DEVELOPMENT OF SALT TOLERANT F₁ WHEAT CROSSES AND ANALYSIS OF THEIR GENETIC AND QUANTITATIVE TRAITS USING ONE WAY DIALLEL ANALYSIS

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Abstract

One of the most important restraining and abiotic stress factors for wheat crop cultivation is high soil salinity. This study was conducted at the greenhouse of Institute of Tropical Agriculture, Universiti Putra Malaysia during season 2017. The objective of study was to develop F₁ crosses as well as investigated of the genetic and agronomic performance of F₁ crosses under various concentrations of NaCl. The three salt susceptible wheat genotypes (Abo-Graib, Forat, and Dijla) and one high salt tolerant genotype (G8) were selected for crossing. The spikes of the parents were crossed in 4× 4 half diallel crosses to obtain a total of 6 [(4(4+1)/2] crosses. The obtained seeds were planted under four concentrations of NaCl (0, 50, 100 and 150 mM). In both parents and their F₁ crosses, grain yield exhibited positive correlation with spikes number/plant, grains number per spike and weight of 1000 grain. Abo-Graib G8, Dijla G8, and Forat G8 crosses showed superiority in grain yield related to the spikes number/plant, grains number per spike and the 1000 grain weight. Highly significant variances (p≤0.01), of both general and specific combining ability, were obtained which referred to important of both additive and non-additive gene effects for the above- mentioned traits. The estimated value of σ^2s was higher than its σ^2g for all five traits which indicated the preponderance of non-additive gene action. The traits were controlled by dominance effects because the ratio of σ^2g / σ^2s for all traits was less than one

*Keywords***:** Combining ability; diallel analysis; grain yield; wheat; NaCl

Introduction

High soil saltiness is one of the important factors that limit the productivity of major field crops (Chandra *et al.*, 2014; Cheeseman, 2016). In arid and semi-arid areas, accumulation of salts in soils leads to a high reduction of grain yield (Khaled *et al.*, 2016; Nouri *et al.*, 2017). Many negative impacts on the growth of a plant such as osmotic stress, ion toxicity, and nutritional imbalance or all of these factors are caused by salinity (Gupta and Huang, 2014; Cabot *et al.*, 2014). All these factors adversely affect the plant growth, physiological and biochemical metabolism (Pirasteh-Anosheh *et al.*, 2016; Hazman *et al.*, 2016). To achieve optimal food production in saline areas, the most convenient option is the development of salt tolerant crops/ genotypes (James *et al.*, 2011; Munns *et al.*, 2012). Estimates of combining ability are helpful in determining the wheat lines breeding value by proposing the proper utilization in a breeding program. In examing combining ability, the most commonly utilized experimental program is the diallel analysis. In this program, Sprague and Tatum (1942) introduced the meaning of GCA and SCA. The GCA is a measurement of the additive genic action, and the SCA is supposed to be a variation from additivity. Crossing a line to others lines supplies the performance mean of the line in all its combinations. This direction, when expressed as a change from the average of all crosses, is noun the line general combining ability. Any particular cross, then, has a predicted value which is the sum of the general combining abilities of its two parental lines. The cross may, however, deviate from this prospective value to a greater or lesser range. This variation is named the specific combining ability of the two

lines in combination. Statistically, the general combining abilities are main effects, and the specific combining ability is an interaction.In plant breeding, diallel crosses are used to acquire information inheritance of different traits, the study of general and specific combining ability, and heritability. Griffing (1956a) proposed four methods of diallel crossing: Method 1 (full diallel). The parents, F₁, and reciprocals included (p² total entries, where p is the number of parents). Method 2 (half diallel). Parents and F₁'s included, but no reciprocals [p (p + l)/2 total entries]. Method 3 F₁'s and reciprocals included, but no parents (p² – P total entries) and Method 4. F₁'s included, but no reciprocals or parents [p (p-l)/2 total entries]. Particularly half or partial diallel is extensively used in crop breeding programs (Yanchuk 1996). Understanding of general combining ability (GCA) and specific combining ability (SCA) is helpful in the selection of parents. Combining ability is used for the recognition of parents with better general combining ability and parental combinations with better specific combining ability. Masood *et al.* (2014a) indicated that the inbred lines perhaps utilized for the synthetic varieties development through pure line selection, selection of pedigree or recurrent backcross selection while higher specific combining ability indicated that the inbred lines might be used to develop hybrids to improve grain yield of wheat through heterosis breeding program. Masood *et al.* (2014b) concluded that the selection of suitable parents produce the highest weight of 1000 grain and grain yield per plant be used for the development of synthetic and hybrids. Masood *et al.* (2014c) clarified from these findings that combinations of viz., 9705 × AARI-11, 9703 × Millat-11 and 9705 × Millat-11 will be the best appropriate F₁ hybrid crosses, having best specific combining

