

GENETICAL ANALYSIS FOR YIELD AND ITS ATTRIBUTES IN BREAD WHEAT USING THE FIVE PARAMETERS MODEL

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ABSTRACT

The present work was carried out at Etay-Elbaroud Agriculture Research Station Behera governorate during four seasons from 2007/ 2008 to 2010/2011. Three crosses were made among four parents, namely Gemniza 9 × Irena, Sids 1× Sakha 93 and Sids 1× Irena. Five populations (P₁, P₂, F₁, F₂ and bulk of F₃) for each cross were used in this investigation. Highly Significant positive heterotic effect was found in the 2nd cross for grain yield and its attributes i.e., number of spikes/plant, number of kernels/spike and 1000-kernel weight and grain yield/plant, being 8.69%, 9.78%, 6.71% and 9.78% in the same respective order. Meanwhile, Negative significant heterotic effects were obtained in the 3rd cross for both number of spikes/plant (-17.45%) and number of kernels/spike -3.08% led to a reduction in grain yield/plant with a value being (-10.37%). Complete dominance was found for number of spikes/plant and 100-kernel weight in the first cross whereas, overdominance ($p>1$) was detected for grain yield and its attributes in the 2nd cross. The other types of dominance were also found.

Inbreeding depression estimates were significant with a positive value for number of spikes/ plant in the first and third cross, number of kernels/ spike and grain yield/ plant in all crosses. On the other side, inbreeding depression was negatively significant for number of spikes/ plant in the second cross and for 100-kernel weight in the second and third cross. Additive gene effects were positive and significant for number of kernels/ spike in the second and third cross and 100-kernel weight in the first cross. Dominance gene effects were found to be significant for all studied characters with the exception of number of kernels/ spike in the first and second cross indicating that dominance played a major role in the inheritance of such characters. Significant and positive (E_1) values were found for 100-kernel weight in the studied crosses. While, negative values were obtained for number of spikes/ plant in the third cross, number of kernels/ spike in all crosses, and grain yield/ plant in the second and third cross. Moreover, (E_2) values were found to be positive and significant for 100-kernel weight in the third cross only. On the other hand, significant negative (E_2) values were detected for number of spikes/ plant and number of kernels/ spike in the three crosses, for 100-kernel weight in the second cross, and grain yield/ plant in both the second and third cross. Narrow sense heritability estimates were ranged from 39.35% for number of spikes/ plant in the third cross to 94.32% for grain yield/ plant in the second one. The parent-off spring regression heritability estimates were high and ranged from 58.85% for number of spikes/ plant in the third cross to 95.65% for grain yield/ plant in the second one. The expected genetic advance (Δg) for number of spikes/ plant was ranged from 3.87 to 10.17 for the selected 5% of F₂ compared with the actual genetic gain which was ranged from 5.07 to 9.37 in the studied crosses. Meanwhile, the expected gain for grain yield/plant was ranged from 21.05 to 36.26 gm.whereas, the actual gain was ranged from 18.46 to 26.81 gm.

INTRODUCTION

Wheat is the most important cereal crop, it is a staple diet for more than one third of the world population and contributes more calories and protein to the world diet than any other cereal crop.

The wheat breeders are concentrating to improve the yield by developing new varieties with desirable genetic make up in order to overcome the consumption pressure of ever increasing population (Memon *et al.*, 2005 and 2007). High grain yield has been the main objective in wheat breeding program. The inheritance of grain yield in wheat has been the subject of intensive studies (Sharma *et al.*, 2002; Heidari *et al.*, 2005 and Rebetzke *et al.*, 2006). Wheat grain yield is a complex character determined by several attribute traits. The true knowledge of the gene action for various bread wheat traits is useful in making decision with regard to appropriate breeding system. Abd-Allah Soheir and Abd EL-Dayem (2008), found that there were positive and significant additive gene effects for number of spikes/ plant, number of kernels/ spike and grain yield/ plant. The additive gene effects played a major role in controlling the genetic variation for number of spikes/ plant. In a study conducted by Amein (2007),. Meanwhile, the dominance gene effects played a major role in controlling the genetic variations for 1000-grain weight and grain yield/ plant. Sallam (2008) pointed out the importance of both additive and dominance gene effects in the inheritance of 1000-grain weight, however the dominance gene effect was more in magnitude than in a favorable conditions. Conversely, Fethi and Mohamed (2010), reported that dominance and dominance \times dominance epistatic effects were more important than additive effects and other epistatic components for the grain yield.

