

**DETECTING EPISTASIS, GENETIC CORRELATIONS
AND NEW RECOMBINANT LINES FOR GRAIN
YIELD AND ITS COMPONENTS IN BREAD
WHEAT (*Triticum aestivum* L.) USING
TRIPLE TEST CROSS ANALYSIS**

Salama, S.M.

**Central Lab. for Design and Statistical Anal. Res., A.R.C.,
Giza, Egypt**

Accepted 6/ 8/2007

ABSTRACT: In two crosses of bread wheat (Sakha 93 x Gemmeiza 7 and Giza 168 x Gemmeiza 9) triple test cross analysis was applied to study gene action, genetic correlations and predicating of new recombinant lines for days to heading, plant height, flag leaf area, number of spikes/plant, number of grains/spike, 1000-grain weight, spike grain weight and grain yield /plant. Results revealed that epistatic gene effects played an important role in the genetic system for the studied characters for the two crosses. The types of epistasis (additive x additive, additive x dominance and dominance x dominance) were significant for all studied characters. Both additive and dominance genetic components were significant and involved in the genetic system for most characters in both crosses. The average degree of dominance was in the range of overdominance for number of spikes/plant in the first cross and spike grain weight for the second cross. While for the remaining characters, additive gene effects were more pronounced. The (F) value was positive and significant for 1000-grain weight in two crosses, suggesting that dominant genes controlled these characters were unidirectional. The highest proportion of inbreds exceeded to outperform parental range in cross 1 for days to heading and flag leaf area. Epistasis, additive and dominance genetic correlations indicated that positive and significant epistasis, additive and dominance genetic correlation were obtained between grain yield/plant with number of spikes/plant, number of grains/spike and 1000 grain weight in both crosses.

Key words: Wheat, additive dominance, epistasis, genetic correlation.

INTRODUCTION

Choice of the most efficient breeding methodology mainly depend upon the type of gene action controlling the genetic variation. Therefore, unambiguous tests of the genetic components help the breeder for rightful decision making about the most effective breeding method to be applied. The knowledge of genetic correlation which occurs between characters helps the breeder to improve the efficiency of selection by using favourable combination of characters and to minimize the retarding effect of negative correlations. The triple test cross analysis (Kearsey and Jinks, 1968) the unique design providing unambiguous test for epistasis, detect and estimates the additive and dominance genetic components. Using triple test cross analysis of wheat by Ketata *et al.* (1976), Singh and Singh (1976) indicated the importance of additive, dominance and epistasis gene effects in the inheritance of yield and its components in wheat. The results of Nanda *et al.* (1983), Iqbal Singh *et al.* (1989), Eissa (1994 a, b and c) reported significant epistasis for grain weight/spike and grain yield/plant. The epistasis was mainly due to

additive x additive type of epistasis for these characters. Triple test cross analysis in wheat was used by Singh 1989, Katiyar and Ziauddin (1996). They indicated that additive and dominance gene effects played the great role in the inheritance of grain yield/plant. The genetic correlations between yield and yield attributes were reported by Eissa (1994 c); Al-Kaddoussi (1996) and Salama *et al.* (2006). They indicated the presence of genetic correlation between grain yield / plant and 1000-grain weight in wheat.

MATERIALS AND METHODS

The present investigation was carried out at Tag El-Ezz Research Station, Agriculture Research Center during four successive winter seasons, from 2003 to 2007. The starting materials for triple test cross was the F_1 and their grand parents (P_1 and P_2) the two studied wheat crosses. The first cross Sakha 93 x Gemmeiza 7 and the second cross was Giza 168 x Gemmeiza 9. The F_1 's were selfed to produce F_2 's grains. The obtained materials (F_1 's grains and F_2 's grains) together with the parental genotypes were sown to produce F_1 's and F_2 's plants. Thirty

