

ESTIMATION OF GENETIC VARIANCE COMPONENTS IN TWO BREAD WHEAT CROSSES

Marwa M. El-Nahas⁽¹⁾ and S. A. Arab⁽²⁾

⁽¹⁾ Agronomy Dep., Faculty of Agric., Minufiya University,

⁽²⁾ National Gene Bank and Genetic resources, Agricultural Research Center, Giza.

(Received: Apr. 13, 2014)

ABSTRACT: *This investigation aimed to study the potentiality of heterosis expression, heritability, expected genetic advance, nature of gene actions for some quantitative traits in two bread wheat crosses. Four parental genotypes (Gemmeiza 9, Sakha 8, Sakha 69 and Shandaweel 1) were chosen for the present study on the base of wide variability. Six populations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) were used to estimate genetic parameters. The results showed that, useful heterotic effects in all studied traits except, heading date and plant height in both crosses. Heterosis in grain yield per plant did not reached the level of significance (-3.55% and 3.02% in the first and second cross, respectively). Inbreeding depression values were highly significant for nearly all studied traits in the two crosses. Additive gene effects (a) and dominance gene effects (d) were highly significant for most studied traits. The three epistatic types: additive x additive (aa), additive x dominance (ad), dominance x dominance (dd) were highly significant for most studied traits in both crosses. The aforementioned were accompanied with significant estimates of both E_1 and E_2 epistatic scales in most studied traits. High heritability estimates in broad sense were detected for nearly all studied traits. Also, high estimates of narrow sense heritability were detected for number of productive tillers per plant and number of spikelets per main culm ear in both crosses. High genetic advance under selection was associated with high narrow sense heritability estimates for mostly all studied traits.*

Key words: *Wheat, Gene action, Heterosis, Heritability, Genetic advance, Additive, Dominance, Six parameters model.*

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important and strategic cereal crop all over the world. In Egypt, wheat is the main winter cereal crop. Increasing wheat productivity is a national target to fill the gap between wheat consumption and production. The total national wheat production reached about 8.80 million tons from 1.34 million hectares (FAO, 2012). Plant breeder needs continuous knowledge about the nature of gene action and genetic systems controlling the inheritance of wheat traits in order to formulate the most efficient breeding programmes to bring out the quick improvement.

Six parameters analysis provides information on the relative importance of average effects of the genes (additive effects), dominance deviations, and effects due to non allelic genetic interactions. This

helps in determining genotypic values of the individuals and, consequently, the mean genotypic values of families and generations (Viana 2000). Generation mean analysis, is a simple and useful technique for estimating gene effects of polygenic trait. Its greatest merit goes to the ability of estimating epistatic gene effects (additive x additive (aa), dominance x dominance (dd) and additive x dominance (ad)), (Singh and Singh, 1992).

The objectives of the present study were to investigate the genetic variance using six parameters model (Gamble 1962), heritability and expected genetic advance under selection for grain yield and some of its components in two selected crosses.

MATERIALS AND METHODS

The present experimental was carried out at the Experimental farm, Faculty of Agriculture, Minufiya University at Shebin El-

Kom during the three successive seasons 2010/2011, 2011/2012, 2012/2013. Four common wheat varieties were used to establish the experimental materials for this investigation. Name, pedigree and origin of these varieties were presented in Table (1).

Parents were crossed in 2010/2011 to obtain F_1 seed of the two crosses. In 2011/2012 season, part of the obtained hybrid seeds of the two crosses Gemmeiza 9 x Sakha 8 and Shandaweel 1 x Sakha 69, were sown and the rest saved to the next season. F_1 plants were self-pollinated and backcrossed to both parents to obtain F_2 and backcross seeds. The six populations P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 were sown using randomized complete block design with three replicates in 2012/2013 growing season. Each block comprised 15 rows of F_2 generation, 10 rows of BC_1 and BC_2 and 5 rows of other three non-segregated populations i.e. P_1 , P_2 and F_1 . The rows were 3.0 meters long with 20 cm between rows and 10 cm between plants within rows. Normal agricultural wheat practices were applied as usual for the ordinary wheat fields in the area. Data were recorded on 30 randomly selection competitive plants in each entry for P_1 , P_2 and F_1 and 90 plants for BC_1 and BC_2 and 100 plants for the F_2 . The studied characters were heading date (day), number of productive tillers per plant, plant height(cm), main culm ear length(cm), number of spikelets per main culm ear, number of grains per main culm ear, main culm ear yield (g), number of

grains per ear, ear yield (g), 1000 grain weight(g) and grain yield per plant(g).

