ESTIMATION OF SOME GENETIC PARAMETERS IN BREAD WHEAT CROSSES USING DIALLEL ANALYSIS

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ABSTRACT

A half diallel analysis of eight bread wheat, parents [Shandaweel 1(P1), Sids 12 (P2), Giza 168 (P3), Gemmiza 9 (P4), Sids 4 (P5) as local cultivars and three lines (Line 11(P6), Line 13(P7) and line 26 (P8)) from (CIMMYT)]. The 28 F_1 and 28 F_2 which were drived from the crosses between the parents, were carried out at Mallawy Agricultural Research Station, ARC, during three successive seasons of 2013/2014, 2014/2015 and 2015/2016 to estimate the genetic prameters of flag leaf area (cm^2), grain filling rate (g day^{-1}), no. of spikes $plant^{-1}$, no. of kernels $spike^{-1}$, grain yield $plant^{-1}$ (g) and 100-kernel weight (g). The analysis of variance revealed that mean squares due to genotypes were highly significant for all of these characters. Also, the non-additive gene effect was important than the additive gene effect for most traits. The degree of dominance was over-dominance for all traits except for no. of kernels $spike^{-1}$ was partial dominance. Moderate narrow sense heritability was observed in all traits in F_2 generations. The lowest value of inbreeding depression was observed in cross Sids 12×Giza 168. Grain yield $plant^{-1}$ had strong correlation with grain filling rate and no. of spikes $plant^{-1}$, and also between flag leaf area and 100-kernel weight. The parent Sids 12 had a maximum domininat genes for flag leaf area, grain yield $plant^{-1}$, no. of spikes $plant^{-1}$, 100-kernel weight and grain filling rate, beside Line 13 for grain filling rate. These two promising genotypes can be used as a donors in multiple traits breeding programme to develop high yielding wheat genotypes.

Key words: *Wheat (Triticum aestivum L.), Diallel, Heritability, Inbreeding depression, Correlation, Grain yield, Additive-dominance model*

INTRODUCTION

Wheat is the most widely cultivated cereal crop all over the world and ranks the first crop in Egypt. The productivity of wheat in Egypt has increased during the last years. Wheat production supplies only 45% of its annual domestic demand. Wheat cultivated area amounted about 1.3 million hectares (3.2 million faddans) in 2018, producing a total of 8.35 million tons of wheat grains with an average of 2.65 ton fed^{-1} (17.63 ard. fed^{-1}) (Economic Affairs Egypt 2018).

Grain yield of wheat is a complex trait consisting of various components and other complementary traits affecting yield response (Farshadfar *et al* 2014 and Jatoi *et al* 2014).

Diallel analysis has been widely utilized to investigate genetic structure of crop plants for various traits and has been used to generate useful information about general combining ability (GCA) and specific combining ability (SCA) (Jinks and Hayman (1953), Hayman (1954 a and b) and Griffing (1956). In addition, Singh and Chaudhary (1979) stated that diallel analysis gives an opportunity to the plant breeders for chosen the msost efficient selection method to estimate several genetic parameters.

Information about inheritance patterns are helping scientists to propose future breeding strategies for specific objectives. Amna Nazir *et al*

2014 and Farooq *et al* 2015 reported that additive with partial dominance type of gene action was observed for tillers plant^{-1}, grain yield plant^{-1} and 1000-grain weight. While over-dominance type of gene action was observed for flag leaf area (Inamullah *et al* 2005), tillers plant^{-1}, 1000-grain weight and grain yield plant^{-1} (Nazeer *et al* 2013).

Heritability is the the proportion of genetic variation to the total phenotypic variation (Mwadzingeni *et al* 2017). It is an important tool to assess the magnitude of genetic variation transferred to the progenies and also provides a better estimate of selection efficiency (Abdolshahi *et al* 2015).

Narrow sense heritability assesses the extent of additive genotypic variation which is primarily responsible for modifying the genetic makeup of a population, and also assists as a guide to the reliability of phenotypic variability in a breeding program (Ahmad *et al* 2016). Correlation coefficient analysis may be utilized as a vital tool to gather the information about right reason and effective association between yield and related components (Abd El-Mohsen and Abd ElShafi 2014). Many resarchers reported that grain yield plant^{-1} was attributable to traits such as spike length, tillers plant^{-1}, grains spike^{-1},1000-grain weight and harvest index (Moustafa 2007 and Baloch *et al* 2013).

Yagdi and Sozen (2009) reported that, the selection criteria to grain yield were found with the traits of 1000-grain weight and tillers per plant.

Therefore, the present study was carried out to investigate inheritance by determining gene action, heritability and correlation using 8×8 half diallel cross in bread wheat to assist the breeders to develop high yielding wheat genotypes.

MATERIALS AND METHODS

This study was conducted at the Experimental Farm of Mallawy Agric. Res. Station, ARC, Egypt, during the winter seasons of 2013/2014, 2014/2015 and 2015/2016. Eight parents of bread wheat genotypes i.e., Shandaweel 1(P1), Sids 12 (P2), Giza 168 (P3), Gemmiza 9 (P4), Sids 4 (P5) as local cultivas and three lines (Line 11(P6), Line 13(P7) and line 26 (P8)) from (CIMMYT) (Table 1). These parents were crossed in a half diallel. In winter growing season of 2013/2014, the parents were sown in two sowing dates with two weeks interval in order to synchronize the flowering time for crossing purposes. Hand emasculation and pollination

were performed to produce enough F_1 seeds of all possible combinations of eight parents without reciprocal.