Heritability estimate plays an important role for planning the breeding strategy. The heritability of a character determines the extent to which it is transmitted from one generation to the next and it is a valuable tool when used with other parameters in predicting genetic gain that follows in selection for that character (Afiah *et al.*, 2000; Baloch *et al.*, 2003 and Ansari *et al.*, 2004 and 2005). The heritability values become a measure of the genetic relationship between parents and progeny, hence considerable research work has been carried out to incorporate the desirable genes in the present wheat varieties to increase the productivity of the crop (Memon *et al.*, 2007). Low, medium, and high narrow sense heritability estimates have been reported for yield and yield components in wheat by many researchers among whom were (Moustafa, 2002; Hendawy, 2003; EL-Sayed, 2004; Abdel-Nour ,Nadya *et al.*, 2005 and Abd Allah, Soheir and Abd EL-Dayem, 2008).

The present study was carried out to obtain information about genetic variance, gene action, heritability, actual and expected genetic gain from selection in three bread wheat crosses to elucidate the breeding value of these crosses that could be utilized for improving wheat yield in the breeding programs .

MATERIALS AND METHODS

Four bread wheat genotypes were chosen to form three crosses, viz., Gemmeiza 9 \times Irena, Sids 1 \times Sakha 93, Sids 1 \times Irena. Table (1) shows names, pedigree and the origin of the parental genotypes.

Table 1: Names, pedigree and origin of parental cultivars and lines.

Parent	Pedigree	Origin
Gemmeiza 9	Ald "S" / Huac "S"// CMH74A.630/ Sx CGM4583-5GM -5GM-1GM-0GM	Egypt
Sids 1	HD 2172/ PAVON "S"// 1158.57/MAYA74"S" SD46-4SD-1SD-0SD	Egypt
Sakha 93	Sakha 92/ TR810328 S8871-1S-2S-1S-0S	Egypt
Irena	BUC/FLK/MYNA/Vul CM 91575	Mexico

The experimental work of the present study was carried out at Etay Elbaroud Agriculture Research Station Behera governorate during four successive seasons from 2007/ 2008 to 2010/ 2011. In the first season (2007/ 2008), the parental genotypes were crossed to obtain F₁ seeds for the three studied crosses. In the second season (2008/ 2009), the hybrid seeds of the three crosses were sown to give the F₁ plants. These plants were selfed to produce F₂ seeds. Moreover, the same parents were crossed again to have enough F₁ seeds. The new hybrid seeds and part seeds obtained from F₁ selfed plants (F₂ seeds) were kept in refrigerator to the final experiment. In the third season (2009/ 2010), three F₁ seeds were sown to produce F₁ plants, which were selfed to produce F₂ seeds. In addition, the F₁ and F₂ plants were selfed to produce F₂ and F₃ seeds, respectively. In the fourth season (2010/ 2011) the obtained seeds of the five populations, P₁, P₂, F₁, F₂ and F₃ of the three crosses were evaluated using a randomized complete block design with three replications. Rows were 3m long, spaced 20 cm apart, the plants within rows were spaced 10 cm apart. Two rows were devoted for each parent and F₁ progenies, five rows for F₂ generation and 20 rows for F₃ families for each cross. Data were recorded on individual guarded plants for number of spikes/ plants, number of kernels/ spike, 100-kernel weight (g) and grain yield/ plant (g).

Various biometrical parameters in this study would only be calculated if the F₂ genetic variance was found to be significant. Heterosis was expressed as the percentage deviation of F₁ mean performance from better parent values (heterobeltiosis). Inbreeding depression was calculated as the difference between the F₁ and F₂ means expressed as percentage of the F₁ mean. The T-test was used to determine the significance of these deviations where the standard error (S.E) values were calculated as follows:

$$\bar{F}_1 - \bar{BP} = \sqrt{(\overline{VF}_1 + \overline{VBP})} \quad (\text{S.E for better parent heterosis})$$

$$\bar{F}_1 - \bar{F}_2 = \sqrt{(\overline{VF}_1 + \overline{VF}_2)} \quad (\text{S.E for inbreeding depression})$$

Potance ratio (P) was also calculated according to Peter and Frey (1966). In addition, F₂ deviation (E₁) and F₃ deviation (E₂) were measured as suggested by Mather and Jinks (1971).

