ESTIMATION OF ADDITIVE, DOMINANCE AND DETECTION OF EPISTASIS USING TRIPLE TEST CROSS   AND

LINE × TESTER ANALYSIS IN BREAD WHEAT

H.I. Hendawy
National wheat Res. Prog. Field crops Res. Institute, (ARC) .

ABSTRACT: *The triple test cross progenies were develoved to study the components of genetic variation for seven traits, viz, grain yield / plant, number of days to heading, number of days to maturity, plant height, number of spikes / plant, number of kernels / spike and 100 – grain weight in three wheat crosses to determine the superior parents and hybrid combinations in respect to grain yield / plant and its components throught line xtester analysis. Ninteen bread wheat varieties and or lines were crossed with three testers. Significant epistasis is present for all characters studied. Additive x additive epistatic type of gene action was found to be much larger in magnitudes than additive x dominance and dominance x dominance. (J+L) epistatic types for number of days to maturity, plant height, number of spikes /plant and 100–grain weight. Both additive and dommance genetic components play an important role in the inheritance of number of kernels / spike, 100 – grain weight and grain yield / plant.*

Due to the presence of epistasis for most of the characters studied selection in the later segregation generating would be more effective for the improvement of these characters. The average degree of dominance (H/D)½ resulted partial dominance for all traits studied. Line xtester analysis revealed that the nature of gene effects were predominantly non-additive for all traits studied . Two wheat lines L1 and L7 exhibited significant GCA effects for, number of spikes / plant, number of kernels / spike and grain yield / plant. The three – way superior Crosses (F1 with each L8 and L11 and Gem.9 with L7 and Sakha94 with L4, L5,12 and L17 F1 With L8 and L11 showed the highest SCA effects for grain yield and its contributing characters.

Key words: additive, dominance . epistasis, combining ability, triple test cross, line x tester, Triticum aestivum L.

INTRODUCTION

A study of components of genetic variation would help the breeders in deciding the appropriate breeding method. A good genetic model, in fact, 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, which 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, it was absent for plant height. Nanda et al (1982) indicated the importance of epistasis component in the genetic control of plant height. Epistasis plays a major role in the inheritance of quantitative taits in several crops particalarly in pea (Narsinghani et al 1982). A greater importance of epistasis was also reported in wheat by Eissa (1994) komber (2001) and Hendawy et al (2007).

The objectives of this study are to establish, 1- The existence of epistasis and to determine the additive (D) and dominance (H) variances conditioning quantitive traits using the triple test cross analysis. 2- Estimates of general and specific combining ability using lines x testers analysis.

MATERIALS AND METHODS

The field work of this study was carried out at Sers El – Iaian Agricaltural Research station during three successive seasons 2004 / 2005, 2005 / 2006 and 2006 / 2007.

In the first season, two high yielding wheat cultivars, which showed wide adaptation in winter season and differed in most of there agronomic traits i.e., Gemmeiza. 9 (p1) and Sakha 94 (p2) were crossed to obtain their F1 (Gemmeiza. 9x Sakha 94) and here after used as three tester.

During 2005/2006, winter season each of the three testers p1, p2 and their F1 were crossed to the 19 divergent origin bread wheat cultivars and or lines, the name and pedigree of these genotypes are presented in table (1) to produce 57 crosses. i.e. 19 L1i, 19 L2i and 19 L3i progeny families of a triple test cross design. The cross p1 x p2 was also repeated to get fresh F1 grains. All plant materials, the 57 families (crosses), 19 parents and the three testers, were grown in a randomized complete block design with three replicates in 2006 / 2007, each progeny families were grown in a 3m. long row,. with 30 cm. between rows and plants within rows were 10 cm. All the normal agronomic practices were followed as usual in an ordinary wheat field in the area of study. Random Samples of fifteen guarded plants were chosen at harvest for recording the different seven traits examined i.e. grain yield / plant and six of its attributes.

Table (1) The names and pedigree of the parental genotypes.