Table 1. The designation number, pedigree and origin of the eight parental genotypes used in this investigation.

Parents	Name	Pedigree	Origin
P1	Shandaweel1	SITE/MO/4/NAC/TH.AC //38*PVN/3/MIRLO/BUC.	Egypt
P2	Sids 12	BUC//7C/ALD/5/MAYA74/ON//1160-147/3/BB/GLL/4/CHAT"S"/6/MAYA/VUL//CMH74A.630/4*SX	Egypt
P3	Giza 168	MIL/BUC//SERI	Egypt
P4	Gemmiza 9	ALD"S"/HUAC"S"//CMH74A.630/SX.	Egypt
P5	Sids 4	MAYA"S"/MON"S	Egypt
P6	Line 11	WAXWING*2	CIMMYT
P7	Line 13	WHEAR/S0K0LL.	CIMMYT
P8	Line 26	R0LF07*2/KIRITATI.	CIMMYT

In 2014/2015 growing winter season, seeds of the 28 F_1 hybrids of the diallel cross and the 8 parents were sown in order to produce the F_2 seeds and to make crosses between the parents for the reproduction of F_1 seeds. In the third winter season of 2015/2016, all genotypes (28 F_1, 28 F_2 and 8 parents) were evaluated in a randomized complete block design with three replicats. Each genotype was planted in three rows with 2 meter length. The distance between plants, within row and between rows was 20 cm. Agricultural practices were carried out as recommended for commercial wheat production and the weeds were controlled by hand.

A random sample of 10 guarded plants per plot for parental and F_1 hybrids and 20 plants per plot for F_2 populations were taken for measuring the characters of flag leaf area (cm^2), grain filling rate (g day^{-1}), no. of spikes plant^{-1}, no. of kernels spike^{-1}, grain yield plant^{-1} (g) and 100-kernel weight (g) for each plant were recorded.

Flag leaf area: Data on length and width of flag leaf were recorded by taking a sample of flag leaves from each plant after 120 days from planting and calculated as leaf length × maximum width × 0.75, according

to Montogomery (1911).

Grain filling rate was estimated as follows:

$$\text{Grain filling rate} = \frac{\text{Grain yield per plant (g)}}{\text{days to Maturity} - \text{days to anthesis}}$$

Diallel analysis and components of genetic variance were estimated according to **Hayman (1954 a** and **b).**

Estimation of inbreeding depression**:** inbreeding depression (ID%) were calculated using the following formulae as recorded by **Paul *et al* 1987**

$$\text{ID\%} = \frac{F_1 - F_2}{F_1} \times 100$$

Test of significance of inbreeding depression is performed by testing the difference ($F_1 - F_2$), using the following t-test according to (Al-Rawi and Kohel 1969):

$$t = (F_1 - F_2) \sqrt{\frac{MSeF_1}{b_1c_1} + \frac{MSeF_2}{b_2c_2}}$$

Where:

F_1 = the mean value of the F_1 generation,

F_2 = the mean value of the F_2 generation,

$MSeF_1$ = mean square of error F_1- analysis,

$MSeF_2$ = mean square of error F_2- analysis,

b_1c_1= number of the replication and sample size of the F_1 generation.

b_2c_2 = number of the replication and sample size of the F_2 generation.

Statitical analysis: Data were subjected to analysis of variance to sort out significant differences among genotypes (Steel *et al* 1997). Scaling tests were employed to test the adequacy of additive-dominance modal following Mather and Jinks (1982).

RESULTS AND DISCUSSION

Performance of wheat genotypes

The analysis of variance revealed that mean square due to genotypes was significant for all stutied chrachters (Table 2), indicating a diversity among the genotypes. The highest values for grain filling rate (g day^{-1}), no. of spikes plant^{-1} and grain yield plant^{-1} (g) were recorded for Shandaweel 1 (P1) (0.85 g, 15.0, and 46.62 g, respectively). no. of kernels spike^{-1} (102) and 100-kernel weight (5.72g) for Sids 4 (P5) and flag leafe area (44.8 cm^2) for the parent Line 26 (P8).

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Table 2. The mean performance of 8 bread wheat parents, and their F$_1$ and F$_2$ generations for flag leaf area (cm^2), grain filling rate (g day^{-1}), no. of spikes plant^{-1}, no. of kernels spike^{-1}, 100-kernel weight (g) grain yield plant^{-1} (g) and inbreeding depression (ID%) of the hybrids.

