Original Article

TRIPLE TEST CROSS ANALYSIS AND SIX POPULATIONS WERE USED TO DETERMINE GENETIC VARIABILITY AND DIVERSITY FOR YIELD AND ITS COMPONENTS IN BREAD WHEAT

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DOI: 10.47750/pnr.2023.14.02.319

Abstract

Joint scaling test x2 and non-allelic interaction scaling test (A, B, and C) and a six-parameter model was used to assess the effectiveness of the genetic model and calculates the genetic elements for days to heading, flag leaf area, (number of spikes / plant, number of grains/spike , 1000 - grain weight and grain yield/ plant (g) using six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) and triple test crosses analysis of two wheat crosses; 1. Gemmeiza11 X Misr1 and 2. Gemmeiza 12 X Misr2. A randomized complete block design with three replications was used. The obtained results indicated the importance of additive genetic variance (D) in the genetic control of days to heading and flag leaf area for Gimmeiza 12 X Misr2 in tow methods analysis and number of spikes / plant in two crosses in tow method analysis. Heritability in narrow sense was more than 0.50. While the dominant type controlling for the remaining traits in two crosses was determined to be the dominance genetic variance (H), the value of $(H/D)^{05}$ was more than one for these characters and heritability in narrow sense was less than 0.50. Joint scaling test (X2) and non-allelic interaction (A, B, and C) demonstrated that a basic genetic model was sufficient to explain the inheritance of number of spikes/plant for Gemmeiza 12 X Misr1, epistasis played a great role of controlling remaining characters in two crosses. Additive (d) and additive X dominance (j) were significant for days to heading and number of grains /spike (1st and 2nd crosses), 1000 grain weight and grain yield / plant for 2nd cross. The digenic interaction type dominance X dominance (l) controlling days to heading (1st and 2nd crosses), Number of spikes per plant (1st cross), number of grains per spike, weight in 1000 grains, and yield in grains per plant (2nd cross). The main limiting variables for selecting the best breeding technique are thought to be an understanding of the type of gene action controlling mechanism of the yield and yield components paired with the reproduction system. These information are of great interest for plant breeder to release high yielding wheat cultivars as well as early mature ones.

Introduction

The sort of gene activity governing the genetic variety is what primarily determines the most successful breeding technique to be applied, such information is helpful for the breeders to predict in early generation of breeding. Programme, the potential of recombinant lines that could be derive following a series of selfing generations in this respect, The importance of dominance was discovered to be greatly influenced by additive and dominance gene effects. heading date, number of grains/spike, and grain yield/plant (**Pawar *et al*. 1988 and Alkadoussi and Eissa 1990)**; area of the flag leaf; quantity of spikes per plant; and weight in grains (**Shehab El-Din, 1997 and Salama, 2002**). The inheritance and genetic model for grain weight/spike were investigated by **Alkaddoussi and Eissa (1989)**. They indicated that digenic model was appropriate to ascertain the genetic model for grain yield/plant. Non - allelic interaction parameters genetic model to test for epistasis were studied by **Salama (2002)**. **Mitkess and Dawla (1983)**, **Chatrath *et al*. (1986)**, **Awaad (1996)** and **Salama**

(2007) revealed that the most common form of gene action influencing the heading data, number of grains/spike, and grain yield/plant was additive. Very limited studies were carried out to study the genetic control of yield and yield attributes characters in wheat **Esmail (2002)** and **Sultan, *et al.* (2005)**. These details are very important for plant breeders to release high-yielding The triple test cross analysis (Kearsey and Jinks, 1968) is a special method that offers a clear test for epistasis and can identify and quantify the genetic components that are additive and dominant.

Singh and Singh (1976) observed the significance of additive, dominance, and epistasis gene effects in the inheritance for wheat yield and its components applying triple test cross analysis of wheat by **Ketata *et al*. (1976)**. **Iqbal Singh *et al*. (1989), Eissa (1994 a, b)**, and **Nanda *et al*. (1983)** all found significant epistasis for grain weight/spike and grain yield/plant. For these features, the epistasis was mostly caused by an additive x additive kind of epistasis. Singh 1989, Katiyar, and Ziauddin (1996) employed triple test cross analysis in wheat and found that additive and dominance gene effects had a significant influence in the inheritance of grain yield/plant. According to **Eissa (1994 c)**, **AlKaddoussi (1996)**, and **Salama *et al*. (2006)**, there are genetic relationships between yield and yield qualities. They claimed there was a genetic link between wheat grain yield/plant and grain weight per thousand. Studying the genetic components of wheat varieties to be used in breeding programs was the goal of this investigation. In order to boost the grain yield of wheat, it was done to outline compression between triple test cross and six populations.

