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GENETIC BEHAVIOUR OF SOME ECONOMIC CHARACTERS IN THREE WHEAT CROSSES

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ABSTRACT

This study was carried out at Sakha Agricultural Research Station (ARC) during the three successive seasons 2015/16, 2016/17 and 2017/18 to determine the genetic factors controlling inheritance of yield and its components for the three bread wheat crosses Sakha95 x Misr1, Sakha 95 x Gemmiza 12 and Gemmiza 12 x Misr1. Analysis of variance showed significant differences among the generation means for all studied traits. Results revealed that the epistatic gene effects cannot be ignored when establishing a breeding program to improve wheat populations for the studied traits. The inheritance of all studied traits was controlled by additive and non-additive genetic effects, with greater values of dominance gene effects than the additive in most cases. Heterosis relative to the better performing parent was significant for the number of tillers/plant and number of grains/spike in the third cross, plant height in the first cross and weight of grains/spike in the first and second crosses. The average degree of dominance revealed the existence of over-dominance towards the better parent for all traits except plant height in the second cross, grain yield per plant in the first and second crosses as well as number of grains/spike in the second and third crosses. Narrow sense heritability estimates displayed moderate values in most cases. The highest broad and narrow sense heritability values were associated with the highest values of genetic advance, especially for number of grains/spike in the second and third crosses, indicating sufficient improvement of yield by selection. The outcome of this study is providing insights to wheat breeders to improve yield potential, release new wheat cultivars with high performance and enhance Egyptian wheat germplasm.

Key words: ***Gene action, Heterosis, Heritability, Genetic advance.***

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is the most important cereal crop in the world and most importantly in Egypt. Increasing wheat yield to reduce the gap between production and consumption is the main target for wheat breeders by developing new cultivars with desirable genetic makeup (Shehab El-Din, 1993).In the early stage of the breeding programs, the direct estimate of yield is quite difficult, because grain yield is complex and driven by many factors. Therefore, the yield components could be used as selection criteria for yield improvement.

Utilization of six populations in generation means analysis is a simple and useful method for computation of genetic effects for the quantitative traits and its greatest merit reside in the capability to measure the epistatic effects such as, additive × additive, additive × dominance and dominance × dominance types (Novoselovic *et al* 2004).

Singh *et al* (2004) and Devi *et al* (2013), suggested that heterosis over better performing parent (heterobeltiosis) can be useful for determining true heterotic cross combinations. High heritability estimates associated with in high genetic advance for yield components in wheat offer better scope for selection of genotypes in early segregating generations (Singh and Chatrath 1992 and Memon *et al* 2005). The heritability may indicate that certain morphological traits that influence grain yield in wheat are more heritable than yield itself (Fethi and Mohamed 2010) and it is a valuable tool when used in conjunction with other parameters in predicting genetic gain that follows the selection for that character. Plant breeder are interested in the estimation of gene effects in order to formulate the most advantageous breeding procedures for improvement of the attribute in question. Therefore, breeders need information about nature of gene action, heterosis, inbreeding depression, heritability and predicted genetic gain from selection for plant height, yield and yield components. The major factors, that must be considered and which may limit progress in the analysis of quantitative genetic variation are the number of genes involved, the type of gene action and the genotype-environment interaction (Erkul *et al* 2010 and Ansari *et al* 2005). Based on the evaluated genetic parameters, selection in advanced generations might be effective for some grain yield traits, due to dominance and epistatic effects (Erkul *et al* 2010). The present study was carried out to obtain information about gene action and other genetic parameters for some characters in three bread wheat crosses. This information would be used in the approval of efficient breeding strategies in wheat breeding.

MATERIALS AND METHODS

The present investigation was carried out at Sakha Res. St., ARC, Egypt, during the three successive seasons 2015/2016, 2016/2017 and 2017/2018. The three bread wheat cultivars ; Sakha95, Misr1 and Gemmeiza12 Table (1) were more adapted in Egypt and proved to produce high yield. The parent cultivars of hexaploid wheat were sown at three planting dates to secure enough hybrid seeds. In 2016/2017 season, F_1 plants were selfed to produce F_2 seeds and backcrossed to the parents to produce BC_1 and BC_2 seeds.

