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GENETIC PARAMETERS OF EARLINESS AND OTHER AGRONOMIC CHARACTERS IN TEN BREAD WHEAT CROSSES

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ABSTRACT

Ten bread wheat crosses derived form five different genotypes were sown to estimate potance ratio, inbreeding depression, heritability, genetic advance and correlation coefficient, among eight earliness and agronomic characters such as days to heading, days to maturity, Grain filling period, Grain filling rate, Number of spikes/plant, Number of kernels /spike, 100-Kernel weight and Grain yield per plant. The experiment was carried out from 2009/2010 to 2011/2012 seasons at Sakha Agric. Res. Station, ARC, Egypt. The t-test of differences between parents of each cross was significant in most studied crosses. The genetic analysis showed that genetic variance among F_2 plants was genetically different for all studied characters in the ten crosses. Moreover, values of potence ratios were more than unity for most studied characters in all crosses. For inbreeding depression, estimates were significant or highly significant negative for most characters in most crosses except for kernel weight which was positive for most crosses. The obtained results indicated that heritability in broad sense (h^2b) ranged from moderate to high for most studied characters. With regard to expected genetic advance, values for most studied characters were moderate in all studied characters. Also, significant positive correlation coefficients among most studied characters in all crosses were detected. The best crosses for improving earliness characters were Gem. 9 × L. 2, Sh. 1 × L. 2 and L.2 × L.3. On the other hand, the favorable crosses for increasing yield and yield components characters were Gem. 9 × Sh. 1, Gem. 9 × L. 1 and Sh. 1 × L. 3. These crosses may be used in breeding program for developing characters under study.

Keywords: Bread Wheat, Heritability, Genetic Advance, Correlation Coefficients***.***

INRODUCTION

Wheat (*Triticum aestivum* L., Graminae) is the world most cultivated since its cultivation is easier, ecologically suitable and contain high amount of nutrients. Wheat is cultivated in an area more than 3 million feddans a with a production about 8.5 million tons in Egypt.

Emphasis is given to explore the ways and means to increase the production of wheat to meet the increasing demand of food grains for the growing population. Currently it is not possible to increase the area of wheat due to other competing crops and rusticated supply of irrigation water. Use of cultivars with better yield potential and wide range of adaptability is of prime importance for increasing wheat production. Thus, development of high yielding wheat cultivars has always been a major objective of wheat breeding programs throughout the world. Extensive testing of wheat genotypes under varying environments has been practiced for screening relatively stable cultivars.

Therefore, in Egypt, early maturity is one of the important objectives in spring wheat breeding program. Earliness in wheat has several advantages, for instance, early maturing cultivars are highly needed to fit in new crop intensive rotation as planting cotton after wheat and planting wheat after harvesting short duration vegetable crops, etc. Also, wheat cultivars that can be harvested early provide farmers with more time to grow another crop such as Fahl berseem. Moreover, earliness ensures timely crop harvest and may also protect wheat from biotic and abiotic stresses such as disease, heat and drought (Poehlman and Sleper 1995). Early heading and maturity cultivars in wheat are advantageous in areas where temperature rises greatly during the grain filling phase (or late sowing) as in Upper Egypt. They also provide more options for farmer to adopt diverse crop pattern, and potential drought escape mechanism (Mahar *et al.* 2003) .

Heritability is a parameter which is widely used in the establishment of breeding programs and formation of selection indexes (Falconer, 1985). The high heritability associated with high genetic advance for main quantitative characters in wheat offer better scope of selecting desirable genotypes in early segregating generations (Memon *et al*., 2005). Knowing the correlations between characters is of great importance for success in selection in breeding programs. The analysis of correlation coefficient is the most widely used method among numerous methods that can be used for this purpose. Inbreeding depression is defined as the deviation of F_1 mean from F_2 one of the same hybrid, and generally high positive values are desirable for yield in wheat.

This research are carried out to:

1- study some heritable characters of existing wheat genotypes to be used in breeding program for improvement of genetic potential.