Materials and methods

The current study was conducted over the duration of three winter growing seasons -2016/2017, 2017/2018, and 2018/2019 at Tag EI-Ezz Research Station, Dakhlia Governorate Agriculture Research Center. In 2016/2017 season the parental wheat genotypes of local origin were grown and two crosses were made by hand; Gemmeiza11 X Misr1 and Gimmeiza12 X Misr2. The parent wheat genotypes' pedigree is displayed in (Table, 1). In the second growing season of 2017/2018, seeds from two F_1 plants were seeded, and the F_1 plants were selfed to create F_2 seeds. The F_1 plants were then crossed with P_1, P_2, and F_1 to produce backcross 1 (BC_1) (F_1 X P_1), backcross 2 (BC_2) (F_1 X P_2), and P_1 X P_2 (F_1 seeds), respectively. On November 20, 2018, triple test crosses of the two crossings and received seeds from the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) were seeded, and the results were assessed using a randomized full block design with three replications. Rows were 2 meters long. The distance between rows was 20 cm, and the distance between plants was 10 cm. The plot measured $6m^2$ (2x3 m). Two rows each for each parent, F_1 and backcrosses, and five rows for F_2 generations make up the experimental plot. The approved agricultural methods for producing wheat were used.

Table (1) pedigree of the studied parental wheat genotypes

Serial number	**Genotypes**	**Pedigree**
1	**Gemmeiza11**	**Maya 74/ on // 1160 .147/3/Bb/Gall /4 /Cha „S„**
2	**Misr1**	***T. aestivum* / Bon // Cno /7CCno /Mfd // Man „S„**
3	**Gemmeiza12**	**Vcm / Cmo 67 „S„ /7C/3/Kal / Bb**
4	**Misr2**	**Giza 155 //Pit62 //LR64/3/Tzpp/ Knott**

2- Recorded data:

The characters that were analyzed were days to heading (day) and flag. Leaf area (cm^2), number of spikes per plant, number of grains per spike, weight per 1000 grains (g), and plant yield of grains (g). In each replication, 50 F_2 plants were labeled, 20 BC_1 and BC_2 plants, and 10 individual plants for each of the parental genotypes and F_1s were used to collect data.

3- Biometrical analysis:

The "t" statistical test was applied to test the differences between parental genotypes for the examined characters before taking the biometric analysis into account.

a- Testing for the genetic model:

The scaling test A, B and C were applied, the following formulas were used by **Mather and Jinks (1982)** to determine whether non-allelic interactions existed:

$A = 2\ Bc_1 - P_1 - F_1$.

$B = 2\ Bc_2 – P_1,-F_1$, and

$C = 4\ F_2 – 2\ F_1 - P_1 – P_2$

The **Cavalli (1952)** joint scaling test was used to determine whether the genetic model governing the investigated features was adequate. When there was no nonallelic interaction, the simple genetic model (m), (d), and (h) was used due to the unknown biased effect of nonallelic interaction, whereas when there was nonallelic interaction, the analysis was carried out using the six-parameter genetic model of **Jinks and Jones (1958)** to estimate the interaction types involved:

m = Mean of F_2.

d= Additive gene effects = $B_1, - B_2$

h= Dominance gene effect = $F_1 – 4\ F_2 - (1/2)\ P_1 - (1/2)\ P_2 + 2\ B_1 + 2\ B_2$,

i= Additive x Additive = $2\ B_1 + 2\ B_2 – 4\ F_2$,

j= Additive x Dominance = $B_1 – (1/2)\ P_1 - B_2 + (1/2)\ P_2$ and

I= Dominance x Dominance= $P_1 + P, + 2\ F_1 + 4\ F_2 – 4\ B_1 – 4\ B_2$.

Using the "t" test as an impact, the importance of genetic components was evaluated.