Statistical analysis:

The t-test was used to examine the existence of genetic variance between parental means. Statistical procedures used herein would only be computed if the F_2 genetic variance was found to be significant. A one tail (F) ratio was used to examine the existence of genetic variance within the F_2 population. Heterosis (H), was expressed as percent increase of the F_1 mean performance above the respective better parent. Inbreeding depression (I.d) was measured as the average percent decrease of the F_2 from the F_1 . The F_2 deviation (E_1) and backcrosses deviation (E_2) were calculated according to (Marani, 1968). The validity of some estimates was examined by t-test. Nature of gene action was studied according to the relationships illustrated by (Gamble, 1962). In this procedure the means of the six populations of each cross were used to estimate six parameters of gene action. A test of significance of these parameters was conducted by the t-test. Heritability was estimated in both broad and narrow senses for F_2 generation, according to (Mather's procedure, 1949). The predicted genetic advance under selection (ΔG) was computed according to (Johnson *et al*, 1955). This genetic gain represented as percentage of the F_2 mean performance was also obtained following (Miller *et al*, 1958).

Table 1: Name, pedigree and origin of the parental wheat varieties used in the study.

Name	Pedigree	Origin
Gemmeiza 9	Ald“S”/Huac“S”//CMH74A.630/5X CGM4583-5GM-1GM-0GM	Egypt
Sakha 8	Indus 66 x Norteno,,s,,/PK3418-65-ISW-OS	Egypt
Sakha 69	Inia/RL4220//7C/Yr“S”CM15430-25-65-0S-0S	Egypt
Shandaweel 1	CAZO/KAUZ//KAUZ.CMBW90 Y327OTOPM-02010M-02010Y-3M-OSH	Egypt

Estimation of genetic variance components in two bread wheat crosses

RESULTS AND DISCUSSION

Means and variance of the studied traits for P₁, P₂, F₁, F₂, BC₁ and BC₂ of the two crosses are shown in Table (2). Generally, the differences between each two parents were found significant. The genetic variances within F₂ populations were also significant for all studied traits in both crosses. Consequently, the various

genetical parameters were computed. The existence of the significant genetic variability in F₂ populations in spite of the insignificant differences between the parental cultivars for some characters in the two crosses, might suggest that the genes of similar effects were not completely associated in the parental cultivars i.e. these genes are dispersed (Mather and Jinks, 1982).

Table (2): Means (\bar{X}) and variances (S^2) of P₁, P₂, F₁, F₂, BC₁ and BC₂ populations of the two crosses I [Gemmeiza 9 (P₁) x Sakha 8 (P₂)] and II [shandaweel 1 (P₁) x Sakha 69 (P₂)] for all studied traits.

