

GENETICAL STUDIES ON YIELD AND SOME AGRONOMIC CHARACTERS IN SOME BREAD WHEAT (*Triticum aestivum*, L.) CROSSES

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ABSTRACT

Parents ($P_1 \times P_2$), F_1 , F_2 , Bc_1 and Bc_2 of three bread wheat (*Triticum aestivum*, L.) crosses IRENA / PBW343, IRENA / GEMMEIZA 9 and Gemmeiza 9 / SIDS 7 were grown during the three successive seasons, 2003/2004, 2004/2005 and 2005/2006 at the experimental farm of El-Gemmeiza Agric. Res. Station, ARC, Egypt. The non-allelic interaction, scaling tests (A,B,C and D) coupled with six types of gene action were estimated in addition to determining the adequacy of genetic model controlling the genetic system of the inheritance of some economic traits. Heading date, maturity date, plant height, number of spikes/plant, number of kernels/spike, 100 kernel weight and grain yield/plant were studied.

Analysis of variance indicated significant differences among the studied generations for all studied traits. Results indicated the presence of non-allelic interaction for the significant values in all traits and crosses except few cases in which the values did not reach the significant levels. In the six parameters model, the additive component (a) as well as dominance component (d) were significant in most cases. Additive x additive (aa) was significant in all cases except heading date and number of spikes/plant in the second cross (IRENA/GEMMEIZA 9) and number of spikes/plant and grain yield/plant in the third cross. Additive x dominance (ad) component was insignificant in the second cross (IRENA/GEMMEIZA 9) and third cross (GEMMEIZA 9/SIDS7) for number of spikes/plant and 100 kernel weight. Also, dominance x dominance (dd) was significant for all traits in all crosses except number of spikes/plant for second cross.

Significant positive or negative heterosis values based on better parents values were obtained for all crosses and traits except in case of maturity date for the second cross. All crosses showed significant inbreeding depression except heading date in the first cross (IRENA/PBW 343). High heritability estimates in broad sense were observed for all studied traits for all crosses. Narrow sense heritability ranged from 13.89% to 66.34% for heading date in first and third cross, respectively. High genetic advance was associated with high heritability estimates for 100 kernel weight and grain yield/plant. Moderate to low genetic advance were detected for other traits in the three crosses.

INTRODUCTION

Wheat is the most important cereal crop in Egypt and world wide. In Egypt, increasing grain yield of cereal crops is considered one of the important national goals to face the growing needs of the populations therefore, it has become necessary to develop genotypes which consistent by showing superior performance.

The plant breeder is interested in the estimation of gene effects in order to formulate the most advantageous breeding procedures for improving his breeding program. Therefore, breeders needs information about nature of gene action, heterosis, inbreeding depression, heritability and predicted genetic gain from selection for earliness, agronomic characters, yield and

yield components. Since decision making about effective breeding system to be used is mainly dictated by type of gene action controlling the genetic variation, such information is helpful for the breeders to predict in early generation the effective breeding program. The potential of new recombination lines that could be derived of a lowing series of selfing generations. Since, genetic information obtained from multi populations (P_1 , F_2 , F_1 , F_2 , Bc_1 and Bc_2) are considered the one which may be give detailed genetic information of the employed genotypes.

Many investigators studied the type of gene effect in wheat genotypes and reported that partial dominance was relatively more important than additive in the inheritance of grain yield, while additive genetic effect were predominated in the expression of plant height and heading date Amaya *et al.* (1972). Partial dominance of genes were important in expression of heading date, plant height and kernel weight. Also, high values of heritability and no significant epistatic effect were detected in the inheritance of these traits Singh *et al.* (1985). Meanwhile, Khalifa *et al.* (1997) and El-Sayed *et al.* (2000), found that additive-dominance model were adequate for revealing the inheritance of grain yield and its components. On the other hand, Amawate and Behl (1995) revealed that the dominance gene effect were more important than additive one in most traits which showed presence of both types of gene effects. Results of Sharma *et al.* (1998) and Yadav and Nersinghani (1999) indicated that additive gene effects were predominant for yield and yield components, though non-additive gene effects were also important. Hamada (2003), Tammam (2005) and Abd El-Majeed (2005) revealed that additive and dominance components were significant for most traits studied.

The present work was undertaken to study the behavior of gene action and other genetic parameters of seven traits in three wheat crosses by using their six population P_1 , P_2 , F_1 , F_2 , Bc_1 and Bc_2 .