ability for two traits each, to fit for breeding programs. Therefore, these parents and F_1 genotypes having superior performance can be further combined with other lines in the hybrid breeding programs or selection of the most appropriate parents based on their performance. Diallel mating gives information about the type of genetic actions controlling the plant traits in an F_1 generation (Harriman and Nwammadu, 2016). Additive and non-additive gene actions determine the prospect of possible utilization of heterosis of the hybrids (Hei *et al.*, 2016). This study aimed to develop F_1 crosses as well as investigated of the genetic and agronomic performance of F_1 crosses under various concentrations of NaCl.

Materials and Methods

In April 2017, four wheat genotypes namely Abo-Graib, Dijla, Forat (salt susceptible) and G8 (salt tolerant) which selected based on their salt tolerance were planted under controlled conditions during the growth period (18-35°C) and relative moisture between 50-60% in the greenhouse of Institute of Tropical Agriculture, Universiti Putra Malaysia (Table 1). The seeds were planted in a small plot grain drill at 300 plants per m^2 (Wajid *et al.*, 2004). In making crosses, the wheat spikes were emasculated 1-2 days before anthesis and immediately covered with glassine bags to prevent open pollination. Two days after emasculation the spikes of parents were crossed in 4× 4 half diallel crosses [(4 (4+1)/2] to obtain a total of six crosses (Table 2 and 3).

After that, the seeds of each F_1 cross and their parent were collected. Small pots containing Ultisol soil, gathered from the surface of the ground (0-15 cm) from the experimental fields at the Faculty of Agriculture, Universiti Putra Malaysia were used for planting the seeds. The chemical and physical properties of soil are described in Table 4. Soil pH was increased from 4.92 to 7 by adding 2 t/ha (2 g/pot) ground magnesium limestone (GML) (Fauziah, 2010). From each genotype, ten seeds per pot under four concentrations of NaCl (0 mM, 50 mM, 100 mM, and 150 mM) were planted. 10 × 4 factorial experiment in a Randomized Complete Block Design (RCBD) with three replications was used in this study. The N, P, and K concentration was maintained by adding 0.2 g NH_4NO_3 (200 kg/ha) and 0.2 g KH_2PO_4 (200 kg/ha) to every pot. A similar amount of these nutrients was added after 20, 40 and 60 days of sowing. At maturity stage, the studied traits were measured.

Table 1: A pedigree of wheat parents

Sr. No	Genotype	Pedigree
1	Abo – Graib (**Susceptible**)	Ajeeba x Inia 66R X Mexico 24
2	Dijla (**Susceptible**)	6H American genotypes x Maxipak
3	Forat (**Susceptible**)	5H American genotypes x Maxipak
4	G8 (**tolerant**)	F5 genotypes (ICARDA)

Table 2 : Crossing program

Varieties	Dijla ♂ (Susceptible)	Forat ♂ (Susceptible)	G8 ♂ (tolerant)
Abo-Graib ♀	F_1	F_1	F_1
Dijla ♀		F_1	F_1
Forat ♀			F_1

Table 3 : Progenies derived from crossing between their parents

Genotypes	
Abo-Graib	Parent
Dijla	Parent
Forat	Parent
G8	Parent
Abo-Graib Dijla	F_1 cross
Abo- Graib Forat	F_1 cross
Abo-Graib G8	F_1 cross
Dijla Forat	F_1 cross
Dijla G8	F_1 cross
Forat G8	F_1 cross