Character	Statistics	Cross I						Cross II					
		P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
1) Heading date, days	\bar{X}	94.68	88.11	91.61	89.84	94.52	92.63	86.23	87.11	89.41	88.84	91.22	93.03
	S^2	6.02	9.13	10.51	36.55	24.22	22.31	7.13	9.32	11.72	39.35	33.21	29.08
2) Number of productive tillers per plant	\bar{X}	9.80	8.00	8.20	8.80	8.10	7.80	9.23	11.31	9.85	9.11	8.33	8.47
	S^2	0.91	1.12	1.31	3.90	2.80	2.50	3.71	5.32	6.53	20.83	12.92	13.71
3) Plant height, cm	\bar{X}	113.6	104.6	111.5	114.3	112.2	100.6	112.3	108.7	110.5	109.8	111.8	100.4
	S^2	14.31	12.33	17.78	120.33	62.32	78.71	9.17	12.31	16.71	99.83	63.22	84.33
4) Main culm ear length, cm	\bar{X}	13.22	12.71	12.51	16.69	14.02	13.32	13.23	12.62	13.81	16.72	11.33	10.71
	S^2	0.26	0.81	0.52	1.63	1.42	0.86	0.57	0.62	0.75	2.09	1.71	1.62
5) Number of spikelets per main culm ear	\bar{X}	24.06	22.00	23.02	20.68	22.67	21.70	22.82	23.31	23.72	19.80	22.38	21.11
	S^2	0.68	1.24	1.60	4.26	3.42	2.28	0.47	0.44	0.78	5.17	3.37	3.22
6) Number of grains per main culm ear	\bar{X}	75.30	63.30	78.20	71.30	85.70	74.80	67.70	73.70	79.30	71.62	66.31	68.23
	S^2	31.50	26.70	37.30	118.30	77.20	75.60	28.02	35.21	36.22	83.17	57.82	61.33
7) Main culm ear yield, g	\bar{X}	3.90	2.70	3.70	3.40	3.40	2.90	2.91	2.82	3.31	3.27	2.62	2.33
	S^2	0.18	0.11	0.14	0.81	0.61	0.52	0.31	0.37	0.42	0.87	0.66	0.68
8) Number of grains per ear	\bar{X}	55.40	45.20	49.70	42.80	44.30	41.70	51.61	47.65	63.22	53.71	54.35	48.41
	S^2	38.10	39.80	35.70	132.90	91.70	81.8	46.07	54.78	67.41	108.51	82.12	88.66
9) Ear yield, g	\bar{X}	2.80	2.04	3.02	2.82	2.22	2.31	1.66	1.96	2.31	2.79	2.19	2.36
	S^2	0.12	0.15	0.18	0.43	0.29	0.32	0.14	0.16	0.22	0.47	0.34	0.38
10) 1000-grain weight, g	\bar{X}	50.50	46.80	48.30	43.70	41.70	39.20	47.50	41.14	44.30	48.01	46.70	44.80
	S^2	21.10	20.30	19.20	44.90	34.20	33.30	21.72	25.92	33.41	78.36	52.70	58.30
11) Grain yield per plant, g	\bar{X}	22.50	16.20	21.70	23.90	21.50	19.80	21.72	23.79	24.51	26.16	22.62	24.82
	S^2	17.80	11.50	13.90	50.60	37.70	34.40	33.20	39.10	42.30	88.71	63.35	68.31

Heterosis

Heterosis was estimated as the percent increase of the F_1 mean performance above the respective better parent values. No useful heterotic effects were detected in both crosses for heading date and plant height (Table 3). Similar results were obtained by (El-Massry, 2009 and Koumber, 2011). As for the second cross (Shandaweel 1 x Sakha 69) had exhibited highly significant useful heterosis in main culm ear length, number of spikelets per main culm ear, number of grains per main culm ear and number of grains per ear. Concerning, main culm ear yield and ear yield, highly significant useful heterosis in both crosses had detected. Highly significant useful heterosis was also detected by (Hendawy *et al*, 2007 and El-Shaarawy and Morad, 2011).

Inbreeding depression

Inbreeding depression is measured as the percent deviation of F_2 from F_1 mean performance (Table 3). Inbreeding depression values were highly significant for nearly all traits in the two crosses under investigation. It was interesting to note that, heterosis in F_1 generation should be followed by appreciable reduction in F_2 generation, since the two parameters are two sides of the same phenomena. The present results agreed with this expectation in most cases studied. On the contrary, this expectation was not fulfilled in some cases, where significant heterosis and insignificant inbreeding depression were obtained. The contradiction between heterosis and inbreeding depression estimates could be due to the presence of linkage between genes in these materials (Van der Veen, 1959). These results agree with Dawwam *et al*, 2010 and Koumber and El-Gammaal, 2012.

F_2 performance (E_1):

F_2 mean performance had significantly deviated from the average of the F_1 and mid-parent value (E_1) for all studied traits except, number of productive tillers per plant and main culm ear yield in the first cross and heading date and plant height in the second cross (Table 3). The highly expressive F_2

deviation (E_1) would indicate the presence of epistasis in the inheritance of these traits. These results are agreed with (El-Massry 2009, Dawwam *et al* 2010 and Koumber 2011).

Backcross-performance (E_2):

When no effects of epistasis were assumed, backcross performance would be expected to be near the average of F_1 and recurrent parent performance. Appreciable deviation from this expected value, however, will be observed if epistasis was found to be operated in the inheritance of the trait in view. E_2 was found to be significant for all studied traits in the both crosses except grain yield per plant in both crosses under investigation (Table 3). The F_2 deviation (E_1) was accompanied by backcross deviation (E_2) in sixteen cases and that would ascertain the presence of epistasis in such large magnitudes as to warrant great deal of attention in wheat breeding program for improving these traits.