MATERIALS AND METHODS

The present study was carried out at El-Gemmeiza Agric. Res. Station A.R.C., Egypt, during three successive seasons 2003/2004, 2004/2005 and 2005/2006. This study aimed to estimate, heterosis, heritability and type of gene action of some quantitative characters in three bread wheat crosses. Four bread wheat (*Triticum aestivum* L.) genotypes i.e. IRENA, PBW 343, GEMMEIZA 9 and SIDS 7, were chosen for this study on the basis of their diversity in origin Table (1). In 2003/2004 season, three crosses were made, $P_1 \times P_2$, $P_1 \times P_3$ and $P_3 \times P_4$ to produce F_1 hybrids. In 2004/2005 season some F_1 plants of each cross were backcrossed to each of the two parents to produce the backcrosses (Bc_1 and Bc_2). The rest of the F_1 plants were selfed to produce F_2 generation. In 2005/2006 season, the six populations, P_1 , P_2 , F_1 , F_2 , Bc_1 and Bc_2 of three crosses were sown in a randomized complete block design with four replications. Each replicate for every cross was planted with 40 grains in two rows for each of the two parents and F_1 , 100 grains in five rows of each of the two backcrosses and 160 grains in eight rows for the F_2 population. Plants were sown in rows, 2.0

m long and 30 cm apart and 10 cm within rows. Recommended field practices for wheat production were adopted in all growing seasons.

Table (1): The name, pedigree and origin of the four parental bread wheat genotypes.

Parents	Name	Pedigree	Origin
P ₁	IRENA	BUC/FLK/MYNA/VUL CM 91575-28Y-OM-OY-1M-OY	Mexico
P ₂	PBW 343	ND/VG9144//KAL/BB/3/YACO/4/VEE#5 CM 5836-4Y-OM-OY-8MOY-01ND	Mexico
P ₃	Gemmeiza 9	ALD"s//SHUAC//CMH74A.630/SX GM4583-5GM-1GM-OGM	Egypt
P ₄	Sids 7	Maya"s//Mon"s//CMH74A.592/3/Sakha8*2 SD10002 -8SD -1SD -1SD - 0SD	Egypt

Data were recorded on 25, 25, 75 and 60 plants for both parents, F₁, F₂ and backcrosses of each cross for every replicate. Data were recorded on individual guarded plants for heading date, maturity date, plant height, number of spikes/plant, number of kernels/spike, 100 kernel weight and grain yield/plant.

Statistical and genetic analysis:-

To determine the presence or absence of non-additive interactions, scaling test as outlined by Mather (1949) was used. The quantities A, B, C and D and their variances were calculated to test the adequacy of the additive-dominance model in each case where:-

$$A = 2 \overline{Bc_1} - \overline{P_1} - \overline{F_1}$$

$$B = 2 \overline{Bc_2} - \overline{P_2} - \overline{F_2}$$

$$C = 4 \overline{F_2} - \overline{F_2} - \overline{P_1} - \overline{P_2}$$

$$D = 2 \overline{F_2} - \overline{Bc_1} - \overline{Bc_2}$$

The variance of these estimates were calculated as follows:-

$$V(A) = 4V(\overline{Bc_1}) + V(\overline{P_1}) + V(\overline{F_1})$$

$$V(B) = 4V(\overline{Bc_2}) + V(\overline{P_2}) + V(\overline{F_2})$$

$$V(C) = 16V(\overline{F_2}) + 4V(\overline{P_1}) + V(\overline{P_1}) + V(\overline{P_2})$$

$$V(D) = 4V(\overline{F_2}) + V(\overline{Bc_1}) + V(\overline{Bc_2})$$

The standard error of A, B, C and D was obtained by taking the square root of their respective variances. T-test was calculated by dividing the effects of A, B, C and D on their respective standard error.

Type of gene effects estimated according to Gamble (1962) as follows:-

$$m = \overline{F_2}$$

$$a = \overline{Bc_1} - \overline{Bc_2}$$

$$d = \overline{F_1} - \overline{F_2} - \frac{1}{2}(\overline{P_2}) - \frac{1}{2}(\overline{P_1}) + 2(\overline{Bc_1}) + 2(\overline{Bc_2})$$

$$aa = 2(\overline{Bc_1}) + 2(\overline{Bc_2}) - (\overline{F_2})$$

$$ad = (\overline{Bc_1}) - \frac{1}{2}(\overline{P_1}) - (\overline{Bc_2}) + \frac{1}{2}(\overline{P_2})$$

$$dd = (\overline{P_1}) + (\overline{P_2}) - 2(\overline{F_1}) + 4(\overline{F_2}) - 4(\overline{Bc_1}) - 4(\overline{Bc_2})$$