Genotype	Pedigree
Lines (L) L1	CHEN / AEGILOPS SQUARROSA (TAUS) // BCN / 3 / VEE # 7 CMSS 93 B 01854 T – 040 Y – 27 Y – 010 M – 010 M – 5 Y – 0 M – 0 S .
L2	C 182–24/C 168. 3/3/CNO/7 C*2// CC/TOB// MYNA"S" VOC "S"/4 / SAKHA 8. CGM 7905 – 3 GM – 2 GM – 1 GM – 0 GM.
L3	PF 70354 / ALD "S" // VEE "S" // CHIL / 2* STAR. CGM – 79/5 – 4 GM – 3 GM – 1 GM – 0 GM.
L4	CHOIX / STAR / 3 / HE 1 / 3* CNO 79 // 2* SERI. CMSS 93 YO 2712 T – 40 Y – 010 Y – 010 M – 010 Y – 6 M – 0 Y ONUB.
L5	SW 89. 5181 / KAUZ. CMSS 93 B 00824 S – 5 Y – 010 M – 010 Y – 010 M – 6 Y – 0 M – 0 SH.
L6	WEAVER / ENAC / TH. AC // 3* PVN / 3 / MIRLO / BUC. CMSS 93/ 3 B 002235 – 24 Y – 010 M– 010 Y– 010 M– 10 Y– 0 M– 0 SD.
L7	MAYON "S" // CROW "S" / VEE "S" ICW 90 – 0382 – 5 AP – 0TS – 0 BR – 2 AP – 0 L – 0 AP – 0 SD.
L8	MAYA"S"/MON"S"/4/CMH 72428/MRC//JUP/3/582/5/A 2 SAKHA 8/6/ SAKHA 69. SD 10157 – 1 SD – 1 SD – 2 SD – 0 SD – 0 S.
L9	HUBARA – 5 ICW 94 – 0329 – 0 L – 3 AP – 2 AP – 2 AP – 0 AP.
L10	(GEMMIZA. 7). CMH 74 A. 630 / 5 X // Seri 82 / 3 Agert. CGM 4611 – 2 GM – 3 GM – 1 GM – 0 GM.
L11	PF 70354 / Ald "S" // Vee "S" // Chil / 2* Star. CGM 7915 – 4 GM – 3 GM – 1 GM – 0 GM.
L12	B1 / Ban / swef 2.
L13	Bloudan / 3 / Bb / 7 c*2 // y 50 E / KaJ 3 / C 182 – 24 / C / 68 – 3 / 3 cno / 7 C*2 // Cc // Tib Sannine "s".
L14	NS 732 / HER // SHI #4414 / CROW "S". ICW 91 – 0182 – OBR – 2 AP – 1 AP – 0 AP.
L15	PARENTS 47 A–4–ISAKHA 61/ Mildress M 073/ P 01// t. aet–Bon / CNO–7C.
L16	VEE "S" / TS 1 // CHM 79. 959 / 2* CNO 79 SD – 2919 – 1 SD – 2 SD – 0 SD.
L17	(Sids. 4). MAYA "S" / Mons // CMH 74 A – 592 / 3 / Giza 157 2 SD 10001 – 2 sd – 3 sd – 2 sd – 0 sd.
L18	SKAUZ 2 / SRIMA CMBW 91 MO 2694 F – OTOPY – 7 M – 010 Y – 010 M – 010 Y – 0 S.
L19	CAZO / KAUZ // KAUZ CMBW 90 Y 3279 – OTOPM – 010 M – 010 Y – 3 M – 0 SH.
Esters (T) T. 1	(Gemmiza . 9) ALD "S" / HUAC // CMH 74 A. 630 / SX CGM 4583 – 5 GM – 1 GM – 0 GM.
T.2	Gem. 9 X Sakh . 94
T.3	(Sakha 94). OPATA / RAYON // KAUZ. CMBW 90 Y 3180 – OTOPM – 3 Y – 010 M – 010 M – 010 Y – 10 M 015 Y – 0 Y – 0 AP – 0 S.

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.

where; $Iijk = m + gij + rk + eijk$.

$Iijk$: Denotes the phenotypic value of the cross between tester Li and J in replication k.

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

Gij: Denotes the genotypic value of the cross between tester Li and line j.

RK: Denotes the effect of replication k.

$Eijk$: Denotes the error associated with the cross ij in replication.

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.

The overall epistasis was partitioned into (I) type of epistasis (additive x additive) and (J and L) types of epistasis i.e. additive x dominance and dominance x dominance; respectively. The estimation of additive (D) and dominance (H) genetic components and the correlation coefficient (r) between sums $L1i + L2i$ and difference $L1i - L2i$ 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 analysis of variance for all traits studied i.e.. are presented in Table (2) Genotypes, hybrids and parents mean square estimates were found to be highly significant for all traits studied except 100 – grain weight, 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 except 100 – grain weight,. Also, the data given in table (2) indicated highly significant mean squares for lines for all traits studied. Tester mean squares were found to be highly significant for grain yield / plant.

