ESTIMATION OF EPISTASIS, ADDITIVE AND DOMINANCE COMPONENTS OF GENETIC VARIANCE USING TRIPLE TEST CROSS AND LINE X TESTER ANALYSES IN BREAD WHEAT

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Abstract

The triple test cross progenies were evaluated to study the components of genetic variance for four traits, viz, grain yield/plant, number of spikes/plant, number of kernels/spike and 100-grain weight. The superior parents and hybrid combinations in respect to studied characters were also determined through line x tester analysis. Seventeen bread wheat varieties and lines were crossed with three testers. Significant epistasis was present for all characters studied. Additive x additive epistatic type of gene action was found to be much larger in magnitude than additive x dominance and dominance x dominance (J+L) epistatic types for number of spikes/plant, 100-grain weight and grain yield/plant. Both additive and dominance genetic components played an important role in the inheritance of all studied traits . Due to the presence of epistasis for most of studied characters, selection in the later segregating generations would be more effective for the improvement of these characters. The average degree of dominance $(H/D)^{1/2}$ ***resulted partial dominance for all traits studied. Line x tester analysis revealed that the nature of gene action was predominantly non-additive for most studied traits. Five wheat lines, viz. L6, L11, L13, L16 and L17 exhibited significant general combining ability effects for all studied traits. The superior crosses*** $(T_1)P_1$ ***Gemmiza 10 with each of L1, L2, L3, L4, L5 and L9;*** T_2 (F_1)***each of with L5, L6, L8, L13, L14 and L17; and*** (T_3) ***Line # 1 with each of L7, L11 and L15) showed the highest specific combining ability effects for grain yield and its contributing characters.***

Key words: ***Additive, Aominance, Epitasis, Combining bility, Triple test cross, Line x Tester, Triticum aestivum.***

INTRODUCTION

Information on the components of genetic variation would help the plant breeder in deciding the appropriate breeding method. A good genetic model, is which enables the breeder to have precise and unbiased estimates of all components of genetic variance. A design, which is a simple extension of the design III of Comstock and Robison (1952) has been proposed by Kearsey and Jinks (1968). This design, known as a "triple test cross" provides not only a precise test for epistasis but also gives unbiased estimate of additive (D) and dominance (H) components, if epistasis is absent. Further, this approach is independent of both the gene frequencies and the mating system of the population to be investigated. In this respect, Ketata *et al* (1976) and Singh and Singh (1978) revealed the importance of epistatic gene effects in controlling heading date but, not for plant height. Nanda *et al* (1982) indicated the importance of epistasis component in the genetic control of plant height. Epistasis played a major role in the inheritance of quantitative traits in several crops particularly in pea (Narsinghani *et* al 1982). A great importance of epistasis was also reported in bread wheat by Eissa (1994), Kumber (2001), Hendawy et al(2007) and Hendawy (2008).

The objectives of this study were to: (1) establish, the existence of epistasis and to determine the additive (D) and dominance (H) variances conditioning quantitative traits using the triple test cross analysis and (2) estimate general and specific combining ability using lines x tester analysis.

MATERIALS AND METHODS

The field work of this study was carried out at El-Giza Research Station, Egypt during 2007/2008 and 2008/2009 seasons. In 2009/2010 season, the final experiment was conducted at Kafer El-Hamam, El-Sharkya, Egypt. In the first season, 2007/2008 two high yielding bread wheat (*Triticum aestivum*), which showed wide adaptation in winter season and differed in most of their agronomic traits i,e., Gemmeiza 10 (P_1) and the promising line# 1 (P_2) were crossed to obtain their F_1 (gemmeiza 10 x Line #1) and here after used as three testers.

During 2008/2009 winter season, each of the three testers P_1, P_2 and their F_1 were crossed to 17 divergent origin bread wheat cultivars and lines. The name and pedigree of these genotypes are presented in Table (1). Fifty one crosses were produced i.e 17 L_{1i}, 17 L_{2i}, 17L_{3i} progeny families of a triple test cross design. The cross P_1 x P_2 was also repeated to get more F_1 grains. All plant materials i.e., the 51 families (crosses), 17 parents and the three testers were grown in a randomized complete block design with three replications in 2009/2010 season. Each experimented plot consisted of one row 4m long, with 30 cm. between rows and distance between plants within row was 10 cm. All the normal agronomic practices were followed as recommended in the area. Random samples of ten guarded plants from each plot were chosen at harvest for recording the different four traits examined i.e., grain yield/plant and its components no. of spikes/plant, no. of kernels/spike, 100-grain weight and grain yield/plant.