The variance values needed in this concern were obtained as follows:-

$$Vm = V(\overline{F_2})$$

$$Va = V(\overline{Bc_1}) + V(\overline{Bc_2})$$

$$Vd = V(\overline{F_1}) + 16V(\overline{F_2}) + \frac{1}{4}V(\overline{P_2}) + \frac{1}{4}V(\overline{P_1}) + 4V(\overline{Bc_1}) + 4V(\overline{Bc_2})$$

$$Vaa = 2V(\overline{Bc_1}) + 2V(\overline{Bc_2}) + 16V(\overline{F_2})$$

$$Vad = V(\overline{Bc_1}) + \frac{1}{4}V(\overline{P_1}) + V(\overline{Bc_2}) + \frac{1}{4}V(\overline{P_2})$$

$$Vdd = V(\overline{P_1}) + V(\overline{P_2}) + 4V(\overline{F_1}) + 16V(\overline{F_2}) + 16V(\overline{Bc_1}) + 16V(\overline{Bc_2})$$

The standard error of a, d, aa, ad and dd was obtained by taking the square root of their respective variances. T-test values were calculated by dividing the effects of a, d, aa, ad and dd on their respective standard errors.

The amount of heterosis was expressed as the percentage deviation of F_1 mean performance from better-parent values. Inbreeding depression was calculated as the difference between the F_1 and F_2 means expressed as a percentage of the F_1 mean. T-test was used to determine the significance of these deviation where the standard error (S-E) was calculated as follows:

S-E for pater-parent heterosis calculated as follows:

$$(\overline{F_1} - \overline{BP}) = (V\overline{F_1} + V\overline{BP})^{1/2}$$

And S-E for inbreeding depression were estimated as follows:

$$(\overline{F_1} - \overline{F_2}) = (V\overline{F_1} + V\overline{F_2})^{1/2}$$

Heritability in both broad and narrow sense were estimated according to Mather (1949), predicted genetic gain from selection (Δg) was calculated according to Johanson *et al.* (1955).

RESULTS AND DISCUSSION

1-Mean performance:-

Means and variances of the studied traits in the three crosses for the six populations, P_1 , P_2 , F_1 , F_2 , Bc_1 and Bc_2 are presented in Table (2). The analysis of variance indicated that there were significant differences among the studied generations in all characters under this study. Therefore, needed parameters were computed.

In general, the mean performance of Bc_2 cross 1 and cross 2 and P_2 in cross 3 were the earliest in heading date. Bc_1 , F_2 and P_2 were the best as early maturing for the crosses 1, 2 and 3, respectively. For plant height, F_2 in crosses 1, 2 and 3 were the highest values. For number of spikes/plant, F_2 , P_1 and F_1 have the highest values for the crosses 1, 2 and 3, respectively. On the other hand, F_1 , P_2 and F_2 were the best in number of kernels/spike for the crosses 1, 2 and 3, respectively. P_1 , F_1 and F_2 have the heaviest kernel weight for the crosses 1, 2 and 3, respectively. Meanwhile, F_2 in crosses 1 and 2 and F_1 in cross 3 recorded the highest grain yield/plant.

Table (2) :- Means (\bar{x}) and variances (S^2) of P_1 , P_2 , F_1 , F_2 , Bc_1 and Bc_2 populations of the three wheat crosses for the studied traits.

Traits	Cross I ($P_1 \times P_2$)						Cross II ($P_1 \times P_3$)						Cross III ($P_3 \times P_4$)					
	P_1	P_2	F_1	F_2	Bc_1	Bc_2	P_1	P_2	F_1	F_2	Bc_1	Bc_2	P_1	P_2	F_1	F_2	Bc_1	Bc_2
Heading date	\bar{x} 99.97	92.30	91.40	92.10	92.08	90.93	100.97	101.63	104.30	96.20	99.91	92.57	108.37	90.53	90.60	92.23	98.00	95.37
	S^2 1.34	1.10	0.78	2.16	2.03	1.99	1.48	0.92	2.17	1.98	1.56	1.57	2.45	1.32	1.32	7.10	5.39	4.10
Maturity date	\bar{x} 149.78	151.40	150.07	149.33	146.60	151.40	154.10	155.77	155.87	150.20	152.87	151.17	156.23	144.93	150.30	155.30	147.53	153.75
	S^2 1.28	1.14	1.90	2.65	2.05	1.99	1.06	0.86	1.89	1.73	1.52	1.98	1.93	1.28	3.25	2.75	2.61	
Plant height	\bar{x} 110.70	108.47	106.57	113.30	106.00	112.00	107.53	113.07	107.00	118.63	112.30	112.30	116.07	113.60	114.07	116.20	114.47	110.27
	S^2 41.66	30.95	25.36	223.50	197.00	148.00	21.84	22.68	18.62	275.56	156.80	295.40	14.20	10.69	10.48	25.75	20.47	19.30
No. of spikes/plant	\bar{x} 10.20	9.17	8.93	13.73	10.13	11.00	9.07	9.54	9.10	9.50	9.20	9.40	14.70	13.71	16.83	12.80	13.20	13.23
	S^2 13.50	13.20	11.88	19.62	19.50	14.78	12.44	11.10	10.30	16.21	15.20	14.10	10.63	10.06	6.07	18.84	16.37	12.38
No. of kernels/spike	\bar{x} 65.88	59.53	70.97	63.40	59.47	69.96	70.00	73.50	67.66	69.00	71.90	71.07	80.17	71.93	75.00	88.28	78.60	72.90
	S^2 156.40	135.29	110.52	196.40	179.36	175.00	161.10	149.78	32.70	263.81	230.23	176.90	127.18	85.99	83.93	185.10	157.79	138.97
100- kernel weight	\bar{x} 5.71	4.04	5.38	5.36	5.55	5.43	4.42	4.64	4.61	4.09	4.47	4.49	5.05	5.11	5.09	5.40	5.05	5.07
	S^2 37.83	30.45	25.09	96.10	72.62	62.36	74.00	42.5	18.95	165.80	131.60	109.20	10.10	9.46	9.39	16.78	15.33	11.98
Grain yield/plant	\bar{x} 23.61	21.40	20.20	34.41	22.09	22.61	23.24	21.28	10.90	23.65	21.24	22.20	45.61	43.25	53.66	50.79	48.81	52.26
	S^2 147.26	105.55	105.30	210.53	192.48	156.05	141.12	130.36	91.21	174.58	164.44	143.55	71.95	65.17	57.78	95.37	83.89	81.37