Genotypes	Flag Leaf area (cm^2)		Grain filling rate (g day^{-1})		No. of spikes Plant^{-1}		No. of kernels spike^{-1}		100 kernels weight		Grain yield plant^{-1} (g)		ID%
Parents													
Shandaweel- (P1)	33.3		0.85		15		85		4.25		46.62		
Sids-12 (P2)	42.5		0.74		10		87		4.38		38.27		
Giza-168(P3)	42.2		0.85		12		75		4.31		42.19		
Gemmiza-9 (P4)	41.6		0.71		11		68		5.15		36.55		
Sids-4 (P5)	42.6		0.54		6		102		5.72		32.93		
Line- 11 (P6)	36.9		0.83		11		80		4.64		40.65		
Line- 13 (P7)	38.0		0.70		11		74		4.10		33.04		
Line- 26 (P8)	44.8		0.76		12		61		4.92		38.53		
Parental mean	40.2		0.75		10.9		79		4.69		38.60		
Hybrids													
Hybrids	F$_1$	F$_2$	F$_1$	F$_2$	F$_1$	F$_2$	F$_1$	F$_2$	F$_1$	F$_2$	F$_1$	F$_2$	
P1 x P2	45.1	39.7	0.82	0.75	11	10	78	79	4.76	4.68	40.98	34.53	15.74**
P1 x P3	41.6	37.2	0.81	0.77	12	12	94	78	3.52	4.23	40.55	39.24	3.23
P1 x P4	41.1	35.3	0.77	0.55	10	11	86	82	4.96	4.78	42.35	42.14	0.50
P1 x P5	54.7	51.5	0.77	0.69	11	7	96	91	4.76	5.44	47.24	34.00	28.03**
P1 x P6	41.2	39.4	0.96	0.73	12	11	79	84	5.35	3.62	47.13	34.48	26.84**
P1 x P7	53.3	37.7	0.86	0.81	12	11	72	77	5.51	5.04	46.06	41.58	9.73**
P1 x P8	41.4	36.6	0.88	0.63	12	12	75	65	5.19	5.52	44.34	41.43	6.56
P2 x P3	46.2	39.0	0.71	0.77	9	11	90	73	4.72	4.78	36.86	36.74	0.33
P2 x P4	39.7	38.4	0.75	0.82	9	10	81	90	5.23	4.22	39.23	36.07	8.06
P2 x P5	50.9	45.0	0.74	0.62	7	11	101	72	5.76	5.42	41.75	37.96	9.08*
P2 x P6	43.3	39.5	0.93	0.70	11	9	82	86	5.16	4.08	47.84	31.10	34.99**
P2 x P7	44.6	39.2	0.76	0.72	10	10	68	77	6.03	4.86	40.98	36.68	10.49**
P2 x P8	49.0	42.5	0.84	0.69	8	9	95	83	5.53	4.83	42.72	36.82	13.81**

Table 2. Cont.

Genotypes	Flag Leaf area (cm^2)		Grain filling rate (g day^{-1})		No. of spikes Plant^{-1}		No. of kernels spike^{-1}		100 kernels weight		Grain yield plant^{-1} (g)		ID%
Parents													
Shandaweel-(P1)	33.3		0.85		15		85		4.25		46.62		
Sids-12 (P2)	42.5		0.74		10		87		4.38		38.27		
Giza-168(P3)	42.2		0.85		12		75		4.31		42.19		
Gemmiza-9 (P4)	41.6		0.71		11		68		5.15		36.55		
Sids-4 (P5)	42.6		0.54		6		102		5.72		32.93		
Line- 11 (P6)	36.9		0.83		11		80		4.64		40.65		
Line- 13 (P7)	38.0		0.70		11		74		4.10		33.04		
Line- 26 (P8)	44.8		0.76		12		61		4.92		38.53		
Parental mean	40.2		0.75		10.9		79		4.69		38.60		
Hybrids													
Hybrids	F$_1$	F$_2$	F$_1$	F$_2$	F$_1$	F$_2$	F$_1$	F$_2$	F$_1$	F$_2$	F$_1$	F$_2$	
P3 x P4	44.8	32.6	0.72	0.50	10	10	84	76	4.50	4.87	38.13	37.25	2.31
P3 x P5	47.2	43.5	0.76	0.66	9	7	83	84	5.94	4.70	43.31	29.04	32.95**
P3 x P6	45.7	41.4	0.83	0.76	12	8	80	76	4.81	4.98	43.54	30.61	29.70**
P3 x P7	50.5	36.0	0.74	0.58	11	13	79	62	4.71	4.86	40.64	39.64	2.46
P3 x P8	47.5	40.6	0.84	0.46	12	9	80	75	4.55	4.68	42.92	30.89	28.03**
P4 x P5	47.3	43.8	0.82	0.71	10	12	93	38	4.69	6.03	43.81	28.22	35.59**
P4 x P6	38.5	44.5	0.78	0.71	12	10	80	67	4.32	5.33	40.81	34.71	14.95**
P4 x P7	42.9	37.9	0.69	0.60	9	14	80	47	5.22	5.43	35.48	35.24	0.68
P4 x P8	45.4	43.4	0.82	0.55	10	10	81	66	5.39	5.41	42.66	35.00	17.96**
P5 x P6	43.9	39.7	0.69	0.57	10	9	70	71	5.09	5.34	35.65	33.85	5.05
P5 x P7	55.9	48.2	0.65	0.60	7	9	95	71	5.71	5.37	37.08	34.54	6.85
P5 x P8	48.5	46.2	0.72	0.73	9	10	84	59	5.59	6.15	41.11	34.10	17.05**
P6 x P7	37.5	40.6	0.71	0.74	13	11	58	50	4.96	6.54	36.46	33.87	7.10
P6 x P8	47.8	37.8	0.90	0.63	13	11	72	75	5.12	4.87	46.64	38.58	17.28**
P7 x P8	42.8	39.3	0.94	0.75	16	10	58	63	5.28	5.49	48.29	34.59	28.37**
Hybrid mean	45.7	40.6	0.79	0.67	10.5	10.2	81	72	5.08	5.06	41.95	35.46	
Grand mean	44.4	40.5	0.78	0.69	10.6	10.3	81	74	5.00	4.97	41.20	36.18	
L.S.D. 5%	14.04	11.24	0.247	0.282	5.56	4.89	30.8	36.2	1.57	1.76	11.72	11.50	

Regarding to the hybrids, the data illusterated in Tabe 2 shwoed that the crosses were differed among them for the studied traits in F$_1$ and F$_2$ generations.