Statistical analysis

The procedure for detecting epistasis was done according to the method outlined by Kearsey and Jinks (1968). The analysis is based on the following model:

Data of the triple test cross families L1i, L2i and L3i were firstly subjected to the conventional analysis of variance to test the significance between families. The mean squares of deviations L1i + L2i – 2L3i (overall epistasis) were tested against pooled error to determine the presence of epistasis.

Table 1. The Names, origin and pedigree of bread wheat cultivars and lines used in this study.

Genotypes	Name	Pedigree	Origin
Lines (L)			
L_1	*Gemmeiza9*	*Ald"s"/HUA//CMH74A,630/sx*	*Egypt*
L_2	*Sakha 93*	*Sakha92/TR810328*	*Egypt*
L_3	*Giza 168*	MRL/BUC//SERI	*Egypt*
L_4	*Sids 1*	*HD21/PAVON"S"//1158.57/MAYA74"S"*	*Egypt*
L_5	*Sakha 94*	*OPATA/RAYON//KAVZ*	*Egypt*
L_6	*Chil "s"*	*BTY/JUP*	*CIMMYT*
L_7	*Line # 2*	*BL1133/3/CMH79A-955*2/CN079//CMH79A.955/BOW"S"*	*Egypt*
L_8	*Line # 3*	*Seri82/4/SPN//MCD/CAMA/3/NZR*	*Mexico*
L_9	*HUBARA-5*		*ICARDA*
L_{10}	*ATTILA*		*ICARDA*
L_{11}	*MILAN*	*V"s"73.600/MRL/3/BOW//YR/TRF*	*CIMMYT*
L_{12}	*Debira*		*India/Syria*
L_{13}	*Line # 4*	*SKAUZ 2/SRIMA*	*ICARDA*
L_{14}	*Line # 5*	*PFAU/Milan*	*CIMMYT*
L_{15}	*Line # 6*	*Vee"s"SWM6525/4/TRM//KAL/Bb/3/Crops"s"/PIY "s"*	*CIMMYT*
L_{16}	*Line # 7*	*ALD/CEP75630//CCP75234/PT7219/3/BUC/BJY/4/SARA//JUP/BJY/3/KAUZ/4/BABAX/5/FRTL*	*ICARDA*
L_{17}	*Sids 12*	*BUC//7C/ALD/5/MAYA7410N/1160.147/3/BB/GLL/4/CHAT"s"/6/MAYA/VUL/CMH74A.630/4*SX*	*Egypt*
Testers			
T_1	*Gemmeiza 10 (P_1)*	*MAYA74"S"10N/1160-147/3/BB/g/LL/4/CHA7"S"/5/CROW"S"*	*Egypt*
T_2	(F_1)	*Gemmiza 10 x Line # 1*	*Egypt*
T_3	Promising Line #1 (P_1)	*MAYON"S"//CROW"S"/VEE"S"*	*Egypt*

$L_{ijk} = M + G_{ij} + RK + E_{ijk}$

Where :

L_{ijk} = Denotes the phenotypic value of the cross between tester L_i and Lj in replication k.

M = Denotes the mean of all single and three way crosses.

G_{ij} = Denotes the genotypic value of the cross between tester L_i and Line j.

RK = Denotes the effect of replication k.

E_{ijk} = Denotes the error associated with the cross ij in replication K.

The overall epistasis was partitioned into (i) type of epistsis (additive x additive) and (J and L) types of epistasis i.e. additive x dominance and dominance x dominance. The estimation of additive (D) and dominance (H) genetic components and correlation coefficient (r) between sums L_{1i}+L_{2i} and differences L_{1i} - L_{2i} were obtained to detect the direction of dominance according to Jinks and Perkins (1970). Average degree of dominance was calculated as $(H/D)^{1/2}$.

The data were also subjected to Line x tester analysis using methodology which is fully described by Kempthorne (1957) and Singh and Chaudhary (1985).

RESULTS AND DISCUSSION

The mean performance of the triple test cross fifty one families for the four studied traits are presented in Table (2). The analysis of variance for all traits studied are presented in Table (3). Genotypes, hybrids and parents mean squares were found to be highly significant for all studied traits, indicating the presence of genetic variability among hybrids and their parents. Hybrids *vs* parents mean square estimates, as an average heterosis overall crosses, were found to be highly significant for all traits. Also, the data given in Table (3) indicated highly significant mean squares due to lines for all studied traits.

