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UTILIZATION OF TRIPLE TEST CROSS IN BREAD WHEAT F2 POPULATIONS. 1- PREDICTING OF NEW RECOMBINANT LINES AND GENETIC CORRELATIONS

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ABSTRACT: *Epistasis, additive and dominance components of genetic variation for yield and some yield related traits were assessed through triple test cross technique in bread wheat. Two genotypes of bread wheat, Gemmeiza 11 and Line 1, and their F1 progeny were used as a testers to crossed with twenty random selected F2 plants from the previous cross (Gemmeiza11 × Line 1) to produce L1i (P1 × F2i), L2i (P2 × F2i) and L3i (F1i × F2i) respectively. The sixty families (L1 (20) + L2 (20) + L3 (20)) were sown at Experimental Farm of Gemmeiza Agriculture Research Station to study gene action, predicting of new recombinant lines and genetic correlation for some quantitative traits. The mean squares of the analysis of variance revealed significant differences among triple test cross (T.T.C) families for all the traits studied indicating that L1i, L2i and L3i families were significantly different from each other, providing evidence for adequate amount of genetic variability. Epistasis was found an important part of genetic variation for all traits studied. Partitioning of total epistasis into (i) type and (j +L) types of epistasis revealed that (i) type of epistasis (additive x additive) was found to be significant and highly significant for most traits studied except plant height, main spike length, number of spikelets per main spike and kernels per spike. However, (J+ L) additive × dominance, dominance × dominance, types were also highly significant for most traits studied except number of days to heading. The additive genetic variances (D) was found to be much larger in magnitudes than the dominance genetic variance (H) for number of days to maturity, number of spikes per plant, number of kernels per main spike, grain yield per plant and 1000-kernels weight and that resulted in $(H/D)^{½}$ to be less than one. The results showed that the $\hat{F}$ value (covariance of sums / differences) was found to be significant and positive or negative for number of days to maturity and flag leaf area revealing that the dominance was unidirectional among parents. The prediction results revealed that it could be feasible to predict as early as possible for transgressive segregants and the highest proportions of recombinants which outperform parental range for number of spikes per plant, followed by number of days to maturity, grain yield per plant, flag leaf area and plant height. Thus the breeder should give a great emphasis to the promising cross are the most frequent ones and having high values for new recombinants for yield, therefore, the breeder should pay great emphasis for considering these promising cross in wheat breeding program. Results of genetic correlation generally revealed presence of significant additive, dominance and epistatic genetic correlations among some traits suggesting common genetic pool, pleiotropy or linkage. Since additive genes is a fixable type, therefore, selection based on such type may indicate that indirect selection via, main spike length, number of kernels per main spike, number of spikes per plant and 1000-kernels weight would be effective in improving grain yield and enhance its importance as selection criteria. Meanwhile, the great part of traits showed non-significant genetic correlations and confirmed that T.T.C mating system was useful in break up undesirable linkage to obtain new recombinant lines.*

***Key words**: Wheat, Triple test cross, epistasis, additive, dominance, prediction and genetic correlation.*

INTRODUCTION

Wheat is the most important cereal crop in Egypt. It is the major crop in winter season, the local production of wheat is not sufficient to cover the local consumption in Egypt. Increasing wheat production to narrowing the gap between production and consumption is considered the main goal of breeder in Egypt as well as in most countries all over the world (Shehab El-Din,1993).

The initial stage of wheat breeding programs is to develop cross populations having high genetic variation in order to improve new wheat cultivars. Desired genotypes from these cross populations are selected using suitable selection methods. Selection of the efficient breeding method depends to large degree on understanding of the genetic scheme controlling the traits to be selected. In plant breeding, various mating designs and arrangements are used by breeders and geneticists to generate improved plants. The selection of suitable parents and good mating designs are keys to the successful plant breeding schemes (Khan *et al.,* 2009). Thus mating designs developed and applied for investigation inheritance of quantitative traits have helped to understand the nature of genetic variation, which in turn were useful in formulating appropriate breeding methods and improving selection efficiency (Kearsey and Pooni, 1996).