In 2017/18 season, the six populations, i.e. P_1, P_2, F_1, F_2, BC_1 and BC_2 of the three crosses were sown in a randomized complete block design with three replications. Seeds were sown in rows of 4 m long, and 20 cm apart. The plants within rows were 10 cm apart. Four rows were devoted for each parent, F_1 progenies, and BC_1 and BC_2 and ten rows for F_2 generation of each cross.

Table 1. The pedigree of three parental bread wheat cultivars used in the present study.

Parent code	Genotype	Pedigree
P1	**Sakha 95**	**PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBLL1. CMA01Y00158S-040POY-040M-030ZTM-040SY-26M-0Y-0SY-0S.**
P2	**Misr 1**	**OASIS/SKAUZ//4*BCN/3/2*PASTOR. CCMSSOYO1881T-050M-030Y-O3OM-030WGY-33M-0Y-0S.**
P3	**Gemmiza 12**	**OTUS/3/SARA/THB/VEE CMSS97Y00227S-5Y-010M-010Y-010M-2Y-1M-0Y-0GM**

All recommended field practices for wheat production were adopted in all growing seasons. Data were recorded on individual guarded plants for a number of tillers/plant, plant height, grain yield/plant (g), number of grains/spike and weight of grains/spike (g).

Data analysis targeted the differences among crosses and differences among parental genotypes for each cross was performed using the T-test before considering the biometrical analysis according to Allard (1999). Type of gene effects was determined according to Gamble (1962) based on, simple genetic model (m, d, and h) was applied when epistasis was absent, whereas in the presence of non-allelic interaction the analysis was proceeded to estimate the inter-action types involved using the six parameters genetic model. The genetic parameters indicating hetrosis over the better parent, inbreeding depression, mean degree of dominance $(H/D)^{1/2}$ and heritability in broad and narrow sense according to Mather and Jinks (1982) and Wynn *et al.* 1970 and predicted genetic gain as mean percent from selection (Δg %) according to Allard (1999) were calculated.

RESULTS AND DISCUSSION

Generation means of the six populations differed significantly for most studied yield traits, indicating the presence of genetic variability for these traits in the studied materials and revealing that level of the differences between generations' means could be subjected to statistical-genetic analyses.

Results of the mean performance and variance for the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the three crosses for different traits are presented in Table (2).

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 three bread wheat crosses for the studied traits.

Genotypes		Parameters	No. of tillers /plant	Plant height (cm)	Grain yield /plant (g)	No, grains /spike	Weight of grains /spike (g)
Sakha 95	P_1	$\bar{x}$	25.20a	136.60a	57.71a	75.20a	3.03a
		S^2	17.50	15.60	111.20	17.82	0.31
Misr 1	P_2	$\bar{x}$	18.73c	126.10c	44.17c	68.60c	2.31b
		S^2	21.75	25.10	102.37	18.94	0.26
Cross 1 (Sakha 95 x Misr 1)	F_1	$\bar{x}$	21.60b	137.50a	44.94c	74.00ab	2.42b
		S^2	22.94	41.90	121.11	19.31	0.38
	F_2	$\bar{x}$	20.97bc	136.75a	40.27d	71.57b	2.22b
		S^2	58.32	247.20	228.44	40.00	0.89
	Bc_1	$\bar{x}$	24.27a	136.44a	49.47b	71.55b	2.94a
		S^2	50.16	207.40	195.79	35.05	0.73
	Bc_2	$\bar{x}$	21.10bc	133.41b	42.06cd	71.65b	2.50a
		S^2	46.71	147.30	169.44	31.27	0.80
Sakha 95	P_1	$\bar{x}$	25.20a	136.60a	57.71a	75.20a	3.03a
		S^2	17.50	15.60	111.20	17.82	0.31
Gemmiza 12	P_3	$\bar{x}$	15.53d	104.33b	36.90b	49.57d	1.75b
		S^2	12.33	23.68	105.19	38.81	0.33
Cross 2 (Sakha 95 x Gemmiza 12)	F_1	$\bar{x}$	19.07c	102.83b	31.00c	58.93b	2.05b
		S^2	31.72	54.63	119.33	54.48	0.39
	F_2	$\bar{x}$	22.49b	103.63	35.32b	52.73cd	1.90b
		S^2	102.84	107.99	286.20	192.95	0.46
	Bc_1	$\bar{x}$	22.55b	105.00b	35.26b	56.07bc	1.84b
		S^2	111.79	85.81	241.02	133.20	0.33
	Bc_2	$\bar{x}$	21.77bc	101.33b	29.66c	53.93c	1.78b
		S^2	63.58	75.90	210.62	136.93	0.54
Gemmiza 12	P_3	$\bar{x}$	15.53a	104.33b	36.90b	49.57c	1.75b
		S^2	12.33	23.68	105.19	38.81	0.33
Misr 1	P_2	$\bar{x}$	18.73a	126.10a	44.17a	68.60a	2.31a
		S^2	21.75	25.10	102.37	18.94	0.26
Cross 3 (Gemmiza 12 x Misr 1)	F_1	$\bar{x}$	17.07a	104.67b	33.32b	54.67b	1.97ab
		S^2	37.72	34.37	156.79	318.71	0.47
	F_2	$\bar{x}$	16.80a	103.40b	42.31a	53.41b	1.82b
		S^2	86.45	54.29	307.58	407.67	0.63
	Bc_1	$\bar{x}$	16.53a	101.87b	36.17b	55.59b	1.90ab
		S^2	68.82	37.68	212.79	388.41	0.64
	Bc_2	$\bar{x}$	17.80a	102.33b	36.32b	48.72c	1.57b
		S^2	75.00	59.68	288.93	215.45	0.46

