

## Genetic Variability and Heterosis in F<sub>1</sub> and F<sub>2</sub> Generations of Diallel Crosses among Seven Wheat Genotypes

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### ABSTRACT

In order to study the effect of heterosis and nature of genetic on plant height and yield traits were studied in a 7x7 diallel cross without reciprocals and their F<sub>2</sub> generation in wheat to define and select an efficient and prospective material for immediate use in hybridization programs to improve grain yield of wheat in Egypt. Parents, F<sub>1</sub> and F<sub>2</sub> were evaluated for quantitative traits in 2016/2017 season. Significant genotype mean squares and its components (parents and crosses) were obtained for all traits in both generations. Significant heterosis in F<sub>1</sub> generation was obtained for all studied traits. Heterosis of grain yield/plant relative to mid parent varied from 4.64 to 75.50% in F<sub>1</sub> crosses. The P2xP3, P1xP4 and P2xP5 were the best crosses for grain yield heterosis. General (GCA) and specific (SCA) combining ability mean squares were significant for all traits. MS (GCA)/ MS (SCA) ratios indicated the relative importance of additive and non-additive gene action in their inheritance for all the traits. The nine crosses i.e. P1xP2, P1xP6, P2xP5, P2xP6, P4xP5, P4xP6, P5xP6 and P5xP7 had significant and positive  $\delta_{ij}$  effects in F<sub>1</sub> and F<sub>2</sub> generations and contained Inter-and inter-allelic interactions. Generally, no wide differences in the genetic parameters in F<sub>1</sub> and F<sub>2</sub> generations were detected. Highly significant and larger (in magnitude) values of dominance component (H<sub>2</sub>) than additive were obtained for all studied traits resulting in more values of (H<sub>1</sub>/D)<sup>0.5</sup> which were more than unity in both generations. High heritability values (in a broad-sense) along with medium or low ones in narrow-sense were exhibited in both generations, indicating that most genetic variances were due to non-additive genetic effects. The regression line passed through the origin in spike length and No. of spikes/plant in F<sub>1</sub> generation and 1000-grain weight in F<sub>2</sub> generation, revealed a presence of complete dominance. Meanwhile, it intersects the Wr axis above the origin in plant height in both generations, 1000-grain weight in F<sub>1</sub>, No of spike/plant and Spike length in F<sub>2</sub>, reflecting partial dominance.

**Keywords:** Wheat, Diallel analysis, Gene action, Combining ability.

### INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most important cereal crop in Egypt. Increasing wheat production to narrowing the gap between production and consumption is vital in Egypt. Big variation in wheat productivity in different parts of the country should be reduced to achieve a projected high productivity, through diversification of wheat breeding programs and developing new set of wheat varieties with high yielding. Heterosis depends on the balance of different combinations of gene effects as well as on the distribution of plus and minus alleles in the parents of a mating system. In self-pollinated crops, like wheat, the scope for utilization of heterosis depends mainly upon the direction and magnitude of heterosis. Heterosis over better parent may be useful in identifying the best crosses but these hybrids can be of immense practical value if they involve the best cultivars of the area (Prasad *et al.* 1998). Production of wheat hybrid seed is expensive and the economics of the commercial production of hybrid wheat have not yet been worked out. The economic feasibility would be considerably improved if sufficient heterosis were retained in the F<sub>2</sub> generation to render its production value. The segregation that occurs in an F<sub>2</sub> generation could, however, cause problems.

Wheat breeding programs mostly involve hybridization, evaluation and selection of desirable

genotypes. The assessment of combining ability and determining gene action are elementary tools for selection of ideal genotypes. Advancement in the yield of this important crop species requires adequate information regarding the nature of combining ability of the parents available in a wide array of genetic material to be used in the hybridization program and also the nature of gene actions involved in the expression of quantitative and qualitative traits of economic importance. Diallel mating design has been extensively used to analyze the combining ability effects of wheat genotypes and also to provide information regarding genetic mechanism controlling grain yield and other traits. According to Farooq *et al.* (2010) and AL Saadon *et al.* (2017), the combining ability is a most reliable biometrical tool to circumvent plant breeding programs. The diallel analysis also provides a unique opportunity to test a number of lines in all possible combinations. The present study is aimed at estimating heterosis in F<sub>1</sub> and comparing combining ability obtained from F<sub>2</sub> crosses with those of F<sub>1</sub> resulting from a set of diallel crosses for certain quantitative traits of wheat.

### MATERIALS AND METHODS

Seven parents of bread wheat representing a wide range of variability were selected for this study (Table 1).

**Table1. The code number, name and pedigree of the studied parental bread wheat varieties and lines.**

Code No.	Name	Pedigree
P1	Giza 171	Sakha 93 /Gemmeiza 9 GZ003 – 101-1GZ -1GZ – 2 GZ -0GZ
P2	Shandaweel 1	Site // MO /Nac/th.Ac./3*pvN/3/Mir 10/Buc Cmss93Boo567s-72Y-010M-010Y-010M-OHTY
P3	Sids 13	ALMAZ.19=KAUZ"S"/TSI/SNB"S"/IICSBW1-0375-4AP-2AP-030AP-0APS-3AP-0APS-050AP-0AP-0SD
P4	Misr 1	OASIS / SKAUZ //4*BCN/3/2*PASTOR CMSS00Y01881T-050M-030Y-030M-030WGY-33M-0Y-0S
P5	Gemmeiza 10	CG5820-3GM-1GM-2GM-0GM.
P6	Line1	Aj863//7C/ERA/2BUC/S887.17-301
P7	Line2	TUKURU/PASTOR CMSS99MOO728-040M-030Y-030M-31Y-3M-0Y

There were crossed in all possible combinations giving seeds of F<sub>1</sub> 15 crosses In 2015/16 season, hybrid seeds were sown to obtain F<sub>2</sub> seeds and parents were re-

crossed for obtaining adequate F<sub>1</sub> seeds. The crosses were made at the Experimental Farm of Etay El-Baroud Agricultural Research, El-Bheira governorate. In 2016/17 season, the experiment involved parents, F<sub>1</sub> hybrids and F<sub>2</sub> crosses was conducted in a randomized complete block design with four replications. Plots of parents and F<sub>1</sub>'s consisted of two rows and F<sub>2</sub> consisted four rows 3 meter long and 30 cm wide, plants within row were 20 cm apart. The recommended agricultural practices for wheat production were applied. Data were recorded on individual plant basis: 10 for F<sub>1</sub> and parents and 30 guarded plants for F<sub>2</sub> were randomly chosen from each plot. The following traits were measured: plant height, No. of spikes plant<sup>-1</sup>, No. of grains/spike, spike length, 1000 grain weight, grain yield/plant, biological yield/plant and harvest index.

Heterosis relative to better parent was computed according to Bhatt (1971) as a deviation of F<sub>1</sub> mean performance from the better parent mean value. General and specific combining ability estimates were determined according to Griffing (1956) for method 2 model 1. The genetic parameters were estimated using the procedure

described by Hayman (1954 a and b). Heritability in narrow-sense was estimated according to Mather and Jinks (1971) for F<sub>1</sub>'s data, and Verhalen and Murray (1969) for the F<sub>2</sub>'s data.

## RESULTS AND DISCUSSION

Analysis of variance of both F<sub>1</sub> and F<sub>2</sub> generations for all studied characters is shown in Table 2. Genotypes, parents, crosses and parent vs crosses mean squares were significant for all traits in both F<sub>1</sub> and F<sub>2</sub> generations except, parent vs. crosses for harvest index indicating the presence of diversity in the material and sufficient amount of genetic variability adequate for further biometrical assessment. The parents vs crosses mean squares were large in magnitude in F<sub>1</sub> analysis than F<sub>2</sub> ones for all studied traits except harvest index. These findings are reasonable and might be due to inbreeding depression existing the F<sub>2</sub> which would reduce the heterosis effects. Significant differences among genotypes for grain yield and related traits in different sets of material of wheat were reported by Seleem and Kumber (2011).

**Table 2. Significance of mean squares from ordinary and combining ability analysis for all characters studied in F<sub>1</sub> and F<sub>2</sub> generations.**