Most of the designs used in the estimating the genetic components of variation assume the absence of epistasis. However, in this respect, Esmail (2007), El-Massry (2009) and Morad (2012) mentioned that epistasis was predominating for most studied traits in wheat. Among all the designs available for estimation of gene action, Triple test cross is considered the most efficient model as it provides not only a precise test for epistasis, but also unbiased estimates of additive and dominance components if epistasis is absent (Singh and Yunus, 1986). This design is most flexible in that it can be applied to any population with any level of inbreeding, any gene frequency and degree of linkage disequilibrium or gene correlation. An understanding of genetic factors, determination of agronomic traits is a primary step for breeding studies. The magnitude of additive effects is particularly useful to the wheat breeder involved in developing pure line varieties.

The aim of many selfing programmes is to produce recombinant inbred lines to be used directly or in producing F1 hybrid or multiple cross hybrid. The best source of the genetical parameters required for predicting the properties of recombinant inbred lines is the F_2 triple test cross (Kearsey and Jinks, 1968; Jinks and Perkins, 1970; Pooni and Jinks, 1979; Pooni, *et al.*, 1978).

The knowledge of genetic correlation, which occurs between characters, can help the breeder to improve the efficiency of selection by using favorable combinations of traits and to minimize the retarding effect of negative correlations. The reliability of genetic components estimated from TTC makes computed correlations from them more reliable. In wheat, the correlation of components of genetic variance was computed using TTC analysis by Eissa (1994 c), Alkaddoussi (1997), Menshawy (2008) and Morad (2012).

The objectives of this study are to study:
1) Existence of epistasis and to determine the additive (D) and dominance (H) variances of quantitative traits. 2) To make prediction for studied traits that help the breeders to identify the favorable combinations to improve the efficiency of selection, 3) To compute the genetic correlation among various traits and partitioning it to epistasis , additive and dominance correlations.

MATERIALS AND METHODS

The present study was conducted at Experimental Farm of Gemmeiza Agriculture Research Station, Egypt during the four successive seasons of 2009 / 2010, 2010 / 2011, 2011 / 2012 and 2012/2013. In the first season (2009/2010), two genotypes of bread wheat, differ in most of their agronomic traits namely Gemmeiza 11 and Line1, were crossed to obtain their F1 progeny (Gemmeiza 11× Line1). The pedigree of bread wheat genotypes are

illustrated in the Table (1). In the second season (2010/2011), the F1 plants were selfed to produce F2 grains. In 2011/2012 growing seasons, the obtained materials F1, F2 and the parental genotypes were sown. Twenty random F2 plants were crossed, as males, back to its respective parents P1, P2 and F1 (P1 × P2) to produce L1i (P1 × F2i), L2i (P2 × F2i) and L3i (F1i × F2i) respectively. In 2012/2013 growing season, the sixty families (L1 (20) + L2 (20) + L3 (20)) were sown in a randomized complete block design with three replicates.

Each replication consisted of 60 rows. Row length was 2 m with 30 cm apart and plant to plant spacing was 10 cm. Data were recorded using ten random plants from each family in each replication for number of days to heading, flag leaf area, number of days to maturity, number of spikes per plant, plant height, main spike length, number of spikelets per main spike, number of kernels per main spike, main spike yield, grain yield per plant and 1000- kernels weight.

Biometrical analysis:

Before proceeding to analysis, the families subjected firstly to the conventional one way analysis of variance for the L1i, L2i, L3i sets of families for every trait separately outlined by Kearsey,M. and H.S. Pooni (1996). This analysis provides a test for the significance between families terms. Test of epistasis were carried out according to Kearsey and Jinks (1968), Jinks *et al.* (1969) and Jinks and Perkins (1970).

The mean squares for deviations ($\overline{L_{1i}}$ + $\overline{L_{2i}}$ – 2$\overline{L_{3i}}$) was used for detection of epistasis. The overall epistasis was partitioned into (i) type of epistasis (additive x additive) and (i + j) type due to additive x dominance and dominance x dominance gene interactions. The estimation of additive (D) and dominance (H) genetic components and the correlation coefficient (r) between sums ($\overline{L_{1i}}$ + $\overline{L_{2i}}$ + $\overline{L_{3i}}$) and differences ($\overline{L_{1i}}$ - $\overline{L_{2i}}$) were obtained to detect the direction of dominance, according to Jinks and Perkins (1970). Average degree of dominance was calculated as the formula $(H/D)^{1/2}$, where H and D are the dominance and additive variance components respectively. Also, the F value was computed from the covariance of sums / differences which equal to (-1/8F), where F is the association dispersion of dominant alleles in the parental lines, having a maximum value of 1 if all the dominant alleles are associated in P_1 and having a minimum value -1 if all dominant genes are in P_2.