Means within each column followed by the same letter are not statistically different at 5% level of probability (Duncan 1955).

Significant differences were observed among most genotypes for measured traits. Generally, the differences between each two parents were found to be significant. Significant variance was detected for all traits in the three crosses. Generally, the mean performances of F_1 and backcross population were considerably higher than the best parent in most traits which indicated a high heterotic effects. Data also revealed that the variance of F_2 and BC's respectively was larger for all traits than P_1, P_2 and F_1. This indicates that environmental fluctuation has marked effects on the expression of these traits. These results are in harmony with those obtained by Koumber and El-Gammaal (2012). Therefore, parents are precisely selected to find the desired recombination in the segregating generations. The parental differences in response to their genetic background were found to be significant in most traits under investigation. The F_2 populations had also significant differences for all studied traits in the three studied crosses (El-Awady 2011).

Scaling test

Scaling test A, B, C and D presented in Table (3) illustrated for all the studied traits in the three crosses were significant, except few cases which indicate the presence of non-allelic interactions and the inadequacy of the simple model in interpreting the differences between population means. Also, the scaling test estimates for insignificant ones (number of tillers/plant in that first and third crosses) indicate the absence of non-allelic interactions and the additive-dominance model is adequate in this case. The significance of any one of these scales is taken to indicate the presence of non-allelic interaction. Hence, data indicate the presence of non-allelic interaction for all the studied characters. Scaling test and genetical analysis of generation means to give estimates of additive (a), dominance (d) and three epistatic effects additive x additive(aa), additive x dominance(ad) and dominance x dominance(dd) according to the relationships illustrated by Gamble(1962) are presented in Table (3). Scaling tests were significantly different from zero for all traits in the three crosses, indicating that the additive-dominance model is adequate to interpret the gene effects. These findings indicated that the six parameter model is valid to explain the nature of gene action for these traits. Meanwhile, A, B, C or D scaling tests were insignificant ones, indicating the interactive model failed to explain the type of gene action in this case.