Using the **Mather (1949)** and **Mather and Jinks (1971)** method, the genetic components of variation for each character in the examined crosses were divided into additive (D), dominant (II) genetic variance, and environmental variance (E):

Ew = Y. (VP1 + VP2 + 2VF1).

D = 4 VF2 - 2 (VB 1 + VB2).

H = (VB1 + VB2 - VF2 - Ew) and

F = (VB2 – VB1,)

$(H/D)^{0 \cdot 5}$ = Average degree of dominance

$F/ (DxH)^{0 \cdot 5}$

presents scant evidence that the amount or sign of dominance at different loci is particularly consistent.

Heritability in narrow sense (Tn) and Heritability in broad sense (Tb) were estimated. plants were randomly labeled from each cross and crossed back to their grandparents (P_1 and P_2) and F_1 between then to produce three types of families L_1 (F_{2i} x P_{1i}), L_2 (F_{2i} x P_{2i}) and L_3 (F_{2i} x F_{1i}) in each cross. On November 10th, the triple test cross families (L_1, L_2 and L_3) were planted using a randomized complete block design with tree replications together with the parents, F_1 and F_2 in each cross. Rows were 3 meters long and 20 cm apart. Plant to plant spacing was 10 cm. Data were triple test crosses recorded on ten competitive plants from each family in each replication for day 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:

The data were statistically analysed using the traditional two-way analysis of variance before moving on to the biometric analysis. 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:

Thirty values of ($L_{1i} + L_{2i} - 2L_{3i}$) were used in the test of epistasis. To test for general epistasis, I=1 to 30 with 30 degrees of freedom was utilized. Epistasis was divided into an item with one degree of freedom, and the J and L varieties of epistasis were tested (dominance x dominance and additive x dominance).

2- Detecting additive genetic variation:

The presence of an additive component variance is detected and estimated using the variance component of ($L_{1i} + L_{2i} + L_{3i}$).

3- 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 **Comostock and Robinson (1952).**

4- Detecting dominance variation:

The presence of dominance variance is examined using the variance component of (L_{1i}-L_{2i}).

5- Estimation of the genetic contributions to variance:

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 ⅛ F. The correlation coefficient of sums/differences was used to test the significance of "F" value (**Jinks *et al.*, 1969**).

6- Predicting the properties of recombinant lines:

In accordance with **Jinks and Pooni (1976), Pooni and Jinks (1978), Toledo *et al.* (1984), and Hayward *et al.* (1993)**.

7-Genetic correlations:

The means of triple test cross families in each character were computed and used to calculate the following simple genetic correlations; epistasis ($L_{1i} + L_{2i} - 2L_{3i}$), dominance ($L_{1i}$-$L_{2i}$) and additive ($L_{1i} + L_{2i} + L_{3i}$), **Kearsy and Jinks, (1968)**; **Jinks and Perkias, (1970)** and **Kearsey *et al.*, (1987).**

Results and discussion

1- Mean performance:

Before considering the biometrical analysis for the studied characters, the "t" statistical test was applied for testing parental genotypes involved. The "t" value was significant; suggesting that employed displayed enough amount of genetic variability. Thus, genetic differences for the genes controlling the studied characters were detected (Table, 2).

Mean and Standard error of the six populations (P_1, P_2, F1, F_2, BC1 and BC_2) of two wheat crosses for studied characters are given in (Table, 2). According to the mean of F_1 as compared with its standard error (S.E.).

Table 2 : Mean performance $\pm$ standard error of the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the two Egyptian wheat crosses for studied characters