Table (2) Mean square from analysis of variance of (L1i,L2i and L3i) triple test cross hybrid and line x tester analysis for all trails studied.

Source of variance	d.f	No. of days to heading	No. of days to maturity	Plant height	No. o spikes/ plant	No. of kernels/ spike	100-grain weight	Grain yield/ plant
Replications	2	** 3.48	** 16.74	** 94.19	** 60.67	** 21.91	0.37	** 18.89
Genotypes	78	** 103.72	** 36.99	** 186.89	** 52.4	** 342.7	0.86	** 480.28
Hybrids	56	** 76.2	** 23.54	** 126.27	** 33.57	** 197.83	0.87	** 418.77
Parent	21	** 174.44	** 73.17	** 271.22	** 88.17	** 745.03	0.84	** 600.96
Hybrids Vs Parent	1	** 158.57	** 30.16	** 1810.58	** 355.47	* 6.79	1.23	** 1391.24
Lines	18	** 188.75	** 80.52	** 252.61	** 93.2	** 857.77	0.91	** 607.67
Testers	2	33.44	36.33	77.78	68.11	** 97.48	0.61	** 546.67
Lines Vs testers	1	** 198.89	** 14.56	** 993.22	** 37.76	** 10.76	0.01	** 588.24
P1 Vs P2	2	** 30.08	** 30.08	** 8.33	** 65.33	** 70.08	0.98	** 183.68
Error	156	4.02	2.2	11.47	1.85	31.76	0.16	60.84
GCA	-	0.25	0.07	0.79	0.09	0.19	0.001	1.64
SCA	-	15.76	4.81	12.3	7.73	49.18	0.191	65.38
GCA/SCA	-	0.02	0.01	0.06	0.01	0.004	5.24	0.03

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

Lines vs testers mean squares were highly significant for all traits except 100 – grain weight. The mean performance of the two parent p1 (Gemmeiza.9) vs p2 (Sahka 94) were significantly different from each other in all traits except, 100 – grain weight. 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 of difference between two parents is not met, the estimates are biased to an unknown extent (kearsy and Jinks 1968, Jinks et al. 1969, Eissa 1994, komber 2006 and Hendawy et al 2007)

The estimates of general (GCA) and specific (SCA) combining ability variance in table (2) revealed that the nature of the gene effects was predominantly non – additive for all traits under investigation.

Analysis of variance for testing the presence of epistasis in the inheritance of all traits studied are presented in Table (3). Significant epistasis was detected for all characters studied. Further, partitioning of epistatic effect revealed that mean square estimates due to additive x additive (I) epistatic type were found to be highly significant for all characters under investigation except for number of kernels / spike, same results were obtained by Esmail (2007) and Hendawy et al (2007).

Table (3) Analysis of variance for testing the presence of epistasis in triple test cross for all traits studied.

Source of variance	on	No. of days to heading	No. of days to maturity	Plant height	No. o spikes/ plant	No. of kernels/ spike	100-grain weight	Grain yield/ plant
Total of epistasis	19	** 384.09	** 164.32	** 163.69	** 769.54	** 801.94	** 5.68	** 1045.07
i- types epistasis	1	** 74.12	** 606.94	** 11060.28	** 173.69	0.02	** 9.04	** 420.4
J+I epistasis	18	** 401.31	** 139.73	** 197.84	** 163.13	** 846.5	** 5.5	** 1079.77
i- types epistasis x block	2	1.18	61.11	35.81	20.22	9.18	2.72	150.57
J+L epistasis x block	36	48.86	15.38	55.08	15.11	201.27	1.31	346.37
Total epistasis x block	38	46.35	17.79	54.07	15.38	191.16	1.38	336.07

* ** Significant 0.05 and 0.01 probability, levels respectively
(I) = additive x additive, (J) = additive x dominance,
(L) = dominance x dominance.

