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GENETIC ANALYSIS OF DIALLEL CROSSES IN WHEAT UNDER STRESS AND NORMAL IRRIGATION TREATMENTS

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ABSTRACT

Eight bread wheat genotypes were crossed in a8x8half diallel scheme in 2015/2016.Parents and their 28 F1 crosses were evaluated under normal and stress conditions during 2016/2017 in two field experiments. The results of analysis of variance were significant for all studied traits. The highest mean values were detected by parents P2, P2,P8, P2,P6 and p2 for plant height, spike length, no of spike/ plant, 1000-kernel weight, biological yield/ plant and grain yield/ plant in the combined analysis, respectively. While, the highest mean values were recorded under combined analysis with crosses P1xP6 for biological yield/ plant and the cross P2xP4 for grain yield / plant. Mean squares for both general (GCA) and specific (SCA) combining ability estimates were highly significant for all studied traits. The ratios between GCA and SCA exceeded the unity for all studied traits, revealing that additive and additive x additive types of gene action are more important than non-additive gene action in controlling these traits. The parental P6 exhibited positive and significant ĝi effects spike length, no of spikes/ plant, 1000-grain, biological yield/ plant and grain yield/ plant. The highest desirable SCA effects were obtained with the crosses P1xP6, P1xP7, P2xP4, P3xP7, P3xP8, P4xP8, P5xP8 and P6xP7 for grain yield/ plant which exhibited significant and positive ŝij effects

Key words*: Wheat, heterosis, combining ability, drought stress, GCA and SCA.*

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the major cereal crop in Egypt as well as several other countries. World average cultivated area of wheat reached 221.73[1] million hectares in 2017; the total production was 751.36* million metric tons, with an average productivity of 3.39* metric tons per hectare. Egypt grew in 2017, 1.25* million hectares and produced 8.10* million metric tons of grains, with an average yield of 6.43* metric tons per hectare. With increasing population, it could hardly satisfy only 55% of local requirements. The increasing gap between production and consumption necessitates increasing wheat production in Egypt. Increasing the productivity of wheat through an efficient breading program to overcome this problem.

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[1] Foreign Agricultural Service / USDA Office of Global Analysis
http://www.pecad.fas.usda.gov

- (1 metric ton per hectare = 100 grams per square meter, 1 hectare (ha) = 10,000 square meters).

Drought stresses can occur at any stage of plant growth and development, thus illustrating the dynamic nature of crop plants and their productivity. Drought is the most widespread and limiting crop productivity. There are definitions of drought, which include precipitation, evapo-transpiration, potential evapotranspiration, temperature, humidity and other factors individually or in combination (**Prasad et al., 1998**). Also selection for genotypes with increased productivity in drought environments has been an important of many plant breeding programs, the biological basis for drought tolerance is still poorly understood.

Knowledge of genetic behavior and type of gene action controlling target traits is a basic principle for designing an appropriate breeding procedure for the purpose of genetic improvement. Hence, the success of any selection or hybridization breeding program for developing drought-tolerant varieties depends on precise estimates of genetic variation components for traits of interest consisting of additive, dominant and non-allelic interaction effects **(Farshadfar et al., 2008; Nouri et al., 2011)**.

The diallel cross designs are frequently used in plant breeding research to obtain information about genetic properties of parental lines or estimates of general combining ability (GCA), specific combining ability (SCA) and heritability **(Baker, 1978; EL- Maghraby et al., 2005 and Iqbal et al., 2007)**. In addition, the diallel cross technique was reported to provide early information on the genetic behavior of these attributes in the first generation **(Chowdhry et al., 1992 and Topal et al., 2004).** To establish a sound basis for any breeding program aimed at achieving high yield, breeders must have information on the nature of combining ability of parents, their behavior and hybrid combinations performance **(Chawla and Gupta, 1984)**. Combining ability analysis helps in the identification of parents with high GCA and parental combinations with high SCA. Based on combining ability analysis of different characters, higher SCA values refer to dominance gene effects and higher GCA effects indicate a greater role of additive gene effects controlling the characters **(Sprague and Tatum, 1942)**. The main objectives of the present investigation were to: 1) Identify superior parents and cross combinations from 8x8 diallel cross of bread wheat parental genotypes for drought avoidance and tolerance traits. 2) estimate the magnitude of heterosis, GCA and SCA to improve wheat productivity under drought condition. 3) estimate susceptibility index (SI) for yield and yield components.

MATERIALS AND METHODS

This investigation was carried out at the Experiment, Research Station of Moshtohor Faculty of Agriculture, Benha University, Kalubia Governorate, Egypt during the two successive seasons 2015/2016 and 2016/2017. Eight genotypes of wheat representing a wide range of diversity for several agronomic characters and drought resistance measurements were selected for the study. The names, pedigree and origin of these varieties are presented in Table (1).