In F$_1$ generation the crosses P5×P7, P1×P6, P6×P7, P2×P5, P2×P7 and P7×P8 recorded the heighest values for flag leafe area (55.9 cm^2), grain filling rate (0.96 g day^{-1}), no. of spikes plant^{-1} (13.0), no. of kernels spike^{-1} (101), 100-kernel weight (6.03 g) and grain yield plant^{-1} (48.29 g), respectively.

In F$_2$ generation the crosses P1×P5, P1×P7, P4×P7, P1×P5, P6×P7 and P1×P4 recorded the heighest values for flag leafe area (51.5 cm^2), grain

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filling rate (0.81 g day^{-1}), no. of spikes plant^{-1} (14.0), no. of kernels spike^{-1} (91), 100-kernel weight (6.54 g) and grain yield plant^{-1} (42.14 g), respectively.

Maximium inbreeding depression "ID" was found in cross P4×P5 (35.59%), but the lowest was in cross P2×P3 (0.33%) (Table 2). The cross P1×P4 gave the heaviest grain yield plant^{-1} (42.14 g) and lower value of inbreeding depression (0.50%) indicating that, this cross had highly additive gene effect more than dominant gene effect for grain yield plant^{-1}. These results indicated that the cross P1×P4 maybe promising to improve wheat grain yield through selection.

Analysis of variance

Data presented in Tables (3, 4) showed that all studied characters were significantly differed. Two scaling tests were applied according to Mather and Jinks (1982) for testing the validity of additive-dominance model. The first test was the joint regression coefficient test, followed by analysis of variance of Wr+Vr and Wr-Vr for the confirmation of absences of non-allelic interaction. Wheres, Vr = the variance of an array (one cultivar and all the crosses involving it), Wr = the covariance between the parents and their off-spring in an array.

Table 3. Mean squares from the analysis of variance and scaling test for adequacy of additive-dominance model in F$_1$ bread wheat generation.

Traits	Mean Squares (Anova)	Regression slop		Mean squares		Remark
		b=0	b=1	Wr+Vr	Wr-Vr	
Flag leaf area (cm²)	74.323**	-0.0296	7.216**	959.64**	931.83**	Both tests suggested inadequacy of the model
Grain filling rate (g day^{-1})	0.023**	3.57 *	1.28	0.000096	0.00001	FA
No. of spikes plant^{-1}	11.648**	2.39	4.41**	33.83 **	6.32	Both tests suggested inadequacy of the model
No. of kernels Spike^{-1}	357.92**	2.404	2.574 *	12615.78	3308.88	PA
Grain yield plant^{-1} (g)	51.755**	8.481 **	1.148	603.63	69.40	FA
100-kernel weight (g)	0.933**	2.66 *	2.24	0.30	0.15	FA

Partial adequacy = PA   Full adequacy = FA

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Table 4. Mean squares from the analysis of variance and scaling test for adequacy of additive-dominance model in F_2 bread wheat generation.

Traits	Mean Squares (Anova)	Regrestesion slop		Mean	squares	Remark
		b=0	b=1	Wr+Vr	Wr-Vr	
Flag Leaf area (cm^2)	47.647**	0.623	3.549*	303.284*	194.23	Both tests suggested inadequacy of the model
Grain filling rate (g day^{-1})	0.030**	1.03	0.75	0.00023	0.000049	Model is PA
No. of spikes plant^{-1}	9.019**	1.92	0.81	25.81	24.30 **	Both tests suggested inadequacy of the model
No. of kernels Spike^{-1}	493.419*	1.245	3.425 *	101876.9**	43998.4**	Both tests suggested inadequacy of the model
Grain yield Plant^{-1} (g)	49.888*	0.673	1.257	841.98	367.50	PA
100-kernel weight (g)	1.173**	-0.05	7.36 **	0.170	0.171	PA

Partial adequacy = PA   Full adequacy = FA

Additive-dominance model was found to be adequate for grain filling rate, grain yield plant^{-1} and 100-kernel weight in F_1 generation. This result was in agreement with that reported by Amna Nazir *et al* (2014). Additive-dominance model was partial adequate for grain filling rate, grain yield plant^{-1} and 100-kernel weight in F_2 generation and no. of kernels spike^{-1} in F_1 generation (Tables 3, 4). The data showed also that there were inadequacy for leaf area, no. of spikes plant^{-1} in F_1 and F_2 generation and no. of kernels spike^{-1} in F_2 generation.

The additive component "D" was significant and lower than the value of component of variation due to dominance effect "H_1" in the plus direction and in the minus direction ("H_2"), for no. of kernels spike^{-1} in F_1 and F_2 generation (Tables 5, 6) indicating the preponderance of non-additive gene effect for controlling this trait. These results were in harmony with those reported by Kamaluddin *et al* (2007), Seleem and Koumber (2011) and Moustafa (2013). Also, grain yield plant^{-1} was controlled by more non-additive gene than additive gene effect in the tow generations, these results are in concordance with those reported by Moustafa (2007), Mandal and Madhuri (2016) and Natasa *et al* (2017). Unequal values (UV) of "H_1" and "H_2" suggested that, positive and negative alleles were unequal among parental cultivars.

Table 5. Components of variation for studied characters in F1 generation.