Nature of gene action:

Genetical analysis of generation means were calculated according to relationships illustrated by (Gamble, 1962) which gives estimates of six parameters model i.e. mean effect (m), additive (a), dominance (d), the three epistatic types additive x additive (aa), additive x dominance (ad) and dominance x dominance (dd). The estimated mean effects parameter (m), which reflects the contribution due to the overall mean plus the locus effects and interaction of the fixed loci. These effects were highly significant for all traits in both crosses (Table 3). Additive gene effects (a) were highly significant for all studied traits except number of productive tillers per plant in both crosses and number of grains per ear and ear yield in the first cross only. These results would suggest the potential for obtaining further improvements for these traits (Table 3). Dominance gene effects (d) were significant for all studied traits except, number of grains per ear in both crosses, grain yield per plant in first cross and number of productive tillers per plant in second cross. These suggested that the dominant factors played a great role in

Estimation of genetic variance components in two bread wheat crosses

Table 3

Table 3

Estimation of genetic variance components in two bread wheat crosses

the inheritance of these traits (Table 3). Significant additive x additive (aa) epistatic types were detected for all studied traits except, number of grains per ear in first cross and number of productive tillers per plant in second cross (Table 3).

The estimated values of additive x dominance (ad) type of digenic epistasis was highly significant for plant height in both crosses, heading date, main culm ear length, number of grains per main culm ear and ear yield in first cross and number of spikelets per main culm ear, main culm ear yield and number of grains per ear in second cross (Table 3).

The epistatic type dominance x dominance (dd) was significant for all studied traits except number of spikelets per main culm ear in both crosses (Table 3). It is worth to mention that the three epistatic types (aa, ad and dd) were found to be accompanied by significant estimates of both E_1 and E_2 epistatic scales in most studied traits and that would ascertain the presence of epistasis in such large magnitude as to warrant great deal of attention in a wheat breeding programs. Also, the heterotic effects previously mentioned might due to both dominance and epistasis. The presence of both additive and non-additive gene action in mostly all studied traits would indicate that selection procedures based on the accumulation of additive effects should be successful in improving all traits under investigation. However, to maximize selection advance, procedures which are know to be effective in shifting gene frequency when both additive and non-additive genetic variances are involved would be preferred. Similar results were previously reported by (Hendawy *et al* 2007, El- Massry 2009, Dawwam *et al* 2010, Koumber 2011 and Hammad 2014).

Heritability and genetic advance:

Heritability is one of the most important parameter for determination the genetic behavior of metric traits. It is expressed as the proportion of the variance attributed to the average effect of genes. However, the most important function of the heritability in the genetic study of quantitative traits as its

predictive role. It expresses the reliability of the phenotypic value as a guide to the breeding value. The possible advance through selection based on phenotypic value can therefore, be predicted only from knowledge of the degree of correspondence between phenotypic value and breeding value. The degree of correspondence is measured by heritability estimates. The heritability estimates enter into almost every formula connected with breeding methods and many practical decisions about the techniques followed depends on its magnitude. Heritability in both broad and narrow sense and genetic advance under selection were calculated and the obtained results are presented in Table (4). High heritability estimates in broad sense were mostly observed for all studied traits. Narrow-sense heritability estimates were high for number of productive tillers per plant and number of spikelets per main culm ear in both crosses. Meanwhile, high narrow-sense heritability values were detected for heading date, plant height, main culm ear length, number of grains per main culm ear, main culm ear yield and number of grains per ear in the first cross. Moderate narrow sense heritability values were obtained for 1000-grain weight and grain yield per plant in both crosses and heading date, plant height, main culm ear length, number of grains per main culm ear, main culm ear yield, number of grains per ear and ear yield in the second cross. This results show no low narrow sense heritability were detected. The differences in magnitudes of both broad and narrow sense heritability estimates found for most traits under investigation would ascertain the presence of both additive and non-additive gene action in the inheritance of most traits in the two crosses as previously obtained from gene action parameters studied Table (3).

Genetic advance under selection given in Table (4) showed the possible gain from selection as percent increase in the F_3 over the F_2 mean when the most desirable 5% of the F_2 plants were selected. Genetic advance under selection (ΔG %) was high in magnitudes for all studied traits.