Types of gene effects were estimated according to Hayman model (1958) as described by Singh and Chaudhary (1985) as follows:

$$m = \bar{F}_2 \quad (\text{mean effect of } F_2)$$

$$d^* = \frac{1}{2} \bar{P}_1 - \frac{1}{2} \bar{P}_2 \quad (\text{additive effect})$$

$$h = \frac{1}{6} (4 \bar{F}_1 + 12 \bar{F}_2 - 16 \bar{F}_3) \quad (\text{dominance effect})$$

$$l = \frac{1}{3} (16 \bar{F}_3 - 24 \bar{F}_2 + 8 \bar{F}_1) \quad (\text{dominance} \times \text{dominance})$$

$$i = \bar{P}_1 - \bar{F}_2 + \frac{1}{2} (\bar{P}_1 - \bar{P}_2 + h) - \frac{1}{4} l \quad (\text{additive} \times \text{additive})$$

The variance of these estimates were computed as follows:

$$V_m = VF_2$$

$$V_{d^*} = \frac{1}{4} (VP_1 + VP_2)$$

$$V_h = \frac{1}{36} (16 VF_1 + 144 VF_2 + 256 VF_3)$$

$$V_l = \frac{1}{9} (256 VF_3 + 576 VF_2 + 64 VF_1)$$

$$V_i = VP_1 + VF_2 + \frac{1}{4} (VP_1 + VP_2 + V_h) + \frac{1}{16} V_l$$

The standard errors of additive (d^*), dominance (h), dominance \times dominance (l), and additive \times additive (i) were obtained by taking the square root of respective variances. Also, "T" test values calculated by dividing the effects of d^* , h , l and i by their respective standard errors.

Heritability was calculated in both broad and narrow senses according to Mather (1949) and parent off-spring regression according to Sakai (1960). Furthermore, the expected and actual genetic advance (Δg) was computed according to Johanson *et al.* (1955).

Likewise, the genetic gain represented as percentage of the F_2 and F_3 mean performance (Δg %) was estimated using the method of Miller *et al.* (1958).

RESULTS AND DISCUSSION

Parental differences in response to their genetic background were found to be significant in most studied characters. The F_2 genetic variances were also significant for all characters in the three crosses. Means and variances of the five populations (P_1 , P_2 , F_1 , F_2 and F_3) for the studied characters in the three crosses are presented in Table (2).

Heterobeltiosis, Potence ratio (P), inbreeding depression percentage, E_1 , E_2 and different gene actions for yield and its attributes are given in Table (3).

Table 2: Means (\bar{x}) and variances (S^2) of the studied characters of the five populations (P_1 , P_2 , F_1 , F_2 and bulk F_3 families) in three bread wheat crosses.