Component of variance	Flag leaf area (cm²)	Grain filling rate (g day⁻¹)	No. of spikes plant⁻¹	No. of kernels spike⁻¹	Grain yield plant⁻¹ (g)	100-kernel weight (g)
D	4.332± 5.453	0.0007±0.0022	1.33±1.44	108.01**±24.63	-1.66 ±6.40	-0.17±0.24
H_1	57.323**±12.535	-0.0088±0.0051	-0.28±3.32	185.67**±56.61	-8.87±14.70	-0.20±0.55
H_2	47.730**±0.906	-0.0045±0.0044	0.67±2.89	139.46**±49.25	1.29±12.79	-0.1 ±0.47
F	-2.211±12.884	-0.009 ± 0.0052	-3.53±3.42	31.43 ±58.19	-17.96±15.11	-0.39±0.56
E	9.992**±1.818	0.0098**±0.0007	3.35**±0.48	51.28**±8.21	22.93**±2.13	0.47**±0.08
$\sqrt{H1/D}$	3.638	3.546	0.459	2.066	2.31	1.085
UV	0.208	0.130	0.606	0.188	0.036	0.138
hn	26.90	24.43	35.76	41.62	11.67	12.78

Table 6. Components of variation for studied characters in F2 generation.

Component of variance	Flag leaf area (cm²)	Grain filling rate (g day⁻¹)	No. of spikes plant⁻¹	No. of kernels spike⁻¹	Grain yield plant⁻¹ (g)	100-kernel weight (g)
D	7.233±3.715	-0.0022±0.0046	0.71±1.26	106.74*±42.18	-7.16±10.51	0.06±0.18
H_1	211.596**±8.539	0.096**±0.0109	36.39**±2.90	2235.02±96.97	196.87**±24.15	4.41**±0.41
H_2	103.876**±7.429	-0.0002±0.0095	2.12±2.52	1396.65**±84.37	-33.34±21.01	1.92**±0.36
F	5.92±8.777	-0.0267*±0.011	-2.48±3.00	137.52±99.68	-41.42±24.82	-0.46±0.42
E	7.091**±1.238	-0.0267±0.0112	3.99±0.42	51.70**±14.06	28.43**±3.50	0.24±0.06
$\sqrt{H1/D}$	5.409	6.606	7.16	4.58	5.24	8.573
UV	0.123	0.008	0.015	0.156	0.04	0.109
hn	53.46	58.45	56.07	47.11	57.44	55.74

This was also supported by the ratio of "UV" ($H_2/4H_1$) which were not equal 0.25 for all traits in F_1 and F_2 generation indicating presence of positive and negative alleles in unequal frequency. The present finding was in harmony with the finding of Amna Nazir *et al* (2014) and Kumar *et al*

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(2018). Component "F" values (covariation of additive and dominance effect) in Tables 5, and 6 shwoed that, all studied tarits in the two generations were insignificantt except for grain felling rate in F_2. These results indicating that "F" has an imorportant role in dominant genes when it was significant and displaying unimportant one when it was insignificant (Rabbani *et al* 2011).

The environmental effects "E" had significant effect on all studied traits in the two generations except for the characters of grain filling rate, no. of spikes plant^{-1} and 100-kernel weight in F_2 generation (Tables 5 and 6). These results are in harmony with thoes reported by Seleem and Koumber (2011).

The relationship between Wr/Vr indicated that, there were over dominance in F_1 generation for grain filling rate, grain yield plant^{-1} and 100-kernel weight (Figures 3, 9 and 11), and also in F_2 generation for grain filling rate and no. of spikes plant^{-1} (Figures 4 and 6), respectively. These results are in harmony with those reported by Shehzad *et al* (2015), and Khahani *et al* (2017). In the other hand, data presented in Fig. 5 showed partial dominance for no. of spikes plant^{-1} and no. of kernels spike^{-1} in F_1 generation (Fig. 7), and for flage leaf area, no. of kernels spike^{-1}, grain yield plant^{-1} and 100-kernel weight in F_2 generation (Figures 2, 8, 10 and 12a) respectively, these results are in agreement with those obtatanied by Yao *et al* (2014) and Ahmad *et al* (2016).

Two types of non-allelic gene interaction were detected for flage leaf area in F_1 generation and 100-kernel weight in F_2 generation. The Wr/Vr line was concave upwards indicated complementary non-allelic interaction in the flage leaf area in F_1 generation (Fig. 1b), while it was concave downwords indicating duplicate non-allelic interaction in 100-kernel weight for F_2 generation (Fig. 12b). These results are in harmony with Moustafa (2007).

The degree of dominance ($\sqrt{H1/D}$) and the graphical represntation indicated partial dominance in No. of spikes plant^{-1} in F_1 generation, this result are in agreement with the preview mentioned results of Wr/Vr (Fig. 5) and harmony with Amna Nazir *et al* (2014) and Farooq *et al* (2015). Meanwhile, ($\sqrt{H1/D}$) was over dominance in No. of spikes plant^{-1} in F_2, grain yield plant^{-1} and 100-kernel weight in F_1 generations (Fig. 6, 9 and 11). These results are agree with reported by Moustafa (2007).