individual F_2 plants were randomly labeled from each cross and crossed back to their grand parents (P_1 and P_2) and F_1 between them to produce three types of families L_1 ($F_{2i} \times P_{1i}$), L_2 ($F_{2i} \times P_{2i}$) and L_3 ($F_{2i} \times F_{1i}$) in each cross. The triple test cross families (L_1 , L_2 and L_3) together with parents, F_1 and F_2 in each cross were sown on 10th November 2006 using a randomized complete block design with three replications. Row length was 3m with 20 cm apart. Plant to plant spacing was 10 cm. Data were recorded on ten arandomand competitive plants from each family in each replication for days to heading (day), plant height (cm) flag leaf area (cm)², number of spikes/plant, number of grains/spike, 1000-grain weight (g.), spike grain weight (g.) and grain yield / plant (g.).

Biometrical Analysis

Before proceeding to the biometrical analysis the obtained data were statistically analysed using the conventional two way analysis of variance. The triple test cross analysis was carried out according to Kearsey and Jinks, (1968) and Jinks and Perkins, (1970). Before proceeding to biometrical analysis the analysis of variance for (L_1 , L_2 , L_3) as well as (L_1 , L_2) types of families was

carried out separately to obtain the error variance for testing epistasis, additive and dominance gene effects.

Test for epistasis

For test of epistasis thirty values of ($L_{1i} + L_{2i} - 2L_{3i}$), $I=1$ to 30 with 30 degrees of freedom was used to test for overall epistasis. The item epistasis was partitioned into an item by one degree of freedom, testing for J and L types of epistasis (dominance x dominance and additive x dominance).

Detecting additive genetic variation

The variance component of ($L_{1i} + L_{2i} + L_{3i}$) is used to detect and estimate the presence of additive component variance.

Detecting North Carolina Design (N.C.N) additive"

The variance component of ($L_{1i} + L_{2i}$) is employed to detect the additive genetic components according to Comstock and Robinson (1952).

Detecting dominance variation

The variance component of ($L_{1i}-L_{2i}$) is used to test for the presence of dominance variance.

Estimation of the genetic components of variation

The estimation of D and H components were obtained

according to Jinks and Perkins (1970). The direction of dominance (F) was completed from the covariance of sums ($L_{1i} + L_{2i}$) / differences ($L_{1i} - L_{2i}$) which equal to $-1/8 F$. The correlation coefficient of sums/differences was used to test the significance of "F" value (Jinks *et al.*, 1969).

Predicting the properties of recombinant lines

The method were applied according (Jinks and Pooni 1976), Pooni and Jinks (1978), Toledo *et al.* (1984) and Hayward *et al.* (1993).

Genetic correlations

The means of triple test cross families in each character were computed and used to calculate the following simple genetic correlations, epistatic ($L_{1i} + L_{2i} - 2L_{3i}$), dominance ($L_{1i} - L_{2i}$) and additive ($L_{1i} + L_{2i} + L_{3i}$). [(Kearsey and Jinks, (1968) and Kearsey *et al.*, (1987)].

RESULTS AND DISCUSSION

Mean squares of the analysis of variance Table 1 revealed significant different between families in terms of all characters for the two wheat crosses. These results might be suggested that L_{1i} , L_{2i} and L_{3i} triple test cross families were

significantly different from each other, revealing presence of fair amount of genetic variability which could be assessed by means of triple test cross analysis.

Test for epistasis

Mean squares for epistasis Table 2 provide evidence for significant overall epistasis for all studied characters in two crosses. In this respect similar results were reported by Nanda *et al.* (1983) and Iqbal, Singh *et al.* (1989). When the overall epistasis was partitioned to I type additive x additive, additive x dominance, and dominance x dominance (J + L) type, results indicated significance, of both types for all studied characters. The important role of (I) type epistasis was much larger in magnitude than the (I) and (L) type for most studied characters, revealing the important role of (I) type (additive x additive) in the genetic control of these characters. Standard hybridization and selection procedures could take advantage of epistasis if this additive type are present. Therefore, selection in early segregating generation would be effective to improve these characters. In this respect (Eissa 1994, and Iqbal Singh *et al.*, 1989) found similar results. The type of epistasis (J + L) are not fixable by