2-Gene effects:-

The choice of the most efficient breeding procedures depends, to large extent, on the knowledge of the genetic system controlling the characters to be selected. The estimates of various types of gene effects contributing to the genetic variability are presented in Table (3).

Scaling test A, B, C and D in Table (3) showed that all the studied characters in the three crosses were significant except twelve out of eighty four estimates. These results, in general, indicated the presence of non-allelic interaction. On the other hand, if scaling test A, B and C were significant this may indicate the inadequacy of the simple model in computing the differences between population means. Also, the scaling test estimates for the excepted traits (insignificant ones) indicated the absence of non-allelic interactions and have the additive-dominance model is adequate. These results were in agreement with those of Sirvastava *et al.* (1992), Hamada *et al.* (2002), Hamada (2003), Tammam (2005) and Abd El-Majeed (2005).

The mean parameter (m) for all studied attributes of the three crosses which reflect the contribution due to the over all mean plus the locus effects and interaction of the fixed loci, was highly significant except number of spikes/plant in the second cross.

Additive gene effect (a) was positive and significant for heading date in the three crosses, maturity date in the second cross, plant height and number of kernels/spike in the third cross and 100 kernel weight in the first cross. On the other hand, it was negative and significant for maturity date in both first and third crosses, plant height, number of spikes/plant and number of kernels/spike in the first cross, and grain yield/plant in the second and third crosses. While, it had positive or negative and insignificant values for plant height and number of kernels/spike in the second cross, number of spikes/plant and 100 kernel weight in both second and third crosses, and grain yield/plant in the first cross. These results indicated that the potentiality of improving the performance of these traits using the pedigree selection program may be more effective, Abul-Nass *et al.* (1993).

In autogamous crops, i.e., wheat and barley, the breeder is usually aiming to isolate parental combinations that are likely to produce desirable homozygous segregants. The utility of attempts in identifying such pure lines is facilitated by the preponderance of additive genetic effects in self pollinating crops, Joshi *et al.* (1966).

The estimates of dominance(d) effects were significant for all studied traits except; number of spikes/plant in the second cross. The estimates of dominance were positive and significant for heading date in both second and third crosses, maturity date in the second cross, number of spikes/plant in the third cross, number of kernels/spike and 100 kernel weight in both first and second cross and grain yield/plant in the third cross and they were negative and significant for heading date and number of spikes/plant in the first cross, maturity date in both first and third crosses, plant height in the three crosses, number of kernels/spike and 100 kernel weight in the third cross and grain yield/plant in both first and second crosses. These results indicating the importance of dominance gene effects in inheritance of these traits.

Table (3) :- Scaling test and gene action parameters of the studied traits in the three wheat crosses.