SOV	df	Mean squares									
		Days to maturity	Plant height	No. of spikes plant <sup>-1</sup>	No. of grains spike <sup>-1</sup>	Spike length	1000-grain weight	Grain yield plant <sup>-1</sup>	Biological yield	Harvest index	
F <sub>1</sub> diallel cross											
Blocks	3	2.61**	5.86**	1.30*	8.12**	0.95**	2.67	18.13	3.85**	9.23	
Genotypes	20	17.09**	103.77**	18.97**	104.67**	2.34**	16.36**	235.36**	756.97**	133.51**	
Parent (P)	5	8.83**	191.96**	36.42**	21.22**	1.57**	46.58**	275.59**	852.42**	171.88**	
F <sub>1</sub> hybrid (h)	14	3.39**	76.04**	9.07**	91.55**	2.51**	7.69**	206.41**	546.37**	128.60**	
P vs h (heterosis)	1	340.67**	129.22**	112.32**	867.92**	3.55**	8.28**	573.11**	4396.44**	1.40	
Error	60	0.40	0.14	0.29	0.32	0.03	1.13	18.84	0.51	11.25	
GCA	5	2.60**	102.72**	3.77**	28.11**	1.78**	13.62**	122.46**	319.49**	26.12**	
SCA	15	6.58**	15.12**	7.05**	36.83**	0.49**	3.12**	65.88**	233.13**	49.75**	
Error	60	0.13	0.05	0.10	0.11	0.01	0.38	6.28	0.17	3.75	
GCA/SCA		0.40	6.79	0.53	0.76	3.62	4.37	1.86	1.37	0.53	
F <sub>2</sub> generation											
Blocks	3	2.58**	0.94	0.26	3.39**	0.03	0.12	23.69**	16.94**	11.02**	
Genotypes	20	9.78**	97.69**	19.81**	75.14**	1.75**	23.16**	156.08**	323.70**	112.86**	
Parent (P)	5	16.30**	132.60**	26.67**	48.09**	1.53**	43.66**	254.79**	850.23**	167.01**	
F <sub>2</sub> hybrid	14	8.17**	88.53**	18.49**	76.49**	1.87**	18.08**	129.31**	155.15**	102.08**	
P vs F <sub>2</sub> hybrid	1	2.89**	71.57**	5.10**	210.43**	0.65**	1.70**	99.03**	535.65**	3.55**	
Error	60	0.36	0.30	0.14	0.37	0.04	0.06	0.31	0.35	0.27	
GCA	5	5.15**	73.20**	2.12**	13.05**	1.15**	19.24**	72.43**	138.86**	31.87**	
SCA	15	2.72**	20.95**	7.89**	28.47**	0.42**	4.43**	46.20**	99.05**	39.26**	
Error	60	0.12	0.10	0.05	0.12	0.01	0.02	0.10	0.12	0.09	
GCA/SCA		1.89	3.49	0.27	0.46	2.74	4.34	1.57	1.40	0.81	

\* p<0.05; \*\* p<0.01

Mean performance values of the parents, F<sub>1</sub> and F<sub>2</sub> generations for all traits are presented in Table 3. For days to maturity, the F<sub>2</sub> hybrids: P1xP3, P1xP4, P1xP6 and P5xP6 had the lowest values. On the other hand, for F<sub>1</sub> hybrids: P5xP6, P6xP7, P4xP6 and P2xP4 had the lowest values too. For plant height, the lowest values were detected by F<sub>1</sub> hybrids: P3xP7, P1xP3 and P1xP6 and F<sub>2</sub> hybrids P3xP7, P1xP3 and P2xP7, whereas three F<sub>2</sub> hybrids P1xP7, P1xP4 and P1xP5 had the highest values. Dwarf plants are more lodging resistant whereas tall plants are preferred for straw purpose thus preference depends upon the breeding objective, EL-Hosary and Abdelwahed (2015)

Four F<sub>1</sub> hybrids (P1xP3, P1xP2, P1xP4 and P1xP6) had the highest number of spikes plant<sup>-1</sup> as well as two F<sub>2</sub> hybrids P1xP3 and P1xP2.

For No. of grains spike<sup>-1</sup>; the P7 and the two F<sub>1</sub> hybrids P2xP5 and P1xP6 as well as the F<sub>2</sub> crosses P2xP5, P1xP6 and P1xP2 expressed the highest values for this trait. The F<sub>1</sub> hybrids P1xP7 and P1xP2 were the highest hybrids for spike length as well as three F<sub>2</sub> hybrids; P1xP7, P2xP5 and P1xP4. As for 1000-grain weight, the F<sub>1</sub> hybrid P5xP6 exhibited the highest weight.

With regard to biological yield, two F<sub>1</sub> hybrids (P1xP6 and P5xP6) as well as the three F<sub>2</sub> hybrids P2xP4 and P4xP5 expressed the highest values. As for harvest index, the two F<sub>1</sub> hybrids P2xP3 and P1xP4 exhibited the highest values as well as the F<sub>2</sub> hybrids.

For grain yield/plant; one F<sub>1</sub> hybrids (P1xP4) and two F<sub>2</sub> hybrid (P1xP4 and P2xP3) as well as P7 showed the highest values. The high yield plant<sup>-1</sup> of the P7 could

be attributed to its high No. of grains/spike and No. of spikes/plant. On the other hand, the high grain yield/plant of the one aforementioned F<sub>1</sub> hybrids and the two F<sub>2</sub> hybrids could be attributed to the high values of No. of spikes plant, No. of grains/spike and grain yield/plant. Therefore, these crosses could be efficient for prospective wheat breeding programs aiming at improving wheat grain yield.

**Table 3. Mean performance of all studied genotypes (parents, F<sub>1</sub> and F<sub>2</sub> generations) for all studied traits.**

Genotype	Days to maturity	Plant height	No. of spikes plant <sup>-1</sup>	No. of grains spike <sup>-1</sup>	Spike length	1000-grain weight	Grain yield plant <sup>-1</sup>	Biological yield	Harvest index
Parents									
P1 (Giza 171)	148.33	101.69	10.10	70.47	11.90	36.12	43.07	119.80	35.95
P2 (Shandaweel 1)	144.67	105.84	10.79	65.22	12.92	44.20	30.13	98.22	30.68
P3 (Sids 13)	148.33	92.68	12.48	65.22	11.37	43.07	24.57	114.25	21.51
P4 (Misr 1)	146.00	100.63	12.54	69.68	12.30	36.15	30.82	108.85	28.31
P5 (Gemmeiza 10)	147.67	103.63	10.50	69.80	12.58	45.05	31.64	80.27	39.42
P6 (Line1)	145.33	102.92	13.40	68.83	13.06	40.75	42.27	98.12	43.08
P7 (Line2)	144.33	83.15	20.27	72.30	13.48	36.72	51.87	131.80	39.35
F <sub>1</sub> crosses									
P1xP2	143.67	100.98	17.70	82.43	14.43	41.23	50.90	134.23	37.92
P1xP3	141.33	88.63	19.50	76.13	12.27	40.98	49.00	125.70	38.98
P1xP4	141.67	100.61	16.67	80.50	13.36	38.23	61.48	137.76	44.63
P1xP5	143.33	99.90	17.65	74.04	13.61	38.15	49.15	136.93	35.90
P1xP6	142.33	89.12	17.54	84.10	13.52	40.45	45.07	144.77	31.13
P1xP7	142.67	98.79	14.87	74.58	14.88	42.52	42.03	129.13	32.55
P2xP3	141.33	95.86	12.87	79.10	11.93	41.83	48.00	97.17	49.43
P2xP4	140.67	95.80	13.84	80.89	13.29	40.43	34.01	100.89	33.71
P2xP5	142.67	102.55	15.12	88.37	13.72	41.17	47.12	120.04	39.26
P2xP6	143.33	102.69	16.94	82.35	13.55	40.25	48.90	130.99	37.33
P2xP7	141.67	92.00	13.64	75.18	13.07	43.07	37.51	124.87	30.04
P3xP4	142.33	93.36	12.82	65.94	11.62	40.48	32.00	100.73	31.77
P3xP5	141.33	96.08	17.08	76.45	11.80	42.78	24.81	129.97	19.09
P3xP6	141.00	99.91	14.32	69.97	11.82	41.63	41.15	113.92	36.13
P3xP7	141.67	84.79	14.95	75.79	12.65	41.15	46.37	136.14	34.06
P4xP5	141.67	100.07	15.29	75.13	12.62	40.12	39.37	114.80	34.29
P4xP6	140.33	94.93	15.94	75.80	12.57	40.00	28.79	130.45	22.05
P4xP7	142.33	91.46	14.90	70.27	13.47	39.55	38.39	113.66	33.78
P5xP6	139.67	99.18	15.53	70.57	13.50	45.22	42.56	141.52	30.07
P5xP7	141.00	94.75	14.45	69.46	13.49	40.22	39.82	122.96	32.38
P6xP7	140.33	90.02	14.70	73.39	11.64	41.92	43.33	118.15	36.68
LSD 5%	1.03	0.61	0.88	0.92	0.26	1.73	7.09	1.17	5.48
LSD 1%	1.37	0.81	1.17	1.22	0.34	2.30	9.43	1.56	7.28
F <sub>2</sub> generation									
P1xP2	149.33	99.58	17.72	79.72	12.41	39.40	37.97	112.00	33.90
P1xP3	144.33	89.65	18.75	69.72	11.70	37.93	41.03	116.25	35.29
P1xP4	144.67	103.18	10.47	71.32	13.27	37.53	47.48	109.79	43.25
P1xP5	145.33	103.00	11.11	66.05	13.21	37.27	37.95	105.38	36.01
P1xP6	144.67	92.32	10.42	79.74	12.24	36.98	36.61	116.62	31.39
P1xP7	146.00	107.00	12.61	61.37	13.97	41.53	40.22	106.68	37.70
P2xP3	145.00	92.24	7.69	73.25	11.00	38.67	47.29	98.43	48.04
P2xP4	146.67	90.75	14.92	74.13	13.00	41.65	44.40	119.43	37.17
P2xP5	147.67	101.82	12.34	80.19	13.42	43.92	40.40	111.52	36.23
P2xP6	145.00	101.25	10.72	76.00	12.93	42.98	39.23	107.29	36.57
P2xP7	145.67	90.67	10.85	69.57	12.44	41.72	32.38	103.47	31.29
P3xP4	148.33	92.17	12.04	65.97	11.52	40.52	30.25	94.61	31.97
P3xP5	147.67	93.58	12.55	65.02	11.60	43.70	23.06	99.44	23.19
P3xP6	146.67	96.50	11.17	67.90	11.38	42.15	30.31	99.70	30.40
P3xP7	147.00	85.11	11.93	71.84	11.65	41.37	29.99	109.69	27.34
P4xP5	145.00	97.80	14.14	69.16	12.47	38.43	29.75	119.14	24.97
P4xP6	145.00	92.09	14.08	67.58	12.30	42.55	30.97	104.36	29.67
P4xP7	149.00	97.10	10.85	70.00	12.00	39.42	33.91	99.88	33.95
P5xP6	144.67	96.67	11.25	71.46	12.34	42.02	30.25	103.58	29.20
P5xP7	149.33	93.25	12.14	66.12	12.45	45.62	30.62	110.05	27.82
P6xP7	146.00	93.72	12.20	69.54	11.20	43.20	29.22	99.09	29.48
LSD 5%	0.98	0.90	0.61	0.99	0.33	0.41	0.91	0.97	0.856
LSD 1%	1.31	1.20	0.82	1.31	0.44	0.54	1.21	1.28	1.139