Table 1. Mean squares of the analysis of variance (L_1 , L_2 and L_3) and (L_1 and L_2) sets of triple test cross families for the studied characters in two Egyptian wheat crosses

Characters	Days to heading (day)		Plant height (cm)		Flag Leaf area (cm) ²		Number of spikes/plant		Number of grains/spike		1000-grain weight (g.)		Spike grain weight (g.)		Grain yield/plant (g.m)		
	Cross		Cross		Cross		Cross		Cross		Cross		Cross		Cross		
	D.F	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Between (L_{11} , L_{21} , L_{31}) within families	89	** 12.360	** 11.710	** 16.856	** 15.340	** 8.651	** 12.364	** 1.324	* 2.007	** 9.631	** 8.540	** 11.643	** 12.165	** 0.210	** 0.199	7.520	5.361
Within families replicates	2430	0.210	0.302	0.641	0.422	0.350	0.614	0.162	0.148	0.530	0.401	0.652	0.831	0.010	0.014	0.641	0.512
Between (L_{11} , L_{21}) Families	59	** 9.62	** 9.841	** 14.693	** 9.918	** 9.932	** 13.264	** 1.531	** 1.482	** 9.911	** 7.562	** 6.754	** 8.936	** 0.231	** 0.179	8.174	7.533
Within Families within replicates	1620	0.221	0.340	0.710	0.653	0.412	0.963	0.113	0.207	0.478	0.602	0.690	0.708	0.013	0.012	0.591	0.793

selection and would hence not favourable for developing pure line cultivars. Therefore, population improvement through pedigree method might given a good response (Jensen, 1970).

Detection and estimation of additive, dominance, and genetic components

Analysis of variance for sums $L_1 + L_2 + L_3$ and $L_1 - L_2$ Table 3 indicated that the additive genetic variances were significant for all studied characters in two methods of estimates geneaction of additive. The analysis of variance for differences ($L_{1i} - L_{2i}$) Table 3 indicated that the dominance genetic variance was significant for all studied characters. These results provide evidence for the presence of additive and dominance genetic system controlling the studied characters in these crosses. Similar results were obtained by Singh and Singh (1976), Eissa (1994 a), Al-Kaddoussi (1996) and Salama *et al* (2006).

The estimates of additive (D), dominance (H) and direction of dominance (F) shown in Table 4, indicated that the magnitude of the dominance components were larger than the corresponding

additive one for number of spikes/plant (1st cross) and 1000-grain weight for both crosses resulting in $(H_1/D)^{0.5}$ more than one and confirming the role of overdominance gene effects in the genetic control for these characters, whereas, the remaining characters, the additive gene effects was found characters the additive gene effects was found to be the predominant type similar to these found by (Eissa 1994a and Salama *et al.*, 2006).

The (F) value were positive and significant for 1000-grain weight in both crosses, explaining that dominance seemed to be acting in one direction. The remaining characters possessed dominance was ambidirectional, the F value was insignificant.

Predicting the properties of new recombinant lines

The aim of many selfing programmes is to produce recombinant inbred lines to be used directly or in producing F_1 hybrid or multiple cross hybrid. Such inbreds can be extracted by breeding methods. All these methods are slow and labour. To overcome these problems predicting can be made from observations made on the early generations. Prediction results

Table 4. Estimates of additive (D) dominance (H) and direction of dominance (F) in two wheat crosses for the studied characters