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Table 7. Correlation coefficient for pairs of studied characters in the parents and F₁ generation (upper value) and in the the parents and F₂ generation.

| Traits		grain filling rate (g day⁻¹)	No. of spikes Plant⁻¹	No. of kernels spike⁻¹	Grain yield plant⁻¹ (g)	100-kernel weight (g)
Flage leaf area (cm²)	F_1	-0.101	-0.335 **	0.234 *	0.058	0.262 **
	F_2	-0.252 **	-0.279 **	-0.076	-0.199 *	0.347 **
Grain filling rate (g day⁻¹)	F_1		0.651 **	-0.178	0.849 **	-0.085
	F_2		0.668 **	0.095	0.859 **	-0.274 **
No. of spikes Plant⁻¹	F_1			-0.468 **	0.596 **	-0.459 **
	F_2			-0.339 **	0.697 **	-0.197 *
No. of kernels spike⁻¹	F_1				-0.040	-0.142
	F_2				0.148	-0.629 **
Grain yield plant⁻¹ (g)	F_1					0.012
	F_2					-0.192 *
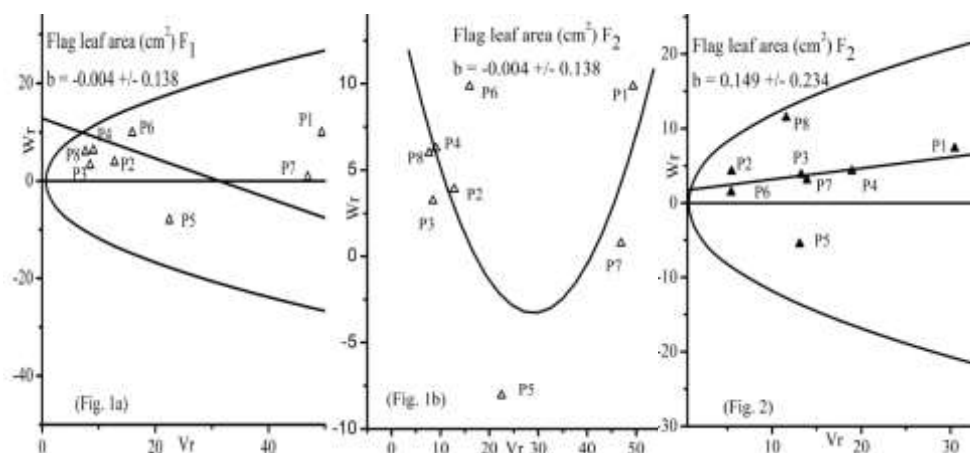
Fig. (1a, 1b and 2). The Wr/Vr graphs for flag leaf area (cm²) at F₁ (Fig. 1a and Fig. 1b) and F₂ generations (P1 = Shandawee1, P2= Sids 12, P3= Giza 168, P4 = Gemmiza 9, P5= Sids 4, P6= Line 11, p7= line 13, P8 = line 26).
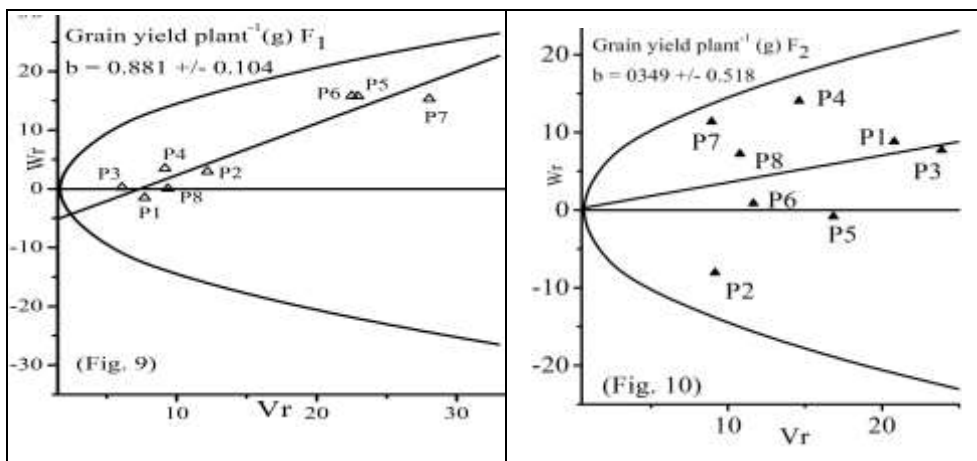
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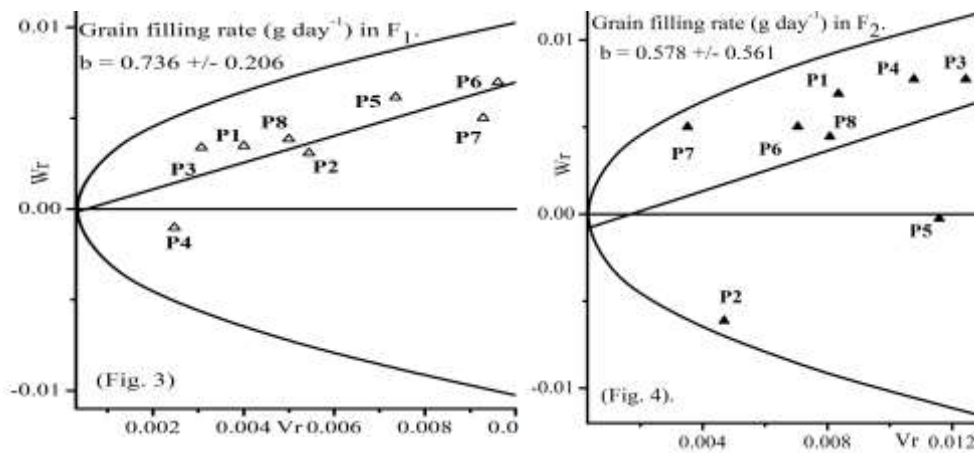
Fig. (3 and 4). The Wr/Vr graphs for grain filling rate (g day^{-1}) at F$_1$ and F$_2$ generations (P1= Shandawee1, P2= Sids 12, P3= Giza 168, P4= Gemmiza 9, P5= Sids 4, P6= Line 11, p7= line 13, P8= line 26).
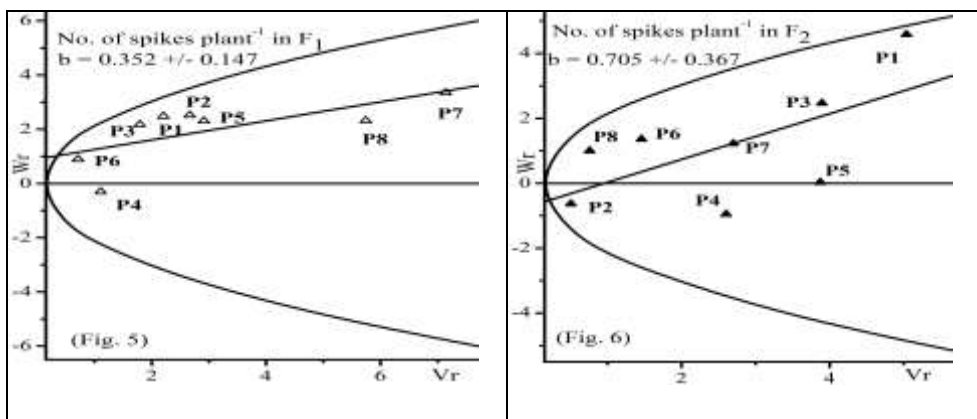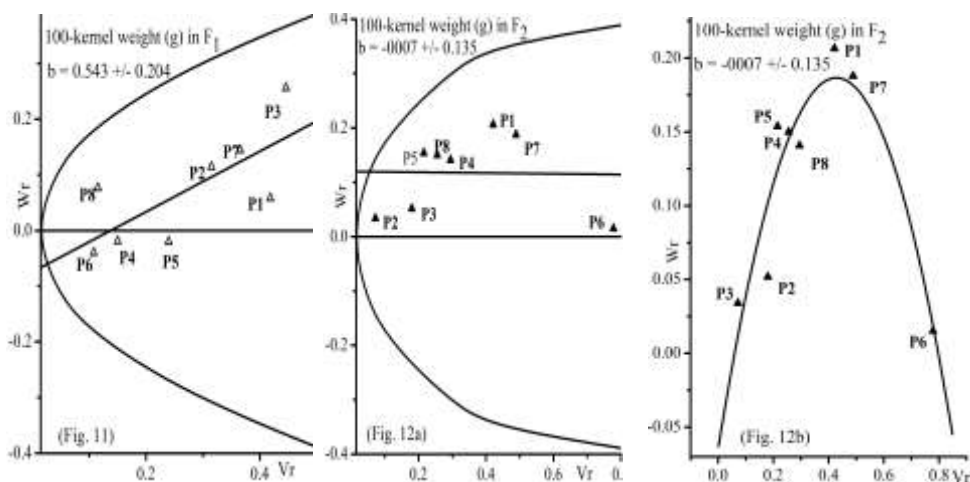