Additive x dominance (J) epistatic type and dominance x dominance (J+L) epistatic type mean square estimates were detected to be highly significant for all traits studied. The additive x additive epistatic type (I) was found to be much larger in magnitudes than additive x dominance (J) and dominance x dominance epistatic type (L) for number of days to maturity, plant height, number of spikes / plant and 100 – grain weight, indicating that fixable components of epistasis were more important than non – fixable one in the inheritance of these traits. In self – fertilized crop like wheat, the fixable component of epistasis could be easily exploited. The presence of epistasis could have important implications, in a breeding programme. Standard hybridization and selection procedures could take advantage of epistasis if it is additive x additive type as in all traits except for number of kernels / spike. These results would ascertain the results prevously obtained from the line x

tester analysis Table (2) A greater importance of epistasis was also reported in wheat by komber (2006), Esmail (2007) and Hendawy et al (2007).

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 (4). The mean square estimates due to sums (L1i + L2i) were found to be highly significant for all traits except for 100 – grain weight. Also, mean square estimates due to differences (L1i – L2i) were also found to be highly significant for all characters under investigation, except 100 – grain weight. These results would, indicate that both additive and dominance genetic components play an important role in the inheritance of all characters studied the results abtained from line X tester analysis as previousely mentioned indicated that non-additive genetic variance was predominant in the inheritance of all traits studied. 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 large magnitude that effect the estimation of both additive and dominance genetic variation obtained from triple test cross. Similar results were obtained by Singh et al (1989) Eissa (1994), Pawar et al (1996), Komber (2001), El–Nahas (2005). and Hendawy et al (2007).

The estimates of additive (D) and dominance (H) components in Table (4). indicated that, both additive and dominance components in of gene effects play an important role in the inheritance of number of kernels / spike, 100 – grain weight and grain yield / plant. The (D) component was significant for number of days to heading, number of days to maturity, plant height and number of spikes / plant. However, the additive components were larger in magnitude than dominance for all traits except number of kernels / spike, 100 – grain weight and grain yield / plant, Consequently, it could be concluded that selection procedures based on accumulation of additive effects would be successful in improving all traits studied. However, to maximize selection advance, procedures which are known to be effective in shifting gene frequency when both additive and non–additive genetic variance are involved would be preferred. The same results were also obtained by Singh (1981), Singh et al (1989), Eissa (1994), Komber (2006), and Hendawy et al. (2007).

The degree of dominance $(H/D)^{1/2}$ was less than unity for number of days to heading, number of days to maturity, plant height and number of spikes/ plant, suggesting the role of partial dominance in the inheritance of these traits and ascertain the fact that in self pollinated crops, most genes are homozyous and the over – dominance is rare. Genetic advance in genetic systems with over – dominance and epistasis are slower than when gene effects are purely additive or paritially dominant. (Wang et al. 2004).

The direction of dominance and types of genes exhibiting dominance were detected by calculating the correlation coefficients between sums (L1i + L2i) and differences (L1i – L2i) (Table 4). If (R) is negative and significant, then increasing type of genes are dominant and vice versa. The correlation coefficients between sums and differences were found to be negative for number of days to heading, plant height and 100 – grain weight, however, the remaining traits showed positive correlation coefficients of sums and differences and both directions were insignificant hence the dominance was ambidirectional.

Table (4) Mean square from analysis of variance for sums, difference and estimates of additive(D), dominance (H) and degree of dominance in triple test cross analyses.

Source of variance	on	No. of days to heading	No. of days to maturity	Plant height	No. o spikes/ plant	No. of kernels/ spike	100-grain weight	Grain yield/ plant
Sums (L1i+L2i)	18	** 116.58	** 32.83	** 232.84	** 76.22	** 331.24	2.05	** 675.57
Error	36	6.03	4.14	24.83	3.851	61.95	0.27	171.34
Difference (L1i+L2i)	-	** 71.45	** 19.92	** 127.63	** 45.71	** 435.04	1.08	** 668.04
Error		6.03	3.76	22.05	2.84	34.21	0.25	136.67
D	-	** 147.4	** 38.25	** 277.35	** 96.49	** 359.04	0.3	** 84.04
H	-	** 87.23	** 21.54	** 140.77	** 57.16	** 534.45	1.06	** 708.49
(H/D)1/2	-	0.77	0.75	0.71	0.77	1.22	1.88	2.090
R.	-	0.05	0.04	0.07	0.14	0.15	0.01	0.19

* ** significant at 0.05 and 0.01 probability levels respectivaly
(R) correlation coefficients between suns (L1i + L2i) and defrerences (L1i – L2i)

Estimaties of general combining ability (GCA) effects of the nineteen parental lines and three testers are presented in table (5). High positive values of GCA effects would be of interest in all traits studied except number of days to heading, number of days to maturity and plant height. High negative value would be preferred from the wheat breeder point of view. Results reveald that the seven lines L10, L11, L12, L13, L15 and Sids. 4 giving significant negative GCA effects for number of days to heading proving to be good combiners for wheat breeding to develop early genotypes, while lines L12, L15 and Sids. 4 exhibited significant negative GCA effects and prove to be good combiners in early heading and early maturity.