Table (1): The code no, name, pedigree and source of the studied parental varieties and lines.

NO	Entry name	Pedigree	Source
1	Yakora Rojo	Ciano 67/Sonora 6411 Klien Rendidor/3/1L815626Y-2M-1Y-0M-302M	CIMMYT
2	Gemiza 7	CMH74 A. 630/5x//Seri 82/3/Agent (Gemiza 7)	Egypt
3	Giza 168	MRl/BUG/SEPI CM933046-8M-OY-OM•2Y-O3-OGZ.	Egypt
4	Gemiza 11	BOW"S"/KVZ"S"//7C/SER182/3/GIZA 168/SAKHA61. GM7892-2GM-1GM-2GM-1GM-0GM.	Egypt
5	Sakha 93	S 92/TR 810328 S8871-1S-2S-1S-0S	Egypt
6	Sides 12	BUC//7C/ALD/5/MAYA74/ON//1160.147/3/BB/GLL /4/CHAT"S"/6/MAYA/VUL//CMH74A.630/ 4*SXSD7096-4SD-1SD-1SD 0SD	Egypt
7	Sahel 1	NS 732/PIMA//Veery'S'	ICARDA
8	13-ssd-43	S.S.D/ Giza 170/ Sakha 93	Egypt

The line no 8 was developed in Department of Agronomy, Fac. of Agic. at Moshtohor, Banha Univ. by Prof. Dr. M. El-Badawy

The parents were crossed in a 8x8 diallel cross excluding reciprocals in 2015/2016 growing season giving a total of twenty-eight crosses. In 2016/2017 two experiments using randomized complete block design with three replications were carried out. Each experiment contained the eight parents and their resulting 28 F_1's. The sowing date was on 4th Dec. 2016. The first experiment was irrigated only once after planting irrigation and the second one was normally irrigated five irrigations. Plots of parents and F1's consisted of one row, 3 m-long, with spacing of 30 cm between rows and 20 cm between plants. The dry method of planting was used in this study. The other cultural practices of growing wheat were practiced. The amounts of total rainfall during the evaluating season were recorded in Table (2).

Ten guarded plants from parents and the F_1's were selected randomly from each plot for recording observations on different characters. The characters studied were, Plant height(cm), spike length (cm), No .of spikes /plant, 1000- kernel weight (g), biological yield/ plant and grain yield/ plant (g).

Heterosis for each trait was computed as parents *vs*. crosses sum of squares was obtained by partitioning the genotypes sum of square to its components. Analysis of variance was conducted as outlined by Steel and Torrie (1980) for all characters. The analysis of GCA and SCA was done following the procedure given by Griffing (1956) using Method II Model I. The combined analysis of the two experiments was carried out whenever homogeneity of mean squares was detected (Gomez and Gomez 1984). Percentages of heterosis relative to mid (MP) and better (BP) parents were calculated according to Fonsecca and Patterson (1968) as follows:

MP= (value of F_1- mean of the two parents/mean of the two parents)×100.

BP= (value of F_1- value of the best parent/value of the best parent)×100.

Table 2. Monthly averages of temperature, relative humidity (R.H.) and total rain fall during 2016/2017 season at Kalubia (Moshtohor).

Months	Temperature C		R.H. (%)	Rain fall mm/month
	Min.	Max.		
Dec.2016	19.7	9.2	51.3	0.5
Jan.2017	17.7	6.1	55.9	1.6
Feb.2017	20.4	7.8	47.2	0.8
Mar.2017	25.8	11.4	37.3	0.4
Apr.2017	29.1	14.4	38.9	0.3
May.2017	34.5	19.0	32.1	----

RESULTS AND DISCUSSION

Analysis of variance for yield and its components under drought and normal irrigation and combined analysis across the mention environments are presented in Table 3. Results indicated that mean squares due to irrigation treatments (Environments) were highly significant for all studied traits indicating overall differences between the two environments of study.

Genotypes mean squares were highly significant for all studied traits indicating wide diversity between all genotypes used in this work. Moreover, significant mean squares between genotypes and environment interaction were detected for No of spikes/plant, biological yield/ plant and grain yield/ plant. This result indicated that genotypes responded differently to different environments for the mention traits.

Mean squares due to parents were highly significant for all traits in drought stress, normal irrigation and combined across them, indicating that these parents are differently in the aforementioned significant traits. Moreover, mean squares due to the interaction between parents and environments were significant for No of spike/ plant, Biological yield/ plant and grain yield/ plant. Such result indicated that wheat parents responded differently to stress and non-stress conditions for these traits. For the

Table (3) Mean squares for yield and its components under drought stress condition and normal irrigation as well as the combined over them.