The proportion of superior inbreds, that outperform their parental range, is equal to the normal probability integral corresponding to the value [d] /√ D while, the range of inbred lines is m ± 2√ D . The [m] and [d] values derived from the expectations of TTC families were, m = $\overline{L_3}$ and [d] = $\overline{L_1}$ - $\overline{L_2}$ (Jinks and Ponni, 1976). The proportions of recombinant lines corresponding to the probability level were obtained using Fisher and Yates (1963) Tables.

Epistasis, additive and dominance correlation coefficients were computed from ($\overline{L_{1i}}$ + $\overline{L_{2i}}$ – 2 $\overline{L_{3i}}$), ($\overline{L_{1i}}$ + $\overline{L_{2i}}$ + $\overline{L_{3i}}$) and ($\overline{L_{1i}}$ - $\overline{L_{2i}}$) respectively.

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

Name	Pedigree	Origin
Gemmeiza 11	BOW"S"/KVZ"S"//7C/SERI82/3/GIZA168/SAKHA61 GM7892-2GM-1GM-2GM-1GM-0GM	Egypt
Line 1	Sakha 93 /Sids 6 CGZ (16) 3GM-2 GM-OGM	Egypt

RESULTS AND DISCUSSION

The mean squares of the analysis of variance (Table 2) revealed significant and highly significant differences among triple test cross (T.T.C) families for all the traits studied indicating that L1i , L2i and L3i T.T.C families were significantly different from each other , providing evidence for adequate amount of genetic variability and assured the variability between parents. Likewise, the results indicated that L1i, L2i and L3i families were significantly different from each other in most studied traits confirming the presence of high amount of genetic variability which could be assessed by means of triple test cross analysis. These results are in generally agreed with those obtained by Menshawy (2008) , El-Nahas, Marwa (2010) and Morad (2012).

The average performance of $\overline{L_1}$, $\overline{L2}$ and $\overline{L_3}$ TTC families for all traits are given in Table (3). The data revealed that mean of back crosses exhibited significant differences for most traits studied.

Test of epistasis:

The comparison ($\overline{L_{1i}}$ + $\overline{L_{2i}}$ – 2 $\overline{L_{3i}}$) was used by kearsy and Jinks (1968) and Jinks and Perkins (1970) as a test for epistasis (Table 4). The data revealed highly significant overall epistasis for all traits studied indicated the important role of epistasis in the control of these traits. These result are similar to those reported by Sadat and Sokhansanj (2004) , Hendawy *et al.*, (2009) and Morad (2012).

Further partitioning of epistasis to its component parts revealed that (i) type of epistasis (additive x additive) was found to be significant and highly significant for most traits studied except plant height, main spike length, number of spikelets per main spike and kernels per spike . These results indicated the importance of (i) type of epistasis in the inheritance of these traits. Similar results were reported by Zaazaa *et al.* (2012) and Abd El-Rahman, Magda (2013).

The rest type of epistatic components i.e. additive x dominance and dominance x dominance (J+ L) types were highly significant for most traits studied except number of days to heading indicate that (J+ L) types are not fixable by selection and not favorable for developing pure lines for these traits. The (J+ L) types epistasis has also been found to be less important than (i) type of epistasis in wheat Eissa (1994 a), Salama(2007) and Hendawy (2008) .

Generally, The results revealed the important role of (I) type was much larger in magnitude than (J + L) type for most traits studied reflecting the importance of additive x additive in the genetic system controlling such traits.

From the results obtained, it has been concluded that which one of the above traits an epistatic component plays an important role. Epistasis cannot therefore be ignored when plant breeders are planning breeding programs to improve these traits in wheat. Therefore, the fixable components of epistasis (i) type could be easily exploited in developing homozygous germplasm by standard hybridization and selection procedures in early segregating generations would be effective to improve these traits. The rest types of epistasis i.e. (J) and (L) are not fixable by selection in self-pollinated crops such as wheat, and therefore are not useful for developing pure line cultivars. They may be useful in the development of hybrids. Therefore, population improvement through pedigree method might be giving a good response for releasing genotypes Eissa (1994b), Salama (2007) and Farshadfar, *et al.* (2008).