Table (5) General combining ability effects of the parental lines and testers for all traits studied.

Parental liens	No. of days to heading	No. of days to maturity	Plant height	No. o spikes/ plant	No. of kernels/ spike	100- grain weight	Grain yield/ plant
Line 1	2.43**	1.16	3.71	1.86**	6.67**	0.06	6.92**
2	-0.35	1.5**	8.71**	1.98**	2.9	0.76**	-1.64
3	6.43**	1.72**	6.15**	-1.43**	7.01**	0.46**	6.56**
4	4.43*	1.5**	-1.29	0.55	0.12	-0.13	-2.5
5	1.32*	1.83**	1.26	1.22**	-3.33	-0.44**	-8.73**
6	-0.01	-0.39	-3.52**	1.34**	-1.11	-0.33**	-12.66**
7	-0.68	0.16	-1.63	1.28**	12.34**	0.12	10.33**
8	6.1**	3.16**	-1.07	-049	-1.22	-0.38**	-0.35
9	-2.79**	0.28	-0.4	1.44**	-5.66**	-0.06	-4.09
10	-4.57**	-0.84	-5.74**	-1.16	-0.55	0.31*	-7.68**
11	-1.57*	-0.84	-5.18**	1.39**	-7.33**	-0.23	8.06**
12	-2.57**	-1.72*	4.82**	2.95**	-0.11	-0.23	-2.35
13	-1.57*	-0.06	6.15**	1.01	-5.88**	-0.08	8.96**
14	0.54**	2.16**	5.04**	-1.80**	-4.44*	-0.05	2.03
15	-5.67**	-3.83**	-1.18*	-1.54**	-1.99	0.37**	-9.24**
16	1.21	-2.5**	-5.51**	-4.23**	-6.77**	0.32*	0.64
17	-5.78**	-3.5**	-2.96**	-2.10**	6.45**	0.11	0.02
18	-0.78	-0.73**	-5.18**	-4.42**	-0.22	-0.11	4.9
19	3.88**	0.94	-2.18**	2.17**	3.12	-0.47**	0.78
Testers							
T 1	1.54**	1.0**	-1.01	-1.07**	0.57	0.23**	-7.42**
T 2	0.38	-1.09**	4.64**	-0.58**	-0.01	-0.13*	-0.91
T 3	-1.92**	0.09	-3.64**	1.65**	-0.57	-0.09	8.33**
lines L.S.D							
0.05	1.32	0.99	2.24	0.9	3.72	0.26	5.15
0.01	1.74	1.29	2.95	1.18	4.9	0.34	6.79
Testers L.S.D							
0.05	0.52	0.39	0.89	0.36	1.48	0.10	2.05
0.01	0.69	0.51	0.17	0.47	1.95	0.14	2.7

T1 = G.9   T2 = G.9 × S.94   T3 = S. 94

*   **   Significant at 0.05 and 0.01 level of probability, respectively.

Nine parental lines showed significant negative GCA effect. Nine parental lines exhibited highly significant positive GCA effects for number of spikes / plant proving to be good combiners for this traits. L1, L3, L7 and sids. 4 (L17) giving highly significant positive GCA effect for number of kernels / spike four parental lines showed to be good combiners for 100 – grain weight. Five wheat lines L1, L3, L7, L11 and L13 were good general combiners for grain yield / plant. The tester cultivar exhibited highly significant positive GCA effects for 100–grain weight, while the cultivar Sakha 94 exhibited significant one for number of days to heading (Hamada et al, 2002).

Estimates of specific combining ability effects SCA of the fifty seven crosses for all traits studied are presented in Table (6). Significant negative SCA effects were obtained in eleven crosses for number of days to heading and seven crosses for number of days to maturity, while seven crosses for

plant height. Significant positive SCA effects were observed in ten crosses for number of spikes / plant, for number of kernels /spike. Meanwhile, eight hybrid combinations studied showed significant desirable SCA effects. For 100 – grain weight, six crosses exhibited significant desirable SCA effects. For grain yield/plant, six hybrid combinations showed significant SCA effects. If crosses showed high specific combining ability involve only one good combiner such combinations would throw out desirable transgressive segregates providing that the additive genetic system present in the good combiner and complementary of epistatic effects present in the crosses act in the same direction to produce undesirable plant characteristies and maximize the character in view. Therefore, the most previous crosses might be important in breeding program for traditional breeding procedures.