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

Traits	Cross	Scaling test				Gene action parameter					
		A	B	C	D	m	a	d	aa	Ad	dd
No. of tillers/ plant	1	-2.25	1.87	-3.25	-1.43	20.97**	1.17	2.50	-	-	-
	2	4.83	8.95**	11.09**	-1.34	22.49**	2.77	1.38	2.68	-2.06	-16.45**
	3	0.47	-0.20	-1.20	-0.73	16.80**	-1.27	1.40	-	-	-
Plant height	1	-1.21	3.23	9.29*	3.64	136.75**	3.03	-1.13	-7.28	-2.22	5.26
	2	-29.43**	-4.50	-32.07**	0.933	103.63**	3.67*	-19.50**	-1.87	-12.47**	35.80**
	3	-5.27**	-26.10**	-26.17**	2.60	103.40**	-0.47	-15.75**	-5.20	10.42**	36.57**
Grain yield/plant	1	-3.70	-4.99	-30.68**	-10.99**	40.27**	7.41**	15.99**	21.99**	0.64	-13.30
	2	-18.18**	-8.57*	-15.31**	5.72	35.32**	5.60*	-27.75**	-11.44	-4.81**	38.20**
	3	2.13	-4.84	21.52**	12.12**	42.31**	-0.15	-31.45**	-24.24**	3.49	26.95**
No. of grains/ spike	1	-6.11**	0.70	-5.50*	-0.05	71.57**	-0.11	2.20	0.10	-3.41**	5.31
	2	-22.00**	-0.63	-31.70**	-4.53	52.73**	2.13	5.62	9.07	-10.68**	13.57
	3	6.94	-25.83**	-13.87	2.51	53.41**	6.87*	-9.43	-5.01	16.38**	23.90
Weight of grains/ spike	1	0.43	0.27	-1.30**	-1.00**	2.22**	0.44**	1.75*	2.00**	0.08	-2.70**
	2	-1.40**	-0.23	-1.26**	0.19	1.90**	0.05	-0.73**	-0.38	-0.58**	2.02**
	3	0.08	-1.14**	-0.70*	0.18	1.82**	0.33**	-0.42	-0.36	0.61**	1.42**

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

m = mean, a: additive, d: dominance, aa: additive × additive, ad: additive × dominance, dd: dominance × dominance effects.

These results are similar to those reported by Zaazaa *et al* (2012) and Moussa (2010). Estimates of the six parameters (Table 3) revealed that the estimated mean effects (m) for all studied traits which reflect the contribution due to the overall mean plus the locus effects and interactions of the fixed loci were highly significant in the three crosses. Additive gene effect (a) was positive and significant for grain yield/plant and weight of grains /spike in the first cross; plant height and grain yield/plant in the second cross; and number of grains/spike and weight of grains/spike in the third cross. These results indicate that improving the performance of these traits may be more effective by using the pedigree selection program (Abul-Nass *et al* 1993).

The estimates of dominance effects (d) were positive and significant for grain yield/plant and weight of grains/spike in the first cross; meanwhile, negative and significant dominance effects were recorded for plant height and grain yield/plant in the second and third cross; and weight of grains/spike in the second cross. These results indicated the importance role of dominance gene effects in the inheritance of these traits. On the other hand, significance 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 traits may be practiced in the early generations but it would be effective in the late ones. Similar results were obtained by Hendawy (2003), Abd El-Rahman (2013) and Abd El-Hamid and Ghareeb (2018).

Moreover, positive and significant additive x additive (aa) epistatic gene effects were detected for grain yield/plant and weight of grains/spike in the first cross. Estimates of dominance x dominance gene effects and additive x dominance (ad) were positive and significant for plant height, number of grains/spike and weight of grains/spike in the third cross. Values of dominance x dominance (dd) gene effects were positive and significant for plant height, grain yield/ plant and weight of grains/spike in the second and third crosses. These results indicate that the inheritance of these traits was affected by the duplication effect of epistatic genes. Positive and significant results confirm the importance role of dominance x dominance gene interactions in the genetic system which controls these traits. Similar results were reported by Sheikh *et al* (2009) and Moussa (2010).

Generally, the dominance and dominance x dominance effects were more important than additive x additive (aa) with more additive gene effect in the expression of the most studied traits in the three crosses. These results are in line with those previously obtained by Sheikh *et al* (2009) Aykut *et al* (2011). Novoselovic *et al* (2004) identified that significant additive and additive x additive type gene effects could be fixed in their studied populations. Besides, opposite values of dominance and dominance x dominance gene effects indicated the presence of duplicate epistatic effects. This situation complicates using epistatic gene effects in breeding programs. Similar findings were pointed out by Sheikh *et al* (2009), Khattab *et al* (2010), Abd El-Rahman (2013), Al-Naggar *et al*. (2015) and Al-Bakry *et al*. (2017) who reported that selection in later segeregating generations can be advisable to improve of traits governed by dominance gene effects with prevalence of duplicate epistasis.

Table 4. Heterosis (BP%), inbreeding depression, heritability (hb and hn),The average degree of dominance (H/D)1/2and genetic advance from selection (GS%) for the studied traits in three wheat crosses.