Characters	**Heading date (days)**		**Flag leaf area (cm^2)**		**Number of spikes/ plant**		**Number of grains / spike**		**1000-grain weight (g.)**		**Grain yield/ plant (g.)**	
Population	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**
P_1	99.5 +0.23	100.10 +0.19	42.97 +0.29	43.80 +0.34	7.66 +0.11	6.45 +0.09	65.82 +0.36	69.11 +0.31	59.33 +0.29	62.17 +0.38	19.70 +0.10	21.12 +0.08
P_2	93.0 +0.20	92. 5 +0. 13	45.0 +0.18	40.23 +0.20	6.33 +0.13	5.83 +0.15	62.14 +0.29	58.32 +0.28	65.46 +0.24	57.35 +0.31	18.51 +0.14	26.49 +0.07
F_1	96.32 +0. 31	91.85 +0.26	47.24 +0.33	45.81 +0.37	8.13 +0.17	6.92 +0.19	69.18 +0.39	73.81 +0.41	67.28 +0.35	66.53 +0.34	25. 93 +0. 16	24.54 +0.11
F_2	102.01+0.71	99.53 +0.93	46.16 +0.84	44.82 +0.92	7.73 +0.28	6.52 +0.37	68.88 +0.91	72.53 +0.82	66.21 +0.84	65.42 +0.79	24.17 +0.28	23.34 +0.23
BC_1	103.36+0.54	100.52 +0.48	46.02 +0.94	44.51 +0.91	6.82 +0.19	6.14 +0.38	69.88 +0.67	71.93 +0.65	61.72 +0.51	64.81 +0.58	23.09 +0.23	22.08 +0.26
BC_2	92.01 +0.75	90. 10 +0.92	47.93 +0.65	42.13 +0.61	6.98 +0.27	6.73 +0.20	65.16 +0.93	59.99 +0 88	68.16 +0.95	58.35 +0.87	24. 73 +0.26	20.49 +0.16
't'' .test	**	**	**	**	**	**	**	**	**	**	**	**
h= F1 - ½(p1 + p2)	0.07	-4.45**	3.26**	3.79**	1.13 **	0. 78 **	5.20 **	10 09**	4.88 **	6.77 **	6.82**	3.73 **
± S.E	+0.33	+0.28	+0.37	+0.41	+0.18	+0.20	+0.44	+0.45	+0.39	+0.42	+0.18	+0.12

Results indicated that the F_1 was earlier than the early heading for cross-2 (Gimmeiza 12X Misr2) whereas, the F_1 exceeded its high performing parent (HP) for remaining studied characters in two crosses. The results provide evidence for present of over dominance gene effects and increasing alleles were more frequent in the genetic constitution of wheat parental genotypes, and that dominant gene were dispersed. With the exception of cross-2 for days to heading, the F_2 mean of the two examined crosses for each character showed high values from high parents for all analyzed characters in the two crosses. This indicated a sizable level of genetic variability for these characters in the respective crosses. The dominance deviations reflected by the (h) value. Except for days to heading in two crosses, (F_1-MP = F_1 - P_1 + P_2/2) was positive and significant for all examined features. Significant and positive (h) values show that the parental genotypes' genetic make-up was dominated by increasing allele frequencies rather than decreasing ones and by the presence of heterotic effects. However, days to heading at cross - 2 had a negative and significant (h) value, demonstrating the predominance of decreasing alleles over increasing ones and the significance of dominance and I or dominance x dominance gene effects in the genetic control of these traits.

2- Component of genetic variance:

The evaluation of the genetic variance (Table, 3) showed that, for the first cross's days to heading and flag leaf area, number of grains per spike, weight in 1000 grains, and grain yield per plant, the dominance genetic variance (h) was higher in magnitude than the corresponding additive genetic variance (D). The average degree of dominance (H1/D) as a consequence was 0.5, which was greater than one unit. However, it was discovered that additive component (D) was the dominant type controlling for the final character in two crosses. So early segregating generations would benefit from phenotypic selection.

Table 3: Narrow sense heritability (Tn), derived parameters, and genetic variance components for the examined features in two wheat crosses

Characters	Days to heading (day)		Flag leaf area(cm2)		Number of spikes /plant		Number of grains / spike		1000-grain weight (g.)		Grain yield/ plant (g.)	
	1	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**
Genetic parameters												
D	0.2	1.2	0.1	0.9	0.09	0.17	0.72	0.66	0.46	0.29	0.07	0.02
H	1.1	0.6	2.1	0.9	0.	0.	1.44	1. 28	1.52	1.44	0.08	0.10
E	0.0	0.0	0.0	0.	0.02	0.03	0.13	0.12	0.09	0.12	0.02	0.01
F	0.2	0.	-	-0.	0.04	-	0.44	0.37	0.65	0.43	0.02	-
Derived parameters												
√ H/D	2.	0.7	3.4	0.9	0.71	0.70	1.41	1.39	1.81	2.23	1.04	2. 22
F / √ DH	0.4	0.6	-	-	0.19	-	0.43	0.40	0. 77	0.66	0.26	-
Tn	0.	0.6	0.1	0.5	0.60	0.63	0.42	0.41	0.33	0.23	0.48	0.21