Tester mean squares were found to be highly significant for all studied traits. Line *vs* testers mean squares were highly significant for all traits except number of kernels/spike. The mean performance of the two parents P_1 (Gemmeiza 10) *vs* P_2 (Promising Line # 1) and (P_1 + P_2) *vs* F_1 were significantly different from each other in all traits. The unbiased estimates of additive and dominance gene action and the unambiguous test of epistasis would only be achieved when the testers are different from each other. However, when this condition between two parents is not met, the estimates are biased to an unknown extent (Keassey and Jinkes 1968, Jinks *et al* 1969, Eissa 1994, Kumber 2006, Hendawy *et al* 2007 and Hendawy 2008.

The estimates of general (GCA) and specific (SCA) combining ability variance in Table (3) revealed that the nature of the gene effects was predominantly non-additive for all traits under investigation, except for grain yield/plant.

Analysis of variance for testing the presence of epistasis in the inheritance of all studied traits are presented in Table (4). Significant epistasis was detected for all studied characters. Further, partitioning of epistatic effect revealed that mean squares due to additive x additive (i) epistatic type were found to be highly significant for all characters under investigation. Similar results were reported by Esmail (2007), Hendawy *et al* (2007) and Hendawy (2008).

Table 2. Mean performance *of the triple test cross hybrid and line x tester for all studied traits*

A-Hybrids		No. of spikes/plant	No. of kernels/spike	100-grain weight (g)	Grain yield/plant (g)
Gemmeiza9	x P_1	10.33	64.50	3.87	26.22
	x F_1	13.33	56.50	5.19	37.30
	x P_2	13.00	53.27	5.12	32.18
Sakha 93	x P_1	10.67	58.60	4.59	27.48
	x F_1	13.33	55.33	4.06	34.00
	x P_2	12.67	43.65	4.82	37.43
Giza 168	x P_1	14.33	42.52	4.96	30.05
	x F_1	13.00	69.67	4.60	41.78
	x P_2	12.33	60.50	4.79	35.22
Sids 1	x P_1	10.40	75.50	4.79	27.97
	x F_1	14.07	60.00	4.43	39.13
	x P_2	12.73	48.73	5.43	31.67
Sakha 94	x P_1	13.67	46.83	5.50	25.90
	x F_1	17.57	62.30	4.60	42.30
	x P_2	12.77	61.03	4.48	27.90
Chil "S"	x P_1	10.07	57.50	4.97	28.72
	x F_1	20.97	47.87	5.51	55.20
	x P_2	16.00	41.29	5.59	36.40
Line # 2	x P_1	18.03	40.10	4.64	24.38
	x F_1	16.07	43.92	3.35	38.50
	x P_2	9.03	64.73	4.10	35.22
Line # 3	x P_1	13.03	36.30	4.92	22.95
	x F_1	9.07	74.13	6.46	43.95
	x P_2	13.03	62.87	4.35	35.92
Hubara-5	x P_1	11.07	57.58	4.39	27.75
	x F_1	15.10	55.00	4.89	40.38
	x P_2	10.07	38.33	5.80	30.85
Attila	x P_1	18.07	39.43	4.61	24.35
	x F_1	13.03	48.23	6.51	40.49
	x P_2	12.03	70.50	4.05	34.32
Milan	x P_1	15.00	54.33	4.09	32.55
	x F_1	13.03	69.33	4.87	43.38
	x P_2	17.03	95.67	2.77	44.90
Debira	x P_1	11.03	55.97	3.40	20.67
	x F_1	19.07	30.93	5.79	33.67
	x P_2	12.03	55.00	4.49	29.30

Table 2 Cont.