2- evaluate the potential of wheat genotypes for estimation of correlation of various characters among themselves and with grain yield.

MATERIALS AND METHODS

The field work was conducted at the Experimental Farm of Sakha Agricultural Research Station (ARC), Kafer-Elsheikh, Egypt. The experiment was carried out during the three wheat sowing seasons, i.e., 2009/10, 2010/11 and 2011/2012. Five genetically diversed bread wheat parental genotypes representing a wide range of genetic diversity for several characters were used in this study. However, the names and pedigrees of the used genotypes are given in Table 1.

In 2009/10 season, seeds from each of the parental genotypes were grown and all possible parental combinations excluding reciprocals were made among the five parental genotypes. In 2010/11, the F_1 of each cross was selfed to produce F_2 seed. In 2011/2012, four populations of the ten wheat crosses (P_1, P_2, F_1 and F_2) were sown in plots. Each plot consisted of 18 rows ($2P_1$, $2P_2$, $2F_1$ and $12F_2$) in addition to two border rows. Each row was 4m long, 25cm between each adjacent rows and 20cm apart within plants. On the other hand, all other recommended cultural practices were followed.

Table 1: Names and pedigrees of five parental bread wheat genotypes.

Genotype	Name	Earliness	Abbreviation	Cross Name & Pedigree
P_1	Gemmeiza 9	Late	Gem. 9	Ald “S” / Huac"s" // Cmh 74 A. 630 / Sx GM 4583-5GM-1GM-0GM
P_2	Shandaweel 1	Late	Sh.1	SITE/MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC CMSS93B00567S-72Y-010M-010Y-010M-3Y-0M-0HTY-0SH
P_3	Line1	Early	L.1	ATTILA *2/GIZA 168 S.15612-1S-1S-1S-0S
P_4	Line 2	Early	L.2	GIZA 168/5/MAI "S"/PJ//ENU "S"/3/KITO/ POTO. 19//MO JUP/4/K 134 (60) /VEE S. 15410-19S-7S-2S 0S
P_5	Line 3	Early	L.3	KAUZ/ATTILA/7/KVZ/4/CC/INIA/3/CNO//ELGAU/SON 64 /5/ SPARROW "S"/BROCHIS "S"/6/BAYA "S"/IMU S. 15563-9S-3S-1S-0S

The following measurements were recorded on individual plants in each of parents , F_1's and F_2's: Days to heading (DH), Days to maturity (DM), Grain filling period (GFP),Grain filling rate (GFR), Number of spikes/plant (S/P), Number of kernels /spike (K/S), Kernel weight (100-KW) g and Grain yield per plant (GY) g / plant.

Statistical and genetical analyses:-

In each cross, the mean and variance were calculated for (P_1, P_2, F_1 and F_2) generations. The population means and variance were used to estimate the type of gene action. One tail F ratio was calculated to test the significance of F_2 variance and The “ t ” test was used to test the significance of the difference between the two parents in each cross.

Heritability in broad sense was estimated according to Allard (1960); potence ratio was also calculated as suggested by to Smith (1952), inbreeding depression followed the formula of Mather and Jinks (1971). Predicted genetic advance from selection (Δg) was also calculated as described by Johanson *et al* (1955) and Simple correlation coefficients among all studied characters were computed using the formula given by Steel & Torrie (1980).

RESULTS AND DISCUSSION

The data in Table 2 illustrate the (t) test for detecting the differences between the two parents in each cross and (F) test for detecting the significance of the genetic variance among F_2 plants for all characters in all tested crosses. These data indicate that the two parents were significantly different in most characters of most crosses, revealing the diverse of genetic background of most parents.

The (F) test also showed that F_2 plants genetically differed in all crosses for all studied characters. The existence of significant genetic variability in spite of the significance differences between parents obtained herein in most characters may suggest that the genes of favorite effects were not completely associated in the parents, i.e., these genes are dispersed.

Table 2: The t-test of differences between parents and the F - test for significance of the genetic variances among F_2 plants in ten bread wheat crosses for studied characters.