Traits	Cross	Heterosis BP%	Inbreeding depression %	Heritability %		$(H/D)^{1/2}$	GS%
				Broad (h_b)	Narrow (h_n)		
No. of tillers/plant	1	-14.29**	2.92	63.51	33.90	1.32	25.43
	2	-24.34**	-17.96	77.33	29.47	1.80	27.37
	3	9.87**	1.56	68.33	33.64	1.44	38.36
Plant height	1	9.04**	0.55	87.41	56.51	1.05	13.38
	2	-1.44**	-0.78	65.62	50.26	0.78	10.38
	3	-17.00**	1.21	45.88	20.64	1.56	3.03
Grain yield/plant	1	-22.12**	10.39	50.12	40.12	0.71	31.02
	2	-46.29**	-13.95	60.25	42.19	0.93	41.63
	3	-9.69**	-26.97	57.64	36.88	1.06	31.49
No. of grains/spike	1	-1.60	3.28	52.89	34.23	1.04	6.23
	2	-21.63**	10.52	78.55	60.00	0.79	32.56
	3	10.29**	2.30	57.37	51.88	0.46	40.40
Weight of grains/spike	1	4.76**	8.26**	62.64	28.52	1.55	24.96
	2	16.73**	6.94**	23.03	11.86	1.37	8.73
	3	-14.72**	7.38**	38.73	24.28	1.09	21.71

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

Results in Table (4) revealed heterosis over better parent, inbreeding depression percentage and different gene action for the studied traits. The results revealed significant and negative heterotic effects that found for some studied traits among three crosses. Absence of significant heterosis only for number of grains/spike in the first cross could be due to the internal cancellation of heterosis components. By contrast, desired significant and positive heterotic effect over the best performing parent were obtained for number of tillers/plant and grains/spike in the third cross, plant height in the first cross and weight of grains/spike in the first and second crosses. These results indicated that dominance direction was toward the best respective parent in these cases. The significant heterotic effect might be due to the dominance and/or dominance × dominance effects, confirming the previously results, reported by Gad (2010), Khattab*et al* (2010), Koumber and El-Gammaal (2012), El-Shaarawy (2012), Zaazaa *et al* (2012), Abd El-

Rahman (2013) and Abd El-Hamid and Ghareeb (2018). Basd on, significant superiority in yield as well as best performance of hybrids compared to the current commercial cultivars, heterosis over best performing parent may be useful in identifying the best hybrid combinations (Prasad *et al* 1988).

Regarding inbreeding depression, highly significant and positive inbreeding values were obtained for the weight of grains/spike in all three crosses (Table 4). Results from this study displayed significant effects for both heterosis and inbreeding depression, seeming logic since the expression of heterosis in F_1's was followed by a considerable reduction in the F_2 performance due to homozygosity. Also, the reduction in values of non-additive genetic components is logically caused by means of inbreeding depression. The results are in accordance with those reported by Koumber and El-Gammaal (2012) Zaazaa *et al* (2012) and Abd El-Rahman (2013).

The average degree of dominance $(H/D)^{1/2}$ is presented in Table (4). Results revealed values more than unity for all traits, except plant height in the second cross, grain yield/plant in the first and second crosses as well as number of grains/spike in the second and third crosses. These results indicate the presence of over-dominance towards the better parent, suggesting early selection might improve these traits. On the contrary, where the same parameter is less than unity it confirms the role of partial-dominance gene effects underpining these traits. Similar results were obtained by Farooq *et al* (2010), Abd El Rahman (2013) and Abd El-Hamid and Ghareeb (2018).

Heritability estimates depending on magnitudes of its genetic variance components of additive and dominance are presented in Table (4). The highest broad and narrow sense heritabilities were obtained for plant height in the first cross and number of grains/spike in the second cross (87.41, 56.51% and 78.55, 60.00%, respectively). Meanwhile, the lowest estimates for both broad and narrow sense heritabilities were for weight of grains/spike (23.03, 11.86% and 38.73, 24.28%) in the second and third crosses, respectively. Comparison between broad and narrow-sense heritability estimates revealed equal importance of additive and non-additive effects in genetic control of traits. Broad-sense heritability estimates the genetic proportion (additive + dominance + epistasis) of the total phenotypic variation, while narrow-sense heritability estimates only the additive portion. Considerable differences were observed between both broad and narrow-sense heritability in all crosses. This confirms that previous results found by means of gene action estimates of dominance gene action were primarily responsible for the inheritance of most studied traits in these crosses. High narrow sense heritability values indicate that selection may be more effective for improving traits of genotypes in early segregating generations. On the contrary, low and medium narrow sense heritability were estimated for grain yield per plant in the three crosses. These results indicate that environmental and non-additive effects have a larger contribution than addative genetic effects for these traits. These results are similar to those reported by Farshadfar *et al* (2013), Abd El Rahman (2013) and Abd El-Hamid and Ghareeb (2018).