Table (4): Heritability estimates, genetic advance (Δg), and genetic advance expressed as a percent of the F_2 mean ($(\Delta g \%)$) for all studied characters in the two crosses-under investigation.

Characters	Cross	Heritability %		Genetic advance	
		Broad sense	Narrow sense	Δg	$\Delta g \%$
1) Heading date(days)	I	76.61	72.69	9.04	10.06
	II	76.13	41.70	5.38	6.06
2) Number of productive tillers	I	71.50	64.10	2.60	29.50
	II	75.13	72.15	6.76	74.20
3) Plant height (cm)	I	87.60	82.70	18.60	16.34
	II	87.20	52.20	10.74	9.78
4) Main culm ear length (cm)	I	67.40	60.10	1.57	9.40
	II	69.30	40.60	1.22	7.30
5) Number of spikelets per main culm ear	I	72.50	66.20	2.80	13.60
	II	89.20	72.50	3.39	17.15
6) Number of grains per main culm ear	I	73.10	70.80	15.80	22.20
	II	60.10	56.70	10.65	14.80
7) Main culm ear yield (gm)	I	82.70	60.50	1.12	32.90
	II	58.60	45.90	0.88	26.90
8) Number of grains per ear	I	71.50	69.40	16.40	38.40
	II	48.30	42.60	9.14	17.02
9) Ear yield (gm)	I	65.11	58.13	0.78	27.78
	II	63.80	46.80	0.66	23.60
10) 1000-grain weight(gm)	I	55.01	49.60	6.85	15.60
	II	65.50	58.30	10.63	22.10
11) Grain yield per plant (gm)	I	71.52	57.50	8.42	35.20
	II	56.90	51.50	9.99	38.19

Johnson *et.al* (1955) reported that, heritability estimates along with genetic gain upon selection were more valuable in predicting the effect of selection than the former alone. Also, Dixit *et.al* (1970) pointed out that, high heritability is not always associated with high genetic advance, but in order to make your selection more effective,

high heritability should be associated with high genetic gain. In the present study, high genetic gain was found to be associated with high narrow sense heritability mostly for all studied traits. Therefore, selection for these traits might be effective for satisfactory and successful breeding purposes.

Estimation of genetic variance components in two bread wheat crosses

REFERANCE

- Dawwam, H. A., F. A. Hendawy, A.E. El-Zanaty and Marwa M. El-Nahas (2010). Using six populations model for estimating epistatic, additive and dominance genetic variance in bread wheat (*Triticum aestivum* L.). Minufiya J. Agric. Res. Vol. 36 No.4(2):1411-1434.
- Dixit, P. K., P. D. Saxena and L. K. Bahatia (1970). Estimation of genotypic variability of some quantitative characters in groundnut. Indian J. Agric. Sci. 40: 197 – 201.
- El-Massry, L. E. (2009). Detecting of epistasis in bread wheat (*triticum aestivum* L.). M.Sc. Thesis, Faculty of Agric., Minufiya Univ., Egypt.
- El-Shaarawy, G.A. and A.A. Morad (2011). Genetic studies on some bread wheat crosses. Minufiya J. Agric. Res. Vol. 36 No.4:981-996.
- FAOSTAT, (2012). Crop production. <http://faostat.fao.org/site/339/olefau/t.aspx>
- Gamble, E. E. (1962). Gene effects in corn (*Zea mays* L.). 1. Separation and relative importance of gene effects for yield. Can. J. Plant Sci. 42: 339 – 348.
- Hammad, S. M. (2014). Estimation of genetic parameters in three bread wheat crosses. Minufiya J. Agric. Res., 39 No.2(2): 703-710.
- Hendawy, F. A., H. A. Dawwam and Mona. M. Serag El-Din (2007). The detection of the different components of variation in bread wheat (*Triticum aestivum* L.). Minufiya J. Agric. Res., 32 (4): 1071 – 1086.
- Johnson, H.W., H. F. Robinson and R. E. Comstock (1955). Estimates of genetic and environmental variability in soybean. Agron. J., 47: 314 – 338.
- Koumber, R.M.A. (2011). Estimation of genetic parameters for some quantitative traits in two bread wheat crosses (*Triticum aestivum* L.). Minufiya J. Agric. Res. Vol. 36 No.2: 359-369.
- Koumber, R.M.A. and A.A. El-Gammaal (2012). Inheritance and gene action for yield and its attributes in three bread wheat crosses. World. J. Agri.Sci. 8(2): 156-162.
- Marani, A. (1968). Heterosis and inheritance of quantitative characters in interspecific crosses of cotton. Crop. Sci. 8: 299 – 303.
- Mather, K. (1949). Biometrical Genetics. Dover Publications, Inc., London.
- Mather, K. and J. L. Jinks (1982). Biometrical Genetics. (3rd edition), Chapman and Hall, London.
- Miller, P. A., J. C. Williams, H. F. Robinson and R. E. Comstock (1958). Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. Agron. J., 50: 126 – 131.
- Singh, R.P and S. Singh (1992). Estimation of genetic parameters through generation mean analysis in bread wheat. Indian J of Gene. and plant bree. vol 52:369-375.
- Van der veen, J. H. (1959). Test of non-allelic interaction and linkage for quantitative characters in generations derived from two diploid pure lines. Gene. 30: 201 – 232.
- Viana, JMS. (2000). Generation mean analysis to polygenic systems with epistasis and fixed genes. Pesq. Agropec. bras., vol. 35 no.6