Crosses	Test	DH	DM	GFP	GFR	S/P	GY	K/S	KW
Gem.9×Sh.1	T	3.48**	-2.76**	-6.68**	2.49*	0.61	1.75	2.22*	3.91**
	F	7.81**	6.34**	4.41**	2.05**	2.43**	1.89**	2.04**	1.88**
Gem.9 × L. 1	T	33.02**	25.42**	-18.18**	5.92**	7.75**	4.08**	4.63**	4.71**
	F	6.82**	3.29**	5.70**	1.98**	2.79**	2.15*	2.53**	2.81**
Gem.9 × L.2	T	30.80**	22.56**	-15.41**	5.39**	3.19**	3.30**	3.91**	2.00
	F	4.98**	6.63**	3.54**	1.69**	1.93**	1.68**	1.69**	1.69**
Gem.9 × L. 3	T	17.29**	15.33**	-12.50**	5.16**	0.57	4.32**	2.67*	1.50
	F	2.53**	2.49**	2.04*	2.10**	1.51*	2.09**	1.83**	3.12**
Sh.1× L. 1	T	32.65**	28.49**	-14.58**	4.15**	7.79**	2.91**	2.65*	1.51
	F	6.47**	5.62**	2.86**	2.34**	1.89**	2.29**	1.73**	2.68**
Sh.1 × L. 2	T	26.91**	20.15**	-13.56**	-0.16	0.75	-1.07	0.63	1.16
	F	5.84**	6.65**	5.06**	1.83**	1.75**	1.79**	1.86**	1.89**
Sh.1 × L. 3	T	15.98**	17.13**	-6.29**	3.36**	-0.34	2.79**	-0.02	-0.52
	F	4.06**	3.52**	1.78**	2.77**	1.72**	2.93**	1.74**	1.74**
L. 1 × L. 2	T	-2.93**	-6.91**	-1.15	-1.35	-4.65**	-1.51	-1.37	-4.10**
	F	6.92**	10.07**	13.01**	2.28**	2.29**	1.94**	2.16**	2.75**
L. 1 × L. 3	T	-4.38**	-1.43	4.71**	-0.90	-6.59**	0.02	-2.85**	-2.57*
	F	4.55**	10.08**	4.18**	5.00**	2.34**	4.49**	1.93**	1.43*
L.2 × L. 3	T	-2.23*	4.87**	4.94**	0.35	-2.42*	1.58	-1.50	0.77
	F	5.21**	16.83**	4.58**	3.16**	1.63**	3.63**	2.99**	2.39**

***,**Significant at 0.05 and 0.01, probability levels respectively.**
DH: Days to heading DM: Days to maturity GFP: Grain filling period
GFR: Grain filling rate S/P : No. spikes / plant GY: Grain yield/plant
K/S : No. kernels / spike
KW :Kernel weight

Values of potence ratios were more than unity for DH, DM, GFP, S/P, GY and K/S in all crosses except for few cases. This indicate that most characters were governed by over dominance and they have predominated and played the greatest role in the inheritance of most characters. On the other hand, for GFR and KW potence ratio values were less than unity for all crosses. These results indicate that partial dominance was predominated and played the greatest role in the inheritance of these characters. Similar results were obtained by Abd El-Rahman (2008), Aglan (2009), and Batool *et al.*, (2013).

Moreover, data presented in Table 3 indicate that inbreeding depression estimates were significant or highly significant negative for most characters in most crosses except for KW estimates which were highly significant and positive for most crosses. For days to heading, days to maturity and grain filling period the desirable values are the negative ones. These results were in agreement with these of El-Sayed and El-Shaarawy (2006) and Aglan (2009).

Table 3: Potance ratio (P. R.) and inbreeding depression (I. D.) for different characters in ten bread wheat crosses.