Characters	Parameters	P_1	P_2	F_1	F_2	F_3 bulk
Gemmleza 9 × Irena						
No. of spikes/ plant	\bar{x}	20.50	24.80	24.70	22.80	21.45
	S^2	2.84	3.99	4.25	29.15	19.08
No. of kernels/ spike	\bar{x}	68.9	77.5	74.05	68.20	72.10
	S^2	15.71	16.6	20.85	192.50	120.25
100-kernel weight (g)	\bar{x}	5.0	4.51	5.02	5.025	4.25
	S^2	0.028	0.019	0.025	0.216	0.135
Grain yield/ plant (g)	\bar{x}	51.40	61.75	68.40	63.32	59.92
	S^2	16.56	27.57	31.45	342.45	194.09
Sids 1 × Sakha 93						
No. of spikes/ plant	\bar{x}	18.90	22.60	24.75	22.10	18.20
	S^2	4.90	5.95	7.93	50.15	33.50
No. of kernels/ spike	\bar{x}	80.85	72.55	79.30	72.45	72.22
	S^2	14.35	10.95	20.85	259.50	159.50
100-kernel weight (g)	\bar{x}	4.18	4.47	4.77	5.24	4.18
	S^2	0.056	0.042	0.033	0.219	0.136
Grain yield/ plant (g)	\bar{x}	52.5	59.59	65.42	57.10	54.85
	S^2	7.20	11.65	12.75	348.20	185.1
Sids 1 × Irena						
No. of spikes/ plant	\bar{x}	18.25	65.62	21.15	19.83	16.75
	S^2	4.87	6.62	3.32	22.82	17.52
No. of kernels/ spike	\bar{x}	79.65	76.05	77.20	68.54	58.9
	S^2	14.05	21.35	27.52	112.25	75.05
100-kernel weight (g)	\bar{x}	4.09	4.46	4.62	5.01	5.06
	S^2	0.025	0.02	0.026	0.22	0.133
Grain yield/ plant (g)	\bar{x}	52.90	64.6	57.9	52.52	50.7
	S^2	10.10	19.52	12.45	184.45	114.28

Table 3: Heterosis, potence ratio, inbreeding depression and gene action parameters for the studied characters in three bread wheat crosses.

Characters	Cross	Heterosis % over B.P	Potence ratio (P)	Inbreeding depression (%)	Gene action parameters						
					m	d*	h	l	l	E_1	E_2
No. of spikes/ plant	1	-0.40	0.953	7.692**	22.8**	-2.15**	4.867**	-2.133	-1.483	-0.875	-4.45**
	2	8.69**	2.162	-10.71**	22.10**	-1.85**	12.167**	-13.733*	4.467	-0.650	-9.10**
	3	-17.45**	-0.215	6.24**	19.82**	-3.685**	9.033**	-12.91**	2.51**	-1.713**	-9.585**
No. of kernels/ spike	1	-4.45**	0.198	7.90**	68.20**	-4.30**	-6.5	36.4**	-15.95**	-5.425**	-3.05**
	2	9.78**	2.645	12.72**	72.45**	4.15**	5.18	17.04	10.88	-3.633**	-11.765**
	3	-3.08*	-0.361	11.218**	68.54**	1.8**	31.48**	-28.32**	35.70**	-8.985**	-37.25**
100-kernel weight (g)	1	0.40	1.082	-0.10	5.025**	0.245**	2.063**	-4.147**	2.289**	0.138**	-1.275
	2	6.71**	3.069	-9.85**	5.24**	-0.145**	2.513**	-8.907**	1.778**	0.693**	-0.735**
	3	3.59**	1.865	-8.44**	5.01**	-0.185*	-0.393**	-0.773*	-1.109	0.563**	1.225**
Grain yield/ plant (g)	1	10.77**	2.285	7.43**	83.32**	-5.175**	12.453*	-4.587	-9.722	0.833	-5.135
	2	9.78**	2.645	12.72**	57.1**	-3.545**	11.547*	10.187	-4.919	-3.633**	-11.765**
	3	-10.37**	-0.145	9.292**	52.52**	-5.85**	8.44*	4.64	-2.41**	-5.805**	-15.25**

* and ** Indicate significant at 0.05 and 0.01 probability levels, respectively

Highly significant positive heterotic effect was found in the 2nd cross for grain yield and its attributes i.e , number of spikes/plant , number of kernels/spike and 100-kernel weight and grain yield/plant ,being 8.69%,9.78%,6.71% and 9.78% in the same respective order . Meanwhile, 100-kernel weight in the 3rd cross and grain yield/plant in the 1st one gave also a highly significant heterobeltiosis being 3.59% and 10.77%, respectively. Also, insignificant heterotic effect was found for number of spikes/ plant in the negative direction and 100-kernel weight with a positive value in the first cross. Similar trends were reported by Moustafa (2002), Hendawy (2003), EL-Sayed (2004), Abdel-Nour, Nadya *et al.* (2005), Abd-Allah, Soheir (2007) and Abd-Allah, Soheir and Abd EL-Dayem (2008). Negative significant heterotic effects obtained in the 3rd cross for both number of spikes/ plant (-17.45%) and number of kernels/ spike(-3.08%) led to a reduction in grain yield/ plant with a value being (-10.37%). Absence of heterotic effect in the F₁ generation may be due to that some genes show dominance effect in one direction, while the others work in the other side (Singh and Narayanan, 1993). The pronounced heterotic effect recorded for grain yield and its attributes in the 2nd cross (Sids1 X Sakha93) would be of great interest in a breeding program for selecting a recombinants having high yielding ability.