Detection and estimation of additive and dominance genetic variance components

The analysis of variance for sums ($\overline{L_1}$ + $\overline{L_2}$ + $\overline{L_3}$), and differences ($\overline{L_1}$ – $\overline{L_2}$) are presented in Table (5). The results revealed that mean square estimates due to sums were found to be significant and highly significant for all traits studied except main spike length and number of spikelets per

Table 2 , 3

Table 4 , 5

main spike. The mean square estimates due to differences were detected to be significant and highly significant for all traits studied except number of days to maturity, main spike length, number of spikelets per main spike and number of kernels per main spike.

These results would indicate that both additive and dominance genetic variance appeared to predominantly affect all traits measured. Consequently, it could be concluded that selection procedures based on the 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 variances are involved would be preferred. The same results were also obtained by El – Nahas, Marawa (2005), Esmail (2007) , Hendawy *et al.,* (2009) and Koumber (2011).

The estimates of genetic components of variations are given in Table (6).The additive genetic variances (D) was found to be much larger in magnitudes than the dominance genetic variance (H) for number of days to maturity, number of spikes per plant, number of kernels per main spike, grain yield per plant and 1000- kernels weight and that resulted in $(H/D)^{½}$ to be less than one confirming that these traits were influenced predominantly by the additivity of the genes and also the role of partial dominance in the inheritance of these traits. Whereas, the remaining traits the dominance genetic variance (H) was found to be larger in magnitudes than the additive genetic variance and that resulted in $(H/D)^{½}$ to be more than unity confirming the role of the overdominance in the inheritance of these traits . In this regard, El-Massry (2009) and El-Nahas, Marwa (2010).

The direction of dominance and types of genes exhibiting dominance are presented in Table (6). The results showed that the ($\hat{F}$) value was found to be significant (positive or negative) as (r) values indicated for number of days to maturity and flag leaf area revealing that the dominance was unidirectional among parents. On the other hand, the remaining traits have insignificant ($\hat{F}$) values and positive or negative, reflecting ambidirectional dominance. Eissa (1994 a), Salama (2007) and Menshawy (2008) obtained similar conclusion.

It can be concluded that the additive, dominance and epistatic components are important in wheat but as it is an autogamous plant, only the additive component is important to develop pure breeding varieties from any hybridization program. While, additive × additive epistatic type coupled with additive genetic variance were found to be preponderant for all traits except plant height, main spike length, number of spikelets per main spike and number of kernels per main spike indicating the possible improvement of these traits through standard hybridization and selection in early generations. If the rest type of epistasis (J+L) types is predominant this, biparental matings may be attempted in F_2 and subsequent generations and selection may be postponed till late generation to allow sufficient epistasis to get fixed.

Generally, the results obtained here would indicate that epistasis is an integral component of the genetic variance for mostly traits studied and hence detection, estimation and consideration of epistasis is important for the formulation of breeding program to improve wheat population for such traits. If epistasis is ignored no precise conclusion can be drawn about the relative importance of the other component of genetic variation, additive and dominance, where such estimation of additive and dominance would be biased by epistasis to unknown extent as in the present materials (Sood and Dawa, 1999).

Prediction of superior recombinants:

Triple test cross is one of the most useful sources for such information to make prediction of new recombinants lines. These informations will allow predictions of the proportion of inbreds which as good as or superior to better parent or F_1 hybrid. The results of such proportions for traits studied are given in Table (7). The results revealed that it could be feasible to predict as early as possible for transgressive segregants and the highest proportions of recombinants which outperform parental range for number

Table 6 , 7

of spikes per plant (44.43%), followed by number of days to maturity (40.51%), grain yield per plant (34.45%), flag leaf area (28.43%) and plant height (17.10%). In this regard Menshawy (2008) recorded highest proportions of recombinants for grain yield per plant (47.6 %) followed by 100-kernels weight (47.2 %) and number of kernels per spike.

These results revealing that this cross exhibited fair amount of genetic variability and considered valuable further breeding studies aiming to improve yield traits. The obtained high proportion could be explained that the wheat genotypes studied have common genetic pool, and the prevalence of additive gene effects for most traits studied refer that, selection imposed for the traits studied was to intermediate performance.