Traits	Crosses			Scaling test				Gene action parameter						
	I	II	III	A	B	C	D	m	a	d	na	ad	dd	
Heading date	I	II	III	-7.21	-1.84	-6.67	1.19	92.10	1.15	-7.11	-2.38	-2.69	11.43	
	I	II	III	-5.45	-20.79	-26.40	-0.00	96.20	7.34	3.16	0.16	7.67	26.08	
	I	II	III	-2.97	9.61	-11.18	-2.63	92.23	2.63	8.97	17.82	-6.29	-24.46	
Maturity date	I	II	III	-6.65	-1.33	-4.00	0.66	149.33	-4.80**	-1.84	-1.32	-3.99	6.64	
	I	II	III	-4.23	-9.30	-20.81	-3.64	150.20	1.70**	8.22	7.28	2.54	6.25	
	I	II	III	-11.47	11.91	19.44	9.50	155.30	-6.04**	-19.28	-19.00	-11.69	18.56	
Plant height	I	II	III	-5.27	8.96	22.89	9.60	113.80	-6.00**	-22.22	-19.20	-7.12	15.51	
	I	II	III	10.07	4.53	39.92	12.66	118.63	0.00	-28.62	-25.32	2.77	10.72	
	I	II	III	-1.20	-7.13	6.90	7.66	116.20	4.20**	-16.09	-15.32	2.97	23.65	
No. spikes/plant	I	II	III	1.13	5.10	17.69	5.73	13.73	-1.47	-12.22	-11.46	-1.99	5.23	
	I	II	III	-0.37	0.16	0.59	0.40	9.50	-0.20	-1.31	-0.80	-0.27	1.01	
	I	II	III	-5.13	-4.08	-10.87	-0.83	12.80	-0.03	4.29	1.66	-0.53	7.55	
No. kernels/spike	I	II	III	-17.91	9.42	-13.75	-2.63	63.40	-10.49	67.53	59.26	-40.67	-104.77	
	I	II	III	6.14	2.58	-2.82	-3.77	69.00	0.03	7.45	11.54	1.78	-20.26	
	I	II	III	2.03	-1.13	51.02	25.06	88.28	5.70	-51.17	-50.12	1.58	49.22	
100-kernel weight	I	II	III	0.07	6.57	1.30	-2.67	53.57	1.09	6.37	5.34	-3.25	-3.25	
	I	II	III	-2.80	-4.73	-23.07	-7.77	40.91	-0.15	18.33	15.54	0.97	-8.01	
	I	II	III	-0.57	-0.67	12.58	6.91	54.03	-0.25	-13.73	-13.82	0.05	15.06	
Grain yield/ plant	I	II	III	0.37	3.62	52.23	24.12	34.41	-0.52	-50.55	-48.24	-1.63	44.25	
	I	II	III	0.34	4.22	12.28	3.86	23.65	-0.96	-11.08	-7.72	-1.94	3.16	
	I	II	III	-1.65	7.61	6.98	0.51	50.79	-3.45	8.21	-1.02	-4.63	-4.94	

*, ** significant at 5% and 1% probability levels, respectively.

On the other hand, significant of additive (a) and dominance(d) components indicated that both additive and dominance gene effects were important in the inheritance of these traits. Also, selecting desirable characters may be practiced in the early generations but it would be effective in the late ones .Similar results were obtained by El Hosary *et al.* (2000) and Hendawy (2003).

Estimates of epistatic gene effects; additive x additive (aa), additive x dominance (ad) and dominance x dominance (dd) are presented in Table (3). Significant estimates of epistatic gene effects for one or more of these three types of epistatic gene effects in the three crosses for all studied traits were detected. Additive x additive (aa) gene effects were positive and significant in the first cross for number of kernels/spike and 100 kernel weight, the second cross for maturity date , number of kernels/spike and 100 kernel weight and in the third cross for heading date, indicating that two traits had increasing genes and selection for the development of these traits could be effective. Meanwhile, it was negative and significant in case of heading date, maturity date, plant height, number of spikes/plant and grain yield/plant for the first cross, plant height and grain yield/plant for the second cross, and maturity date, plant height, number of kernels/spike and 100 kernel weight for the third cross. These results indicate that the material used in these study have decreasing alleles for these characters and selection to improve it could not be effective except in the case of heading and maturity dates and plant height in which selection will be effective in identifying early dwarf lines.

Data concerning the epistatic gene effects, additive x dominance (ad) revealed different positive and significant estimates in the second cross for heading date, maturity date, plant height and number of kernels/spike, in the third cross for plant height and number of kernels/spike and they were negative and significant in the first cross for all studied characters, in the second cross for grain yield/plant and in the third cross for heading date, maturity date and grain yield/plant. These results indicate that the inheritance of these traits were affected by the duplication effect of epistatic genes.