Table 4 : Chemical and physical properties of soil

Chemical and physical properties of soil	Amount
pH	4.92
Ec	2.10 mM
Bulk density	1.21 $g.cm^3$
Porosity	55.25%
Soil texture	Clay (clay = 57.20 microns, silt = 10.66 microns and sand = 32.14 microns)
Carbon	1.95%
Nitrogen	0.17
Sulfur	0.02
Na	0.02 cmol $(^+)$/kg
K	0.04 cmol $(^+)$/kg

Plant height (cm)

Ten plants height (cm) per experimental unit were measured. Then the mean of plant height was obtained by divided into ten.

Number of spikes per plant

The number of spikes of three plants from each experimental unit was calculated. Then, it was converted per plant.

Number of grain per spike

Ten Spikes from each experimental unit were threshed manually, and grains were separated and calculated. Then the number of grains was divided into ten to obtain a single spike grain number.

Grain yield per plant (g)

At maturity, three plants from each plot were harvested. The spikes also were threshed, and grains were separated and weighed. Then the grain yield (g) of the single plant was computed.

Statistical Analysis

ANOVA design was used for data analysis using SAS program version 9.4. Genotypes means were determined using the LSD (p≤0.01) (Steel and Torrie, 1980). GCA effects of the parents and SCA of the combinations were identified in the half-diallel cross following (Griffing, 1956b) using DIALLEL-SAS program adapted to SAS software version 9.4.

Results and Discussion

Grain yield and its components

Grain yield is the output of many developmental and physiological proceedings that take place during the plant growing stages. It is affected by the spikes number per unit area, grains number spike[-1] and grain weight (Bustos *et al.*, 2013). Therefore, phenotyping can be according to grain number per area unit (GN) and grain weight (GW) to realize variance in grain yield potential (Bustos *et al.*, 2013). According to the results in appendix 7, significant differences (p≤0.01) were presented in the plant height, the spikes number per plant, the grains number per spike, the weight of 1000 grains and the grain yield/plant amongst the six F_1 crosses and their parents under different concentrations of NaCl. The decline in the plant height, the grain yield per plant and its components coincided with increasing salt stress levels.

The control treatment (0 mM) exhibited the highest value of the plant height, the number of spikes/plant, the number of grain/spike, the weight of 1000 grain and the grain yield/plant (79.5 cm, 6.6, 61, 30.7 g and 12.5 g, respectively) (Table 5). While the high concentration of NaCl salt (100 mM) displayed the shortest value of plant height, the lowest number of spikes/plant, the lowest number of grain/spike, the lowest weight of 1000 grain and the lowest grain yield/plant (67 cm, 4.7, 55.6, 22.2 g and 6.2 g, respectively) (Table 5).

Table 5 : Mean comparison of five traits studied by LSD of four concentrations of NaCl

NaCl	Plant height (cm)	No. of spikes / plant	No. of grains / spike	Weight of 1000 grain (g)	Grain yield (g) / plant	Mean
0 mM	79.51[a]	6.69[a]	61.04[a]	30.76[a]	12.54[a]	38.11
50 mM	69.38[b]	4.94[b]	58.58[b]	26.87[b]	7.49[b]	33.45
100 mM	67.06 c	4.78 b	55.62 c	22.28 c	6.20 c	31.19
	np	np	np	np	np	np
Mean	71.98	5.47	58.41	26.64	8.74	34.25
LSD (P=0.01)	1.25	0.40	1.14	0.84	0.75	

Means followed by same letters within a column are not significantly different at p=0.01

The plant height reduction with increasing salinity may be due to the presence of supernumerary salts in the root zone (Singla and Garg, 2005; Mirzaei *et al.*, 2011) which reduced the water and essential nutrients uptake. The reduction in grains number is the major reason for grain yield decrease under salinity stress that may be due to ionic toxicity and osmotic stress generated by the excessive salts present in the soil (Munns *et al.*, 2016).