Means followed by the same letter for each tested parameter are not significantly different By Duncan's test (P < 0.05)

**Heterosis**

Mean squares for parents vs hybrids in F<sub>1</sub> generation, as an indication of average of heterosis in F<sub>1</sub> across all crosses were significant for all the studied traits (Table 2). The heterotic effects relative to mid parent are presented in Table 4. The most significant and desirable negative heterosis relative to mid parent was exhibited by

four crosses (P3 xP6, P1xP3, P5xP6 and P3xP5) gave the highest heterotic value for days to maturity, four crosses (P1xP6, P1xP3, P2xP4 and P4xP4) while, cross P1xP7 had most significant and desirable positive heterosis relative to mid parent for plant height. Also in positive direction the most significant and desirable heterosis relative to mid parent was exhibited by eight crosses P1xP3, P1xP5,

P1xP2, P1xP4, P1xP6, P2xP5, P2xP6, P3xP5 and P4xP5 for No. of spike plant<sup>-1</sup>, eight crosses (P2xP5, P2xP6, P2xP3, P1xP2, P1xP4, P1xP6, P2xP4 and P3xP5) for No. of grains spike<sup>-1</sup>, eight crosses (P1xP7, P1xP2, P1xP5, P1xP4, P1xP6, P2xP5, P2xP4 and P5xP6) for spike length, four crosses P1xP7, P4xP7, P6xP7 and P1xP4 for 1000 grains weight, six crosses P5xP6, P1xP5, P2xP5, P2xP6, P3xP5 and P1xP6 for biological yield and four crosses P2xP3, P1xP4, P1xP3 and P3xP6 for harvest index.

Concerning grain yield plant<sup>-1</sup>, ten crosses (P1xP4, P2xP3, P2xP5, P3xP6, P1xP2, P1xP3, P1xP5, P2xP4, P3xP7 and P4xP5), showed significant positive heterotic effects. These hybrids exhibited heterosis for one or more of the contributing traits. Significant positive heterotic effects relative to higher yielding parent were obtained by Fonseca and Patterson (1968). Innamullah *et al.* (2006) and Shah *et al.* (2018) reported heterosis in several crosses of bread wheat for maturity traits, plant height, spike length, No. of grains/plant and 1000 grains weight. Prakash (2006) and EL-Hosary and Abdelwahed (2015) reported heterosis for yield and yield components in wheat as manifestation of dominant gene action.

**Combining ability**

The analysis of variance for both general (GCA) and specific (SCA) combining abilities show that the mean squares were highly significant for all studied traits in both generations (Table 2) which indicates the importance of both additive and non-additive gene effects in the inheritance of such traits. The relative importance of additive and non-additive gene action is essential for the development of an

efficient hybridization program. The concept of combining ability as a measure of gene action refers to the capacity or ability of genotype to transmit superior performance to its crosses. The value of an inbred line depends on its ability to produce superior hybrids in combination with other inbreds. If both GCA and SCA mean squares are significant, it is vital to determine the type of gene action which is important in determining the performance of progeny. To overcome such situation the magnitude of mean squares can be used to assume the relative importance of general and specific combining ability mean squares which were highly significant. Hence, GCA/ SCA ratio was used to reveal the nature of genetic variance involved. The ratio of MS GCA/ MS SCA (Table 2) displays the relative importance of additive and non-additive gene action effects in their inheritance. Therefore, selection for some traits in early generations would be effective in developing the high yielding varieties in wheat breeding programs. The preponderance of additive genetic variation for yield and some of its related characters in F<sub>1</sub> and F<sub>2</sub> generations indicate that the parents involved in these crosses could be selected based on their GCA values. The genetic variance was previously reported to be mostly due to additive for yield traits by El Hosary *et al.* (2012), Gomaa *et al.* (2014) AL Saadon *et al.* (2017) and Rahul *et al.* (2017). On the other hand, the non-additive genetic variance was previously reported to be the most prevalent for plant height, No. of spike plant<sup>-1</sup> for No. of kernels spike<sup>-1</sup>, 1000-grain weight and grain yield plant<sup>-1</sup> by Mohammad *et al.* (2009), Abdel Nour *et al.* (2011) and Rahul *et al.* (2017).

**Table 4. Heterosis percentage relative to mid parent for studied traits in the studied F<sub>1</sub> wheat crosses.**

Crosse	Days to maturity	Plant height	No. of spikes plant <sup>-1</sup>	No. of grains spike <sup>-1</sup>	Spike length	1000-grain weight	Grain yield plant <sup>-1</sup>	Biological yield	Harvest index
P1xP2	-1.93**	-2.68**	69.41**	21.51**	16.30**	2.67	39.08**	23.14**	13.82
P1xP3	-4.72**	-8.80**	72.67**	12.21**	5.41**	3.51	44.89**	7.41**	35.69**
P1xP4	-3.74**	-0.55	47.29**	14.88**	10.43**	5.81*	66.43**	20.50**	38.90**
P1xP5	-3.15**	-2.69**	71.36**	5.57**	11.16**	-6.00**	31.59**	36.89**	-4.75
P1xP6	-3.06**	-12.89**	49.26**	20.74**	8.29**	5.24*	5.62	32.86**	-21.22**
P1xP7	-2.51**	6.89**	-2.07	4.48**	17.25**	16.75**	-11.46	2.64**	-13.56
P2xP3	-3.53**	-3.43**	10.55**	21.28**	-1.73	-4.13*	75.50**	-8.53**	89.45**
P2xP4	-3.21**	-7.21**	18.67**	19.93**	5.43**	0.64	11.61	-2.56**	14.29
P2xP5	-2.39**	-2.09**	42.05**	30.90**	7.61**	-7.75**	52.58**	34.51**	12.01
P2xP6	-1.15**	-1.63**	40.07**	22.87**	4.32**	-5.24*	35.08**	33.43**	1.23
P2xP7	-1.96**	-2.64**	-12.15**	9.33**	-0.98	6.45**	-8.51	8.57**	-14.21
P3xP4	-3.28**	-3.41**	2.48	-2.23**	-1.84	2.21	15.55	-9.70**	27.53**
P3xP5	-4.50**	-2.11**	48.60**	13.24**	-1.48	-2.89	-11.72	33.63**	-37.33**
P3xP6	-4.73**	1.79**	24.61**	3.63**	-1.34	-5.50**	46.43**	17.13**	18.59*
P3xP7	-3.19**	-3.55**	-8.70**	10.23**	1.80	3.15	21.32*	10.66**	11.92
P4xP5	-3.52**	-2.02**	32.72**	7.73**	1.41	-1.19	26.06*	21.41**	1.26
P4xP6	-3.66**	-6.73**	22.94**	9.45**	-0.87	4.03	-21.23*	26.06**	-38.24**
P4xP7	-1.95**	-0.47	-9.14**	-1.01	4.51**	8.55**	-7.13	-5.54**	-0.16
P5xP6	-4.66**	-3.97**	29.93**	1.80**	5.32**	5.40**	15.16	58.67**	-27.10**
P5xP7	-3.42**	1.46**	-6.09*	-2.24**	3.50**	-1.63	-4.64	15.96**	-17.78
P6xP7	-3.11**	-3.24**	-12.67**	4.00	-12.27**	8.22**	-7.94	2.78**	-11.02
LSD 5%	1.03	0.61	0.88	0.92	0.26	1.73	7.09	1.17	5.48
LSD 1%	1.37	0.81	1.17	1.22	0.34	2.30	9.43	1.56	7.28

\* p<0.05; \*\* p<0.01

**General combining ability effects**

General combining ability effects  $\hat{g}_i$  of individual parent for each trait from both F<sub>1</sub> and F<sub>2</sub> generations are presented in Table 5.

The estimates of  $\hat{g}_i$  effects obtained from F<sub>2</sub> generation were similar to those of F<sub>1</sub> generation in most cases. High positive response would be of interest for all studied traits except for days to maturity the best cross

combination for earliness in maturity is preferred and plant height since short stature is preferred due to non-liability to lodging and progressive response to increased rate of fertilizer. Therefore, negative combining ability effects regarding days to maturity and plant height are preferred in wheat.