S.O.V.	df	plant height (cm)	spike length(cm)	No. of spikes /plant	1000 kernel weight (g)	Biological yield/plant (g)	Grain yield/plant (g)
Drought environment							
Rep	**2**	41.82	7.34**	17.81*	100.51**	7.96	0.3
Genotypes (G)	**35**	163.82**	2.55**	102.81**	56.12**	4046.34**	141.80**
Parent (P)	**7**	123.61**	2.62	95.07**	73.90**	2320.86**	119.96**
Cross (C)	**27**	178.29**	2.53*	90.55**	53.37**	4247.56**	152.00**
P vs C.	**1**	54.57*	2.67*	488.02**	5.76	10691.64**	19.1*
Error	**70**	28.19	1.3	5.49	16.02	77.59	9.23
Normal environment							
Rep	**2**	7.16	1.9	3.39	5.33	2.16	6.72
Genotypes (G)	**35**	176.69**	4.50**	114.25**	70.14**	4683.45**	179.64**
Parent (P)	**7**	288.20**	4.69**	70.93**	114.22**	7645.45**	182.67**
Cross (C)	**27**	146.43**	4.58**	125.90**	60.67**	4012.33**	180.58**
P vs C.	**1**	213.00**	0.93	102.93**	17.19	2069.68**	132.89**
Error	**70**	23.56	1.18	4.58	9.18	80.31	14.61
Combined analysis							
Irrigation (I)	**1**	5726.03**	102.78**	2681.12**	443.19**	363533.47**	3985.17**
Rep/ I	**4**	24.49	4.62**	10.6	52.92**	5.06	3.51
Genotypes (G)	**35**	301.97**	5.70**	155.57**	117.43**	6221.16**	230.37**
Parent (P)	**7**	374.62**	6.63**	154.87**	181.57**	7009.63**	254.07**
Cross (C)	**27**	285.38**	5.55**	142.26**	104.35**	5836.61**	228.07**
P vs C.	**1**	241.60**	3.37*	519.60**	21.42	11084.74**	126.37**
G x I	**35**	38.54	1.34	61.50**	8.83	2508.63**	91.07**
p x I	**7**	37.2	0.68	11.12*	6.55	2956.68**	48.57**
C x I	**27**	39.35	1.55	74.19**	9.69	2423.28**	104.51**
P.vs.C x I	**1**	25.97	0.22	71.35**	1.52	1676.59**	25.62
Error	**140**	25.87	1.24	5.04	12.6	78.95	11.92

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

exceptional traits, insignificant mean squares between parents and environments were detected, indicating that parents behaved similarly in stress and non-stress conditions.

Mean performance

Results in Table (4) showed the average of plant height, yield and its components traits at the combined across irrigation treatments. It's clear that the parental line (P_1) gave the lowest mean value for plant height. On the other hand, P2 was the tallest parent. Plant height for crosses ranged from 72.50 cm (P1xP3) to 97.75cm (P6xP7). Moreover, the crosses P2xP4, P2xP7, P3xP7, P4xP5, P4xP8 and P6xP8 did not differ significantly than the tallest hybrid P6xP7. Some farmers usually prefer higher plant due to the high price of hay. On the other hand, this plant must be given high yield for grain and behave resistant to lodging. The highest parents mean value for spike length (12.92cm) was detected for P2. However, eight crosses P2xP3, P2xP4, P3xP4, P3xP7, P4xP6, P4xP7, P4xP8 and P7xP8 exhibited highest values for spike length. For No. of spike/ plant the parent P8 and the cross P1xP4 give the highest number of spikes/ plant. Heavier 1000-kernel weight were detected for P2, P4, P6, P1xP6, P2xP4, P2xP6, P2xP8, P4xP5, P4xP8, P5xP8, P6xP7 and P6xP8. The parental No 6 (P_6) gave the highest mean value for biological yield/ plant and ranked the first parents for this traits. Moreover, the cross P1xP6 exhibited the highest crosses for biological yield/ plant. Parent No 2 (P_2) and the cross P2xP4 gave the highest mean values for grain yield / plant. Therefore, these crosses could be efficient for prospective wheat breeding programs aiming at improving wheat grain yield.

Heterotic effects

Mean squares for parents *vs* crosses in F_1 generation, as an indication of average of heterosis in F_1 across, all crosses were significant for all the studied traits except, 1000-kernel weight at both and across environments and spike length at normal irrigation environment (Table 2). Meanwhile, significant interaction between P vs C and environments were detected for No of spikes/ plant and biological yield/ plant. Its mean that, heterotic effect was differed from environment to another for the mention traits. On the other hand, heterosis in the other traits were stable in front of environment changes.