Significant variances were observed among different genotypes at p≤0.01 under different concentrations of NaCl. The Abo-Graib genotype , Abo-Grab×Forat cross, and Forat genotype were shorter (66.6 cm, 66.6 cm and 66.5 cm, respectively), compared with the others, while Dijla genotype was the tallest one (84.7 cm) in descending order of plant height (Table 6). The higher number of spikes per plant (8.7) and the higher number of grains per spike (65.5) was exhibited by Abo-Graib× G8 cross compared with a lower value of the number of spikes per plant (4.3, 4.5, 4.7, 4.7 and 4.7) which was produced by G8, Dijla, Abo-Graib genotypes, Abo-Graib×Dijla, and Abo-Graib×Forat cross,

respectively. In addition, the lowest number of grains per spike (46) was shown by Forat genotype. The Dijla genotype and Abo-Graib×Dijla cross displayed a higher weight of 1000 grain (32.8 g, and 31.5 g, respectively) compared with the others (Table 6). For the grain yield/plant, Abo-Graib×G8 cross showed its superiority through the production of the highest amount of grain yield per plant (13.9 g). On the other hand, the lower values of this trait (6.2 g, 7.2 g, and 7.2 g) were offered by Forat, Dijla and G8 genotypes, respectively (Table 6) compared with the other genotypes. The grain yield was mostly stated by changes in a number of spike/plant and grain number/spike more than in grain weight, in agreement with the findings of Subira *et al.* (2015). This result highlights the importance of spike number and number of grain for increasing grain yield. Therefore, the larger number of spikes and grains could combine to improve grain yield potential despite expecting of partial compensation. Thus, grain yield was co-limited by source and sink for modern wheat genotypes.

Table 6 : Mean effect of traits studied in four parents and their six F_1 progenies under various concentrations of NaCl

Genotypes and F_1 hybrids	Plant height (cm)	No. of spikes / plant	No. of grains / spike	Weight of 1000 grain (g)	Grain yield (g) / plant	Mean
Abo-Graib (parent)	66.67[e]	4.72[de]	51.50[f]	28.50[c]	7.78[de]	31.83
Dijla (parent)	84.78[a]	4.56[e]	48.11[g]	32.89[a]	7.21[ef]	35.51
Forat (parent)	66.50[e]	4.67[de]	46.06[h]	28.33[c]	6.25[f]	30.36
G8 (parent)	71.52[d]	4.37[e]	63.07[bc]	25.15[e]	7.23[ef]	34.27
Abo-Graib×Dijla	77.67[bc]	4.72[de]	58.56[de]	31.56[ab]	8.78[cd]	36.26
Abo-Graib×Forat	66.67[e]	4.78[de]	57.33[e]	27.61[cd]	8.05[de]	32.89
Abo-Graib×G8	71.78[d]	8.70[a]	65.52[a]	23.44[f]	13.90[a]	36.67
Dijla×Forat	76.50[c]	5.28[cd]	61.39[c]	30.28[b]	9.86[c]	36.66
Dijla×G8	79.00[b]	5.56[c]	63.81[ab]	27.11[cd]	9.89[c]	37.07
Forat×G8	70.89[d]	7.37[b]	59.30[d]	26.63[d]	12.05[b]	35.25
Mean	73.20	5.47	57.47	28.15	9.10	34.68
L.S.D (p=0.01)	2.13	0.69	1.93	1.43	1.27	

Means followed by same letters within a column are not significantly different at p=0.01