Crosses	Parameter	DH	DM	GFP	GFR	S/P	GY	K/S	KW
Gem.9×Sh.1	P. R.	-1.60	-2.89	8.86	0.01	-10.71	-14.49	39.75	0.41
	I. D.	0.15	0.21	0.37	16.61**	-14.55**	17.13**	11.90**	8.29**
Gem.9 × L. 1	P. R.	-114.08	-31.92	25.92	0.20	18.14	261.04	-537.09	0.54
	I. D.	3.91**	1.18**	-5.38**	32.66**	21.39**	29.11**	-10.34**	6.54**
Gem.9 × L.2	P. R.	107.90	28.44	-25.51	-0.20	-39.90	-211.42	-397.32	0.01
	I. D.	-5.59**	-1.94**	5.71**	10.02**	3.15*	15.12**	-0.63	-5.50**
Gem.9 × L. 3	P. R.	-13.05	0.00	4.32	-0.23	-9.80	-370.06	-190.80	0.25
	I. D.	3.27**	1.84**	-1.57**	-45.24**	-1.74	-46.38**	-11.47**	3.61**
Sh.1 × L. 1	P. R.	115.91	39.53	-16.86	0.11	24.00	213.37	245.68	0.06
	I. D.	-0.53	0.18	1.62**	16.68**	3.22**	18.26**	-1.12	1.46**
Sh.1 × L. 2	P. R.	117.26	42.94	-15.84	0.01	-0.08	93.63	22.33	0.06
	I. D.	-5.55**	-2.52**	3.68**	-18.98**	3.31**	-14.55**	6.13	-0.41**
Sh.1 × L. 3	P. R.	-53.59	-22.83	4.20	0.05	2.72	76.77	-0.27	-0.02
	I. D.	1.44	0.15	-2.89**	16.65**	1.61	14.17**	4.18	1.89**
L. 1 × L. 2	P. R.	2.83	0.13	0.84	0.03	-15.40	76.19	-0.70	0.03
	I. D.	-2.18**	-2.56**	-3.28**	-35.89**	-13.02**	-37.09**	5.80	-21.07**
L. 1 × L. 3	P. R.	-9.11	3.00	25.01	0.02	51.75	-0.77	66.24	0.03
	I. D.	-6.17**	-1.34**	7.55**	-75.88**	-28.59**	-61.73**	-16.74**	-3.38**
L.2 × L. 3	P. R.	-18.27	27.01	-20.86	-0.01	28.83	-109.23	200.43	0.12
	I. D.	-7.20**	-7.17**	-7.12**	-41.60**	-28.50**	-51.36**	-49.61**	11.76**

***,**Significant at 0.05 and 0.01, probability levels respectively.**

DH: Days to heading DM: Days to maturity GFP: Grain filling period
GFR: Grain filling rate S/P : No. spikes / plant GY: Grain yield / plant
K/S : No. kernels / spike KW :Kernel weight

Heritability estimates in broad sence and expected genetic advanced for all studied characters are presented in Table (4). Generally, heritability values in broad sense were slightly high in the ten studied crosses for all studied characters, except for few cases where the value were moderate. In these cases, the environmental variances were higher than the genetic ones. These results revealed that the genetic variance was mostly attributed to additive effects for most studied characters. Regarding to expected genetic advance, values for most studied characters were moderate. This indicates that selection for these characters could be possible in early generations; but, it would be better if it was delayed to later generations. For the rest cases, the expected genetic advance estimates were low, indicating that selection for these characters would be effective in late generations only. Moreover, this suggests that these characters are controlled by non-additive gene effects, and that the inheritance of such characters is influenced by environment rather than genotype. Similar results were obtained by Memon *et. al*., (2007), Aglan (2009), Yagdi and Sozen (2009), Wani *et.al*., (2011), Tripathi *et. al.,* (2011) and Hussain *et. al.,* (2013)

Table 4: Heritability in broad sense (H^2b) and genetic advance (GS) for eight characters in ten bread wheat crosses.