Char.	Days to heading (day)		Plant height (cm)		Flag Leaf area (cm) ²		Number of spikes/plant		Number of grains/spike		1000-grain weight		Spike grain weight (g.)		Grain yield /plant (g.)	
	Cross		Cross		Cross		Cross		Cross		Cross		Cross		Cross	
Param.	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
D	2.404	2.189	3.362	3.184	1.658	1.937	0.224	0.422	1.837	1.579	2.279	2.314	0.043	0.039	1.218	0.930
H	2.138	1.229	2.512	1.668	1.242	1.308	0.271	0.289	1.671	1.016	1.727	1.695	0.039	0.048	0.984	0.893
(H/D) ^{0.5}	0.943	0.749	0.864	0.723	0.865	0.821	1.100	0.828	0.953	0.802	0.870	0.732	0.952	1.109	0.899	0.980
F	**	**	**	**							*	**				
r.sums/differences	-165.231	-191.92	-144.31	-190.32	163.61	149.82	96.532	85.717	53.506	163.615	151.933	140.657	0.301	0.226	5.824	6.697
	0.430	0.752	-0.808	-0.971	0.162	0.2263	0.141	-0.012	0.002	-0.079	0.386	0.651	0.039	0.057	-0.039	0.177

given in Table 5 revealed that it could be feasible to predict as early as possible for transgressive segregants which outperform parental range for days to heading and flag leaf area in cross 1, expect to throw reasonable proportion of recombinant lines that outperform parental range. In this respect Eissa and Awaad (1993) and Al-Kaddussi (1997). The highest proportion of recombinant lines in cross 2 were obtained for grain yield / plant (46.812).

Genetic correlation

Separation out the genetic correlation to its components of epistasis, additive, and dominance were computed for all studied characters. Epistasis (rE) genetic correlation Table 6 indicated that positive and significant correlation between flag leaf area with number of grains / spike, 1000-grain weight and grain yield/plant on the other hand were found in cross 1; Flag leaf area and 1000 grain weight in cross 2, and between number of grains/spike and grain and grain yield/plant for both crosses, between number of grains/spike with spike grain weight and grain yield / plant for both crosses. At the same time, between 1000-grain weight and grain yield / plant for both crosses

and between spike grain weight and grain yield/plant for cross 2.

Additive (rA) genetic correlation Table 7 revealed that the additive genes effects of flag leaf area were significantly correlated with those controlled 1000-grain weight in both crosses; number of spikes / plant with grain yield/plant for both crosses; 1000-grain weight and for spike grain weight and grain yield/plant in both crosses, between spike grain weight and grain yield/plant in both crosses.

The dominance (rD) genetic correlation Table 8 indicated that positive and significant correlation between dominance genes controlling 1000-grain weight with spike grain weight in cross 2 and between grain yield/plant with those of flag leaf for cross 2; number of spikes / plant, number of grains/spike, 1000-grain weight for both crosses and grain yield/plant in cross 1. Results of genetic correlation, generally, revealed the presence of significant additive and dominance genetic correlations for yield and its contributing characters. These result is expected, since yield is the and product of its components characters. Such genetic correlation may be due to a common genetic control,

Table 5. Predicting of range of inberd lines and the proportion of inberds expected to fall outside their parental range for studied characters

Characters	Cross No.	L ₃ (m)	(L ₁ -L ₂) (d)	(L ₁ +L ₂ +L ₃) (D)	Range of inberds		Probability $\frac{(d) D}{d\sqrt{D}}$	P max $m+h\sqrt{H/D}$	2 nd cycle of F ₁ -F ₂ $\sqrt{\frac{1}{2} D + \frac{1}{4} H}$	Proportion of inberds falling outside parental range%
					$m \pm 2 \sqrt{D}$					
Days to heading (day)	1	98.662	-3.616	2.404	101.762	95.561	2.333	111.371	2.748	99.03
	2	94.523	-4.512	2.189	97.481	91.565	3.051	133.227	4.127	11.442
Plant height (cm)	1	96.651	-5.502	3.363	106.319	92.983	3.001	121.728	1.087	13.499
	2	91.388	-5.383	3.184	94.956	87.82	3.017	137.412	2.599	13.062
Flage leaf area (cm) ²	1	44.293	-2.110	1.658	46.869	41.717	1.638	54.977	2.495	51.55
	2	38.951	1.718	1.937	41.733	36.169	1.235	50.382	2.507	10.935
Number of spikes/plant	1	7.813	0.261	0.224	8.759	6.867	0.551	8.033	1.209	29.116
	2	8.291	0.314	0.422	9.590	6.991	0.483	11.487	1.430	31.561
Number of grains/spike	1	52.323	1.253	1.837	55.025	49.621	0.927	61.012	5.086	17.879
	2	49.141	2.748	1.579	51.655	46.627	2.186	71.138	7.783	14.629
1000-grain weight (g.)	1	42.530	0.763	2.279	45.556	39.510	0.505	51.888	5.581	30.854
	2	40.515	1.239	2.314	43.557	37.473	0.814	57.346	6.000	20.897
Spike grain weight (g.)	1	2.293	-0.042	0.043	2.707	1.879	0.203	2.777	2.893	42.074
	2	2.268	0.110	0.039	2.662	1.874	0.558	2.606	1.926	29.116
Grain yield/plant (g.)	1	17.533	0.417	1.218	19.741	15.325	0.378	20.864	3.734	35.569
	2	16.558	0.083	0.930	18.487	14.63	0.086	17.742	3.421	46.812