The interaction between genotypes×salinity was significantly at p≤0.01 in all studied traits excjept the number of spikes per plant was significantly at p≤0.05. The Dijla genotype and Dijla×G8 hybrid cross under control treatment showed higher values of plant height (87.4 cm, and 85.8 cm, respectively), while from four survived genotypes under 100 mM NaCl, three genotypes which were G8, Abo-Graib×G8, and Forat×G8 offered shorter plants (65.4 cm, 66.7 cm, and 65.6 cm, respectively). Six genotypes (Abo-Graib, Dijla, Forat, Abo-Graib×Dijla, Abo-Graib×Forat, and Dijla×Forat) died during germination stage under 100 mM NaCl, while all genotypes died under 150 mM NaCl during the germination stage because they were very sensitive to the high concentration of salt (Table 7). The highest number of spikes per plant (11) and the highest number of grains per spikes (68.4) were offered by Abo-Graib×G8 cross under control treatment (0 mM). In contrast, the lowest number of spikes per plant (3.3), and (4) were produced by G8 genotype, and Dijla×G8 cross, respectively under 100 mM NaCl. The Abo-Graib, Dijla genotypes, Abo-Graib×Forat, Abo-Graib×Dijla, and Dijla×Forat crosses exhibited higher values of 1000 grains weight (33.4 g, 33 g, 32.7 g, 31.9 g, and 31.9 g, respectively) under 0 mM NaCl. On the other hand, Abo-Graib×G8, Forat×G8 crosses, and G8 genotype produced a lower weight of 1000 grains (20.3 g, 22.1 g, and 22.2 g, respectively) under 100 mM NaCl. Abo-Graib×G8 and Forat×G8 cross offered a higher amount of grain yield per plant (19.9 g, and 17.8 g, respectively) under control treatment, while the least value of grain yield per plant (4.1 g) was produced by G8 genotype under 100 mM NaCl. The Forat×G8, Abo-Graib×G8, and Dijla×G8 hybrid crosses were more tolerant to salinity compared with the other genotypes under 100 mM NaCl through producing high grain yield per plant (7.4 g, 7.3 g, and 6.0 g, respectively) (Table 7) that may be due to reduction in the content of Na^+ and increasing the content of K^+ and K^+/Na^+ ratio in their leaves. Therefore, they were categorized as salt tolerant wheat genotypes and may be recommended for cultivation in salty areas.

Table 7 : Five traits mean comparison by LSD of four genotypes and their six F$_1$ crosses under 0, 50 and 100 mM of NaCl

Genotypes	Plant height (cm)					No. of spikes/plant					No. of grain/spike				
	NaCl (mM)					NaCl (mM)					NaCl (mM)				
	0	50	100	150	Mean	0	50	100	150	Mean	0	50	100	150	Mean
Abo-Graib (parent)	75.4[d]	57.9[d]	np	np	66.7	5.7[d]	3.8[de]	np	np	4.8	63.0[b]	40.0[f]	np	np	51.5
Dijla (parent)	87.4[a]	82.1[a]	np	np	84.8	5.3[d]	3.8[de]	np	np	4.6	49.7[d]	46.6[e]	np	np	48.2
Forat (parent)	78.2[bcd]	54.8[d]	np	np	66.5	5.7[d]	3.7[e]	np	np	4.7	48.7[d]	43.4[e]	np	np	46.1
G8 (parent)	78.6[bc]	70.6[c]	65.4[b]	np	71.5	5.8[d]	4.0[de]	3.3[b]	np	4.4	68.6[a]	64.9[a]	55.8[b]	np	63.1
Abo-Graib×Dijla	79.8[b]	75.6[b]	np	np	77.7	5.6[d]	3.9[de]	np	np	4.8	58.7[c]	58.4[c]	np	np	58.6
Abo-Graib×Forat	77.4[bcd]	55.9[d]	np	np	66.7	5.7[d]	3.9[de]	np	np	4.8	62.2[b]	52.4[d]	np	np	57.3
Abo-Graib×G8	77.1[bcd]	71.6[c]	66.7[b]	np	71.8	11.0[a]	9.3[a]	5.8[a]	np	8.7	68.4[a]	66.0[a]	62.1[a]	np	65.5
Dijla×Forat	79.1[b]	73.9[bc]	np	np	76.5	5.9[d]	4.7[cd]	np	np	5.3	61.9[b]	60.9[bc]	np	np	61.4
Dijla×G8	85.8[a]	80.7[a]	70.6[a]	np	79.0	7.2[c]	5.4[c]	4.0[b]	np	5.5	66.4[a]	64.1[ab]	60.9[a]	np	63.8
Forat×G8	76.2[cd]	70.9[c]	65.6[b]	np	70.9	9.1[b]	7.0[b]	6.0[a]	np	7.4	62.9[b]	59.4[c]	55.6[b]	np	59.3
Mean	79.5	69.4	67.01	np	72.0	6.7	5.0	4.8	np	5.5	61.1	55.6	58.6	np	58.4
LSD (p=0.01)	2.9	3.7	2.9	-		1.2	0.9	1.0	-		2.9	3.2	2.6	-	