Generally, it could be concluded from the prediction results that the breeder should give a great emphasis to the promising cross are the most frequent ones and having high values for new recombinants for yield, therefore, the breeder should pay great emphasis for considering these promising cross in wheat breeding program.

Genetic correlation

The kind of relationships, which may occur among characters, is important for selection breeding programs. Partitioning of the total genetic correlation to its components of epistasis, additive and dominance genetic correlations illustrated in Table (8). The results obtained provide evidence for positive and significant correlation between epistatic gene effects controlling between number of spikelets per main spike and main spike length, between number of kernels per main spike and main spike length, between main spike yield and each of main spike length and number of kernels per main spike, between grain yield per plant and each of number of spikes per plant, main spike length and number of kernels per main spike. On the other side, significant negative epistasis correlation between number of spikelets per main spike and plant height.

Concerning the additive genetic correlations indicated positive and significant additive correlation between flag leaf area and number of days to heading , between number of spikes per plant and number of days to maturity, between main spike length and plant height, between number of spikelets per main spike and main spike length , between number of kernels per main spike with those of number of days to maturity, plant height, main spike length, between main spike yield with those of main spike length , number of spikelets per main spike and number of kernels per main spike , between grain yield per plant with those of number of days to maturity , number of spikes per plant, number of spikelets per main spike, number of kernels per main spike and main spike yield. On the contrary, it was found negative and significant additive genetic correlation between plant height and flag leaf area, between 1000-kernels weight with those of no of days to heading and flag leaf area.

Regarding dominance genetic correlation the results indicated positive and significant correlation between dominant genes controlling number of spikelets per main spike and main spike length , between number of kernels per main spike and each of main spike length and number of spikelets per main spike, between main spike yield and each of main spike length and number of kernels per main spike , grain yield per plant and each of number of days to maturity and main spike yield , between 1000-kernels weight and each of main spike yield and grain yield per plant . On the other hand, the results revealed significant negative dominance correlation between number of days to maturity and number of days to heading. Similar conclusion were obtained by Eissa (1994c), Salama (2007) and Morad (2012) using triple test cross in wheat.

Results of genetic correlation generally revealed the presence of significant additive, dominance and epistatic genetic correlations among some traits. Meanwhile, the great part of traits showed non-significant genetic correlations and confirmed that T.T.C mating system was useful in break up undesirable linkage to obtain new recombinant lines. In

Table 8

this regard, Menshawy (2008) and Morad (2012) reported the efficiency of triple test cross for obtaining new recombinant lines in wheat.

Generally, the results of genetic correlations revealed that additive and dominance gene effects controlling yield and its components were significantly asSsociated with each other, suggesting common genetic pool, pleiotropy or linkage. Since additive genes is a fixable type, therefore, selection based on such type may indicate that indirect selection via, main spike length, number of kernels per main spike, number of spikes per plant and 1000-kernels weight would be effective in improving grain yield and enhance its importance as selection criteria.

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إستخدام التلقيح الاختبارى الثلاثى في عشائر الجيل الثانى لقمح الخبز
1. التنبؤ بالتراكيب الوراثية الجديدة وتقدير الارتباط الوراثى

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الملخص العربى

أجرى هذا البحث فى مزرعة محطة البحوث الزراعية بالجميزة – مركز البحوث الزراعية وذلك فى اربعة مواسم متتالية هى 2010/2009 ، 2011/2010 ، 2012/2011 ، 2013/2012 باستخدام هجين من قمح الخبز

(جميزة 11 × سلالة 1). وذلك بغرض اختبار التفاعل غير الاليلى وتقدير الفعل الجينى المضيف والسيادى والتنبؤ بالتراكيب الوراثية الجديدة وكذلك دراسة الارتباط الوراثى وتجزئته الى مكوناته للصفات التالية : عدد الايام من الزراعة حتى طرد السنابل – مساحة ورقة العلم – عدد الايام من الزراعة حتى النضج – عدد السنابل على النبات – طول النبات – طول السنبلة الرئيسية – عدد السنيبلات فى سنبلة الساق الرئيسية – عدد الحبوب فى سنبلة الساق الرئيسية – محصول سنبلة الساق الرئيسية –ومحصول النبات الفردى – وزن الألف حبة. وقد استخدم لهذا طريقة تحليل التلقيح الاختبارى الثلاثى(Triple test cross) طبقا (Kearsey and Jinks , 1968) .

