساسية وجود إرتباط موجب تام بين ثلاثة أزواج من أدلة تحمل الاجهاد وهى (المتوسط الهندسى للانتاجية GMP ، دليل تحمل الاجهاد STI) ، (دليل نسبة الحساسية للاجهاد SSPI ، دليل التحمل TOL) و (معامل الاختلاف CV ، دليل الحساسية للاجهاد SSI) حيث يعطى كل زوج من هذه الدلائل نتائج متطابقة بالنسبة لترتيب التراكيب الوراثية للقدرة على تحمل الاجهاد الملحى مما يشير إلى وجوب الاكتفاء باستخدام دليل واحد من الادلة المرتبطة وان استخدامهما معا يعتبر مضيعة للوقت والجهد. اتضح من نتائج التحليل العنقودى أن التراكيب الوراثية المختبرة أمكن تقسيمها إلى خمسة مجموعات (متشابهة فى داخلها) متباينة فيما بينها وذلك تبعا لصفة محصول الحبوب وأدلة تحمل الاجهاد. وقد تضمنت المجموعة الخامسة تحديدا على سلالتين مبشرتين (L 2 ، L 17) يتميزان بمحصول حبوب متوسط فى كل من التربة العادية والملحية كما انهما حققتا اقل نسبة انخفاض محصولى عند الزراعة فى التربة الملحية وبناء عليه فقد جاءت السلالتان فى المرتبة الاولى والثانية من حيث القدرة على تحمل الاجهاد الملحى. يتضح من نتائج هذه الدراسة ان التراكيب الوراثية المستخدمة تتميز بالتنوع الوراثى مما يمكن أن يساهم بشكل كبير في برامج تحسين محصول القمح وذلك عن طريق التهجين بين التراكيب الوراثية التى تتبع مجموعات (Clusters) مختلفة.