The parental line P1 (Giza 171) exhibited significant desirable  $\hat{g}_i$  effect among all the tested parents for all

studied traits in both F<sub>1</sub> and F<sub>2</sub> except for the, Days to maturity, plant height in negative direction and 1000- grain weight in F<sub>1</sub> and plant height in negative direction, No. of spikes plant<sup>-1</sup> and 1000- grain weight in F<sub>2</sub> generation. The parental variety P<sub>2</sub> (Shandawel 1) gave significant desirable  $\hat{g}_i$  effects for most studied traits in both F<sub>1</sub> and F<sub>2</sub>. But, it gave significant undesirable or insignificant  $\hat{g}_i$  effects for other traits. The variety P<sub>3</sub> (Sids 13) expressed significant negative  $\hat{g}_i$  effects and seemed to be the good combiner for plant height in both F<sub>1</sub> and F<sub>2</sub>. Thus it could be utilized to reduce plant height in wheat. Also, the variety P<sub>4</sub> (Misr 1) expressed significant negative  $\hat{g}_i$  effects and seemed to be the good combiner for days to maturity in both F<sub>1</sub> and F<sub>2</sub>.

The parental line P<sub>5</sub> (Gemmeiza 10) expressed significant desirable  $\hat{g}_i$  effects for spike length and 1000-kernel weight in F<sub>1</sub> generation and for spike length, 1000-kernel weight and No. of spikes plant<sup>-1</sup> in F<sub>2</sub> generations. The parental line P<sub>6</sub> (Line 1) expressed significant desirable  $\hat{g}_i$  effects for days to maturity, No. of spikes/plant, 1000-grain weight and biological yield/plant in F<sub>1</sub> generations, while days to maturity, No. of grains/spike, 1000-grain weight and harvest index in F<sub>2</sub> generations. Such obtained results suggested that a great opportunity for selection would be possible for yield and its components having earliness in maturity. Earliness in maturity is essentially a pre-requisite in breeding programme of a crop.

**Table 5. Estimates of parental general combining ability effects for all studied traits in F<sub>1</sub> and F<sub>2</sub> generations.**

Parent	Days to maturity	Plant height	No. of spikes plant <sup>-1</sup>	No. of grains spike <sup>-1</sup>	Spike length	1000-grain weight	Grain yield plant <sup>-1</sup>	Biological yield	Harvest index
F <sub>1</sub>									
P1 (Giza 171)	0.95**	1.04**	0.57**	1.99**	0.32**	-1.43**	6.32**	9.92**	2.10**
P2 (Shandawel 1)	-0.05	3.28**	-0.81**	2.66**	0.32**	1.08**	-0.02	-6.03**	1.66**
P3 (Sids 13)	0.28*	-3.11**	-0.28**	-2.34**	-0.91**	0.92**	-4.05**	-2.97**	-2.41**
P4 (Misr 1)	-0.24*	0.61**	-0.49**	-0.77**	-0.16**	-1.73**	-3.47**	-4.76**	-1.92**
P5 (Gemmeiza 10)	0.21	3.09**	-0.32**	-0.14	0.10**	1.23**	-2.31**	-3.57**	-0.48
P6 (Line1)	-0.61**	1.08**	0.31**	-0.11	-0.03	0.47*	0.83	1.91**	0.60
P7 (Line2)	-0.53**	-5.99**	1.01**	-1.29**	0.35**	-0.54**	2.70**	5.51**	0.45
LSD gi 5%	0.22	0.13	0.19	0.20	0.06	0.38	1.55	0.26	1.20
LSD gi 1%	0.30	0.18	0.25	0.27	0.07	0.50	2.06	0.34	1.59
LSD gi-gj 5%	0.34	0.20	0.29	0.31	0.09	0.58	2.36	0.39	1.83
LSD gi-gj 1%	0.46	0.27	0.39	0.41	0.11	0.77	3.14	0.52	2.43
F <sub>2</sub>									
P1 (Giza 171)	-0.87**	2.95**	0.01	0.73**	0.20**	-2.46**	4.11**	4.83**	2.30**
P2 (Shandawel 1)	-0.32**	1.20**	-0.07	1.76**	0.31**	0.18**	2.61**	0.04	2.42**
P3 (Sids 13)	0.09	-4.46**	-0.28**	-1.73**	-0.73**	0.05	-3.20**	-2.89**	-2.23**
P4 (Misr 1)	-0.47**	0.15	0.26**	-0.66**	-0.11**	-1.01**	-1.93**	0.27*	-2.07**
P5 (Gemmeiza 10)	0.61**	2.75**	-0.50**	0.57**	0.25**	1.90**	-2.56**	-4.06**	-0.75**
P6 (Line1)	-0.39**	0.68**	-0.36**	0.39**	-0.05	1.44**	-0.87**	-3.72**	0.54**
P7 (Line2)	1.35**	-3.27**	0.94**	-1.07**	0.14**	-0.10*	1.84**	5.52**	-0.21*
LSD gi 5%	0.21	0.20	0.13	0.22	0.07	0.09	0.20	0.21	0.19
LSD gi 1%	0.28	0.26	0.18	0.29	0.10	0.12	0.26	0.28	0.25
LSD gi-gj 5%	0.33	0.30	0.20	0.33	0.11	0.14	0.30	0.32	0.29
LSD gi-gj 1%	0.44	0.40	0.27	0.44	0.15	0.18	0.40	0.43	0.38

\* p<0.05; \*\* p<0.01 and r refer to the correlation coefficient between GCA effects for parents and its mean performance.

The parental line P<sub>7</sub> (Line 2) expressed significant desirable  $\hat{g}_i$  effects for days to maturity, plant height, No. of spikes plant<sup>-1</sup>, spike length, grain yield plant<sup>-1</sup> and biological yield plant<sup>-1</sup> in both F<sub>1</sub> and the same traits in F<sub>2</sub> generations except days to maturity. Such obtained results suggested that a great opportunity for selection would be possible for earliness in maturity, yield and its components having a semi-dwarf plant height hence can response to more N fertilizers without least of lodging. These results are in harmony with those obtained by Gurmani *et al* (2007), EL-Shaarawy and Kumber (2010) and Seleem and Kumber (2011), Kumar *et al.* (2017) and AL Saadon *et al.* (2018).

**Specific combining ability effects**

Specific combining ability effects  $\hat{s}_{ij}$  of both F<sub>1</sub> and F<sub>2</sub> for all traits are presented in Table 6, and show highly significant desirable  $\hat{s}_{ij}$  values for some crosses in the F<sub>1</sub> than F<sub>2</sub> generation. This result is expected indicating inbreeding depression in the F<sub>2</sub> reducing the non-additive or increased the additive portion.

As for days to maturity fourteen cross combinations showed significant and negative  $\hat{s}_{ij}$  effects. Cross P5xP6

showed (-2.82) highest significant negative  $\hat{s}_{ij}$  effects followed by P1xP3 (-2.79) and P3xP5 (-2.05) at F<sub>1</sub> generation and followed by P2xP7 and P4xP5 at F<sub>2</sub> generation. With regard to plant height, twelve crosses expressed significant and negative  $\hat{s}_{ij}$  effects at F<sub>1</sub> and F<sub>2</sub> generation, respectively.

Such results indicate that crosses P<sub>1</sub>xP<sub>6</sub>, P<sub>1</sub>xP<sub>3</sub>, P<sub>2</sub>xP<sub>4</sub> and P<sub>4</sub>xP<sub>6</sub> of F<sub>1</sub> and F<sub>2</sub> recorded the highest desirable  $\hat{s}_{ij}$  effects for this trait. As for No. of spike plant<sup>-1</sup>; eleven crosses gave significant and positive  $\hat{s}_{ij}$  effects, four of them (P<sub>1</sub>xP<sub>3</sub>, P<sub>1</sub>xP<sub>2</sub>, P<sub>3</sub>xP<sub>5</sub> and P<sub>2</sub>xP<sub>6</sub>) gave the highest number of spikes plant<sup>-1</sup> significant and positive  $\hat{s}_{ij}$  effects in F<sub>1</sub> and seven crosses in F<sub>2</sub> five of them gave the large number of significant and positive  $\hat{s}_{ij}$  effects (P<sub>1</sub>xP<sub>3</sub>, P<sub>1</sub>xP<sub>2</sub>, P<sub>2</sub>xP<sub>4</sub>, P<sub>4</sub>xP<sub>5</sub> and P<sub>4</sub>xP<sub>6</sub>).

For No. of grain spike<sup>-1</sup>, twelve crosses in F<sub>1</sub> generations had significant positive  $\hat{s}_{ij}$  effects seven of them P<sub>2</sub>xP<sub>5</sub> (11.5), P<sub>1</sub>xP<sub>6</sub> (7.87), P<sub>2</sub>xP<sub>6</sub> (5.45), P<sub>3</sub>xP<sub>7</sub> (5.06), P<sub>1</sub>xP<sub>4</sub> (4.93) and P<sub>2</sub>xP<sub>4</sub> (4.65) gave the highest significant and positive  $\hat{s}_{ij}$  effects in F<sub>1</sub>. Eleven crosses in F<sub>2</sub> and five of them gave the highest significant and positive  $\hat{s}_{ij}$  effects P<sub>1</sub>xP<sub>6</sub> (8.79), P<sub>2</sub>xP<sub>5</sub> (8.02), P<sub>1</sub>xP<sub>2</sub> (7.39), P<sub>3</sub>xP<sub>7</sub> (4.81) and P<sub>2</sub>xP<sub>6</sub> (4.02).

Table 6. Estimates of specific combining ability effects of the parental combination for all studied traits in F<sub>1</sub> and F<sub>2</sub> generations.