The dominance x dominance (dd) gene effect differed according to crosses and characters. Heading date was positive and significant in the first and second crosses; and negative and significant in the third cross. Maturity date, plant height and number of spikes/plant were positive and significant in all crosses except the second cross in number of spikes/plant where it was positive and insignificant, number of kernels/spike and 100 kernel weight were negative and significant in both first and second crosses; and positive and significant for grain yield/plant in both first and second crosses and negative and significant in the third cross. Positive and significant results confirm the importance role of dominance x dominance gene interactions in the genetic system controlling these characters. Similar results were reported by Singh *et al.* (1985), Sirvastava *et al.* (1992) and Tammam (2005).

The absolute relative magnitude of the epistatic gene effects to the mean effects were somewhat variable depending on the cross and the studied trait. Generally, the absolute magnitude of the epistatic effects were larger than additive or dominance effects. Therefore, it could be concluded that homozygous x homozygous and heterozygous x homozygous non- allelic

interactions were more important than the heterozygous x heterozygous interaction in the inheritance of most studied traits. The study further revealed that epistatic gene effects were as important as additive and dominance gene effects for most of the traits. The failure in detecting epistatic gene effects based on the generation mean analysis does not necessarily indicate that non-allelic interactions play no role in the determination of phenotypic value. Nighawan *et al.* (1969) had also reported the importance of all the three types of gene actions. On the other hand, Ketata *et al.* (1976) postulated non-additive gene action of sizable amount for grain yield in wheat. Thus, the system of inbreeding employed in exploiting any character depends on the gene action involved in its expression for predicted gain in selection progress Abul-Naas *et al.* (1993).

3-Heterosis:-

In self-pollinated crops such as wheat, plant breeders have been investigated the possibility of developing hybrid cultivars. Thus, the utilization of heterosis in various crops through the world has tremendously increased the production either for human food or livestock feed. Heterosis is a complex phenomenon which depends on the balance of different combinations of genotypic effect as well as the distribution of plus and minus alleles in the parents. Heterosis is expressed as the percentage deviation of F_1 mean performance from the better or mid-parent of the traits. As it will be expected, better-parent for plant height was the short one and heterosis relative to the mid-parent value may be also effective. On the other hand, a few days for both heading and maturity dates may be the best.

In this concern, percentage of heterosis over better parent values are presented in Table (4). Negative significant heterosis was obtained for heading date in the first and third crosses and maturity date in the third cross. Therefore, these crosses can be utilized in breeding for early heading and or maturity. Plant height heterosis values in the first and second crosses were also negative and significant, so they were suitable for breeding dwarf plant. The third cross had positive and significant heterosis values for number of spikes/plant, number of kernels/spike and grain yield/plant. Positive and significant heterosis was obtained for number of kernels/spike and 100 kernel weight in the first cross, and 100 kernel weight in the second cross. These results were in agreement with those obtained by El-Sayed *et al.* (2000), Hamada *et al.* (2002), Hamada (2003) and Hendawy (2003). Significant and positive better parent heterosis effects for grain yield/plant was detected for cross $P_3 \times P_4$ (17.65%), therefore, it could be concluded that the single cross ($P_3 \times P_4$) exhibited a great potential for commercial hybrid wheat production.

4-Inbreeding depression:-

Inbreeding depression measured the reduction in performance of the F_2 generation due to inbreeding. The results in Table (4), showed a significant positive values for heading date, maturity date and 100 kernel weight in the second cross, number of spikes/plant and grain yield/plant in the third cross; and number of kernels/spike in first cross.

Table (4) :- Heterosis (BP), inbreeding depression , heritability (Bs&Ns), genetic advance upon selection and genetic advance as percentage for the studied traits in three wheat crosses.

Traits	Crosses	Heterosis BP %	Inbreeding depression %	Heritability %		Δg	Δg %
				Broad	Narrow		
Heading date	I	-8.57**	-0.77	51.70	13.89	0.42	0.46
	II	3.30**	7.77**	46.70	36.87	1.12	1.16
	III	-16.40**	-1.80	74.93	66.34	3.64	3.95
Maturity date	I	0.19	0.49	55.85	47.55	1.59	1.07
	II	1.15*	3.64**	48.32	28.04	0.79	0.53
	III	-3.80**	-3.33**	46.77	35.08	1.30	0.84
Plant height	I	-1.72*	-6.78**	85.39	45.64	14.5	12.35
	II	-5.37**	-10.87**	92.36	35.90	12.28	10.35
	III	0.41	-1.87*	54.21	45.55	4.76	4.10
No. of spikes/ plant	I	-12.45**	-53.75**	34.45	25.28	2.31	16.80
	II	-5.89**	-4.40*	30.41	19.25	1.60	16.80
	III	14.49**	23.95**	52.65	47.40	4.24	33.11
No. of kernels /spike	I	10.22**	10.67**	31.81	19.45	5.62	8.86
	II	-7.27**	-1.98*	56.59	45.67	15.28	22.15
	III	4.27**	-17.71**	46.50	39.68	11.12	12.60
100 – kernel weight	I	11.10**	0.35	67.63	59.63	12.05	22.49
	II	3.60**	14.89**	72.68	54.76	14.53	35.51
	III	-0.41	-6.09**	42.33	37.25	3.14	5.82
Grain yield/ plant	I	-14.44**	-70.35**	43.30	34.45	10.30	29.93
	II	-18.67**	-25.13**	30.75	23.58	6.42	27.14
	III	17.65**	5.35*	31.88	26.72	5.37	10.58