The potence ratio (P) indicated over dominance ($p > 1$) towards the higher parent for all studied traits in the second cross , grain yield/ plant in the first cross and 100-kernel weight in the 3rd cross. Nearly complete dominance case $P=1$ was found for both number of spikes/ plant and 100-kernel weight in the first cross .Partial dominance towards the lower parent was found for number of spikes/ plant, number of kernels/ spike, and grain yield/ plant in the third cross only. Moreover, partial dominance towards the higher parent was recorded for number of kernels/ spike in the first cross. Over dominance was obtained for number of spikes/ plant by Abdel-Nour, Nadya and Moshref (2006); for number of kernels/ spike by Abd Allah, Soheir (2007), for 100-kernel weight by Moustafa (2002), Abdel-Nour, Nadya and Moshref (2006); for grain yield/ plant by Abd-Allah, Soheir and Abd EL-Dayem (2008). Partial dominance towards the lower parent was reported for number of kernels/ spike by Moustafa (2002); while, partial dominance towards the higher parent was found for number of kernels/ spike by Abd-Allah, Soheir and Abd EL-Dayem (2008).

Inbreeding depression measured the reduction in performance of F₂ generation from their F₁'s due to inbreeding, Positive and highly significant values were found for number of spikes/ plant in the first and third cross, number of kernels/ spike and grain yield/ plant in all studied crosses. The obtained results for most studied crosses were in harmony with those obtained by Khalifa *et al.* (1997) and Abd-Allah, Soheir and Abd EL-Dayem (2008). However, inbreeding depression was significantly negative in the second cross for number of spikes/ plant and for 100-kernel weight in the second and third cross. Significant negative inbreeding depression values were detected for grain yield and number of spikes/ plant by Farag (2009) and Khattab *et al.* (2010).

Nature of gene action was determined using the five parameters model Table 3. The estimated mean effect of F_2 (m), which reflects the contribution due to the overall mean plus the locus effect and interactions of fixed loci, was found to be highly significant for all studied characters in all crosses. The additive gene effects (d') were found to be significant with a positive values for number of kernels/ spike in the second and third cross. as well as for 100-kernel weight in the first cross. Conversely, the remaining characters in studied crosses which showed a significant and negative additive effect (d').

Dominance gene effects (h) were found to be significant for all studied characters in all crosses, except number of kernels/ spike in the first and second cross indicating that dominance genes played a major role in the inheritance of such characters. When dominance genes are present, it would tend to be in favor of production hybrid wheat, while the existence of the additive gene action in the gene pool encourages the improvement of character by selection program. Dominance \times dominance (l) types of gene action were found to be negative and significant for number of spikes/ plant in the second and third cross, number of kernels/ spike in the third cross and 100-kernel weight in the three crosses.

A significant and positive additive \times additive type of epistasis (i) was detected for number of spikes/ plant and number of kernels/ spike in the third cross, and for 100-kernel weight in the first and second crosses. A negative and significant additive \times additive type of epistasis (i) was detected for number of kernels/ spike and grain yield/ plant in the first and third cross, respectively. The obtained results showed the importance of epistatic types of gene effects in the inheritance of all traits studied, and cannot be ignored when establishing a new breeding program to improve wheat populations for economic traits. The inheritance of all traits studied was controlled by additive and non-additive genetic effects, with greater values of dominance gene effect than the additive one in most cases. Farag (2009) reported that among the epistatic components, the dominance \times dominance was greater in magnitudes than additive \times additive in most studied traits. When additive effects are larger than non-additive one, it is suggested that selection in early segregating generations would be effective, while, if non-additive portion is larger than additive, the improvement of the characters needs intensive selection through later generations.