Fig. (5 and 6). The Wr/Vr graphs for no. of spikes plant^{-1} at F$_1$ and F$_2$ generations (P1= Shandawee1, P2= Sids 12, P3= Giza 168, P4= Gemmiza 9, P5= Sids 4, P6= Line 11, p7= line 13, P8= line 26.

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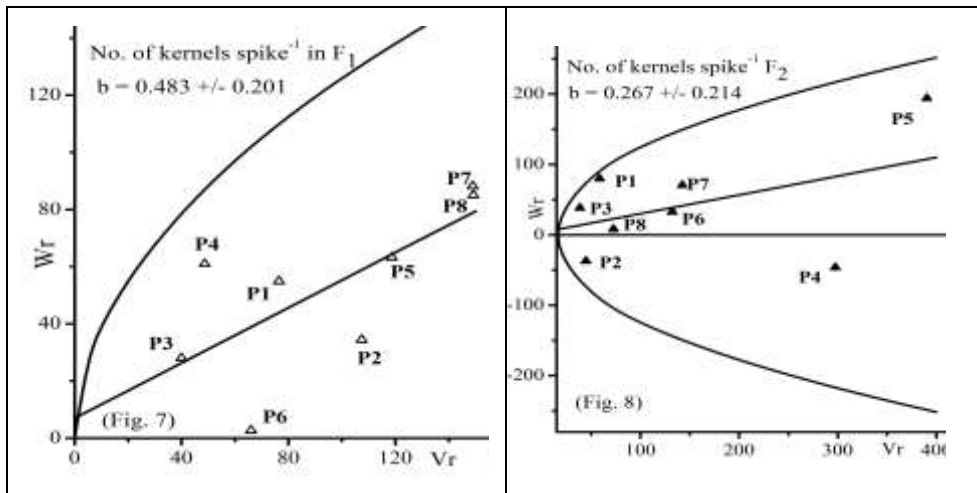
Fig. (7 and 8): The Wr/Vr graphs for no. of kernels spike^{-1} at F$_1$ and F$_2$ generations (P1= Shandawee1, P2= Sids 12, P3= Giza 168, P4= Gemmiza 9, P5= Sids 4, P6= Line 11, p7= line 13, P8= line 26).