Heterosis expressed as the percentage deviation of F_1 mean performance from its mid- and better- parents for yield and its components are presented in Table (5). For plant height the crosses P1xP2 and P2xP3 expressed significant and negative heterotic effects relative to mid parent. However, the cross P2xP5 manifested significant and negative heterotic effects relative to better parent. Whereas, the crosses P1xP5, P3xP7, P4xP5, P4xP8 and P6xP7 expressed the highest significant and positive effects relative to mid and better parent. Significant and negative heterotic effects relative to both mid parent and better parent were also reached by **El- Sayed (1997), Hamada and Taufelis (2001), Bayoumi (2004), Abdel El- Aty et al., (2005), and Abdel- Monwam (2009).** Meanwhile, positive heterotic effects are currently important for straw production for its contribution to animal feed **EL-Hosary and Nour El Deen (2015).**

The most significant and desirable heterosis relative to mid parent were exhibited by the crosses P3xP7, P4xP8 and P7xP8 for spike length, the crosses P1xP5 and P2xP5 for No. of spikes/ plant and the crosses P3xP7, P4xP5 and P5xP8 for for 1000-kernel weight. Significant and positive mid-parent and better- parent heterosis for spike length, no of spikes/ plant and 1000-kernel weight was reported by **Zaied (1995), El- Seidy and Hamada (2000) and El- Borhamy et al., (2008) .** For biological yield/ plant four crosses i.e. P1xP6, P2xP5, P3xP6 and P3xP7 exhibited significant and positive mid parent heterosis. On the other side, positive heterobiltosis for this traits was exhibited by the two crosses P1xP6 and P3xP7. For grain yield/ plant, nine crosses exhibited positive significant mid parent heterosis.

Table 4. Mean performance of the genotypes for yield and its components over the studied environments .

Genotypes	plant height (cm)	spike length(cm)	No. of spikes /plant	1000 kernel weight (g)	Biological yield/plant (g)	Grain yield/plant (g)
P1	70.13	11.25	29.25	38.3	207.5	16.5
P2	95.92	12.92	24.5	50.58	211.17	35.25
P3	79.67	12.08	28.42	35.48	134.92	16.75
P4	80.54	12.08	32.58	46.17	188.25	24.88
P5	75.17	11.42	17.33	40.37	128.67	16.5
P6	88.75	11.92	28.83	49.23	214.33	25.42
P7	82.17	9.33	29.67	39.37	166.5	26.67
P8	83.58	11.17	33.33	39.95	199.17	23.5
1x2	73.67	11.33	16.5	38.77	140.83	18.78
1x3	72.5	9.83	30.83	35.36	167	18.58
1x4	81	12.25	32.33	40.43	192.33	25.33
1x5	86.63	11.08	28.5	37	146.17	16.67
1x6	85.75	11.92	32.17	47.65	229.17	33
1x7	76.46	10.17	28.17	37.5	149.83	27.71
1x8	75.58	10.75	23.33	38.2	123	26.33
2x3	79.5	13.33	22.33	40.53	150	21.67
2x4	92.54	12.58	14.5	50.68	115.33	37.5
2x5	78.17	11.25	25.67	42.72	187.17	22.92
2x6	89.25	12.25	17.33	49.65	209.33	30.6
2x7	91.42	11.33	26.83	41.77	174.67	19.49
2x8	87.85	12.33	21.75	46.1	174.78	25.5
3x4	78.5	13	23.17	42.13	169.17	20.58
3x5	75.92	11.83	24.83	37.93	140	12.33
3x6	82.25	11.83	29.83	41.75	202.83	20.58
3x7	90.75	12.67	22.83	44.28	181.67	27.33
3x8	79.58	11	25.08	39.48	135.5	33.83
4x5	92.33	11.92	25.67	49.2	169.67	21.83
4x6	89.67	12.58	25.58	47.92	201	27.33
4x7	86.42	12.92	28.67	44.83	174.17	26.96
4x8	95.67	12.83	19	45.8	154.67	34.83
5x6	83.42	12.08	23	44.05	159.17	25.21
5x7	82.5	10.58	20.75	42.63	129.67	20.5
5x8	81.5	10.25	27.5	47.38	155.67	27.17
6x7	97.75	11.33	25.5	46.45	204.33	31
6x8	90.42	13.17	23.33	45.82	166.33	30.79
7x8	89.96	12.58	14.25	43.27	90.83	16.25
mean of parents	81.99	11.52	27.99	42.43	181.31	23.18
mean of crosses	84.53	11.82	24.26	43.19	164.08	25.02
mean of Genotypes	83.97	11.75	25.09	43.02	167.91	24.61
L.S.D 5%	8.14	1.78	3.59	5.68	14.22	5.52
L.S.D 1%	10.67	2.34	4.71	7.45	18.65	7.24

Table (5): Heterosis relative to mid and better parent for the studied traits in the combined analysis .