The expected genetic advance from selection for all studied traits in the three crosses is presented in Table (4). Results recorded the highest values for grain yield per plant (41.63%) in the second cross and number of grains/spike (40.40%) in the third cross. Meanwhile, low genetic advance values were obtained for plant height (3.03%) in the third cross and for number of grains/spike (6.23%) in the first one. In the present work, in relation to grain yield/plant, high genetic advance was associated with high heritability values in narrow sense for number of grains/spike in the third cross and grain yield/plant in the second cross. Therefore, selection in these particular populations should be effective and satisfactory in the early segregating generations for successful breeding purposes. These results coincident with those reported by Abd El-Fattah and Mohammad (2009) and Abd El-Hamid and Ghareeb (2018).

CONCLUSION

Results indicated that environmental fluctuation has marked effects on the expression of all traits. Therefore, parents were precisely selected to find the desired recombination in the segregated generations. Also, selecting desirable traits may be practiced in the early generations but it would be more effective in the late ones. Generally, the dominance, dominance x additive and dominance x dominance effects were more important than additive x additive with more additive gene effects in the expression of the most studied traits in the three crosses. These results were confirmed by heterosis values relative to better parent, which may be useful in identifying the best hybrid combination. Degree of dominance revealed values more than unity for most traits in the studied crosses, indicating the presence of over-dominance towards the better parent for most traits and suggesting that early selection might improve these traits.

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السلوك الوراثي لبعض الصفات الإقتصادية لثلاثة هجن من القمح

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أجريت هذه التجربة في محطة البحوث الزراعية بسخا، مركز البحوث الزراعية خلال الثلاث مواسم زراعية ٢٠١٦/٢٠١٥ و ٢٠١٧/٢٠١٦ إلي ٢٠١٨/٢٠١٧ لتحديد المعلمات الوراثية لبعض صفات االمحصول بين العشائر الستة لاستخدامها كمؤشرات للإنتاجية العالية لمحصول الحبوب في ثلاثة هجن من قمح الخبز، وهي Sakha95 x Misr1 و Sakha95 x Gemmiza12 و Gemmiza12 x Misr1. أظهر تحليل التباين اختلافات معنوية بين متوسطات الأجيال لكل الصفات المدروسة. كما أظهرت النتائج أنه لا يمكن تجاهل التأثير التفوقى للجينات عند إنشاء برنامج تربية لتحسين عشائر القمح للصفات المدروسة. كان تأثير الفعل الجيني المضيف وغير المضيف هو المتحكم فى التوارث الا أن قيم التأثير السيادى للجينات كان أكبر من تلك المضيفة في معظم الحالات. وجد أن قوة الهجين بالنسبة للأب الأفضل موجبة وعالية المعنوية بالنسبة لعدد أفرع النبات وعدد حبوب السنبلة في الهجين الثالث، ارتفاع النبات في الهجين الأول، ووزن حبوب السنبلة في الهجينين الأول والثانى. وقد كشفت قيمة متوسط درجة السيادة عن وجود سيادة فائقة لجميع الصفات باستثناء صفة ارتفاع النبات في الهجين الثاني ، ومحصول حبوب النبات في الهجينين الأول والثاني ، وكذلك عدد حبوب السنبلة في الهجينين الثاني والثالث. كما سجلت تقديرات كفاءة التوريث بالمعنى الضيق قيماً متوسطة في معظم الحالات. وقد أشارت أعلى قيم كفاءة توريث بالمعنى الواسع والضيق والمرتبطة بأعلى تقدم وراثي متوقع بالانتخاب لصفة عدد حبوب السنبلة في الهجينين الثاني والثالث لامكانية التحسين الفعال بالمحصول. وتعتبر هذه المعلومات ذات أهمية بالنسبة لمربي القمح لتحسين الإنتاجية، وإستنباط تراكيب وراثية جديدة من القمح مع تعزيز المادة الوراثية للقمح المصري.

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