Table (6) Specific combining ability effects of different crosses for all traits studied.

hybrids	No. of days to heading	No. of days to maturity	Plant height	No. o spikes/ plant	No. of kernels/ spike	100-grain weight	Grain yield/ plant
Gem.9(P1)X							
L1	-3.21**	-2.44**	1.78	3.24**	7.54*	0.95**	4.82
L2	3.29**	2.64**	2.80	-1.89*	-5.55	-0.69**	1.67
L3	-0.08	-0.2	-4.59**	-1.35	-1.99	-0.26	-6.69
L4	-0.76	-2.78**	-0.22	-1.02	3.98	0.32	-3.32
L5	-1.6	-0.02	-3.53	1.93*	-3.44	-0.32	-2.84
L6	2.36*	2.8**	3.74	-0.91	-0.54	0.01	6.16
L7	-1.87	-1.33	-5.66**	-0.31	-0.13	-0.52*	14.25**
L8	2.95*	3.09**	4.36*	-4.53**	0.12	0.51*	-3.07
L9	-1.08	-1.75*	1.3	4.84**	0.01	0.01	-11.17**
L10	1.13	-1.78*	0.78	3.51**	-0.24	-0.06	-9.19*
L11	4.95**	2.31**	-3.87*	-0.51	-4.99	0.27	4.26
L12	-6.08**	-0.53	3.08	-3.01**	5.23	-0.21	4.93
L13	-5.76**	-2.44**	4.23*	-0.79	7.21*	0.53*	4.00
L14	2.73*	1.98*	-1.42	1.93*	-2.22	0.29	7.92
L15	3.03**	0.47	-2.81	-1.14	-4.99	-0.82**	-11.92**
L16	-1.09	-0.56	0.01	-2.71**	-8.02*	0.18	-8.67*
L17	0.73	2.53**	-0.31	-0.03	3.89	-0.46*	7.95
L18	0.36	-198*	0.30	2.47**	4.12	0.27	0.72
L19	0.91	-1.11	-0.78	-0.82	-3.8	-0.07	-10.92*

Table (6) Con.

	No. of days to heading	No. of days to maturity	Plant height	No. o spikes/ plant	No. of kernels/ spike	100-grain weight	Grain yield/ plant
F1(skh.94)X (Gem.9)X L1	-5.27**	0.64	-4.87*	0.36	16.12**	0.56*	7.63
L2	4.36**	0.47	4.08*	0.46	-12.32**	-0.48*	3.29
L3	2.8*	1.22	0.23	-3.04**	6.09	0.40	8.09