ويُمكن تلخيص النتائج المتحصل عليها فى الآتى :

- اظهر تحليل التباين وجود اختلافات معنوية لكل الصفات المدروسة بين عائلات التلقيح الرجعى الثلاثى مما يؤكد على وجود كمية كافية من الاختلافات الوراثي.
- اظهر اختبار التفاعل غير الاليلى وجود اختلافات معنوية لمعظم الصفات المدروسة وكانت انواع التفاعل غير الاليلى معنوية لكل من الطراز المضيف × المضيف والطرازالمضيف × السيادى بالاضافة الى السيادى × السيادى لمعظم الصفات المدروسة.
- اظهر تحليل التباين للتأثيرات الجينية المضيفة معنوية لمعظم الصفات المدروسة . كما اظهرت ايضا التاثيرات الجينية السائدة معنوية لمعظم الصفات المدروسة. مما يعكس اهمية كل من التاثيرات المضيفة والسائدة فى التحكم الوراثى لتلك الصفات .
- كانت قيمة التباين الوراثي السيادى أعلى من قيمة التباين الوراثى المضيف لمعظم الصفات المدروسة.واظهر اتجاه السيادة عدم معنوية لمعظم الصفات المدروسة .
- أوضحت النتائج انه يمكن التنبؤ بنسبة عالية من الإتحادات الجديدة والتى تفوق حدود الابوين لبعض الصفات المدروسة مما يعطى مؤشر لمربى النبات للأنتخاب لهذه الصفات فى الأجيال المبكرة فى برنامج تربية القمح والتى تهدف لزيادة المحصول.
- أظهرت نتائج الارتباط الوراثى وجود ارتباط وراثى معنوى (تفوقى ومضيف وسيادى) بين عائلات التهجين الرجعى الثلاثى لبعض الصفات المدروسة. بينما اظهرت الغالبية العظمى من الصفات عدم وجود ارتباط فيما بينها مما يؤكد فعالية نظام التلقيح الرجعى الثلاثة فى كسر الارتباط وظهور اتحادات وراثية جديدة يمكن استغلالها فى برامج التربية المختلفة .

Table (2): Analysis of variance and mean squares of triple test cross families (L1, L2, and L3) and (L1, L2) for all traits studied.

S.O.V.	D.F	Number of days to heading (days)	Flag leaf area (cm^2)	Number of days to maturity (days)	Number of spikes per plant	Plant height (cm)	Main spike length (cm)	Number of spikelets per main spike	Number of kernels per main spike	Main spike yield (g)	Grain yield per plant (g)	1000-kernels weight (g)
Between L1, L2, L3 families	59	27.63**	130.50**	34.10**	69.90**	64.00**	18.38**	22.236**	760.29**	4.19**	836.90**	130.50**
Between L1	19	11.80**	803.62**	21.35**	30.79**	60.89**	13.24**	16.43**	469.27**	4.86**	304.56**	134.40**
Between L2	19	23.90**	286.12**	63.63**	37.54**	88.75**	6.13**	7.17**	537.74**	2.78**	562.20**	110.86**
Between L3	19	17.49**	1038.53**	18.18**	143.78**	26.56**	11.29**	20.39**	815.87**	3.51**	1535.76**	82.23**
Residual	2	309.90**	9843.62**	26.01**	46.99**	214.29**	250.84**	237.72**	5111.08**	17.58**	1864.53**	738.56**
Within families within replicates	720	0.80	2.03	0.82	1.07	1.32	0.59	0.91	19.77	0.07	5.58	2.10
Between L1, L2 families	39	19.94**	596.53**	42.02**	33.62**	83.88**	21.90**	23.68**	751.53**	4.35**	463.47**	147.43**
Within families within replicates	480	0.78	2.00	0.85	0.91	1.32	0.52	0.90	20.15	0.06	4.76	2.19

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

Table (3): Mean values of F2 triple test cross families for the traits studied.