A-Hybrids		**No. of spikes/plant**	**No. of kernels/spike**	**100-grain weight (g)**	**Grain yield/plant (g)**
Line # 4	**x P_1**	**15.07**	**40.90**	**5.15**	**31.52**
	x F_1	**15.00**	**66.97**	**4.95**	**49.78**
	x P_2	**12.03**	**70.13**	**4.24**	**35.25**
Line # 5	**x P_1**	**14.03**	**36.20**	**4.75**	**23.73**
	x F_1	**15.03**	**52.00**	**6.15**	**47.13**
	x P_2	**10.03**	**82.33**	**4.49**	**38.47**
Line # 6	**x P_1**	**12.03**	**56.83**	**3.73**	**25.52**
	x F_1	**12.07**	**53.30**	**6.71**	**43.47**
	x P_2	**15.07**	**70.67**	**3.70**	**39.63**
Line # 7	**x P_1**	**14.03**	**40.37**	**5.55**	**30.48**
	x F_1	**19.93**	**55.43**	**4.35**	**48.38**
	x P_2	**14.10**	**37.30**	**5.25**	**37.45**
Sids 12	**x P_1**	**14.10**	**46.30**	**5.24**	**33.30**
	x F_1	**16.97**	**78.13**	**4.24**	**56.43**
	x P_2	**11.07**	**58.63**	**5.96**	**47.10**
B-Parents		**No. of spikes/plant**	**No. of kernels/spike**	**100-grain weight (g)**	**Grain yield/plant (g)**
Gemmeiza 9		**14.50**	**67.40**	**4.75**	**28.87**
Sakha 93		**12.67**	**65.83**	**4.71**	**30.23**
Giza 168		**14.77**	**56.23**	**4.24**	**31.74**
Sids 1		**10.63**	**76.00**	**4.80**	**25.43**
Sakha 94		**11.83**	**62.00**	**4.60**	**27.73**
Chil "S"		**15.47**	**57.00**	**4.32**	**36.80**
Line # 2		**10.23**	**71.00**	**4.70**	**20.10**
Line # 3		**14.13**	**60.00**	**4.50**	**27.70**
Hubara-5		**13.33**	**52.67**	**4.30**	**29.57**
Attila		**11.00**	**47.33**	**4.40**	**22.73**
Milan		**16.00**	**68.27**	**4.03**	**36.67**
Debira		**12.33**	**35.33**	**4.67**	**18.87**
Line # 4		**12.67**	**48.00**	**4.37**	**25.50**
Line # 5		**11.50**	**69.67**	**4.20**	**21.60**
Line # 6		**14.13**	**61.67**	**5.30**	**27.40**
Line # 7		**14.40**	**57.33**	**4.87**	**28.63**
Sids 12		**16.00**	**58.33**	**5.42**	**38.57**
C-Testers					
Gemmeiza	**x P_1**	**10.00**	**58.33**	**4.31**	**24.15**
	x F_1	**11.33**	**64.91**	**4.11**	**29.82**
	x P_2	**12.33**	**54.57**	**5.03**	**35.77**
L. S. D	**5%**	**1.673**	**2.79**	**0.378**	**2.577**
	1%	**2.288**	**3.815**	**0.518**	**3.524**

Table 3. Mean square from analysis of variance of (L1i, L2i and L3i) triple test cross hybrid and line x tester for all studied traits

S O V	d.f	No. of spikes/plant	No. of kernels/spike	100-grain weight (g)	Grain yield/plant (g)
Replications	*2*	0.079	2.53	0.123	2.595
Genotypes	*70*	18.78**	469.212**	1.709**	203.801**
Hybrids	*50*	21.706**	542.956**	1.426**	206.984**
Parents	*19*	10.709**	266.4**	0.907**	93.157**
Hybrids vs Parents	*1*	25.858**	635.45**	2.589**	2146.89**
Lines	*16*	10.197**	306**	0.413**	96.446**
Testers	*2*	4.111**	82.21**	0.695**	101.23**
Lines vs Testers	*1*	32.098**	1.11	9.243**	24.386**
P_1 vs P_2	*1*	2.667*	64.879**	0.394**	48.167**
(P_1+P_2) vs F_1	*1*	5.556**	99.546**	0.996**	154.293**
GCA (line)	*16*	13.732**	418.948**	1.426**	161.609**
GCA (Tester)	*2*	72.13**	1329.98**	3.198**	3263.93**
GCA (Average)	*18*	20.22**	520.17**	1.623**	506.311**
SCA	*32*	22.54**	555.77**	2.207**	38.613
Error	*140*	1.093	3.04	0.056	2.593
GCA / SCA		0.897	0.936	0.735	13.112

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

Table 4. Analysis of variance for testing the presence of epistasis in triple test cross for all studied traits

S O V	*d.f*	*No. of spikes/plant*	*No. of kernels/spike*	*100-grain weight (g)*	*Grain yield/plant (g)*
Total epistasis	*17*	448.86**	2161.5**	20.328*	1930.654**
i-type epistasis	*1*	846.683**	1549.247**	38.324**	27931.174**
J+L epistasis	*16*	423.996**	2199.76**	19.204*	305.62**
i-types epistasis x block	*2*	3.385	18.793	0.167	37.257
J+L epistasis x block	*32*	143.071	15.925	9.836	13.841
Total epistasis x block	*34*	134.855	16.093	9.267	15.218

* and ** indicate significant at 0.05 and 0.01 probability levels, respectively.