Significant and positive F_2 deviation (E_1) was found for 100-kernel weight in the three crosses and the first cross only for grain yield/ plant, while negative values were obtained for number of spikes/ plant and number of kernels/ spike in all crosses, and grain yield/ plant in the second and third cross. On the other hand, insignificant F_2 deviations with negative values were detected for number of spikes/ plant in the first and second cross. This may indicate that the epistatic gene effects had a major contribution in the inheritance of these traits.

F_3 deviation (E_2) was found to be positive and significant for 100-kernel weight in the third cross only. On the other hand, significant negative (E_2) values were detected for number of spikes/ plant and number of kernels/ spike in the three crosses, and for 100-kernel weight in the second cross and

grain yield/ plant in both second and third cross. While, insignificant (E_2) values were detected for 100-kernel weight and grain yield/ plant in the first cross. The F_2 deviation (E_1) were accompanied by F_3 deviation (E_2) in most cases indicating the presence of epistasis and should require more attention in wheat breeding programs. Insignificance of (E_1 and E_2) for grain yield/ plant in the first cross indicating a presence of minor contribution of epistatic effects in the inheritance of that trait.

Heritability in both broad and narrow senses, and between generations (parent off-spring regression) are presented in Table (4). High heritability estimates in broad sense were detected for all studied characters and ranged from 81.32% for number of kernels/ spike to 96.34% for grain yield/ plant, in the third and second cross, respectively.

Table 4: Heritability and expected genetic gain versus actual gain for all studied characters in three bread wheat crosses .

Characters	Cross	Heritability %			Expected gain		Actual gain	
		Broad sense	Narrow sense	Parent off spring regression	Δg	% of F_2	Δg	% of F_3
No. of spikes/ plant	1	85.42	71.01	79.18	7.9	34.64	7.12	33.22
	2	84.19	69.73	78.62	10.17	46.03	9.374	51.51
	3	85.45	39.35	58.85	3.87	19.53	5.074	30.29
No. of kernels/ spike	1	89.17	76.69	83.74	21.919	32.14	18.97	26.24
	2	91.97	79.18	86.63	26.276	36.27	22.538	31.207
	3	81.32	72.113	76.71	15.739	22.963	13.69	23.24
100-kernel weight (g)	1	88.43	75.46	82.18	0.722	14.377	0.622	14.636
	2	84.93	70.91	75.48	0.684	13.05	0.573	13.72
	3	88.18	80.14	84.55	0.774	15.46	0.635	12.55
Grain yield/ plant (g)	1	90.82	88.47	90.558	33.725	53.26	25.989	43.373
	2	96.34	94.32	95.65	36.26	63.49	26.807	48.87
	3	93.25	75.23	83.82	21.05	40.07	18.46	36.41

Narrow sense heritability estimates ranged from 39.35% for number of spikes/ plant in the third cross, to 94.32% for grain yield/ plant in the second cross. The parent off-spring regression heritability was found to be of high to moderate and ranged 58.85% for number of spikes/ plant in the third cross to 95.65% for grain yield/ plant in the second cross. The differences in magnitude of both narrow sense and parent off-spring regression heritability estimates for all the studied characters would ascertain the presence of non-additive genes and environmental effects in the inheritance of these characters. The results obtained here are coincident with those reported by EL-Sayed (2004), Abdel-Nour, Nadya *et al.* (2005), Abdel-Nour, Nadya and Moshref (2006), EL-Sayed and EL-Shaarawy (2006), and Abd-Allah, Soheir and Abd EL-Dayem (2008).

The expected genetic gain versus actual gain which are presented in Table (4) showed the possible gain from selection as a percent increase in the F_3 over the F_2 mean when the most desirable 5% of F_2 plants were selected. The results revealed that the expected genetic advance (Δg) for number of spikes/plant was ranged from 3.87 to 10.17 for the selected 5% of F_2 compared with the actual genetic gain which was ranged from 5.07 to 9.37

in the studied crosses .Meanwhile, the expected gain for grain yield /plant was ranged from 21.05 to 36.26 gm. in the F₂ .whereas , the actual gain was ranged from 18.46 to 26.81 gm. In the three crosses. The highest estimates of narrow sense heritability which was associated with the highest genetic advance for number of spikes/ plant and number of kernels/ spike in the first and second cross, and grain yield/ plant in all crosses indicate a presence of sufficient improvement of their variability. These results indicate the possibility of practicing selection in the early generations and can obtain high yielding genotypes.