Table 7 continued

Genotypes	Weight of 1000 grain (g)					Grain yield(g)/plant				
	NaCl (mM)					NaCl (mM)				
	0	50	100	150	Mean	0	50	100	150	Mean
Abo-Graib(parent)	33.4[a]	23.6[de]	np	np	28.5	12.0[bc]	3.6[g]	np	np	7.8
Dijla (parent)	33.0[ab]	32.8[a]	np	np	32.9	8.7[de]	5.7[ef]	np	np	7.2
Forat (parent)	29.8[cd]	26.9[bc]	np	np	28.35	8.2[e]	4.3[g]	np	np	6.3
G8 (parent)	27.9[de]	25.3[cd]	22.2[b]	np	25.1	11.0[cd]	6.5[e]	4.1[b]	np	7.2
Abo-Graib×Dijla	31.9[ab]	31.2[a]	np	np	31.6	10.5[cde]	7.1[de]	np	np	8.8
Abo-Graib×Forat	32.7[ab]	22.6[e]	np	np	27.7	11.6[c]	4.5[fg]	np	np	8.1
Abo-Graib×G8	26.4[e]	23.6[de]	20.3[b]	np	23.4	19.9[a]	14.5[a]	7.3[a]	np	13.9
Dijla×Forat	31.9[ab]	28.7[b]	np	np	30.3	11.6[c]	8.1[d]	np	np	9.9
Dijla×G8	29.4[cd]	27.4[bc]	24.4[a]	np	27.1	14.1[b]	9.6[c]	6.0[a]	np	9.9
Forat×G8	31.1[bc]	26.7[bc]	22.1[b]	np	26.6	17.8[a]	11.0[b]	7.4[a]	np	12.1
Mean	30.8	26.9	22.3	np	26.6	12.5	7.5	6.2	np	8.7
LSD (p=0.01)	2.0	2.4	2.2	-		2.5	1.4	1.5	-	

Means followed by same letters within a column are not significantly different at p =0.01
np means no plants (plants died during germination stage under 100 and 150 mM of NaCl)

Combining ability variances and effects

General and specific combining ability variation and effects were determined to (or "intending to") decoding the architecture of genetic of the features under study. Combining ability describes parental lines breeding value to produce combinations (Hei *et al.*, 2016). The general combining ability refers to additive gene action and specific combining the ability to non-additive gene action (Griffing, 1956b). The combining ability analysis of variance was done for all the five characters (Table 8). Highly significant variances (p≤0.01), of both general and specific combining ability, were obtained which referred to important of both additive and non-additive gene effects for the above-mentioned traits. The estimated value of σ_s^2 was higher than

its σ_g^2 for all five traits which indicated the preponderance of non-additive gene action. The traits were controlled by dominance effects because the ratio of σ_g^2 / σ_s^2 for all traits was less than one. In the same way, the preponderance of non-additive gene effects was reported by Singh *et al.* (2012) for plant height, the number of productive tillers per plant, the number of grain per spike, the weight of grain and grain yield. Selection of suitable genotypes and their crosses in successful hybridization is necessary to create an organized breeding program leading to sustained and rapid improvement. Therefore, the available wheat germplasm in the present study is appropriate for development desirable crosses and varieties. Because, gca effects in the parents, it

was found that three of the parents were observed as good general combiners for all the five traits. Dijal variety for plant height, however, Abo-Graib variety for more number of spikes per square meter, and Abo-Graib, G8 for more number of grains per spike, while Abo- Graib, Dijla, and G8 for the weight of 1000 grain, whereas Abo-Graib and G8 for high grain yield. Corresponding, considering sca effects of the hybrids, it was seen that three of the F_1 crosses were suitable specific combiners for all the five traits. Dijla x G8 combiner was good for all traits studied, while Abo-Graib x G8 and Forat x G8 combiners were suitable for spikes number m^{-2}, the number of grain spike^{-1}, the weight of 1000 grains and grain yield.