I = additive x additive , (J) = additive x dominance

and (L)= dominance x dominance

Additive x dominance and dominance x dominance (J+L) epistatic type mean squares were highly significant for all studied traits. The additive x additive epistatis type (i) was found to be much larger in magnitude than additive x dominance (J) and dominance x dominance (L) epistatic type for number of spikes/plant, 100-grain weight and grain yield/plant, indicating that fixable components of epistatsis were, more important than non-fixable ones in the inheritance of these traits. In self-fertilized crops like wheat, the fixable component of epistasis could be easily exploited. The presence of epistasis could have important implication, in a breeding program by using standard hybridization and progeny selection procedures could take advantage of epistasis if it is of additive x additive type as revealed in all the traits. These results would ascertain the results previously obtained from the line x tester analysis in Table (3). the results indicate also that both additive and dominance genetic components play an important role in the inheritance of all traits under investigation. In this respect a great importance of epistasis was reported in wheat by Singh and Singh (1978), Singh *et al* (1988), Singh and Nanda (1989), Eissa (1994), Esmail (2007), Hendawy *et al* (2007), Kumber (2006), Hendawy (2008), Abdel-Nour and Hassan (2009) and Abdel-Nour and Zakaria (2010).

The analysis of variance for sums (measuring additive genetic variance) and differences (measuring dominance genetic variance) and the estimation of additive (D) and dominance (H) genetic components are presented in Table(5). The mean squares due to sums (L_{1i} + L_{2i}) be highly significant for all traits. Also, mean squares due to differences (L_{1i} - L_{2i}) were also highly significant for all characters under investigation. These results would indicate that both additive and dominance genetic components play an important role in the inheritance of all characters under investigation and these results obtained from line x tester analysis as previously mentioned indicated that non-additive genetic variance was predominant in the inheritance of all studied traits. These contradiction between the results obtained from the two models i.e. triple test cross and line x tester could be due to the presence of epistasis in such a large magnitude that defect the estimation of both additive and dominance genetic variation obtained from triple test cross. Similar results were obtained by *Singh et al (1989), Pawar* Eissa (1994), Pawer *et al* (1996), Kumber (2001), El-Nahas (2005), *Hendawy et al* (2007) and Hendawy (2008).

The estimates of additive (D) and dominance (H) components in Table (5), indicated that both additive and dominance components in gene effects play an important role in the inheritance of number of spikes/plant, number of kernels/spike, 100-grain weight and grain yield/plant. However, the additive components were larger in magnitude than dominance for 100-grain weight and grain yield/plant and consequently, it could be concluded

Table 5. Mean squares from analysis of variance for sums, differences and estimates of additive (D), dominance (H) and degree of dominance in triple test cross analysis for all studied traits.

S O V	*d.f*	*No. of spikes/plant*	*No. of kernels/spike*	*100-grain weight (g)*	*Grain yield/plant (g)*
Sums ($L_{1i} + L_{2i}$)	*16*	18.366**	730.27**	4.139**	172.92**
Error	*32*	1.761	5.762	0.155	2.62
Differences($L_{1i}+L_{2i}$)	*16*	43.058**	1490.21**	2.027**	52.616**
Error	*32*	1.164	8.857	0.157	5.731
D		22.139	966.01	5.312	227.07
H		55.859	1975.137	2.496	62.513
$(H/D)^{1/2}$		1.588	1.43	0.685	0.525
R		-0.246	-0.364**	-0.308**	-0.393**

*** and ** indicate significant at 0.05 and 0.01 probability levels, respectively.**

(R) correlation coefficients between sums ($L_{1i} + L_{2i}$)***and differences*** ($L_{1i} - L_{2i}$)

that selection procedures based on accumulation of additive effects would be successful in improving all studied traits. However, to maximizing selection advance, procedures which are known to be effective in shifting gene frequency when both additive and non-additive genetic variances are involved would be preferred. Similar conclusion was also reported by Singh (1981), Singh *et al* (1989), Eissa (1994), Kumber (2006), Hendawy *et al* (2007) and Hendawy (2008).