On the other hand, significant negative inbreeding depressor values were detected for heading date, maturity date and 100 kernel weight in the third cross, plant height in the three crosses, number of spikes/plant and grain yield/plant in the first and second crosses. number of kernels/spike in the second and third crosses. Significant effects for both heterosis and inbreeding depression were associated with heading date and maturity date in both second and third crosses, plant height in both first and second crosses, number of spikes/plant, number of kernels/spike and grain yield/plant in the three crosses, and 100 kernel weight in second cross. Significant effects for both heterosis and inbreeding depression seems logic since the expression of heterosis in F_1 followed by considerable reduction in the F_2 performance. The contribution between sings for dominance and epistatic effects of most parameters may lead to the observed absence of heterosis effect El-Hosary *et al.* (2000). Also, reduction in values of non-additive genetic components is logically caused by means of inbreeding depression. These results were in agreement with those obtained by Abul- Naes *et al.* (1993) in barley and Hendawy (2003).

5-Heritability:-

Heritability estimate indicates the progress from selection for plant character is relatively easy or difficult to make in breeding program. Plant breeders, through experience, can perhaps rate a series of characters based on their response to selection. Heritability gave a numerical description of this concept. Assessment of heritability of various traits is of considerable importance in crop improvement program, for example, to predict response to selection, Nygust (1991) and to identify optimum environments for selection, Allen *et al.* (1978). Heritability has been estimated in several experimental situations in literature. Standard errors of the estimates or the confidence intervals of heritability are reported for parent-offspring data by Falconer (1982) and others. Exact confidence intervals for heritability were obtained by Knapp *et al.* (1985) when the data were collected.

On progeny mean basis from several environments. The standard errors and confidence interval of response to selection have been given by Bridges *et al.* (1991), Singh *et al.* (1993) and Singh and Ceccarelli (1995). For the standard errors of the estimates of heritability from the data generated in a randomized complete block design or incomplete blocks conducted in an environment(or single trial) and in several environments (or multi-location trials). Using a simulation technique, Singh *et al.* (1993) found that, the distribution of heritability estimated to normal distribution in their cases.

Heritability estimates depending on magnitudes of its genetic variance components of additive and dominance are presented in Table (4). The highest broad sense heritability was obtained for plant height in second cross (92.36%). Meanwhile, the lowest estimate was resultant for number of spikes/plant in the second cross with value (30.41%). Heritability in narrow sense as estimated by using F_2 and backcrosses data, were low for heading date in first cross (13.89%) and high in the third cross (66.34%).

The results reveled also that the genetic variance was mostly attributed to the additive effects of genes for the other studied traits. This confirmed the previous results found by means of gene action estimates of

additive genetic portion, which was mostly predominant. These results were in harmony with those obtained by El-Sayed *et al.* (2000), El-Hosary *et al.* (2000), Hamada *et al.* (2002) and Hendaway (2003).

6-Genetic advance:-

The genetic advance as percentage of the F₂ mean for the studied characters is presented in Table (4). Moderate to high genetic advance ($\Delta g\%$) was detected for plant height, number of spikes/plant, number of kernels/spike, 100 kernel weight and grain yield/plant for the three crosses, heading date for the third cross, and low genetic advance was obtained for the other cases.

In the present work, high genetic advance was found to be associated with high heritability estimates for plant height, 100 kernel weight and grain yield/plant in three crosses. Therefore, selection in those particular population should be effective and satisfactory for successful breeding purposes. Also, moderate and low genetic advance was found to be associated with moderate or low heritability estimates.

As it is well known, expected improvement via selection is directly proportional to heritability. Also, the expected response to selection varies with the phenotypic standard deviation of population means. This figure is a measure of low total variability in these traits and therefore reflects the total response that could be realized by breeding techniques. It is possible to visualize a situation where the heritability is high but little response can be expected, El-Hosary *et al.* (1997).