تقدير مكونات التباين الوراثي في هجينين من قمح الخبز

مروة محمد النحاس^(١) ، سليمان عبد المعبود عرب^(٢)

^(١) قسم المحاصيل - كلية الزراعة - جامعة المنوفية.

^(٢) البنك القومي للجينات والموارد الوراثية - مركز البحوث الزراعية - الجيزة.

المخلص العربي

تهدف هذه الدراسة الى معرفة قوة الهجين والسلوك الوراثي ودرجة التوريث والتحسين الوراثي المتوقع بالانتخاب لصفات المحصول ومكوناته وكذلك طبيعة الفعل الجيني في هجينين من قمح الخبز هما (جميزة ٩ X سخا ٨) و (شندويل ١ X سخا ٦٩) . وذلك باستخدام موديل العشائر الستة وقد اختير اربعة تراكيب وراثية لهذه الدراسة هي جميزة ٩ وسخا ٨ و سخا ٦٩ وشندويل ١ و أجرى هذا البحث في مزرعة كلية الزراعة بشبين الكوم جامعة المنوفية وذلك في ثلاثة مواسم متتالية هي ٢٠١٠/٢٠١١ ، ٢٠١١ / ٢٠١٢ ، ٢٠١٢ / ٢٠١٣ . وكانت الصفات المدروسة هي : ميعاد طرد السنابل (يوم) - عدد الفروع المنتجة للنبات - ارتفاع النبات (سم) - طول السنبل الرئيسية (سم) - عدد السنبيلات في سنبل الساق الرئيسي - عدد الحبوب في سنبل الساق الرئيسي - محصول سنبل الساق الرئيسي (جم) - عدد الحبوب في السنبل - محصول السنبل (جم) - وزن الألف حبه (جم) - محصول النبات الفردي (جم). ويمكن تلخيص النتائج المتحصل عليها فيما يلي:

- ١- أظهرت النتائج وجود قوة هجين معنوية في معظم الصفات المدروسة ما عدا صفتي ميعاد طرد السنابل وارتفاع النبات في كلا الهجينين. وقد سجلت قوة الهجين لصفه محصول النبات الفردي -٣,٥٥ ، ٣,٠٢ % لكل من الهجين الأول والثاني على التوالي عند مقارنتها بالأب الأفضل ولكنها لم تصل الى حد المعنوية.
- ٢- كان تأثير الجينات من النوع المضيف والسيادي معنويا لمعظم الصفات المدروسة.
- ٣- كان فعل الجينات التفوقى بطرزه الثلاثة (المضيف X المضيف) و(المضيف X السيادي) و(السيادي X السيادي) معنويا لمعظم الصفات المدروسة في كلا الهجينين وكان ذلك مصاحبا لمقاييس التفوق E_1 و E_2 وذلك في معظم الصفات المدروسة.
- ٤- تشير النتائج إلى أن كانت قيمه درجة التوريث بمعناها العام كانت عالية لجميع الصفات تحت الدراسة وكذلك أظهرت الكفاءة الوراثية بمعناها الدقيق قيما عالية لكل من صفتي عدد الأفرع المنتجة وعدد السنبيلات في سنبل الساق الرئيسي في كلا الهجينين.
- ٥- كانت القيم العالية للتحسين الوراثي المتوقع بالانتخاب مصاحبة للقيم العالية لدرجة التوريث بالمعنى الدقيق لمعظم الصفات المدروسة.