TTC families	Number of days to heading (days)	Flag leaf area (cm^2)	Number of days to maturity (days)	Number of spikes per plant	Plant height (cm)	Main spike length (cm)	Number of spikelets per main spike	Number of kernels per main spike	Main spike yield (g)	Grain yield per plant (g)	1000-kernels weight (g)
L1	95.09	52.90	146.79	11.55	113.30	14.56	26.58	81.28	4.26	40.68	57.39
L2	94.28	48.77	146.39	11.25	111.61	12.76	24.80	73.04	3.86	37.41	54.70
L3	96.30	60.09	146.96	12.04	112.48	13.94	25.66	77.64	3.83	42.30	57.43
L.S.D. 0.05	1.43	2.28	1.45	1.66	1.84	1.23	1.53	7.12	0.42	3.78	2.32
L.S.D. 0.01	1.88	3.00	1.91	2.18	2.42	1.62	2.01	9.37	0.56	4.98	3.05

Table (4): Analysis of variance and mean squares for test of epistasis for triple test crosses for all traits studied.

S.O.V.	D.F	Number of days to heading (days)	Flag leaf area (cm^2)	Number of days to maturity (days)	Number of spikes per plant	Plant height (cm)	Main spike length (cm)	Number of spikelets per main spike	Number of kernels per main spike	Main spike yield (g)	Grain yield per plant (g)	1000-kernels weight (g)
Overall epistasis	20	4.63 **	187.89 **	3.52 **	11.99 **	4.43 **	1.65 **	2.13 **	92.47 **	0.54 **	98.00 **	11.99 **
(I) type	1	69.41 **	2283.68**	3.68 *	10.81 **	0.02	2.09	0.02	6.10	1.43 **	282.96 **	51.64 **
(J + L) type	19	1.22	77.59 **	3.51 **	12.05 **	4.66 **	1.62 **	2.25 **	97.01 **	0.50 **	88.27 **	9.90 **
Within families Within replicates	720	0.80	2.03	0.82	1.07	1.32	0.59	0.91	19.77	0.07	5.58	2.10

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

Table (5): Analysis of variance and mean squares for "sums" additive (L1+ L2 +L3) and "differences" dominance (L1-L2) in triple test crosses for all traits studied.

S.O.V.	D.F	Number of days to heading (days)	Flag leaf area (cm^2)	Number of days to maturity (days)	Number of spikes per plant	Plant height (cm)	Main spike length (cm)	Number of spikelets per main spike	Number of kernels per main spike	Main spike yield (g)	Grain yield per plant (g)	1000-kernels weight (g)
Between sums	19	1.54 *	60.23 **	3.83 **	6.09 **	4.91 **	0.65	0.96	48.42 **	0.21 **	80.35 **	10.11 **
Within families within replicates	720	0.80	2.03	0.82	1.07	1.32	0.59	0.91	19.77	0.07	5.58	2.10
between differences	19	1.40 *	42.86 **	1.29	2.03 **	4.51 **	0.59	0.85	24.60	0.29 **	35.68 **	6.78 **
Within families within replicates	480	0.78	2.00	0.85	0.91	1.32	0.52	0.90	20.15	0.06	4.76	2.19

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

Table (6): Estimates of additive (D), dominance (H) components, degree of dominance $(H/D)^{0.5}$ and covariance between sums and differences (F) for all traits studied.

Traits / Components	Number of days to heading (days)	Flag leaf area (cm^2)	Number of days to maturity (days)	Number of spikes per plant	Plant height (cm)	Main spike length (cm)	Number of spikelets per main spike	Number of kernels per main spike	Main spike yield (g)	Grain yield per plant (g)	1000-kernels weight (g)
D	0.65	51.73	2.67	4.46	3.19	0.05	0.05	25.47	0.12	66.47	7.12
H	0.83	54.49	0.58	1.49	4.25	0.08	-0.07	5.93	0.31	41.23	6.12
$(H/D)^{0.5}$	1.13	1.03	0.49	0.58	1.15	1.28	-1. 25	0.48	1.58	0.79	0.93
F	9.41	-518.54*	25.08 **	8.14	14.50	-3.39	-0.20	-8.00	-0.84	364.23	-26.19
r	-0.33	0.52 *	-0.57 **	-0.12	-0.16	0.28	0.01	0.01	0.17	-0.35	0.16

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

Table (7): Predicting the range of inbred lines and the proportion of inbreds expected to fall outside their parental range for the traits studied.