crosses	**plant height (cm)**		**spike length(cm)**		**No. of spikes /plant**		**1000 kernel weight (g)**		**Biological yield/plant (g)**		**Grain yield/plant (g)**	
	M.P.	B.P	M.P.	B.P	M.P.	B.P	M.P.	B.P	M.P.	B.P	M.P.	B.P
1x2	-11.27*	-23.20**	-6.21	-12.26	-38.60**	-43.59**	-12.77	-23.36**	-32.72**	-33.31**	-27.43*	-46.73**
1x3	-3.2	-9	-15.71*	-18.62*	6.94	5.41	-4.16	-7.68	-2.46	-19.52**	11.78	10.95
1x4	7.52	0.57	5.01	1.38	4.58	-0.77	-4.26	-12.42*	-2.8	-7.31*	22.46	1.84
1x5	19.24**	15.24**	-2.21	-2.92	22.36**	-2.56	-5.93	-8.34	-13.04**	-29.56**	1.01	1.01
1x6	7.95	-3.38	2.88	0	10.76	9.97	8.87	-3.22	8.65*	6.92*	57.46**	29.84**
1x7	0.41	-6.95	-1.21	-9.63	-4.38	-5.06	-3.43	-4.74	-19.88**	-27.79**	28.38*	3.91
1x8	-1.65	-9.57	-4.09	-4.44	-25.43**	-30.00**	-2.36	-4.38	-39.51**	-40.72**	31.67*	12.06
2x3	-9.44*	-17.12**	6.67	3.23	-15.59*	-21.41**	-5.83	-19.88**	-13.32**	-28.97**	-16.67	-38.53**
2x4	4.89	-3.52	0.67	-2.58	-49.20**	-55.50**	4.77	0.2	-42.25**	-45.38**	24.74**	6.38
2x5	-8.62	-18.51**	-7.53	-12.9	22.71**	4.76	-6.07	-15.55**	10.15*	-11.37**	-11.43	-34.99**
2x6	-3.34	-6.95	-1.34	-5.16	-35.00**	-39.88**	-0.52	-1.85	-1.61	-2.33	0.89	-13.18
2x7	2.67	-4.69	1.87	-12.26	-0.92	-9.55	-7.13	-17.43**	-7.5	-17.28**	-37.06**	-44.72**
2x8	-2.11	-8.41	2.42	-4.52	-24.78**	-34.75**	1.84	-8.86	-14.81**	-17.23**	-13.19	-27.66**
3x4	-2	-2.53	7.59	7.59	-24.04**	-28.90**	3.2	-8.74	4.69	-10.14**	-1.1	-17.25
3x5	-1.94	-4.71	0.71	-2.07	8.56	-12.61	0.02	-6.03	6.23	3.77	-25.81	-26.37
3x6	-2.33	-7.32	-1.39	-2.07	4.22	3.47	-1.44	-15.20**	16.15**	-5.37	-2.37	-19.02
3x7	12.15*	10.45*	18.29*	4.83	-21.38**	-23.03**	18.33*	12.49	20.54**	9.11*	25.91*	2.5
3x8	-2.5	-4.79	-5.38	-8.97	-18.76**	-24.75**	4.68	-1.17	-18.88**	-31.97**	68.12**	43.97**
4x5	18.60**	14.64**	1.42	-1.38	2.84	-21.23**	13.71*	6.57	7.07	-9.87*	5.54	-12.23
4x6	5.93	1.03	4.86	4.14	-16.69**	-21.48**	0.45	-2.67	-0.14	-6.22	8.7	7.54
4x7	6.22	5.17	20.62*	6.9	-7.9	-12.02*	4.83	-2.89	-1.81	-7.48	4.61	1.09
4x8	16.58**	14.46**	10.39	6.21	-42.35**	-43.00**	6.37	-0.79	-20.15**	-22.34**	44.01**	40.03**
5x6	1.78	-6.01	3.57	1.4	-0.36	-20.23**	-1.67	-10.53	-7.19	-25.74**	20.28	-0.82
5x7	4.87	0.41	2.01	-7.3	-11.7	-30.06**	6.94	5.62	-12.14*	-22.12**	-5.02	-23.13*
5x8	2.68	-2.49	-9.23	-10.22	8.55	-17.50**	17.99*	17.38*	-5.03	-21.84**	35.83*	15.6
6x7	14.38**	10.14*	6.67	-4.9	-12.82*	-14.04*	4.85	-5.65	7.31	-4.67	19.04	16.25
6x8	4.93	1.88	14.08	10.49	-24.93**	-30.00**	2.75	-6.94	-19.55**	-22.40**	25.89*	21.15
7x8	8.55	7.63	22.76*	12.69	-54.76**	-57.25**	9.1	8.3	-50.32**	-54.39**	-35.22**	-39.06**

* $p< 0.05$; ** $p< 0.01$

Also, three crosses expressed significant and positive heterosis in the same order relative to better parent. However, the most desirable heterotic effects relative to both mid- and better- parent were detected for the crosses P1xP6, P_3 x P_8 and P4xP8. The cross (P_3x P_8) recorded the highest significant and positive heterosis relative to mid parent and better parent. Significant and positive heterosis effects relative to mid parent and better parent for grain yield/ plant were reported by **Zaied (1995), Hamada et al., (2002), Bayoumi (2004),Abde El- Aty et al. (2005) and Abde El- Aty and El – Borhamy (2007)**.