Table 6. Epistatic (rE) genetic correlation ($L_1 + L_2 - 2L_3$) of the two studied Egyptian wheat crosses for the studied characters

Characters	Cross	Dayes to heading (day)	Plant height (cm)	Flag leaf area (Cm ²)	Number of spikes/plant	Number of grains/spike	1000-grain weight (g.)	Spike grain weight (g.)	Grain yield/plant (g.)
		1	2	3	4	5	6	7	8
(1)	1	-	-0.231	-0.361	-0.341	-0.406*	-0.465*	-0.095	-0.221
	2	-	-0.322	-0.422*	-0.223	0.061	-0.651**	-0.022	0.013
(2)	1	-	-	-0.011	-0.036	0.252	0.267	-0.205	0.401*
	2	-	-	-0.023	-0.314	0.172	0.319	0.007	0.253
(3)	1	-	-	-	-0.001	0.426*	0.718**	0.064	0.506**
	2	-	-	-	-0.152	0.359	0.506**	0.005	0.314
(4)	1	-	-	-	-	-0.161	-0.314	-0.209	0.491**
	2	-	-	-	-	-0.265	-0.097	-0.311	0.652**
(5)	1	-	-	-	-	-	-0.651**	0.427*	0.391*
	2	-	-	-	-	-	-0.301	0.415*	0.474*
(6)	1	-	-	-	-	-	-	0.208	0.506**
	2	-	-	-	-	-	-	0.301	0.771**
(7)	1	-	-	-	-	-	-	-	-0.301
	2	-	-	-	-	-	-	-	0.453**
(8)	1	-	-	-	-	-	-	-	-
	2	-	-	-	-	-	-	-	-

Table 8. Dominance (rD) genetic correlation ($L_1 - L_2$) of the two studied Egyptian wheat crosses for the studied characters

Characters	Dayes to heading (day)		Plant height (cm)	Flag leaf area (Cm ²)	Number of spikes/plant	Number of grains/spike	1000-grain weight (g.)	Spike grain weight (g.)	Grain yield/plant (g.)
	Cross	1	2	3	4	5	6	7	8
(1)	1	-	-0.202	-0.212	-0.152	0.141	-0.075	-0.082	-0.141
	2	-	-0.010	-0.310	-0.161	0.389*	-0.011	-0.082	-0.280
(2)	1		-	-0.151	-0.362	0.516**	0.016	0.151	0.306
	2		-	-0.071	-0.216	0.051	0.175	0.260	0.208
(3)	1			-	0.361	0.481**	0.036	0.052	0.462*
	2			-	0.265	0.562**	0.026	0.033	0.582*
(4)	1				-	-0.262	-0.214	-0.252	0.421*
	2				-	-0.516**	-0.142	-0.307	0.651**
(5)	1					-	-0.388*	-0.262	0.517**
	2					-	-0.517**	-0.361	0.814**
(6)	1						-	0.481**	0.461*
	2						-	0.211	0.716**
(7)	1							-	0.262
	2							-	0.311
(8)	1								-
	2								-

pleiotropy or linkage. Thus, improving efficiency of indirect selection which could be applied to improve yield in wheat.