The negative value "F" together with the ratio F/ $(H1/D)^{.05}$ for flag leaf area (1st and 2nd crosses), number of spikes / plant and grain yield/plant (2nd cross). Thus the decreasing alleles were more frequent But, for the remaining characters in two crosses the increasing alleles exceeded the decreasing ones. Heritability in narrow sense was high for days to heading and flag leaf area (2nd cross) 0.65 and 0.58, respectively, number of spikes/plant (1st cross) (0.60) and (2nd cross) (0.63). Suggesting the importance of straight forward phenotypic selection method to improve characters in this respect **Al Kaddoussi and Eissa (1989)**, **Hassan (1993)** and **Salama (2002)**. However, the heritability values for the remaining traits ranged from 0.12 for flag leaf area

(1st cross) to 0.48 for grain output per plant (1st cross). These findings are consistent with those from **Al Kaddoussi (1996)**, **Sultan *et al*. (2005)**, and **Salama (2007)**.

3- Adequacy of genetic model

With the exception of number of spikes/plant, the non-allelic interaction tests (A, B, and C) for the researched characters (Table, 4) demonstrate the significance of epistasis in the inheritance of the studied characters (2nd cross). The additive dominance model may not be adequate to explain the inheritance of these features, according to significance x2. Thus, the conclusions of **Al Kaddoussi and Eissa (1990)** and **Salama (2002)** are supported by the results. With the exception of the number of spikes/plant in two crosses, the separation of the interaction types using a six parameter genetic model revealed significant (d) gene effects for all studied characters in two crosses, and significant dominance (h) was shown for days to heading (2nd cross) and grain yield/plant (1st cross). **Hassan (1993)** and **Salama (2002)** found comparable results.

Table 4: Testing for non - allelic interaction (A, B and C), x-2 and six para- meters genetic model for studied.

Parameters		**Non-allelic interaction test**			**Joint scaling test**	**Six- parameter genetic model**					
Characters	**Cross**	**A**	**B**	**C**		**M**	**(d)**	**(h)**	**(i)**	**(j)**	**(l)**
Days to Heading (day)	**1**	10.92 **	-1.3	22.9	**	102.01**	11.35**	-17.23	-17.66	8.1-**	11.70**
	2	9.09**	-4.15	21.82**	**	99.53 **	10.42**	21.33 **	-16.88	6.6-2**	11.94**
Flag leaf area (cm²)	**1**	1.83	3.62 **	2.19	**	46.16 **	-1.91	6.51	3.26	-0.-89	-8.71
	2	4.94**	0.23	3.63	**	44.82 **	2.38 *	-2.20	-6.0	0-.59	8.37
Number 0f spikes/plant	**1**	-2.15*	-0.50	0.67	**	7.73**	-0.16	-2.18	-3.28	-0-.82**	5.97 **
	2	-1.09	0.71	-0.04	N.S	6.52**	-0.59	0.44	-	--	-
Number of grains spike	**1**	4.76**	2.36	9.2**	**	68.88 **	4.72 **	-0. 24	-5.44	2.8-8**	1.68
	2	0.94	2.15	15.07**		72.53 **	11.94 **	-16.18	-26.28	6.-54**	37.49**
1000-grain weight (g)	**1**	-3.17*	3.58	5.49	**	66.21 **	-6.44	-15.19	-5.08	- -3.37*	4.67
	2	3 01 *	-7.18	9.1**	**	65.42 **	6.46 **	-8.59*	-15.36	4.05*-	21.62**
Grain yield / plant (g.)	**1**	0.55	5.02 '*	6.61' *	**	24.17 * *	-1.64	5.78**	-1.04	-2.23-**	-4.53
	2	-1.5**	-4.05	2.67 **	**	23.34 **	1.59 **	-0.4.48	-8.22*	1.27-**	13.77**

The most important digenic interaction as computed by the six parameter genetic model were; additive x dominance (j) for days to heading and number of grains/spike (two crosses), 1000-grain weight and grain yield / plant (2nd cross). Significant dominance x dominance (l) were the prevailed type that controlled days to heading (1st and 2nd crosses), number of spikes/plant (1st cross), number of grains/spike, 1000-grain weight and grain yield / plant (2nd cross).