The degree of dominance $(H/D)^{1/2}$ was less than unity confirming the role of partial dominance in the inheritance of 100-grain weight and grain yield/plant, suggesting the effectiveness of phenotypic selection for improving such characters, and ascertain the fact that in self pollinated crops, most genes are homozygous and the over-dominance is rare. Genetic advance in genetic systems with over-dominance and epistasis is slower than when gene effects are purely additive or partially dominant (Wang *et al* 2004).

The direction of dominance and types of genes exhibiting dominance were detected by calculating the correlation coefficients between sums (L_{1i} + L_{2i}) and differences (L_{1i} - L_{2i}).

If (Correlation coefficient) is negative and significant, then increasing type of gene are dominant and vice versa. The correlation coefficients between sums and differences were found to be negative and significant for most studied traits.

The obtained results indicated that epistasis is an integral component of genetic architecture of all traits and hence detection, estimation and consideration of this component is important for the formulation of breeding program to improve wheat population for such economic traits. If epistasis is ignored on precise, conclusion can be drawn about the relative importance of additive, dominance and epistasis where the estimation of additive and dominance genetic components were biased by epistasis to unknown extent as in the present materials. (Sood and Dawa 1999).

Estimates of general combining ability (GCA) effects of the seventeen parental lines and three testers are presented in Table (6). High positive values of GCA effects would be of interest in most traits. The results revealed that lines number 5, 6, 11 and 16 showed desirable CGA effects for number of spikes/plant, and lines number 1, 3, 4, 8, 11, 13, 15 and 17 for number of kernels/spike. Obviously, wheat lines number 6, 8, 9, 10, 14, 16 and 17 showed desirable GCA effects for 100-grain weight. Concerning grain yield/plant wheat lines number 6, 11, 13, 16 and 17 were good donors in this respect. The tester F_1 (Gemmeiza 10 x promising Line # 1) could be considered as an excellent one in breeding programs towards releasing cultivars that are of higher number of spikes/plant, number of kernels/spike, 100-grain weight and grain yield/plant *(Hamada et al2002).* However, it is apparent that the parent which posseses high GCA effects for grain yield/plant might also be high for one or more traits contributing to yield, while the parent which has high GCA effects for one or more of yield components not necessary have high GCA effects for yield itself.

Data presented in Table (7) showed that most hybrids exhibited significant and positive specific combining ability (SCA) effects for yield and yield components, while nine, seventeen, fifteen and nine crosses out of 51 cross parental combinations exhibited significant positive SCA effects for number of spikes/plant, number of kernels/spike, 100-grain weight and grain yield/plant, respectively.

It could be concluded that the parental lines 6, 11, 13, 16 and 17 might be selected as parental materials for wheat breeding programs since the lines no. 6, 11, 13, 16 and 17 had the highest general combining ability effect for most studied traits and they gave high specific combining ability effect with the second tester F_1 (Gemmieza 10 x Promising Line # 1) and also with the third tester P_2 (promising Line # 1).

These parents may be used in suitable selection programs where they possess high amount of additive genetic variance. It could be noticed that the hybrids were the favorable crosses for grain yield *via* some components of yield such as number of spikes/plant, number of kernels/spike and 100- grain weight. These cross combinations expressed significant heterotic effects relative to better parents.

The results concerning general and specific combining ability effects could indicate that excellent hybrid combinations could be obtained from the three possible combinations between the parents of high and low general combining effects i.e high x high, high x low and low x low and consequently it could be concluded that the general combining ability effects of the parental lines were generally unrelated to the specific combining ability effects of their respective crosses. If crosses showing high

Table 6. General combining ability effects of the parental lines and testers for all studied traits.