Crosses	Parameter	DH	DM	GFP	GFR	S/P	GY	K/S	KW
Gem.9 × Sh.1	H^2b	87.19	84.24	77.34	51.23	58.89	47.05	50.92	46.73
	G S	5.69	6.82	4.23	0.37	6.22	13.88	8.99	0.94
Gem.9 × L. 1	H^2B	85.34	69.65	82.47	49.45	64.13	53.40	60.49	64.35
	G S	8.23	3.60	5.05	0.31	7.56	17.20	24.55	0.52
Gem.9 × L.2	H^2B	79.94	84.92	71.78	40.86	48.28	40.51	41.00	40.79
	G S	6.28	5.77	4.84	0.08	2.77	1.01	0.22	-0.54
Gem.9 × L. 3	H^2B	60.55	59.89	51.08	52.45	33.59	52.15	45.49	67.91
	G S	5.75	4.71	1.41	0.33	0.02	12.99	2.67	1.04
Sh.1 × L. 1	H^2B	84.53	82.21	65.06	57.24	46.96	56.32	42.08	62.75
	G S	7.65	5.76	2.40	0.32	2.22	13.86	4.96	0.41
Sh.1 × L. 2	H^2B	82.87	84.97	80.25	45.26	42.80	44.21	46.10	47.18
	G S	6.55	6.93	3.12	0.35	0.72	15.59	1.29	0.29
Sh.1 × L. 3	H^2B	75.34	71.56	43.93	63.87	41.73	65.87	42.69	42.50
	G S	7.91	4.78	1.13	0.37	0.06	19.33	1.11	0.24
L. 1 × L. 2	H^2B	85.55	90.07	92.31	56.20	56.28	48.52	53.67	63.70
	G S	9.54	7.47	11.39	0.05	3.67	-4.85	11.46	0.23
L. 1 × L. 3	H^2B	78.02	90.08	76.06	79.98	57.30	77.73	48.14	29.91
	G S	10.23	7.64	7.61	0.73	8.39	31.40	8.43	-0.44
L.2 × L. 3	H^2B	80.80	94.06	78.19	68.37	38.74	72.43	66.57	58.11
	G S	11.33	9.54	9.10	0.41	0.87	22.83	21.94	0.90

DH: Days to heading DM: Days to maturity GFP: Grain filling period GFR: Grain filling rate
S/P : No. spikes / plant GY: Grain yield / plant K/S : No. kernels / spike KW :Kernel weight

Generally, In the present work, low to moderate genetic advance from selection was associated with moderate to high heritability estimates. Therefore, selection in these particular populations could be effective and satisfactory for successful breeding purpose.

Data in Table 5 show positive significant correlation coefficient between most studied characters in all crosses. Similar results were recorded by Aglan (2009), Waqar-ul-haq and Akram (2010), Mohibullah *et al.,* (2011) and Abd El- Mohsen *et al.,* (2012). These accessions according to the characters indicate significant positive correlation and high genetic variability which can be used for future crop improvement program to introduce new wheat cultivars according to the need of basic agro-climatic condition. In addition, these results showed that these genotypes may provide good source of material for further breeding program. It could also be concluded that grain yield per plant meight be improved by utilizing these different characters in plant populations.

Table 5: Simple correlation for all studied characters in ten bread wheat crosses.