REFERENCES

- Al-Kaddoussi A.R. 1996. Using genetic components for predicting new recombinant lines in some crosses of Egyptian wheat (*Triticum aestivum* L.). Zagazig J. Agric. Res. 23 : 463-475.
- Al-Kaddoussi A.R. 1997. Testing for epistasis, prediction and genetic correlation using North Carolina Design III biometrical approach for Egyptian bread wheat (*Triticum aestivum* L.). Zagazig J. Agric. Res. 24:37-50.
- Comstock R.F. and H.F. Robinson. 1952: Estimation of average dominance of genes. Heterosis, Chap. 30. Iowa State College Press.
- Eissa, M.M. 1994 a. Triple test cross analysis in bread wheat (*Triticum aestivum* L.). Zagazig J. Agric. Res. 21:1-10.
- Eissa, M.M. 1994 b. Detecting epistasis for yield and its components in wheat using triple test cross analysis (*Triticum aestivum* L.). Zagazig J. Agric. Res. 21:11-20.
- Eissa, M.M. 1994 c. Genetic correlation and predicting new recombinant lines in bread wheat using triple test cross analysis, Zagazig J. Agric. Res. 21:12-31.
- Eissa, M.M. and H.A. Awaad. 1993. Predicting of new generation of ten wheat crosses (*Triticum aestivum* L.). Zagazig J. Agric. Res. 20:1683-1693.
- Hayward, M.D.; N.O, Bosemark and Romagosa. 1993. Plant Breeding. Principles and Prospects. 1st ed. Chapman and Hall. London.
- Iqbal Singh, I.S.; S. Pawar and S. Singh. 1989. Detection of genotype x environment interaction in spring wheat through triple test cross analysis. Crop. Improv., 16 : 34 – 37.
- Jensen N.F. 1970. A diallel selective mating system of cereal breeding Crop Sci., 10:629-635.
- Jinks J.L., J.M. Perkins and E.L. Breese. 1969. A general method of detecting additive, dominance and epistasis variation for metrical traits : 11 Application to inbred lines Heredity 24 : 45-57.
- Jinks J.L., J.M. Perkins. 1970. A general method for the detecting of additive, dominance and epistatic components of variations. III

- F₂ and backcrosses populations. *Heredity* 25 : 419 – 429.
- Jinks J.L. and H.S Pooni. 1976. Predicting the properties of recombinant lines derived by single seed descent. *Heredity*, 36 : 253-266.
- Katiyar, PK. and A. Ziauddin. 1996. Detection of epistasis components over two environments in bread wheat *Indian J. Genet.* 56 : 285-291.
- Kearsey, M.J. and J.L. Jinks. (1968). A general method of detecting additive, dominance and epistatic variation for metrical traits *Heredity* 23 : 403 – 409.
- Kearsey, M.J.; M.D. Hayward; F.D. Devey; S. Arcionio; M.P. Eggleston and M.M. Eissa. 1987. Genetical analysis of production characters in *Lolium*. I. Triple test cross analysis of spaced plant performance. *Theor. Appl. Genet.* 75 : 66-75.
- Ketata H.; Smith; L.H. Edwards and R.W. McNew. 1976. Detection of epistatic, additive and dominance variation in winter wheat (*Triticum aestivum* L. Thell). *Crop Sci.* 16 : 1-4.
- Nanda, G.S.P.; S. Singhs and K.S. Gill. 1983. Estimating epistasis through triple test cross in wheat *Indian J. Genet.* 43 : 160-163.
- Pooni H.S. and J.L. Jinks. 1978. Predicting the properties of recombinant inbred lines derived by single seed descent for two or more characters simultaneously. *Heredity* 40 : 349-361.
- Salama, S.M.; S.A. Awaad and Manal M. Salem. 2006. Estimates of genetic components, prediction and genetic correlation in wheat (*Triticum aestivum* L.). Using North Carolina Design III *J. Agric., Sci., Ain Shams Univ., Cairo.* 14 : 265-280.
- Singh, G. 1989. Estimation of gene action through triple test cross in bread wheat. *Indian J. of Agric. Sci.* 59 : 700 – 702.
- Singh, S. and R.B. Singh. 1976. Triple test cross analysis in two wheat crosses. *Heredity* 37 : 173 – 177.
- Toledo J.F.F. de; H.S. Pooni and J.L., Jinks. 1984. Predicting the properties of second cycle hybrids produced by intercrossing random sample of recombinant inbred lines. *Heredity* 53 : 285-292.