Generally, the most biometrical parameters resulted from the first and second cross which were higher in magnitude than those obtained from the third one. Consequently, it could be concluded that the two crosses (Gemmiza 9 × Irena) and (Sids 1× Sakha 93) would be of great interest in a wheat breeding program for making a genetic improvement in grain yield.

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التحليل الوراثي للمحصول ومكوناته في قمح الخبز باستخدام نموذج العشائر الخمس

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أجرى هذا البحث بمحطة البحوث الزراعية- إيتاي البارود-محافظة البحيرة في أربعة مواسم متتالية من ٢٠٠٧/٢٠٠٨ إلى ٢٠١٠/٢٠١١ على ثلاثة هجين من قمح الخبز ناتجة من تهجين أربعة تركيب وراثية وهذه الهجين هي حميزة ٩× أيرينا، سدس ١× سحا ٩٣، سدس ١× ليرينا، واشتملت الدراسة على الأبوين والأجيال الأول والثاني والثالث لكل هجين. وقد أوضح النتائج الاتي :

- ١- كانت قوة الهجين عالية المعنوية في الهجين الثاني لصفة المحصول ومكوناته - بقيم ٨.٦٩% لصفة عدد السنابل / النبات ، ٩.٧٨% لصفة عدد الحبوب/السنبله ، ٦.٧١% لصفة وزن إل ١٠٠ حبة و ٩.٧٨% لصفة محصول الحبوب/النبات بينما أعطى الهجين الثالث قوة هجين سالبة لكل من صفة عدد السنابل/النبات - ١٧.٤٥% وعدد الحبوب/السنبله - ٣.٠٨% مما نتج عنه نقص في محصول الحبوب/النبات بقيمة -١٠.٣٧%.
- ٢- وجود سيادة تامة لصفة عدد السنابل/ النبات ووزن ال ١٠٠ حبة في الهجين الأول بينما كانت هناك سيادة فائقة ($p > 1$) للمحصول ومكوناته في الهجين الثاني .
- ٣- تأثير التربية الداخلية في الجيل الثاني موجباً ومعنوياً لصفة عدد السنابل/ النبات في الهجين الأول والثالث وصفتى عدد حبوب/ السنبله ووزن الحبوب/ النبات في كل الهجين. بينما كان تأثير التربية الداخلية معنوياً وسالباً لصفة عدد السنابل/ النبات للهجين الثاني ووزن المائة حبة في الهجين الثاني والثالث.
- ٤- أظهرت لتأثيرات الوراثة غير المضيفة نوراً هاماً في وراثة جميع الصفات المدروسة لكل الهجين عدا صفة عدد الحبوب/ السنبله في كل من الهجين الأول والثاني.
- ٥- كانت تحرفات الجيل الثاني (E_1) وانحرافات الجيل الثالث (E_2) معنوية لمعظم الصفات في الهجين تحت الدراسة مما يوضح أهمية الفعل الجيني التوقفي في وراثة الصفات.
- ٦- أظهرت كفاءة التوريث بمعناها الواسع قيماً عالية لكل الصفات، كما أظهرت كفاءة التوريث بمعناها الضيق وكذلك الكفاءة الوراثة المحسوبة من الإنحدار بين الأجيال قيماً عالية وكانت مرتبطة بنسبة تصيين وراثي ملحوظ في معظم الصفات المدروسة ما عدا صفة عدد السنابل/النبات في الهجين الثالث.

من نتائج هذه الدراسة فأنه يمكن الاستفادة من الهجين الأول والثاني في برامج تربية القمح للحصول على سلالات جديدة متفوقة في المحصول. كما أن النتائج المتحصل عليها تدل على أن الانتخاب في الأجيال الإنعزالية المبكرة ممكن أن يكون مفيداً ولكن سوف يكون أكثر كفاءة إذا تم تأجيله إلى الأجيال الإنعزالية المتأخرة.

قام بتحكيم البحث

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