Cross	**Character**	**DM**	**GFP**	**GFR**	**S/P**	**GY**	**K/S**	**KW**
Gem.9× Sh.1	DH	0.74**	-0.22**	-0.03**	-0.27**	-0.07**	-0.01	0.17**
	DM		0.49**	-0.04**	-0.16**	0.03**	0.08**	0.20**
	GFP			-0.01*	0.11**	0.12**	0.13**	0.06**
	GFR				0.03**	0.99**	0.12**	0.05**
	S/P					0.04**	0.05**	-0.15**
	GY						0.13**	0.06**
	K/S							0.05**
		DM	GFP	GFR	S/P	GY	K/S	KW
Gem.9 × L. 1	DH	0.86**	-0.89**	0.19**	-0.12**	0.06**	0.05**	0.02**
	DM		-0.54**	0.19**	-0.10**	0.11**	0.03**	0.01*
	GFP			-0.14**	0.10**	0.00	-0.06**	-0.03**
	GFR				0.02**	0.99**	0.13**	0.00
	S/P					0.03**	0.00	0.11**
	GY						0.11**	0.00
	K/S							-0.27
		DM	GFP	GFR	S/P	GY	K/S	KW
Gem.9 × L. 2	DH	0.79**	-0.54**	-0.01	0.06**	-0.06**	-0.04**	0.06**
	DM		0.09**	-0.04**	0.01	-0.02**	0.03**	-0.04**
	GFP			-0.04**	-0.10**	0.07**	0.11**	-0.15**
	GFR				-0.13**	0.99**	0.10**	-0.03**
	S/P					-0.13**	-0.09**	0.12**
	GY						0.11**	-0.05**
	K/S							0.05**
		DM	GFP	GFR	S/P	GY	K/S	KW
Gem.9 × L. 3	DH	0.90**	-0.77**	0.37**	-0.13**	0.30**	0.02**	-0.12**
	DM		-0.43**	0.30**	-0.15**	0.26**	-0.03**	-0.08**
	GFP			-0.34**	0.05**	-0.25**	-0.10**	0.14**
	GFR				-0.05**	0.99**	0.06**	-0.26**
	S/P					-0.04**	-0.12**	-0.10**
	GY						0.05**	-0.25**
								0.02**
		DM	GFP	GFR	S/P	GY	K/S	KW
Sh.1× L. 1	DH	0.94**	-0.66**	0.15**	-0.02**	0.10**	-0.07**	-0.11**
	DM		-0.37**	0.11**	-0.01	0.08**	-0.10**	-0.08**
	GFP			-0.17**	0.05**	-0.09**	-0.03**	0.12**
	GFR				0.12**	1.00**	-0.11**	-0.04**
	S/P					0.13**	0.20**	-0.06**
	GY						-0.11**	-0.04**
	K/S							-0.02**

***,**Significant at 0.05 and 0.01, probability levels respectively.**

DH: Days to heading DM: Days to maturity GFP: Grain filling period GFR: Grain filling rate

S/P : No. spikes / plant GY: Grain yield / plant K/S : No. kernels / spike

KW :Kernel weight

Continu Table 5:

	Character	**DM**	**GFP**	**GFR**	**S/P**	**GY**	**K/S**	**KW**
Sh.1× L. 2	DH	0.92**	-0.24**	0.07**	0.19**	0.05**	-0.16**	-0.08**
	DM		0.17**	0.04**	0.21**	0.06**	-0.16**	-0.07**
	GFP			-0.06**	0.04**	0.03**	0.00	0.02**
	GFR				-0.09**	0.99**	0.01*	-0.13**
	S/P					-0.08**	-0.03**	-0.02**
	GY						0.01*	-0.13**
	K/S							0.29**
	7	DM	GFP	GFR	S/P	GY	K/S	KW
Sh.1× L. 3	DH	0.97**	-0.37**	0.03**	0.03**	0.01	0.24**	0.03**
	DM		-0.14**	0.01**	0.01**	0.01	0.24**	0.00
	GFP			-0.05**	-0.09**	0.01	-0.08**	-0.13**
	GFR				0.06**	1.00**	0.06**	0.02**
	S/P					0.05**	-0.12**	0.04**
	GY						0.05**	0.02**
	K/S							0.09**
	8	DM	GFP	GFR	S/P	GY	K/S	KW
L. 1 × L. 2	DH	0.20**	-0.72**	0.37**	0.04**	0.19**	0.04**	0.08**
	DM		0.53**	-0.09**	-0.06**	0.05**	-0.02**	0.13**
	GFP			-0.39**	-0.08**	-0.13**	-0.04**	0.02**
	GFR				0.15**	0.95**	0.18**	0.02**
	S/P					0.12**	0.07**	-0.05**
	GY						0.17**	0.03**
	K/S							0.03**
	9	DM	GFP	GFR	S/P	GY	K/S	KW
L. 1 × L. 3	DH	0.63**	-0.68**	0.10**	-0.08**	-0.04**	-0.08**	0.16**
	DM		0.14**	-0.10**	-0.02**	-0.06**	-0.17**	0.07**
	GFP			-0.23**	0.08**	-0.01	-0.07**	-0.14**
	GFR				0.01**	0.97**	0.02**	-0.01
	S/P					0.01	0.09**	-0.07**
	GY						0.03**	-0.04**
	K/S							0.10**
	10	DM	GFP	GFR	S/P	GY	K/S	KW
L. 3 × L. 3	DH	0.59**	-0.59**	0.19**	-0.16**	0.05**	-0.06**	0.01*
	DM		0.30**	0.04**	-0.12**	0.12**	-0.01	-0.06**
	GFP			-0.18**	0.07**	0.05**	0.06**	-0.07**
	GFR				0.08**	0.97**	0.11**	0.01**
	S/P					0.08**	0.09**	0.01**
	GY						0.12**	-0.01*
	K/S							0.23**