Combining ability

The analysis of variance for combining ability for plant height, spike length, number of spikes/ plant, 1000-kernel weight, biological yield, and grain yield/ plant, under drought treatment, normal irrigation and combined analysis is presented in Table 6.

General (GCA) and specific (SCA) combining ability mean squares were highly significant for all studied traits in both environments as well as combined analysis except for spike length under drought and normal conditions. Such results indicated that both types of combining ability are important in the inheritance of these traits. Moreover, the ratios between GCA and SCA exceeded the unity for all studied traits, revealing that additive and additive x additive types of gene action are more important than non-additive gene action in controlling these traits. The genetic variance was previously reported to be mostly due to additive effects for plant height by **El Hosary *et al* (2009)**; for spikes/ plant by **El Seidy and Hamada (1997), El Borhamy (2000), Gomaa *et al* (2014)**; for 1000-grain weight by **El Seidy and Hamada (1997), El Borhamy (2000),** and for grain yield/ plant by **El Seidy and Hamada (1997), El Seidy and Hamada(2000),**

Table (6) Combining abilities mean squares for yield and its components under normal irrigation and drought stress condition as well as the combined over them.

S.O.V.	df	plant height (cm)	spike length(cm)	No. of spikes /plant	1000 kernel weight (g)	Biological yield/plant (g)	Grain yield/plant (g)
Drought environment							
GCA	7	146.79**	1.68	46.40**	58.49**	3615.79**	94.33**
SCA	28	31.56**	0.64	31.24**	8.76**	782.02**	35.50**
Error	70	9.4	0.43	1.83	5.34	25.86	3.08
GCA/SCA		4.65	2.63	1.49	6.68	4.62	2.66
Normal environment							
GCA	7	158.34**	3.09**	22.91**	88.19**	2226.62**	121.27**
SCA	28	34.04**	1.1	41.88**	7.18**	1394.78**	44.53**
Error	70	7.85	0.39	1.53	3.06	26.77	4.87
GCA/SCA		4.65	2.81	0.55	12.29	1.6	2.72
Combined analysis							
GCA	7	277.47**	4.50**	60.46**	143.88**	4199.35**	162.32**
SCA	28	56.46**	1.25**	49.71**	12.96**	1542.31**	55.40**
GCA x L	7	27.67**	0.27	8.85**	2.8	1643.06**	53.27**
SCA x L	28	9.14	0.49	23.41**	2.98	634.50**	24.63**
Error	140	8.62	0.41	1.68	4.2	26.32	3.97
GCA/SCA		4.91	3.6	1.22	11.1	2.72	2.93
GCA x L/GCA		0.10	0.06	0.15	0.02	0.39	0.33
SCA x L/SCA		0.16	0.39	0.47	0.23	0.41	0.44

* $p < 0.05$; ** $p < 0.01$

El Borhamy (2000), Abd El-Aty and Katta (2002), El Hosary*et al* (2012), Gomaa *et al* (2014).

The mean squares of the interaction between GCA, SCA and irrigation treatments were significant for all studied traits except both types of combining abilities x E for spike length and 1000-kernel weight. Such result indicated that the additive and non-additive types of gene action differed significantly from one environment to another for these traits. Similar results were reported by **El-Seidy and Hamada (1997), El-Seidy and Hamada (2000).**

The ratio SCA x environment/ SCA was much than higher that of GCA x irrigation/ GCA treatments for all traits indicating that non-additive effects were much more influenced by environments than additive genetic one. Such results are in harmony with those obtained by **El Hosary and Nour El Deen (2015).**

General combing ability (GCA) effects

Test of homogeneity revealed the validity of the combined analysis for the data of the two irrigation treatments. The general combining ability effects $\hat{g}_i$ of each parent for all studied measurements at the combined analysis are presented in Table (7).

Table 7. Estimates of general combining ability effects for yield and its components at the combined analysis.