Cross	Days to maturity	Plant height	No. of spikes plant <sup>-1</sup>	No. of grains spike <sup>-1</sup>	Spike length	1000-grain weight	Grain yield plant <sup>-1</sup>	Biological yield	Harvest index
F <sub>1</sub>									
P1xP2	-0.12	0.15	3.06**	3.43**	0.92**	0.75	3.74	10.49**	-0.10
P1xP3	-2.79**	-5.80**	4.33**	2.13**	-0.02	0.66	5.87*	-1.10**	5.03**
P1xP4	-1.94**	2.45**	1.72**	4.93**	0.33**	0.56	17.77**	12.75**	10.19**
P1xP5	-0.71*	-0.73**	2.53**	-2.16**	0.31**	-2.48**	4.28	10.73**	0.01
P1xP6	-0.90**	-9.50**	1.78**	7.87**	0.35**	0.57	-2.94	13.09**	-5.83**
P1xP7	-0.64	7.23**	-1.58**	-0.47	1.33**	3.65**	-7.85**	-6.16**	-4.27*
P2xP3	-1.79**	-0.81**	-0.92**	4.42**	-0.35**	-1.00	11.21**	-13.69**	15.92**
P2xP4	-1.94**	-4.60**	0.27	4.65**	0.26**	0.25	-3.36	-8.18**	-0.29
P2xP5	-0.38	-0.32	1.38**	11.50**	0.43**	-1.97**	8.59**	9.78**	3.81*
P2xP6	1.10**	1.82**	2.57**	5.45**	0.39**	-2.14**	7.23**	15.25**	0.81
P2xP7	-0.64	-1.79**	-1.43**	-0.55	-0.47**	1.69**	-6.03**	5.52**	-6.33**
P3xP4	-0.60	-0.64**	-1.28**	-5.30**	-0.19*	0.45	-1.35	-11.39**	1.83
P3xP5	-2.05**	-0.39*	2.80**	4.57**	-0.27**	-0.20	-9.70**	16.65**	-12.29**
P3xP6	-1.56**	5.45**	-0.59*	-1.94**	-0.12	-0.60	3.51	-4.87**	3.66*
P3xP7	-0.97**	-2.61**	-0.65*	5.06**	0.33**	-0.07	6.85**	13.74**	1.75
P4xP5	-1.19**	-0.13	1.23**	1.69**	-0.20*	-0.22	4.28	3.28**	2.42
P4xP6	-1.71**	-3.25**	1.25**	2.33**	-0.11	0.42	-9.43**	13.45**	-10.90**
P4xP7	0.21	0.34	-0.48	-2.03**	0.41**	0.98	-1.70	-6.95**	0.98
P5xP6	-2.82**	-1.48**	0.66*	-3.54**	0.56**	2.68**	3.18	23.32**	-4.32*
P5xP7	-1.56**	1.15**	-1.12**	-3.47**	0.16	-1.31*	-1.43	1.15**	-1.86
P6xP7	-1.42**	-1.57**	-1.49**	0.43	-1.56**	1.14*	-1.05	-9.13**	1.36
LSD Sij 5%	0.65	0.39	0.56	0.58	0.16	1.10	4.50	0.74	3.48
LSD Sij 1%	0.87	0.51	0.74	0.78	0.22	1.46	5.98	0.99	4.62
LSD sij-sik 5%	0.97	0.57	0.83	0.87	0.24	1.63	6.68	1.10	5.16
LSD sij-sik 1%	1.29	0.76	1.10	1.15	0.32	2.17	8.89	1.47	6.87
LSD sij-skl 5%	0.91	0.54	0.77	0.81	0.23	1.53	6.25	1.03	4.83
LSD sij-skl 1%	1.21	0.71	1.03	1.08	0.30	2.03	8.31	1.37	6.42
F <sub>2</sub>									
P1xP2	4.08**	-0.80**	5.54**	7.39**	-0.35**	0.88**	-3.52**	1.62**	-3.78**
P1xP3	-1.32**	-5.06**	6.78**	0.89**	-0.02	-0.46**	5.35**	8.80**	2.26**
P1xP4	-0.44	3.86**	-2.04**	1.41**	0.92**	0.21	10.54**	-0.82**	10.05**
P1xP5	-0.84**	1.08**	-0.64**	-5.09**	0.51**	-2.97**	1.64**	-0.91**	1.50**
P1xP6	-0.51	-7.53**	-1.47**	8.79**	-0.16	-2.80**	-1.40**	9.99**	-4.42**
P1xP7	-0.92**	11.09**	-0.58**	-8.13**	1.37**	3.30**	-0.49	-9.19**	2.65**
P2xP3	-1.21**	-0.72*	-4.20**	3.39**	-0.83**	-2.37**	13.11**	-4.23**	14.88**
P2xP4	1.01**	-6.82**	2.49**	3.20**	0.54**	1.68**	8.95**	13.60**	3.85**
P2xP5	0.94**	1.64**	0.68**	8.02**	0.60**	1.03**	5.59**	10.02**	1.59**
P2xP6	-0.73*	3.15**	-1.09**	4.02**	0.42**	0.56**	2.73**	5.45**	0.64*
P2xP7	-1.81**	-3.49**	-2.25**	-0.96**	-0.27*	0.84**	-6.84**	-7.61**	-3.88**
P3xP4	2.27**	0.27	-0.17	-1.47**	0.10	0.67**	0.60*	-8.28**	3.29**
P3xP5	0.53	-0.92**	1.10**	-3.65**	-0.17	0.94**	-5.96**	0.87**	-6.80**
P3xP6	0.53	4.07**	-0.43*	-0.59	-0.09	-0.15	-0.39	0.80*	-0.88**
P3xP7	-0.88**	-3.38**	-0.97**	4.81**	-0.02	0.61**	-3.41**	1.55**	-3.18**
P4xP5	-1.58**	-1.32**	2.14**	-0.59	0.07	-3.26**	-0.53	17.42**	-5.19**
P4xP6	-0.58	-4.96**	1.95**	-1.98**	0.21	1.32**	-1.00**	2.29**	-1.78**
P4xP7	1.68**	4.00**	-2.58**	1.89**	-0.29**	-0.27	-0.77**	-11.43**	3.26**
P5xP6	-1.99**	-2.98**	-0.13	0.67*	-0.12	-2.13**	-1.09**	5.85**	-3.56**
P5xP7	0.94**	-2.46**	-0.54**	-3.22**	-0.20	3.02**	-3.42**	3.07**	-4.18**
P6xP7	-1.40**	0.09	-0.61**	0.39	-1.15**	1.06**	-6.52**	-8.23**	-3.82**
LSD Sij 5%	0.62	0.57	0.39	0.63	0.21	0.26	0.58	0.61	0.54
LSD Sij 1%	0.83	0.76	0.52	0.83	0.28	0.34	0.77	0.81	0.72
LSD sij-sik 5%	0.93	0.85	0.58	0.93	0.31	0.38	0.85	0.91	0.81
LSD sij-sik 1%	1.23	1.13	0.77	1.24	0.42	0.51	1.14	1.21	1.07
LSD sij-skl 5%	0.87	0.79	0.54	0.87	0.29	0.36	0.80	0.85	0.76
LSD sij-skl 1%	1.15	1.06	0.72	1.16	0.39	0.48	1.06	1.13	1.00

\* p<0.05; \*\* p<0.01 and r refer to the correlation coefficient between SCA effects for hybrid and its mean performance.

With respect to spike length, eleven and five crosses exhibited significant and positive  $\hat{s}_{ij}$  effects in F<sub>1</sub> and F<sub>2</sub> generations, respectively. The cross P1xP7 was identified as best cross combination in both generations and can be useful for further improvement of the trait. As for 1000-grain weight, four and twelve crosses exhibited significant and positive  $\hat{s}_{ij}$  effects in F<sub>1</sub> and F<sub>2</sub> generations, respectively. Crosses P1xP7 and P5xP6 in F<sub>1</sub> generation

and P1xP7 and P5xP7 in F<sub>2</sub> generation were identified as best specific cross combination for this trait.

With regard to biological yield plant<sup>-1</sup>, thirteen crosses exhibited significant and positive  $\hat{s}_{ij}$  effects in both generations. Cross P5xP6 and P4xP5 were identified as best specific cross combination for this trait in F<sub>1</sub> and F<sub>2</sub> generations respectively.

For grain yield plant<sup>-1</sup>, six and eight crosses had significant and positive  $\hat{s}_g$  effects in F<sub>1</sub> and F<sub>2</sub> generations, respectively. Inter-and intera-allelic interactions were detected in the crosses P1xP4, P2xP3, P2xP5, P2xP6, P3xP7 and P1xP3 in F<sub>1</sub> generation and P<sub>2</sub>xP<sub>3</sub>, P1xP4, P2xP4, P2xP5, P1xP3, P2xP6, P1xP5 and P3xP4 in F<sub>2</sub> generation (Kumar *et al.*, 2017).

If crosses of high SCA involve both parental lines which also are good combiners, they could be exploited for breeding varieties. Nevertheless, if crosses of high SCA involve only one good combiner, such combinations would throw out desirable transgressive segregates provided that the additive genetic system in the good combiner (as well as complementary and epistatic effects in the crosses) act in the same direction to reduce undesirable characteristics and maximize the character under consideration, in this investigation the crosses P<sub>6</sub>xP<sub>7</sub> may be promise for most of traits, cross P<sub>4</sub>xP<sub>6</sub> for earliness and cross P<sub>1</sub>xP<sub>3</sub> for plant height. These results were in agreement with those reported by Hamada *et al.* (2002) and Muhammad *et al.* (2009).