Fig. (9 and 10): The Wr/Vr graphs for grain yield plant^{-1}(g) at F$_1$ and F$_2$ generations (P1= Shandawee1, P2= Sids 12, P3= Giza 168, P4= Gemmiza 9, P5= Sids 4, P6= Line 11, p7= line 13, P8= line 26).

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Fig. (11, 12a and 12b): The Wr/Vr graphs for 100-kernel weight (g) at F₁, and F₂ (12a and 12b) generations (P1= Shandawee1, P2= Sids 12, P3= Giza 168, P4= Gemmiza 9, P5= Sids 4, P6= Line 11, p7= line 13, P8= line 26).

The graphical figures (Figures 2, 4, 6, 8, 10 and 12a) illustrated that Sids 12 (P2) was found in the nearest to the point of origin indicating that it contating maximum dominant genes in F_2 generation for most studied trait.

Moderate of narrow sense heritability "h (n)" ranged from 47.11 in no. of kernels spike[-1] to 58.45g for grain filling rate in F_2 generation (Table 7). These results indicated that the selection in earlyer generation was more effective for improved these traits. The obtained data are in agreement with reported by Amna Nazir *et al* (2014) and Kumar *et al* (2016).

According the data presented in Table 7, the grain yield plant[-1] was significantly and positively coorelated with grain filling rate and no. of spikes plant[-1] in the two generations, thses results are in line with reported by Abd El-Mohsen and Abd El-Shafi (2014) and Ahmad *et al* (2016). While, flage leaf area and 100-kernel weight in F_2 generation was negatively and significantly correlated with grain yield plant[-1].

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CONCLUSION

Diallel analysis of bread wheat genotypes, in this study, showed that the non additive gene effect was more effective than additive in most studied traits. The degree of dominance was over dominance for all studied characters except for the trait of no. of kernels spike^{-1} it was partial. The lowest values for inbreeding depression was recorded with the cross (Sids 12×Giza 168). Grain yield plant^{-1} had the strongest association between grain filling rate and no. of spikes plant^{-1}. In the present study, the parent Sids 12 contained the maximum domininat genes for flage leaf area, grain yield plant^{-1}, no. of spikes plant^{-1}, 100-kernel weight and grain filling rate. Also, Line 13 for grain filling rate. These findings might indicate that Sids 12 and Line 13 are promising genotypes and could be used as a donor in multiple traits breeding programme to improving wheat yield.

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تقدير بعض القياسات الوراثية لهجن قمح الخبز بإستخدام التحليل الدائرى

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قسم بحوث القمح – معهد بحوث المحاصيل الحقلية– مركز البحوث الزراعية – الجيزة – مصر

أستخدم فى هذه الدراسة طريقة التحليل النصف دائرى لثمانية آباء من التراكيب الوراثية لقمح الخبز المحلية وهم:- شندويل ١،سدس ١٢، جيزة ١٦٨، جميزة ٩،سدس ٤ وكذلك ثلاث سلالات مستوردات من الــ CIMMYT وهى سلالة ١١، سلالة ١٦، سلالة ٢٦ و ٢٨ هجين جيل أول و ٢٨ هجين جيل ثانى. وأجريت هذه الدراسة بمحطة البحوث الزراعية بملوى – مركز البحوث الزراعية فى ثلاث مواسم زراعية متتالية (٢٠١٣/٢٠١٤ – ٢٠١٤/٢٠١٥ – ٢٠١٥/٢٠١٦). وتم دراسة بعض القياسات الوراثية للصفات التالية:- مساحة ورقة العلم (سم٢)، معدل أمتلاء الحبة (جم/يوم)، عدد سنابل النبات، عدد حبوب السنبلة، محصول النبات (جم)، وزن الـــ ١٠٠ حبة (جم). وقد أظهر تحليل التباين وجود فروق عالية المعنوية بين التراكيب الوراثية المستخدمة لجميع الصفات المدروسة. كما أظهرت النتائج المتحصل عليها أن الفعل الجينى غير المضيف كان أكثر أهمية من الفعل الجينى المضيف لمعظم الصفات المدروسة. وأن درجة السيادة كانت سيادة فائقة لمعظم الصفات المدروسة فيما عدا صفة عدد حبوب السنبلة فقد كانت سيادة جزئية. وتلاحظ أن درجة التوريث بالمعنى الضيق كانت متوسطة لكل الصفات المدروسة فى التراكيب الوراثية للجيل الثانى. وأظهر الهجين (سدس ١٢×جيزة ١٦٨) أقل القيم إنخفاضاً فى معامل التربية الداخلية للمحصول كما تبين وجود إرتباط قوى بين محصول الحبوب للنبات وكلاً من معدل إمتلاء الحبوب وعدد سنابل النبات الواحد. كما وجد أن هناك إرتباط قوى بين مساحة الورقة العلم ووزن الـــ ١٠٠ حبة. كما أظهرت نتائج علاقة Wr/Vr أن الأب سدس ١٢ الذى يقع قرب منطقة المنشأ للعلاقة ما بين Wr/Vr للصفات (مساحة ورقة العلم، محصول الحبوب للنبات، عدد سنابل النبات، وزن الـــ ١٠٠ حبة ومعدل أمتلاء الحبوب) وكذلك السلالة ١٣ لصفة معدل أمتلاء الحبوب مما يدل على أنهما يمتلكان أكبر قدر من الجينات السيادية لتلك الصفات. ويمكن أن تستخدم هذه التراكيب الوراثية فى برامج التحسين الوراثى المتعددة لزيادة المحصول.