Parent	plant height (cm)	spike length(cm)	No. of spikes /plant	1000 kernel weight (g)	Biological yield/plant (g)	Grain yield/plant (g)
P1	-6.39**	-0.60**	2.45**	-3.57**	5.21**	-2.21**
P2	2.85**	0.45**	-3.19**	2.42**	6.33**	2.54**
P3	-3.74**	0.19*	1.00**	-3.47**	-9.52**	-3.31**
P4	2.15**	0.65**	0.83**	2.62**	4.16**	2.26**
P5	-2.49**	-0.40**	-1.52**	-0.55*	-16.64**	-4.19**
P6	4.03**	0.32**	0.86**	3.46**	28.96**	2.78**
P7	2.39**	-0.55**	0.05	-0.77**	-7.30**	0.11
P8	1.20**	-0.05	-0.49**	-0.12	-11.21**	2.02**
L.S.D(0.05) gi	0.68	0.15	0.3	0.47	1.18	0.46
L.S.D(0.01) gi	0.89	0.19	0.39	0.62	1.55	0.6
L.S.D(0.05) gi-gj	1.29	0.28	0.57	0.9	2.25	0.87
L.S.D(0.01) gi-gj	1.69	0.37	0.74	1.18	2.95	1.15

* $p< 0.05$; ** $p< 0.01$

Such results are being used to compare the average performance of each parent with other genotype and facilitate selection of parents for further improvement to drought resistance. Results indicate that the parental P_1 gave desirable significant $\hat{g}i$ effects for plant height, no of spike/ plant and biological yield/ plant. P_2 exhibited significant and positive $\hat{g}i$ effects for plant height, spike length, 1000-kernel weight, biological yield/ plant and grain yield/ plant. P3 gave useful significant $\hat{g}i$ effects for plant height, spike length and no of spikes/ plant. P_4 expressed significant and positive $\hat{g}i$

effects for plant height, spike length, no of spikes/ plant, 1000-kernel weight, biological yield/ plant and grain yield/ plant. P_5 seemed good general combiner for plant height and grain yield/ plant. P6 exhibited positive and significant ĝi effects spike length, no of spikes/ plant, 1000-grain, biological yield/ plant and grain yield/ plant. Also, it is considered the best combiner for grain yield/ plant and most of its components. P7 and P8 gave positive and significant combiner for plant height.

Specific combining ability (SCA) effects

Specific combining ability effects $\hat{s}_{ij}$ for the F_1 crosses for the studied traits in the combined analysis are presented in (Table 8).

For plant height, six crosses expressed significant and positive ŝij effects. Moreover, the cross P_1 x P_5 gave the most desirable ŝij effects for plant height. However, three cross combinations i.e. P1xP2, P2xP5 and P3xP4 gave significant and negative ŝij effects for the mention trait. For spike length, five crosses in the combined analysis expressed significant and positive ŝij effects. Moreover, the cross P_7 x P_8 gave the most desirable ŝij effects for this trait. For number of spikes/ plant, nine crosses expressed significant and positive ŝij effects. However, the best ŝij effects (5.29**) were detected for the cross P_2 x P_5.Regarding 1000-kernel weight, five cross combinations expressed significant and positive ŝij effects. The cross P3xP7 being the highest one in this traits and recorded 5.51**. twelve crosses combinations exhibited significant and positive ŝij effects for biological yield/ plant. The best positive ŝij effects were the crosses P_2 x P_5 and P_3 x P_7 in the combined analysis (Table 8). Regarding to grain yield/ plant eight crosses i. e. P1xP6, P1xP7, P2xP4, P3xP7, P3xP8, P4xP8, P5xP8 and P6xP7 exhibited significant and positive ŝij effects.

Table 8. Estimates of specific combining ability effects for yield and its components 'at the combined analysis .

It could be concluded that the previous cross combinations might be of interest in breeding programs towards the development of pure lines varieties for high biological, and grain yields/ plant under drought conditions.