#### Genetic components and heritability

Genetic components and heritability, the half diallel analysis of Hayman method (Hayman 1954 a and b) provided six genetic statistical parameters. They are D, H1, H2, h<sup>2</sup>, F and E (Table 7). Several ratios were derived as given by method of Hayman (1954b) and Jinks (1954) to provide further genetic information about each trait. The additive component (D) reached the significant level of probability for all studied traits in both F<sub>1</sub> and F<sub>2</sub> except No. of spike/plant in F<sub>2</sub> and No. of grains spike<sup>-1</sup> in both F<sub>1</sub> and F<sub>2</sub> generations. These results indicate that the additive and non-additive gene effects were involved in the inheritance of these traits in both generations. Significant values for the dominance component (H1) were obtained for all traits in both generations and large of magnitude than D one. Indicating that the dominance type of gene action was the most prevalent genetic component in inheritance of these traits. These results are in agreement with those reported by Seleem and Kumber (2011) and Farshadfar *et al.* (2012). Highly significant values for dominance components associated with gene distribution (H2) were obtained for all traits in both generations. The H<sub>2</sub> values were smaller than the H1 values for most traits indicating unequal allele frequency in the parents. These agree with findings obtained by Hayman (1954 b). The overall dominance effects of heterozygous loci "h<sup>2</sup>" were highly significant in F<sub>1</sub> generation traits except plant height, 1000 grains weight and Harvest index. However, h<sup>2</sup> were significant for No of grains spike<sup>-1</sup> and Biological yield/plant in F<sub>2</sub> generation, indicating that the dominance effects were mainly attributed to heterozygous phase in all crosses and that dominance was unidirectional for the exceptional traits. On the other hand, insignificant "h<sup>2</sup>" that detected for remain cases revealing that dominance was not unidirectional for these traits. The proportion of dominant to recessive gene in parents KD/KR were more than unity for most studied characters indicating that the dominant alleles govern these in both generations. The distributions of the relative frequencies of dominant versus recessive gene (F) were not significant for days to maturity, plant height, No. of grain spikes<sup>-1</sup>, spike length and grain yield/plant in F<sub>1</sub> generation and plant height, No. of

spike/plant, No. of grain/spikes and spike length in F<sub>2</sub> generation. Thus, it could be concluded that an equality of the relative frequencies of dominant and recessive alleles were present in parents for studied traits. For other cases significant F values were obtained indicating asymmetry of gene frequency among the parental population were detected. The same conclusion was obtained for proportion of genes with positive and negative effects by H2/4H1. The weighted measure of average degree of dominance (H1/D) 0.5 exceeded or approximately equal to unity for studied traits in both generations, indicating that presence of over dominance for these traits. Consequently, selection for any of these traits in the early segregating generations will be of little use. Heritability estimates in both broad and narrow sense for the studied attributes were computed according to Mather and Jinks (1971) In addition, the computed t<sup>2</sup> was low and not significant for most traits as shown in Table 7. High values for heritability in broad sense were obtained for all traits, revealing that most phenotypic variability in each trait was due to genetic causes. High heritability values in broad sense along with medium or low ones in narrow sense were exhibited in both generations, indicating that most genetic variances were due to non-additive genetic effects. These finding support the aforementioned results on genetic components in which H1 estimates played a greater role in the inheritance of these characters. Therefore, the bulk method program for improving such traits might be promising Allah *et al* (2010) and Kumber (2011). in contrast, Ali *et al.* (2008) Fellahi *et al.* (2016) and Nazir *et al.* (2014) they reported moderate to high narrow sense heritability estimates for yield and its related.

#### Graphical (wr/vr) analysis.

Graphical (wr/vr) analysis. Graphical presentation (Vr,Wr) of different traits in F<sub>1</sub> and F<sub>2</sub> generations are given in Figures from 1 to 9. The regression coefficient significantly differed from zero but not from unity for F<sub>1</sub> and in F<sub>2</sub> for all traits, except plant height the regression coefficient insignificant differ from zero were detected, indicating that the genetic system could be deduced to be additive without the complication of non-allelic interaction. For the other cases, regression slope differed from unity, indicating that a complementary type of epistasis was involved. The regression line passed through the origin in spike length and No. of spikes/plant in F<sub>1</sub> generation and 1000-grain weight in F<sub>2</sub> generation, revealed a presence of complete dominance. Meanwhile, it intersects the Vr axis above the origin in plant height in both generation, 1000-grain weight in F<sub>1</sub>, No of spike/plant and spike length in F<sub>2</sub>, reflecting partial dominance. The presence of over dominance, however, was obtained from computing the ratio of H1 to D for these cases (Table 7). This contradiction between the two types of analysis might be an expected result of the presence of complementary type of non-allelic interaction which inflated the ratios of H1 to D and distorted the Vr,Wr (Hayman 1954 b and Mather and Jinks 1971). However, the regression line intersected the Vr below the point of origin in the remaining cases, indicating an over dominance in the inheritance of these cases. The array points scattered along the regression line for all traits in both generations indicating genetic diversity among the parents. The low magnitude of correlation coefficient between parental mean (Yr) and the (Wr+Vr)

might be due to a presence of non-allelic interaction in some parental line or variety. P<sub>1</sub> for spike length, No. of spikes/plant and harvest index; P<sub>2</sub> for No of grains/spike; P<sub>3</sub> for physiological maturity and grain yield/plant; P<sub>5</sub> for spike length and biological yield/plant and P<sub>7</sub> for plant height in F<sub>1</sub> as well as P<sub>1</sub> for spike length, No of grain/spike and No of spike/plant; P<sub>3</sub> for grain yield/plant and Harvest index; p<sub>4</sub> for grain yield/plant; P<sub>5</sub> for physiological maturity, 1000-grain weight and biological yield/plant; P<sub>6</sub> for No of grain/spike; P<sub>7</sub> for physiological maturity, plant height and biological yield plant<sup>-1</sup> in F<sub>2</sub> generation included largest number of recessive genes for

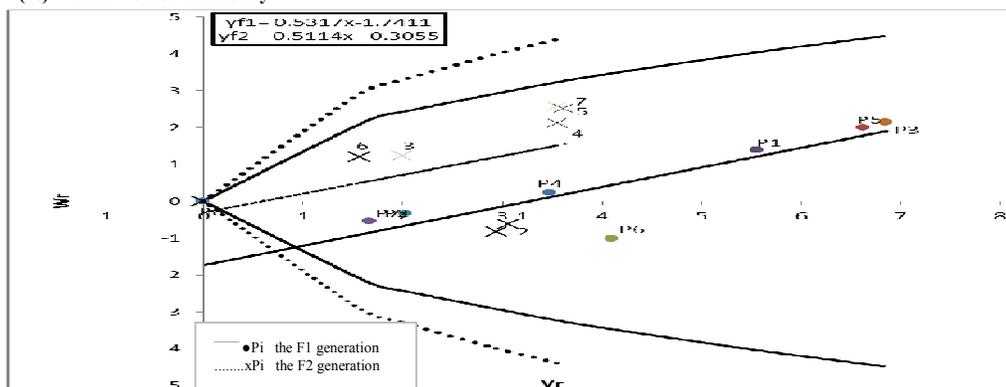
these cases. Meanwhile, the parent P<sub>3</sub> for 1000-grain weight and harvest index; P<sub>5</sub> for plant height; P<sub>6</sub> for spike length, No of spike/plant and grain yield plant<sup>-1</sup>; P<sub>7</sub> for physiological maturity, No of grain/spike and biological yield/plant in F<sub>1</sub> as well as P<sub>1</sub> for 1000-grain weight, biological yield/plant and Harvest index; P<sub>3</sub> for spike length; P<sub>5</sub> for No of spike/plant; P<sub>6</sub> for physiological maturity, plant height, No of spike plant<sup>-1</sup>; P<sub>7</sub> for grain yield/plant and harvest index in F<sub>2</sub> generation seemed to have the highest number of dominant genes. Similar findings have earlier been reported by Salehi *et al.* (2014) and Jadoon *et al.* (2017).