L4	-0.71	0.31	-1.42	-1.86*	-6.66*	-0.18	-9.33*
L5	-2.08	-1.53	1.19	4.9**	0.57	-0.22	1.24
L6	1.02	0.78	2.23	4.03**	-2.13	0.17	-9.03*
L7	0.18	-2.14*	-0.09	-2.99**	-3.22	-0.23	-2.89
L8	-1.19	1.36	-2.14	-1.03	5.35	0.06	11.92**
L9	2.46*	-0.11	-1.11	-1.54	-8.91**	-0.03	-7.08
L10	-0.38	-0.36	-1.09	-0.66	5.34	-0.6**	-5.16
L11	-2.08	0.47	2.19	2.2**	3.56	0.63**	12.24**
L12	1.13	0.56	-0.99	1.4	10.87**	-0.49*	0.61
L13	-2.71*	-0.36	1.36	1.08	1.22	0.13	-6.47
L14	1.59	-0.2	-0.36	-2.49**	-9.66**	0.36	5.86
L15	3.46**	-0.56	-2.66	-1.15	-4.35	0.07	-13.21**
L16	-2.38*	-0.8	1.69	0.03	6.9*	-0.23	8.17
L17	-1.08	1.36	0.97	1.13	-2.54	0.16	5.04
L18	-1.21	-1.56	-7.33**	-0.21	6.42	0.06	5.55
L19	-3.71**	1.53	0.36	3.64**	-2.33	-0.28	4.56
SKh.94 X L1	4.92**	0.02	6.97**	-3.43**	-4.1	0.22	-10.11*
L2	-1.98	0.22	-1.55	1.1	4.65	-0.17	-1.39
L3	8.18**	-0.02	4.14*	-2.72**	0.56	-0.01	-9.77*
L4	-6.19**	-0.20	-2.59	1.62*	-5.21	0.18	11.16*
L5	-4.09**	1.56	-4.33*	-0.1	-6.13	0.27	11.31*
L6	0.4	-0.69	4.36*	-2.49**	-1.55	-0.33	-5.51
L7	3.7**	-0.87	-0.03	2.58**	7.67*	0.06	-5.81
L8	-1.32	6.56**	-1.33	-1.51	-10.02**	-0.11	1.43
L9	4.18**	-6.69**	0.02	4.87**	4.89	-0.08	-4.75
L10	-2.86*	0.14	1.30	-3.36**	5.12	0.18	3.32
L11	7.35**	0.89	-2.45	0.4	-10.91**	-0.83**	-2.08
L12	-6.16**	-1.69*	-0.53	-0.92	-3.66	0.93**	9.34*
L13	-1.19	0.8	-1.92	0.52	14.57**	-0.11	-7.26
L14	2.02	0.78	7.34**	-0.79	9.09**	0.64**	3.53
L15	-5.83**	-.014	0.69	2.63**	-5.66	0.76**	1.02
L16	3.81**	0.64	-8.03**	-1.84*	-3.43	-0.12	-4.55
L17	-0.98	2.11*	5.34**	0.29	-1.24	-0.05	11.29
L18	1.18	-2.14*	-2.64	2.14**	2.67	-0.02	-2.93
L19	-0.19	0.02	-2.7	-2.43**	-1.43	0.07	-8.36*
L.S.D 0.05	2.29	1.69	3.87	1.55	6.44	0.45	8.19
0.01	3.02	2.23	5.11	2.05	8.49	0.59	11.75

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

REFERENCES

Comstock, R.E. and H.F. Robinson (1952). Estimation of average dominance of genes. Eowa State College Press, Ames, Eowa. Chapter. 30

Eissa, M. M., (1994). Triple test cross analysis in bread wheat (Triticum aestivum L.) Zagazig J. Agric. Res., 21:1–10

El – Nahas, M. M. (2005) Triple test cross analysis of some quantitative characters in bread wheat (Triticum aestivum L.) MSc Faculty of Agric. Minufiya Univ. Egypt.

Esmail, R. M. (2007). Detection of genetic components through triple test cross and line x tester analysis in bread wheat. World J. Agric. Sci., 3 (2) : 184 – 190.

Hamada, A. A.; E. H. El-seidy and H. 1. Hendawy (2002). Breeding measurements for heading date, yield and yield components in wheat using line x tester analysis. Annals Agric. Sci. Ain shams univ., 47 (2), 587 – 609.

Hendawy, F.A, H.A. Dawwan and M.M. El-Nahass (2007). The detection of the different components of variation in bread wheat (Triticum aestivum L.) Minufiya J.Agric. Res., 19 (1):2315-2338.

Jink, J. l., J.M. Perkins and E.L. Brease, (1969). Ageneral method of detecting additive, dominance and epistatic variation for metrical traits : II, Application to inbred lines, Heredity, 25 : 45 – 57.

Jinks, J. L. and J. M. Perkins. (1970). A general method for the detection of additive, dominance and epistatic components of variation. Heredity, 25 : 419 – 429.

Kearsey, M. J. and J. L. Jinks (1968). A general method detecting additive, dominance and epistasis variation for metrical traits. Heredity, 23 : 403 – 409.

Kempthorne, O. (1957). An Introduction to Genetic Statistics, pp. 475 – 491. John wiley and Sons. New Youk.

Ketata, H., E. L. Smith; L. H. Edwards and R. W. McNew, (1976). Detection of epistatic, additive and dominance variation in winter wheat (Triticum aestivum L.). Crop Sei., 16 : 1 – 4.

Komber, R. M. A. (2006) Detection of epistasis and estimation of additive and dominance components of genetic variation using triple cross analysis in bread wheat. Egypt, J. of Appl. Sci., 21 : 448 – 461.

Komber, R. M., (2001). Estimation of the different components of genetic variance of some quantitative traits in bread wheat, Ph. D. Thesis, Faculty of Agric. Minufiya univ. Egypt.