Parents		No. of spikes/plant	No. of kernels/spike	100-grain weight (g)	Grain yield/plant (g)
Lines		-1.516**	2.335**	-0.08	-3.551**
		-1.516**	-3.226**	-0.319**	-2.479**
L_3		-0.515	1.807**	-0.025	0.232
L_4		-1.338**	5.657**	0.077	-2.529**
L_5		0.929**	0.968	0.052	-3.418**
L_6		1.939**	-6.867**	0.545**	4.654**
L_7		0.64	-6.171**	-0.782**	-2.751**
		-2.027**	2.013**	0.435**	-1.181*
		-0.326	-5.451**	0.216**	-2.457**
		0.64	-3.032**	0.244**	-2.4**
		1.284**	17.357**	-0.899**	4.826**
		0.307	-8.454**	-0.248**	-7.573**
		0.295	3.579**	-0.027	3.399**
		-0.705*	1.1	0.324**	0.993
		-0.682*	4.513**	-0.095	0.755
		2.284**	-11.387**	0.241**	3.32**
		0.307	5.268**	0.341**	10.16**
Tester T_1		-0.505**	-5.768**	-0.152**	-8.185**
T_2		1.358**	1.837**	0.289**	7.801**
T_3		-0.854**	3.931**	-0.137**	0.384
L.S.D for line g_i	0.05	0.682	1.139	0.155	1.052
	0.01	0.933	1.558	0.212	1.439
L.S.D g_i-g_i	0.05	0.965	1.611	0.219	1.488
	0.01	1.321	2.203	0.299	2.035
L.S.D for tester g_j	0.05	0.286	0.479	0.065	0.442
	0.01	0.391	0.654	0.089	0.604
L.S.D g_i-g_i	0.05	0.406	0.677	0.092	0.625
	0.01	0.555	0.925	0.126	0.855
	0.01	0.933	0.654	0.089	0.604

* and ** indicate significant at 0.05 and 0.01 probability levels, respectively.

Table 7. Specific combining ability effects of different crosses for all studied traits.

Cross	No. of spikes/plant	No. of kernels/spike	100-grain weight (g)	Grain yield/plant (g)
$P_1 x L_1$	-1.384	12.179**	-0.703**	2.501**
$P_1 x L_2$	-1.051	11.84**	0.252	2.695**
$P_1 x L_3$	1.615*	-9.276**	0.331	2.551**
$P_1 x L_4$	-1.495*	19.857**	0.059	3.229**
$P_1 x L_5$	-0.495	-4.121**	0.791**	2.435*
$P_1 x L_6$	-5.106**	14.381**	-0.235	-3.205**
$P_1 x L_7$	4.16**	-3.715**	0.765**	-0.133
$P_1 x L_8$	1.827**	-15.699**	-0.172	-3.136**
$P_1 x L_9$	-1.84**	13.042**	-0.483**	2.94**
$P_1 x L_{10}$	4.194**	-7.521**	-0.294	-0.517
$P_1 x L_{11}$	0.482	-13.01**	0.329*	0.456
$P_1 x L_{12}$	-2.507**	14.435**	-1.009**	0.973
$P_1 x L_{13}$	1.597*	-12.665**	0.524**	0.851
$P_1 x L_{14}$	1.505*	-14.876**	-0.228	-4.527**
$P_1 x L_{15}$	-0.518	2.334**	-0.829**	-2.505**
$P_1 x L_{16}$	-1.484	1.768	0.656**	-0.105
$P_1 x L_{17}$	0.56	-8.954**	0.246	-4.127**
$F_1 x L_1$	-0.247	-3.425**	0.172	-2.401*
$F_1 x L_2$	-0.247	0.968	-0.716**	-6.773**
$F_1 x L_3$	-1.58	10.269**	-0.477*	-1.701
$F_1 x L_4$	0.309	-3.248**	-0.742**	-1.59
$F_1 x L_5$	1.542*	3.741**	-0.55**	2.466*
$F_1 x L_6$	3.931**	-2.857**	-0.137	7.293**
$F_1 x L_7$	0.331	-7.503**	-0.97**	-2.001*
$F_1 x L_8$	-4.003**	14.529**	0.927**	1.872*
$F_1 x L_9$	0.331	2.86**	-0.425*	-0.412
$F_1 x L_{10}$	-2.703**	-6.325**	1.165**	-0.365
$F_1 x L_{11}$	-3.347**	-5.615**	0.674**	-4.696**
$F_1 x L_{12}$	3.664**	-18.204**	0.943**	-2.012*
$F_1 x L_{13}$	-0.391	5.797**	-0.121	3.132**
$F_1 x L_{14}$	0.642	-6.681**	0.731**	2.888**
$F_1 x L_{15}$	-2.347**	-8.804**	1.7**	-0.54
$F_1 x L_{16}$	2.553**	9.229**	-0.989**	1.81
$F_1 x L_{17}$	1.564*	15.274**	-1.196**	3.021*

* and ** indicate significant at 0.05 and 0.01 probability levels of probability , respectively.

Table 7. Cont.