Table 8 : Analysis of variance for combining ability along with estimate of variance for five traits in wheat parents and their F1 crosses

Source of variation	df	Plant height	No of spike m^{-2}	No of grain spike^{-1}	Weight of 1000 grain	Grain yield
				Mean square		
Gca	3	45.03**	380.53**	90.21**	4.18**	2.72**
Sca	6	30.34**	220.65**	60.83**	2.69**	1.54**
Error	18	0.02	0.3	0.2	0.1	0.03
σ_g^2		6.75	25.19	3.62	4.74	2.38
σ_s^2		59.04	38.40	32.18	21.07	14.59
σ_g^2 / σ_s^2		0.11	0.66	0.11	0.23	0.16

** Significant at 1% level; gca, general combining ability; sca, specific combining ability; σ_g^2 / σ_s^2 ratio of gca variance to sca variance

Correlations

To determine agronomical plant traits appropriate for selection for the further improvement of grain yield in bread wheat, the correlation coefficient among various agronomic traits were studied. The results about correlation coefficient of the traits studied have been shown in Table 18. In the current study, the five traits were positively and significantly (p≤0.01) correlated with each other except the relationship between plant height and each of spikes number per m^2, grains number per spike, the weight of 1000 grains and grain yield (ton per hectare) was not significant. While the correlation between grain number per spike and weight of 1000 grain was positively significantly (p≤0.05) (Table 9). The simple correlation coefficient of grain yield was negative and nonsignificant with plant height (r = -0.207). The results of Çifci (2012) also exhibited the relationship between the

grain yield and plant height was nonsignificant (r = 0.184). A positive and robust relationship between grain yield and spikes number per square meter was noted (r = 0.837**). A similar finding was reported by Modhej *et al.* (2012) who showed the correlation coefficient between the grain yield and spike number per square meter was 0.44. A positive and significant correlation between grain yield and grain number per spike were obtained (r = 0.944**). The previous study of Bustos *et al.* (2013) indicated grain yield was linearly associated with grain number in both growing seasons (R^2 = 0.69, p < 0.0001 in season1 and R^2 = 0.71, p < 0.0001 in season 2). Grain yield was positively correlated with the weight of 1000 grain (r = 0.652**). This result is in agreement with the results of Zafarnaderi *et al.* (2013) who presented the relationship between grain yield, and weight of 1000 grain was positive and significant (0.379).

Table 9 : Correlation among five traits in six F_1 crosses and their parents

Traits	No of spikes per m^2	No of grains per spike	Weight of 1000 grain	Grain yield (ton per hectare)
Plant height (cm)	-0.174 [ns]	-0.357 [ns]	0.254 [ns]	-0.207 [ns]
No of spikes per m^2		0.753**	0.348 [ns]	. 0.837**
No of grains per spike			0.434*	0.944**
Weight of 1000 grain				0.652**

[ns]= not significant differences at 0.05 level, * Correlation is significant at 0.05 level, ** Correlation is significant at 0.01 level

Conclusion

From the result of the current investigation it is concluded Abo-Graib G8, Dijla G8, and Forat G8 crosses presented their superiority in grain yield under high concentration of NaCl related to the highest number of spikes per plant, and the number of grains per spike. Highly significant variances, of both general and specific combining

ability, were noted that presented the importance of additive and non-additive gene effects for all the traits. In both parents and their F_1 crosses, grain yield exhibited positive correlation with the spikes number per plant, the grains number per spike and weight of 1000 grain. Abo-Graib G8, Dijla G8, and Forat G8 crosses presented their superiority of grain yield related to the higher number of spikes per plant, the number of grains per spike and the 1000 grain weight.

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