REFERENCES

- Abd El-Majeed, S. A. (2005). Estimation of epistasis, additive and dominance variation in some bread wheat (*Triticum aestivum* L.) crosses. J.Agric.Sci. Mansoura Univ.,30(6): 2999-3011.
- Abul-Naas,A.A.; M.A.Mahrous and A.A.El-Hosary (1993). Genetical studies on grain yield and some of its components in barley (*Hordeum vulgare* L.) Egypt J. Agron., 18 (1-2) 33-46.
- Allen,F.L.; R.E.Comstock and O.C.Resumes (1978). Optimal environment for yield testing. Crop Sci., 18: 747-751.
- Amawate,J.S. and P.N.Behl (1995). Genetical analysis of some quantitative components of yield in bread wheat. Indian J. Genet, 55 (20): 120-125.
- Amaya,A.A.; R.H.Busch and K.L.Lebsock (1972). Estimates of genetic effects of heading date, plant height and grain yield in durum wheat. Crop Sci. 12: 478-481.
- Bridges,J.R.; S.J.Knappand and S.J.Cornliuo (1991). Standard errors and confidence interval estimators for expected selection response. Crop Sci., 31: 253-255.
- El-Hosary,A.A.; M.E.Riad; Nagwa R.Abd El-Fattah and Marial A.Hassan (2000). Heterosis and combining ability in durum wheat. Proc. 9th Conf. Agron., Menufiya Univ. 101-117.
- El-Hosary,A.A.; M.B.Habeeb and A.I.Fahmi (1997). Genetic studies of some quantitative characters in soybean (*Glycine max* L.) Merrill) Menufiya J. Agric. Res., 22(2): 405-419.

- Srivastava, R. B.; S. C. Sharma and M. Yunus (1992). Additive and non additive gene effects for yield and yield components in two crosses of wheat (*T. aestivum* L.). Indian J. Genet, 52 (3): 297-301.
- Tammam, A. M. (2005). Generation mean analysis in bread wheat under different environmental conditions. Menufiya J. Agric. Res., 30 (3): 937-956.
- Yadav, R.K. and V.G.Narsinghani (1999). Gene effects for yield and its components in wheat. Rachis News Letter, 18(2): 79-81.

دراسات وراثية على بعض الصفات المحصولية في بعض هجن قمح الخبز
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أجريت هذه الدراسة بالمزرعة البحثية لمحطة البحوث الزراعية بالجيزة - مركز البحوث الزراعية خلال ثلاثة مواسم زراعية ٢٠٠٣/٢٠٠٤، ٢٠٠٤/٢٠٠٥ و ٢٠٠٥/٢٠٠٦ بغرض دراسة طبيعة الفعل الجيني ونظام التحكم الوراثي والموديل الوراثي الملائم والتنبؤ بالتراكيب الوراثية المباشرة في الأجيال والتي تفوق حدود الأباء الداخلة في التهجين وذلك لسبعة صفات هي تاريخ التزهير، تاريخ النضج، طول النبات، عدد السنابل في النبات، عدد حبوب السنبل، ووزن الحبة ومحصول الحبوب في النبات وذلك في ثلاثة هجن من قمح الخبز هي

١- IRENA x PBW 343

٢- IRENA x GEMMEIZA 9

٣- GEMMEIZA 9 x SIDS 7

- أوضحت النتائج المتحصل عليها من تحليل التباين وجود اختلافات معنوية بين العشائر الوراثية تحت الدراسة لجميع الصفات في جميع الهجن الثلاثة كما لوحظ وجود تباين غير أليلي لمعظم الحالات حيث كانت قيم الفعل الجيني المضيف وكذلك السيادة معنوية لمعظم القيم ماعدا بعض الحالات القليلة.
- كان التفاعل الجيني من نوع المضيف x المضيف معنويا لجميع القيم ماعدا صفة التزهير وعدد السنابل في النبات للهجين الثاني و صفة عدد السنابل في النبات ووزن حبوب النبات في الهجين الثالث. كما لوحظ أن التفاعل الجيني من نوع المضيف x السيادة كان معنويا لكل الصفات المدروسة في هجن الدراسة ماعدا الهجين الثاني والثالث لصفة عدد السنابل في النبات و وزن الحبة. وأظهرت النتائج أن التفاعل الجيني التفوق من النوع السيادة x السيادة كان معنويا لجميع القيم ماعدا عدد السنابل في النبات للهجين الثاني.
- أوضحت النتائج وجود قوة هجين معنوية لأفضل الأبوين في الهجن الثلاثة لكل الصفات ماعدا صفة تاريخ النضج للهجين الأول و صفتي طول النبات ووزن الحبة للهجين الثالث كانا غير معنويين.
- كانت قيم التوريث بالمعنى الواسع عالية لجميع الصفات في جميع الهجن تحت الدراسة أما قيم التوريث بالمعنى الضيق تراوحت بين ١٣,٨٩ إلى ٦٦,٣٤ لصفة التزهير في الهجينين الأول والثالث على الترتيب.