Cross		No. of spikes/plant	No. of kernels/spike	100-grain weight (g)	Grain yield/plant (g)
P_2 x L_1		1.631**	-8.753**	0.531**	-0.101
P_2 x L_2		1.298*	-12.809**	0.463*	-4.077**
P_2 x L_3		-0.035	-0.996	0.146	-0.85
P_2 x L_4		1.187*	-16.609**	0.683**	-1.639
P_2 x L_5		-1.046	0.38	-0.241	-4.517**
P_2 x L_6		1.177	-11.525**	0.372	-4.09**
P_2 x L_7		-4.491**	11.219**	0.206	2.133*
P_{21} x L_8		2.176**	1.169	-0.754**	1.263
P_2 x L_9		1.509	-15.901**	0.908**	-2.528*
P_2 x L_{10}		-1.491	13.817**	-0.87**	0.882
P_2 x L_{11}		2.865**	18.625**	-1.003**	4.238**
P_2 x L_{12}		-1.158	3.769	0.066	1.038
P_2 x L_{13}		-1.146	6.869**	-0.402*	-3.984**
P_2 x L_{14}		-2.146**	21.558**	-0.503*	1.639
P_2 x L_{15}		2.865**	6.469*	-0.881**	3.043**
P_2 x L_{16}		-1.069	-10.998**	0.333	-1.706
P_2 x L_{17}		-2.124**	-6.32*	0.95**	1.105
L.S.D	0.05	1.673	4.833	0.379	2.577
	0.01	2.287	6.608	0.519	3.524
L.S.D SCA	0.05	1.182	1.973	0.268	1.822
	0.01	1.616	2.698	0.367	2.492
L.S.D S_{ij}- S_{kj}	0.05	1.673	4.833	0.379	2.577
	0.01	2.287	6.608	0.519	3.524

* and ** indicate significant at 0.05 and 0.01 probability levels of probability, respectively.

specific combining ability involve only one good generate combiner; such combinations would be desirable for transgressive segregates providing that additive genetic system present in the good generate combiner and complementary if epistatic effects present in the crosses act in the same direction to produce undesirable plant characteristics and maximize the character in view. Therefore, most of the previous crosses might be important for traditional breeding procedures.

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تحديد التفاعل غير الآليلي ، وتقدير التباين الوراثي المضيف والسيادي باستخدام تحليل التهجين الثلاثي الاختباري والسلالة × الكشاف في قمح الخبز

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قسم بحوث القمح – معهد بحوث المحاصيل الحقلية – مركز البحوث الزراعية

أجريت هذه الدراسة في محطة البحوث الزراعية بالجيزة في المواسم ٢٠٠٨/٢٠٠٧ ، ٢٠٠٩/٢٠٠٨ أما الموسم الثالث وهو التقييم فقد تم في الموسم ٢٠١٠/٢٠٠٩ بمحطة البحوث الزراعية بكفر الحمام – محافظة الشرقية - مركز البحوث الزراعية. وذلك بغرض اختبار التفاعل غير الآليلي وتقدير كل من الفعل الجيني المضيف والسيادي لصفات عدد السنابل/نبات، عدد الحبوب/سنبلة، وزن مائة حبة ومحصول حبوب النبات الفردي . ولقد استخدم طريقة تحليل الهجن الثلاثي الاختباري طبقاً لطريقة كيرسي وجينكيز (١٩٦٨) وتحليل السلالة × الكشاف باستخدام طريقة كمبثورن (١٩٥٧).

وكانت النتائج المتحصل عليها كما يلي :

١) كانت قيم التباين الوراثي الراجعة إلى كل من التراكيب الوراثية والهجن والآباء والسلالات وكذلك الكشافات عالية المعنوية لجميع الصفات تحت الدراسة.

٢) التفاعل غير الآليلي لعب دوراً هاماً في توارث الصفات تحت الدراسة وكان التفاعل المضيف × المضيف هو المكون الأعظم في وراثة كل الصفات .

٣) لعب الفعل الجيني المضيف والسيادي دوراً هاماً في توارث جميع الصفات تحت الدراسة .

٤) لعبت السيادة الجزئية دور هام في وراثة معظم الصفات تحت الدراسة .

٥) تم اختيار مجموعة من الهجن تحت الدراسة كأفضل مواد وراثية تفوقت في قدرتها الخاصة وهي الهجن جميزة ١٠ في كل من السلالة ١، ٢ ، ٣، ٤، ٥ و٩ والجيل الأول F_1 مع كل من السلالة ٥، ٦ ، ٨، ١٣ ، ١٤ و ١٧ والأب الثاني وهو السلالة المبشرة مع كل من السلالة ٧، ١١ ، ١٥ ويمكن استغلالها في تحسين القدرة المحصولية في برامج تربية القمح .

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