Parameters / Traits	(m)	(d)	(D)	Range of inbreds	Probability	Proportion of inbreds falling outside parental range %
Number of days to heading	96.30	0.81	0.65	97.91 - 94.69	1.00	15.86
Flag leaf area	60.09	4.13	51.73	74.48 - 45.70	0.57	28.43
Number of days to maturity	146.96	0.40	2.67	150.23 - 143.69	0.24	40.51
Number of spikes per plant	12.04	0.30	4.46	16.26 - 7.82	0.14	44.43
Plant height	112.48	1.69	3.19	116.05 - 108.91	0.95	17.10
Main spike length	13.94	1.80	0.05	14.39 - 13.49	8.05	0.00
Number of spikelets per main spike	25.66	1.78	0.05	26.09 - 25.23	8.21	0.00
Number of kernels per main spike	77.64	8.24	25.47	87.73 - 67.55	1.63	5.15
Main spike yield	3.83	0.40	0.12	4.53 - 3.13	1.14	12.71
Grain yield per plant	42.30	3.27	66.47	58.61 - 25.99	0.40	34.45
1000- kernels weight	57.43	2.69	7.12	62.77 - 52.09	1.01	15.62

Table (8): Epistasis (r_I) genetic correlation, additive (r_A) genetic correlation and dominance (r_D) genetic correlation for all traits studied.

Traits	Type	Number of days to heading	Flag leaf area	Number of days to maturity	Number of spikes per plant	Plant height	Main spike length	Number of spikelets Per main spike	Number of kernels per main spike	Main spike yield	Grain yield per plant
Flag leaf area	r_I	0.222									
	r_A	0.483 *									
	r_D	-0.089									
Number of days to maturity	r_I	0.205	-0.233								
	r_A	0.276	0.147								
	r_D	-0.536 *	0.244								
Number of spikes Per plant	r_I	0.064	0.147	-0.317							
	r_A	0.190	-0.007	0.756 **							
	r_D	-0.150	-0.175	-0.114							
Plant height	r_I	0.212	0.180	-0.127	-0.340						
	r_A	-0.405	-0.455 *	0.271	0.142						
	r_D	0.130	0.339	0.233	0.007						
Main spike length	r_I	-0.112	0.241	-0.087	0.047	0.074					
	r_A	-0.006	-0.294	0.225	-0.061	0.453 *					
	r_D	0.090	0.259	0.037	0.400	0.298					
Number of spikelets per main spike	r_I	-0.003	0.083	0.046	0.027	-0.506 *	0.547 *				
	r_A	-0.011	-0.346	0.249	0.007	0.401	0.909 **				
	r_D	0.004	0.143	0.140	0.324	0.245	0.829 **				
Number of kernels per main spike	r_I	-0.128	0.027	-0.164	0.173	0.083	0.658 **	0.322			
	r_A	-0.056	-0.255	0.636 **	0.301	0.498 *	0.488 *	0.384			
	r_D	-0.199	0.191	-0.011	0.313	0.203	0.600 **	0.677 **			
Main spike yield	r_I	-0.102	0.030	0.059	0.145	-0.080	0.541 *	0.273	0.636 **		
	r_A	0.063	-0.022	0.349	-0.106	0.342	0.594 **	0.473 *	0.661 **		
	r_D	-0.230	0.223	0.246	0.188	0.289	0.596 **	0.413	0.470 *		
Grain yield per plant	r_I	0.230	0.218	-0.357	0.576 **	-0.031	0.479 *	0.269	0.531 *	0.542 *	
	r_A	0.169	-0.149	0.799 **	0.625 **	0.368	0.405	0.453 *	0.643 **	0.482 *	
	r_D	-0.249	0.369	0.527 *	0.198	0.151	0.428	0.376	0.339	0.652 **	
1000- kernels weight	r_I	-0.174	-0.041	-0.006	0.383	-0.282	-0.272	-0.098	-0.313	-0.359	-0.124
	r_A	-0.523 *	-0.530 *	-0.271	-0.400	0.249	0.011	0.063	0.139	0.343	-0.108
	r_D	-0.153	-0.242	0.379	-0.069	0.169	0.178	0.006	-0.084	0.450 *	0.456 *