Nanda, G.S.;P Singh and K.S.Gill(1982) Epistasis. additive and dominance variation in triple test cross of bread wheat Triticum aestivum L.j Indian Theoretical and Applied Genet., b2(1): 49-52.

Narsinghani, V. G., V. S. N. Rao and S. P. Singh (1982). Diallel analysis for quantitative traits in mutant pea. Indian J. Agric. Sci., 52:364 – 367.

Pawar, I. S.; M. Yunus and v. p. Singh (1996). Study of interaction of additive, dominance and epistasis gene effects with environment in wheat. Haryaina. Agric. Univ. J. of Res., 26 (1) : 17 – 21.

Singh, I., I. S. Pawar and S. Singh (1989). Detection of genotype x environment interaction in spring wheat through triple test cross analysis. Crop Improve., 16 : 34 – 37.

Singh, R. K and B. D. Chaudhary (1985). Biometrical Methods in Quantitative Gentic Analysis, Revised Edition. Kalyani Publishers. New Delhi – Ludhiana. India.

Singh, S. and R. B. Singh (1978). Triple test cross analysis in first backcross populations of four wheat crosses. J. Agric. Sci., Camb. 91 : 505 – 508.

Singh, S., (1981). Single tester triple test cross analysis in spring wheat Theo, and Applied Genet., 59 : 247 – 249.

Wang, J.; M. Ginkel, R. Trethowani, G. Ye., I. Delacy., D. Podlich and Coper, (2004). Simulating the effects of dominance and epistasis on selection response in the CYMMYT wheat breeding program using Qu Cim Crop Sci.; 44 : 2006 – 2018.

تقدير التباين الوراثى المضيف والسيادى وتحديد التفاعل الغير اليلى باستخدام تحليل التربل تست كروس والسلالة فى كشاف فى قمح الخير

حمدى إبراهيم هنداوى

البرنامج القومى لبحوث القمح – معهد بحوث المحاصيل الحقلية – مركز البحوث الزراعية

الملخص العربى

أجريت هذه الدراسة فى محطة البحوث الزراعية بالجميزة فى المواسم ٢٠٠٤ / ٢٠٠٥ و ٢٠٠٥ / ٢٠٠٦ و ٢٠٠٦ / ٢٠٠٧ وذلك بغرض اختبار التفاعل غير الليلى واختبار وتقدير كل من الفعل الجينى المضيف والسيادى لصفات عدد الايام من الزراعة حتى طرد السنابل وعدد الايام من الزراعة حتى النضج الفسيولوجى طول النبات وعدد السنابل بالنبات وعدد الحبوب بالسنبلة ووزن ١٠٠ حبة ومحصول النبات الفردى ولقد استخدم لهذا الغرض طريقة تحليل التربل تست كروس طبقا لطريقة كيرسى وجنكنز (١٩٦٨) وتحليل السلالة × كشاف باستخدام طريقة كمبثورن (١٩٥٧).

وكانت النتائج المتحصل عليها كما يلى :–

١– كانت قيم التباين الوراثى الراجعة الى كل من التراكيب الوراثين والهجن والاباء والسلالات وكذلك الكشافات عالية المعنوية لجميع الصفات تحت الدراسة فيما عدا صفة وزن١٠٠حبه

٢– التفاعل الغير اليلى لعب دورا هاما فى توارث الصفات تحت الدراسة وكان التفاعل المضيف × مضيف هو المكون الاعظم فى وراثة كل الصفات ما عدا عدد الايام من الزراعة حتى طرد السنابل وعدد الحبوب بالسنبلة ومحصول النبات الفردى.

٣– لعب الفعل الجينى المضيف والسيادى دورا هاما فى توارث صفات عدد الحبوب بالسنبلة ووزن ١٠٠ حبة ومحصول النبات الفردى.

٤– لعبت السيادة الجزئية دور هام فى وراثة جميع الصفات تحت الدراسة.

٥– تم اختيار مجموعة من الهجن تحت الدراسة كأفضل مواد وراثية تفوقت فى قدرتها الخاصة وهى الهجن جميزة ٩ فى السلالة ٧ وسخا ٩٤ مع كل من السلالة ٤ ، ٥ ، ١٢، والصنف سدس ٤ والجيل الأول مع السلالة ٨، ١١ يمكن استغلالها فى تحسين القدرة المحصولية فى برامج تربية القمح.