**Table 7. Hayman's analysis for all studied traits in F<sub>1</sub> and F<sub>2</sub> generations.**

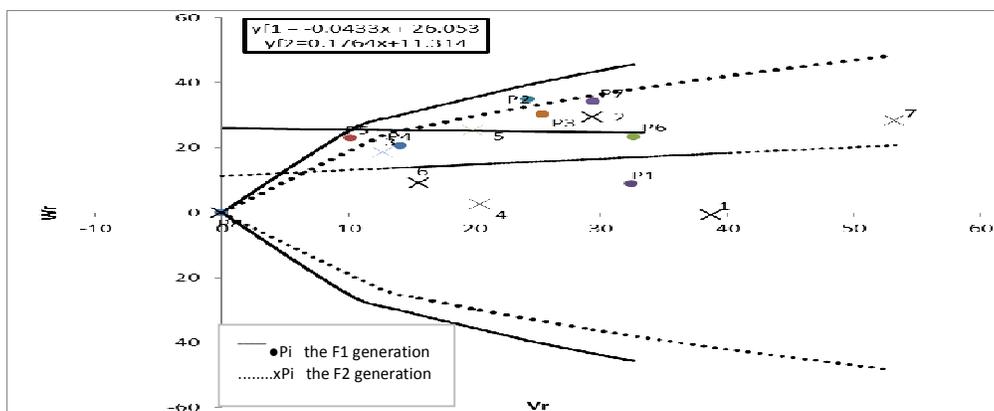
Component	Days to maturity	plant height	No of spikes plant <sup>-1</sup>	No of grains spike <sup>-1</sup>	Spike length	1000-grain weight	grain yield plant <sup>-1</sup>	Biological yield/plant	Harvest index
F <sub>1</sub>									
D	2.78**	63.87**	12.03**	6.88	0.50	15.15**	84.56**	283.94**	54.90**
F	3.42**	27.76**	32.21**	143.07**	2.21**	13.96**	234.08**	980.37**	264.36**
H1	17.58**	59.78**	19.07**	107.37**	1.52*	9.30**	138.96**	678.08**	163.13**
H2	15.96**	54.27**	20.91**	161.85**	0.65	1.36	18.30**	820.23**	-6.85**
H <sup>2</sup>	63.49**	24.05**	23.58**	20.62	0.17	15.47**	141.48**	417.69*	108.57**
E	0.16**	0.11**	0.10	0.20	0.02	0.38	0.37	0.20	2.39*
(H1/D) <sup>0.5</sup>	2.51	0.97	1.64	4.56	2.10	0.96	1.66	1.86	1.10
(H2/4H1)	0.23	0.23	0.15	0.19	0.17	0.17	0.15	0.17	0.15
KD/Kr	1.65	1.58	3.99	1.98	1.17	3.27	3.02	2.31	19.23
h <sup>2</sup> (n.s)	0.11	0.60	0.45	-0.84	-0.12	0.11	-0.13	-0.83	0.05
YD	143.48	100.73	0.20	0.70	0.01	0.01	0.02	0.69	0.002
Yr	151.22	95.36	0.98	0.98	0.98	0.92	0.99	1.00	0.72
r	0.96	0.50	0.14	0.29	0.56	0.44	0.35	0.33	0.36
T <sup>2</sup>	6.90	0.01	0.51	5.08	0.16	0.19	0.07	0.80	1.59
b	0.53	-0.04	0.05	0.14	0.14	0.55	0.57	0.48	0.20
F <sub>2</sub>									
D	5.29**	44.10**	8.84	15.87	0.50**	14.53**	85.59**	283.10**	55.45**
F	11.92**	88.01**	36.18**	131.91	1.99**	21.38**	262.96**	482.82**	197.17**
H1	9.30**	76.51**	27.39*	88.51	1.34**	14.62**	209.75**	299.39**	123.85**
H2	0.47	13.30	0.93	39.19	0.11	0.31	103.86**	99.79**	0.56
H <sup>2</sup>	5.96*	23.84	17.02	46.77	0.49	12.96*	84.04	427.43**	110.19*
E	0.15	0.11	0.05	0.16	0.01	1.21	6.27	0.31	0.22
(H1/D) <sup>0.5</sup>	1.50	1.41	2.02	2.88	2.01	0.17	1.75	1.31	1.89
(H2/4H1)	0.20	0.22	0.19	0.17	0.17	2.16	0.20	0.16	0.16
KD/Kr	2.20	1.47	2.81	3.09	1.65	0.39	1.78	3.74	3.23
H <sup>2</sup> (n.s)	0.52	-0.44	-0.00	-0.61	0.19	0.15	-0.78	0.09	-0.30
YD	0.27	0.19	0.00	0.38	0.04	0.02	0.61	0.01	0.09
Yr	0.96	0.99	0.99	0.99	0.93	0.93	1.00	1.00	0.99
r	0.28	0.17	0.04	0.23	0.48	0.53	0.32	0.21	0.23
T <sup>2</sup>	2.47	0.16	2.05	0.43	4.63	0.04	0.05	2.94	0.29
b	0.51	0.18	-0.21	0.03	0.21	0.68	0.55	0.48	0.20

\* p<0.05; \*\* p<0.01

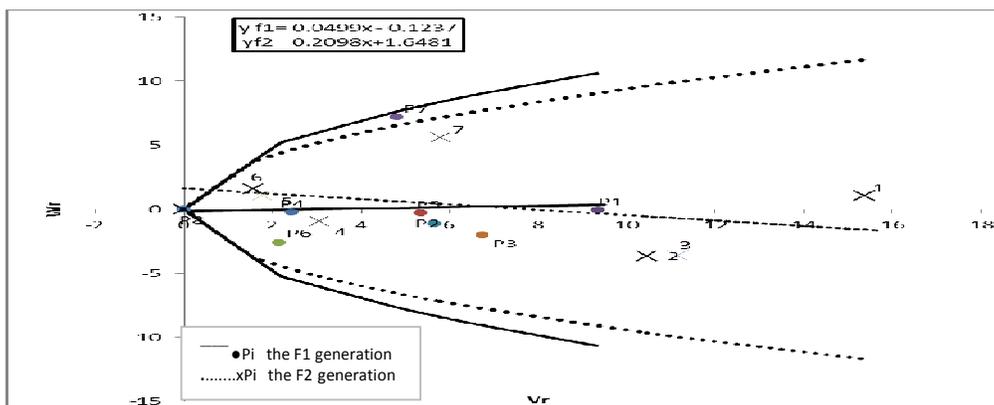
Where: E= the expected environmental component of variation, D= Variation due to additive effect, F= Refers to relative frequencies of dominant Vs recessive genes in the parents, H1 = component of variation due to dominance effects, H2 = Component of variation due to non-additive effects, h<sup>2</sup>= Overall dominance gene effects of the heterozygous loci in all crosses, (H1/D)<sup>0.5</sup> = mean degree of dominance at each locus over alloc, H2/4H1 = measures the average frequency of positive versus negative alleles at loci exhibiting dominance, KD/KR = the ratio of total number of dominant to receive alleles in the parents, h<sup>2</sup> (b.s) = broad sense heritability and h<sup>2</sup> (ns) = narrow sense heritability.



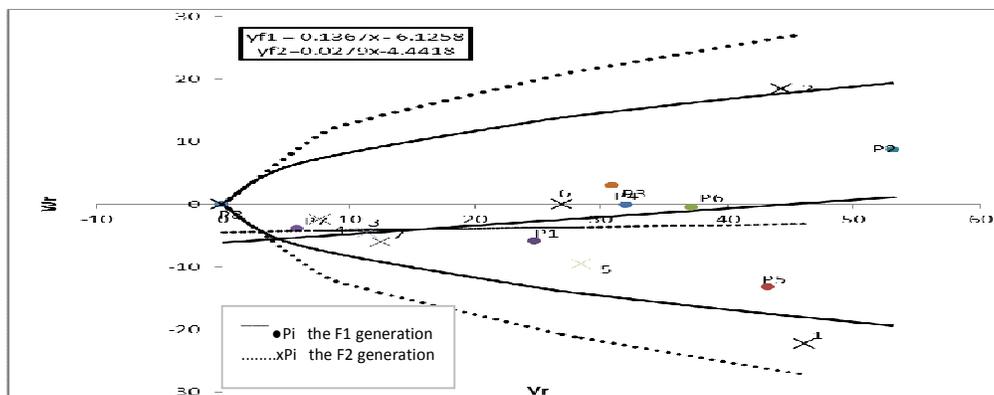
**Fig. 1. Wr/Vr graph for days to maturity in F<sub>1</sub> and F<sub>2</sub> generations.**



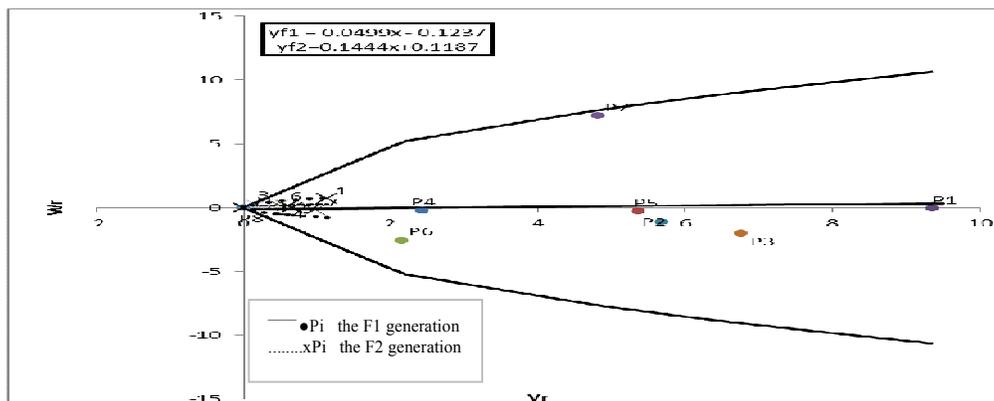
**Fig. 2.  $W_r/V_r$  graph for Plant height in  $F_1$  and  $F_2$  generations.**



**Fig. 3.  $W_r/V_r$  graph for No of spikes/plant in  $F_1$  and  $F_2$  generations.**



**Fig. 4.  $W_r/V_r$  graph for No. of grains/spike in  $F_1$  and  $F_2$  generations.**



**Fig. 5.  $W_r/V_r$  graph for spike length in  $F_1$  and  $F_2$  generations.**

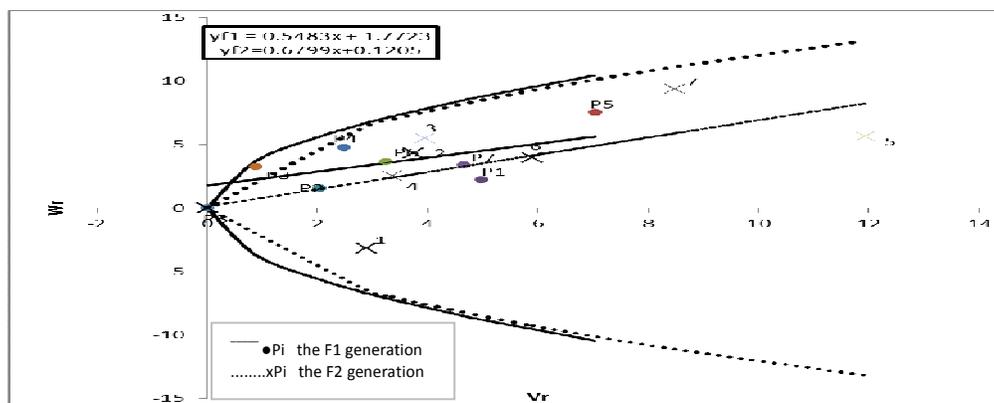


Fig. 6.  $W_r/V_r$  graph for 1000-grain weight in  $F_1$  and  $F_2$  generations.