***,**Significant at 0.05 and 0.01, probability levels respectively.**
DH: Days to heading **DM: Days to maturity** **GFP: Grain filling period**
GFR: Grain filling rate
S/P : No. spikes / plant **GY: Grain yield / plant** **K/S : No. kernels / spike**
KW :Kernel weight

CONCLUSION

The best crosses for improving earliness characters were Gem. 9 × L. 2, Sh. 1 × L. 2 and L.2 × L.3. On the other hand, the favorable crosses for increasing yield and yield components characters were Gem. 9 × Sh. 1, Gem. 9 × L. 1 and Sh. 1 × L. 3. These crosses may be used in breeding program for developing characters under study.

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الدلائل الوراثية لصفات التبكير والمحصول في عشرة هجن من قمح الخبز.

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قسم بحوث القمح - معهد بحوث المحاصيل الحقلية - مركز البحوث الزراعية – مصر.

تمت زراعة عشرة هجن من قمح الخبز ناتجة من خمسة تراكيب وراثية مختلفة لقياس درجة السيادة, التدهور نتيجة التربية الداخلية, درجة التوريث, التحسين الوراثي و معامل الارتباط بين ثماني صفات من صفات التبكير والمحصولية الأخري مثل عدد الأيام حتي التزهير, عدد الأيام حتي النضج الفسيولوجي, فترة إمتلاء الحبوب, معدل إمتلاء الحبوب, طول النبات, عدد السنابل / النبات, محصول النبات, عدد حبوب السنبلة و وزن الحبوب. هذه التجربة اجريت في ثلاثة مواسم من ٢٠٠٩-٢٠١٠ وحتي ٢٠١١-٢٠١٢ بمحطة البحوث الزراعية – سخا – مركز البحوث الزراعية. اجري اختبار (ت) لقياس التباين بين الأبوين في كل هجين فكانت قيم التباين معنوية في معظم الهجن. اظهر التحليل الوراثي للتباين وجود اختلافات وراثية بين نباتات الجيل الثاني في كل الصفات محل الدراسة في كل الهجن. كانت درجة السيادة اعلي من الوحدة لأكثر الصفات المدروسة في كل الهجن. كانت قيم التدهور نتيجة التربية الداخلية معنوية أو عالية المعنوية بالاتجاه السالب لكل الصفات في اغلب الهجن ما عدا صفة وزن الحبة حيث كانت القيم موجبة معنوية لأغلب الهجن. كانت قيم درجة التوريث بالمعني الواسع تتراوح بين متوسطة إلي عالية لكل الصفات المدروسة في كل الهجن.بينما كانت قيم التحسين الوراثي للصفات المدروسة متوسطة لكل الصفات محل الدراسة وكانت قيم معامل الارتباط موجبة معنوية لأكثر الصفات المدروسة في أغلب الهجن. كانت أفضل الهجن لتحسين صفات التبكير هجن جميزة ٩ × سلالة ١, سلالة ١ × سلالة ٢ و سلالة ٢ × سلالة ٣. ومن ناحية أخري لتحسين صفات المحصول ومكوناته كانت الهجن جميزة ٩ × شندويل ١, شندويل ١ × سلالة ١ و شندويل ١ × سلالة ٣.