إكتشاف التفاعل التفوقى والإرتباط الوراثى والتراكيب الوراثية الجديدة
للمحصول ومكوناته فى قمح الخبز باستخدام تحليل التربل تست كروس

سليمان محمد جمعة سلامة

المعمل المركزى لبحوث التصميم والتحليل الإحصائى

مركز البحوث الزراعية - الجيزة - مصر

أجريت هذه الدراسة بمحطة البحوث الزراعية بتاج العز - دقهلية فى الفترة من
عام ٢٠٠٣ إلى ٢٠٠٧ باستخدام هجينين من قمح الخبز المصرى المحلى وهما سخا ٩٣
× جميزة ٧ وجميزة ١٦٨ × جميزة ٩، وذلك بغرض إختبار التفاعل الغير أليلى وإختبار
وتقدير الفعل الجينى المضيف والسيادى والتنبؤ بالإتحادات الجديدة التى يمكن الحصول
عليها بالتلقيح الذاتى المستمر وكذلك دراسة الإرتباط الوراثى وتجزئته لمكوناته من الإرتباط
الراجع للتفاعل غير الأليلى والإرتباط المضيف والإرتباط السيادى لصفات عدد الأيام حتى
طرد السنابل وإرتفاع النبات ومساحة الورقة العظم وعدد السنابل وعدد حبوب السنبل ووزن
الألف حبة ووزن حبوب السنبل ومحصول الحبوب للنبات. وقد أستخدم لهذا طريقة تحليل
التربل تست كروس طبقاً لكيرزى وجنكز ١٩٦٨ وجنكز وآخرون ١٩٦٩ وكيرزى وآخرون
١٩٨٧.

وتلخصت النتائج فى الآتى:

- ١- لعب التفاعل غير الأليلى دور هام فى توارث جميع الصفات المدروسة فى كلا
الهجينين وكان التفاعل المضيف × المضيف والسيادى × السيادى والسيادى ×
المضيف معنوياً لجميع الصفات المدروسة.
- ٢- ساهم كل من الفعل الجينى المضيف والسيادى فى توارث جميع الصفات
المدروسة.
- ٣- كان متوسط درجة السيادة أكبر من الوحدة لصفات عدد السنابل للنبات للهجين
الأول ووزن حبوب السنبل للهجين الثانى مشيراً لأهمية الفعل الجينى السيادى فى

وراثة هذه الصفات، بينما كانت أقل من الوحدة لجميع الصفات الباقية مما يدل على أهمية الفعل الجيني المضيف في توارث هذه الصفات.

٤- كان اتجاه السيادة موجب ومعنوى لصفة وزن الألف حبة فى الهجينين أى أن السيادة فى اتجاه واحد بينما أظهرت باقى الصفات سيادة غير موجهة أى فى اتجاهين مما يظهر التوزيع الغير متمثل لجينات السيادة الموجبة والسالبة بين الآباء لهذه الصفات.

٥- أوضحت النتائج أنه من المتوقع الحصول على نسب معقولة من الإتحادات لصفة عدد الأيام حتى طرد السنابل ومساحة الورقة العلم للهجين الأول.

٦- أوضحت نتائج الارتباط الوراثى وجود ارتباط وراثى موجب ومعنوى بين جينات التفاعل غير الأليلى وكذلك لتأثيرات الفعل الجينى المضيف والسيادى بين صفات محصول الحبوب للنبات مع عدد السنابل وعدد حبوب السنبله ووزن الألف حبة فى كلا الهجينين.