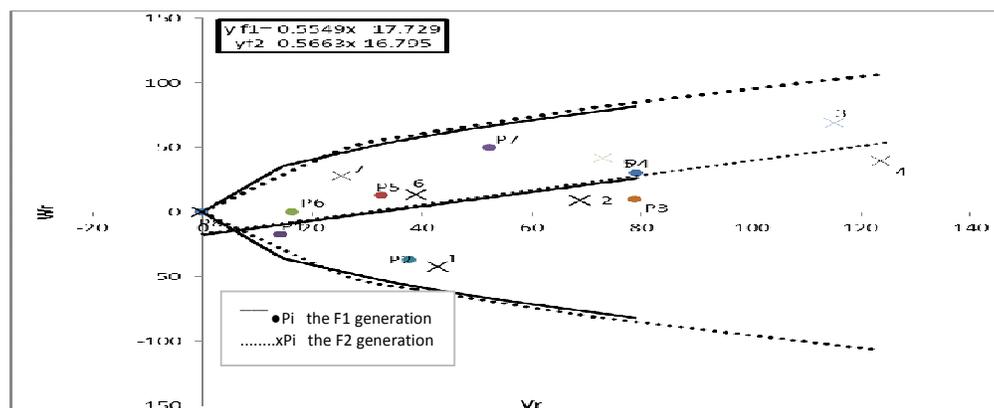


Fig. 7.  $W_r/V_r$  graph for grain yield/plant in  $F_1$  and  $F_2$  generations.

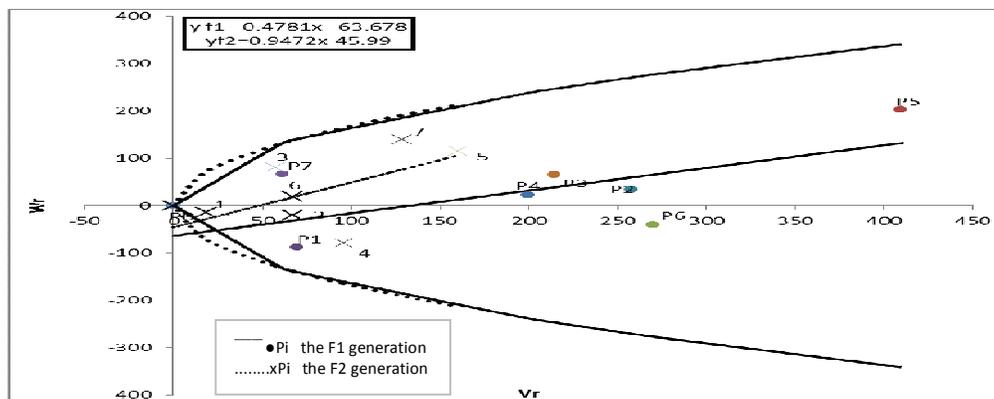


Fig. 8.  $W_r/V_r$  graph for harvest index in  $F_1$  and  $F_2$  generations.

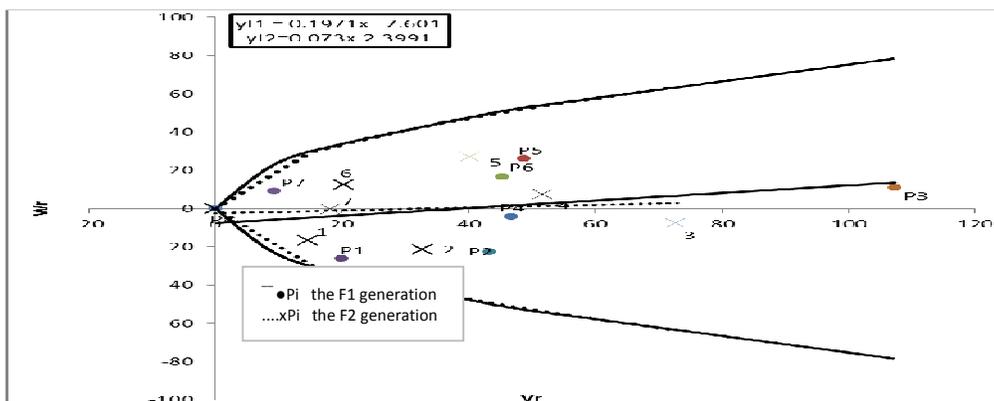


Fig. 9.  $W_r/V_r$  graph for biological yield/plant in  $F_1$  and  $F_2$  generations.

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## التباين الوراثي وقوة الهجين في الجيل الأول والثاني في الهجن التبادلية لسبع تراكيب وراثية من القمح

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يهدف البحث الى تحديد و اختيار الهجن المتميزة لأستخدامها في تحسين محصول حبوب القمح في مصر و دراسة قوة الهجين ، القدرة على التآلف و تقدير الفعل الجيني للمحصول و مكوناته في الجيل الأول و الثاني. اجري التهجين النصف تبادلي بين سبعة أصناف و سلالات من قمح الخبز و تم انتاج حبوب الجيل الأول و الثاني. و قيمت الاباء و الجيل الاول و الثاني معا في تصميم القطاعات الكاملة العشوائية بأربعة مكررات للمحصول و مكوناته في موسم 2016/2017. كان التباين الراجع الى التراكيب الوراثية (الاباء – الهجن) معنويا في الجيل الاول و الثاني في جميع الصفات. و أيضاً، كانت قوة الهجين بالجيل الأول معنوية في كل الصفات تحت الدراسة. تراوحت قيمة قوة الهجين الموجبة و المعنوية مقارنة بمتوسط الابوين من 4.64 الى 75.5% في الجيل الأول. و كانت الهجن (P2xP3 ، P1xP4 ، و P2xP5) افضل الهجن قوة في الهجين لوزن حبوب النبات. كان التباين الراجع للقدرة العامة و الخاصة على التآلف معنويا لكل الصفات المدروسة و النسبة بينهم تشير الى اهمية الفعل الجيني المضيف و غير المضيف في توريث جميع الصفات تحت الدراسة. اظهرت الأب رقم 4 (مصر 1) قدرة عالية على التآلف و مرغوبة لصفة التذكير في كل من الجيل الول و الثاني ، و الاب 3 (سدس 13) لصفة ارتفاع النبات، أما الابوين 6 (سلالة 1) و 7 (سلالة 2) فقد اظهرا قدرة عالية على التآلف لمعظم الصفات تحت الدراسة في الجيلين الول و الثاني. و اظهر ستة هجن في الجيل الاول و الثاني قدرة خاصة على التآلف بينما اعطى سبعة هجن منهم قدرة خاصة مرغوبة في الجيل الثاني لصفة محصول حبوب النبات. أعطت تسعة هجن (P2xP1 ، P2xP1 P6xP2 P5xP2 P6xP1 P5xP4 P6xP4 P6xP5 P7xP5) تأثيرات قدرة خاصة على التآلف عالية المعنوية لمحصول لوزن محصول حبوب النبات في كل من الجيل الاول و الثاني. يمكن استخدام تلك الهجن في برامج التربية. كان تأثير السيادة (H1) معنوي لكل الصفات المدروسة و كان اكبر من الجزء المضيف و كانت النسبة (H1/D)<sup>0.5</sup> اكبر من الوحدة في كل الصفات المدروسة. كانت قيمة كفاءة التوريث بمعناها الواسع كبيرة بالمقارنة بدرجة التوريث بالمعنى الضيق التي ظهرت منخفضة الى متوسطة و هذا يدل على ان الجزء السيادة هو الذي يتحكم في اظهار الصفات. كانت الاليلات المتتحية و السائدة غير متساوية في الأباء لمعظم الصفات و ذلك بأستخدام (H2/4H1) و قيمة (F). و كانت السيادة الفائقة ذات التأثير الأكبر في كل الصفات. أظهرت نتائج التحليل البياني أن صفة عدد السنابل/نبات في الجيل الاول و وزن 1000 حبة في الجيل الثاني بها سيادة تامة و صفة محصول حبوب النبات في الجيل الثاني سيادة تامة. بينما أظهرت صفة عدد السنابل للنبات و طول السنبل في الجيل الثاني سيادة جزئية.