Estimation of genetic variance components in two bread wheat crosses

Table (3): Heterosis, inbreeding depression, and gene action parameters in the two crosses I (Gemmiza 9 x sakha 8) and II (shandawel x sakha69) for all studied characters.

Character	Cross	Heterosis %	Inbreeding depression %	F ₂ deviation E ₁	Backcross deviation E ₂	Gene action parameters					
						m	a	d	aa	ad	dd
1) Heading date(day)	I	3.97**	1.93**	9.58**	26.65**	89.84**	1.89**	15.16**	14.94**	-1.40*	-23.23**
	II	3.68**	0.63	0.8	8.17**	88.84**	-1.81**	-15.88**	13.14**	-1.37	-29.48**
2) Number of productive tillers	I	-10.80**	-7.32**	0.40	-0.90**	8.80**	0.30	-3.80**	-3.40**	-0.30	5.20**
	II	-12.90**	7.51	-0.95*	-3.32**	9.11**	-0.14	-3.26	-2.84	0.90	9.48**
3) Plant height(cm)	I	6.59**	-2.50**	4.00**	-7.80**	114.30**	11.60**	-29.20**	31.60**	7.10**	47.20**
	II	1.65*	0.63	-0.70	-8.80**	109.80**	11.40**	14.80**	-14.80**	9.60**	32.40**
4) Main culm ear length	I	-0.77**	-33.40**	3.96**	1.87**	16.69**	0.70**	-12.53**	12.08**	0.44*	8.35**
	II	4.20**	-21.07**	3.35**	-4.69**	16.73**	0.62**	-21.92**	-22.80**	0.31	32.19**
5) Number of spikelets per main culm ear..	I	-4.32**	10.16**	-2.35**	-1.68**	20.68**	0.97**	6.01**	6.02**	-0.06	-2.66
	II	1.75*	16.50**	-3.59**	-3.29**	19.80**	1.27**	8.44**	7.78**	1.51**	-1.19
6) Number of grains per main culm ear	I	3.85	8.82**	3.85**	13.00**	71.30**	10.90**	44.70**	35.80**	4.90**	-16.8**
	II	7.60**	9.68**	-3.38**	-15.46**	71.62**	-1.92*	-8.80**	-17.40**	1.08	48.32**

Table (3): Cont.

Character	Cross	Heterosis %	Inbreeding depression %	F ₂ deviation E ₁	Backcross deviation E ₂	Gene action parameters					
						m	a	d	aa	ad	dd
7) Main culm ear yield	I	5.12**	8.11**	-0.10	-0.70**	3.40**	0.50**	5.20**	-1.00*	-0.10	2.40**
	II	13.70**	1.21	0.18*	-1.22**	3.27**	0.29**	-2.73**	-3.18**	0.25*	5.63**
8) Number of grains per ear	I	-10.30**	13.80**	-7.20**	-14.00**	42.80**	2.60	-0.20	0.80	-2.50	27.20**
	II	22.50**	15.04**	2.72*	-10.09**	53.71**	5.94**	4.26	-9.32*	3.96**	29.50**
9) Ear yield	I	7.85**	6.62**	0.40**	-0.91**	2.82**	-0.09	-1.62**	-2.22**	-0.47**	4.04**
	II	17.8**	-20.77**	0.73**	0.43**	2.79**	-0.17**	-1.56**	-2.06**	-0.02	1.20**
10) 1000-grain weight	I	-4.35	9.52**	-4.77**	-16.05**	43.70**	2.50**	-13.35**	-13.00**	0.65	45.10**
	II	-6.73**	-8.37**	3.70**	2.88*	48.01**	1.9**	-9.06**	-9.04**	-1.28	-59.72**
11) Grain yield per plant	I	-3.55	-10.13**	3.37**	0.25	23.90**	1.70*	-10.65	-13.00**	-1.45	12.5**
	II	3.02	-6.73	2.53**	0.18	26.16**	-2.20*	-8.00*	-9.76**	-1.17	9.41*

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