cross combinations	**plant height (cm)**	**spike length(cm)**	**No. of spikes /plant**	**1000 kernel weight (g)**	**Biological yield/plant (g)**	**Grain yield/plant (g)**
P1xP2	-6.77**	-0.27	-7.85**	-3.11*	-38.62**	-6.16**
P1xP3	-1.34	-1.51**	2.30**	-0.62	3.4	-0.5
P1xP4	1.27	0.45	3.96**	-1.63	15.05**	0.67
P1xP5	11.54**	0.32	2.48**	-1.9	-10.32**	-1.54
P1xP6	4.14*	0.44	3.76**	4.74**	27.08**	7.81**
P1xP7	-3.51	-0.44	0.57	-1.18	-15.99**	5.20**
P1xP8	-3.2	-0.35	-3.72**	-1.13	-38.92**	1.91
P2xP3	-3.58	0.95*	-0.56	-1.44	-14.72**	-2.17
P2xP4	3.57	-0.26	-8.23**	2.63*	-63.07**	8.08**
P2xP5	-6.16**	-0.55	5.29**	-2.17	29.57**	-0.05
P2xP6	-1.6	-0.27	-5.43**	0.75	6.13	0.66
P2xP7	2.21	-0.31	4.88**	-2.90*	7.73*	-7.77**
P2xP8	-0.17	0.19	0.34	0.78	11.75**	-3.6**
P3xP4	-3.88*	0.41	-3.75**	-0.03	6.61*	-2.98*
P3xP5	-1.82	0.29	0.27	-1.06	-1.75	-4.78**
P3xP6	-2.01	-0.43	2.89**	-1.25	15.48**	-3.50**
P3xP7	8.13**	1.28**	-3.30**	5.51**	30.58**	5.92**
P3xP8	-1.85	-0.89*	-0.51	0.06	-11.68**	10.51**
P4xP5	8.71**	-0.09	1.27	4.12**	14.23**	-0.85
P4xP6	-0.48	-0.14	-1.2	-1.18	-0.04	-2.32
P4xP7	-2.09	1.07**	2.70**	-0.03	9.40**	-0.02
P4xP8	8.35**	0.49	-6.43**	0.29	-6.2	5.94**
P5xP6	-2.09	0.4	-1.43	-1.87	-21.07**	2.01
P5xP7	-1.36	-0.22	-2.87**	0.94	-14.30**	-0.02
P5xP8	-1.18	-1.05*	4.42**	5.04**	15.60**	4.72**
P6xP7	7.37**	-0.19	-0.5	0.74	14.76**	3.49**
P6xP8	1.22	1.15**	-2.13*	-0.54	-19.33**	1.37
P7xP8	2.4	1.44**	-10.40**	1.14	-58.57**	-10.48**
LSD5%(sij)	3.69	0.81	1.63	2.58	6.45	2.5
LSD1%(sij)	4.84	1.06	2.14	3.38	8.45	3.28
LSD5%(sij-sik)	5.46	1.2	2.41	3.81	9.54	3.7
LSD1%(sij-sik)	7.16	1.57	3.16	5	12.51	4.85
LSD5%(sij-skL)	1.82	0.4	0.8	1.27	3.18	1.23
LSD1%(sij-skL)	2.39	0.52	1.05	1.67	4.17	1.61

* $p< 0.05$; ** $p< 0.01$

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التحليل الوراثى للهجن التبادلية فى القمح تحت ظروف الإجهاد والري العادى

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لدراسة قوة الهجين والقدرة علي التآلف لصفات المحصول ومكوناته لثمانية آباء من القمح بالأضافة إلي 28 هجين ناتجة منها بنظام Half diallel وذلك في محطة تجارب بحوث كلية زراعة مشتهر جامعة بنها، حيث تم عمل تجربتين بمزرعة الكلية. في التجربة الأولي تم الري مرة واحدة بعد رية الزراعة بينما التجربة الثانية تم إجراء معاملات الري الطبيعية ، دونت البيانات علي عشرة نباتات فردية أخذت عشوائيا من كل قطعة تجريبية وقدرت قوة الهجين لكافة الصفات المدروسة كنسبة مئوية لإنحراف قيمة الهجين عن قيمة متوسط الأبوين أو قيمة الأب الأفضل. وتم تحليل البيانات باستخدام طريقة الهجن التبادلية (جرفنج 1956) الطريقة الثانية الموديل الأول . وكانت الصفات المدروسة هي : طول النبات (سم) – طول السنبلة - عدد سنابل النبات - وزن 1000 حبه –المحصول البيولوجى – محصول الحبوب/ نبات (جم). كان التباين الراجع للتراكيب الوراثية الآباء والهجن والتفاعل بين الآباء والهجن معنويا لكل الصفات المدروسة تحت ظروف التحليل المشترك.

أظهرت كلا من الآباءP2, P6,P2,P8,P2,P2أعلي قيم لصفات طول النبات ، طول السنبلة، عدد السنابل / النبات ، وزن الـ1000 حبة ، المحصول البيولوجى/ نبات ومحصول حبوب النبات الفردي علي التوالي .كما أظهر الهجين P1xP6أعلي قيم لصفة المحصول البيولوجى للنبات و الهجين P2xP4 لصفة محصول الحبوب للنبات. كان التباين الراجع للقدرة العامة والخاصة علي التآلف معنويا للصفات تحت الدراسة . كانت النسبة بين القدرة العامة/القدرة الخاصة أعلي من الوحدة للصفات تحت الدراسة فى كل من معاملتى الرى و التحليل المشترك. وأظهرت السلالة P6 قدرة عامة علي التآلف لصفات طول السنبلة ، عدد السنابل للنبات، ووزن 1000- حبة والمحصول البيولوجى للنبات و محصول حبوب النبات.أظهرت الهجن P1xP6, P1xP7, P2xP4, P3xP7, P3xP8, P4xP8, P5xP8 , P6xP7 بالنسبة لصفة محصول النبات الفردي قدرة خاصة علي التآلف معنوية.

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