For wheat genotypes to increase grain yield and early mature ones to close the gap between production and consumption in Egypt, this knowledge is very important.

Triple test crosses analysis

Mean squares of the analysis of variance (Table, 5) revealed significant between families terms in 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.

1- Test for epistasis:

Mean squares for epistasis (Table, 6) provide evidence for significant overall epistasis for all studied characters in two crosses in this respect was reported by **Nanda *et al.* (1983)** and **Iqbal, Singh *et al.* (1989)**. When the overall epistasis was divided into the I type (additive x additive), dominance x dominance, and (j + l) type, the results showed that significant both kinds for all analyzed characters.

Table 5: 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	**D.F**	**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)**	
		1	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**
		**	**	**	**	**	**	**	*	**	**	**	**	**	**		
Between (L_{1i}, L_{2i}, L_3) 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_{1i}, L_{2i}) 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**

Table 6: Mean squares for testing of epistasis ($L_1+L_2 - 2L_3$) for the examined features in the wheat crosses.

Mean Squares																	
Characters	**D.F**	**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)**	
		1	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**
Epistasis		**	**	**	**	**	**	**	*	**	**	**	**	**	**	**	**

$(L_{1i}+ L_{2i}- 2L_3)$ families overall	**30**	**13.501**	**16.852**	**17.993**	**21.58**	**5.693**	**4.821**	**6.532**	**4.824**	**6.993**	**11.253**	**19.657**	**17.883**	**0.235**	**0.272**	**5.491**	**5.001**
		**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**
(I) Type	**1**	**27.962**	**39.311**	**52.561**	**47.779**	**26.660**	**19.481**	**22.775**	**16.642**	**23.521**	**46.862**	**55.381**	**35.862**	**0.665**	**0.819**	**7.617**	**6.852**
		**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**
J + L types	**29**	**13.00**	**16.077**	**16.801**	**20.681**	**4.97**	**4.315**	**5.792**	**4.416**	**6.42**	**10.025**	**18.425**	**17.259**	**0.220**	**0.253**	**5.417**	**4.937**
Within families within replicates	**2430**	**0.210**	**0.302**	**0.641**	**0.482**	**0.350**	**0.614**	**0.162**	**0.148**	**0.530**	**0.401**	**0.652**	**0.831**	**0.010**	**0.014**	**0.641**	**0.512**

The importance 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. Therefore selection in early segregating generation would be effective to improve these characters. In this respect (**Eissa 1994**, and **Iqpal, Singth *et al*. (1989)**. The epistasis of (j + l) is not fixable by selection and would hence not favorable for developing pure lines cultivars. Therefore, population improve through pedigree method might be give a good response (**Jensen, 1970**).

2- Detection and estimation of additive, dominance, genetic components:

The additive genetic variance was significant for all analyzed characters in both ways of estimating the additive genetic variance, according to the analysis of variance for sums $L_1+L_2 + L_3$ and L_1-L_2 (Table, 6). The dominance genetic variance was significant for all examined features, according to the analysis of variance for differences $(L_{1i} - L_{2i})$ (Table, 7). These results provide evidence for the presence of additive and dominance genetic system controlling the studied character in these crosses similar results were obtained by **Singh (1976)**, **Eissa (1994 a)**, **Al-Kaddoussi (1996)** and **Salama *et al*. (2006)**.

Table 7: Mean squares of the analysis additive $(L_1 + L_2 + L_3)$ and N.C.M $(L_1 + L_2)$ and dominance $(L_1 – L_2)$ of two wheat crosses for the studied characters.

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)**	
Item	**D.F**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**	**1**	**2**
Additive$(L_1+L_2 +$ $L_3)$ families		**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**
Within families within replicates	**29**	**9.226**	**8.512**	**13.251**	**12.422**	**6.566**	**7.879**	**1.002**	**1.731**	**7.421**	**6.321**	**9.201**	**9.510**	**0.172**	**0.163**	**5.201**	**4.00**

N.C.M. additive	**2430**	**0.210**	**0.302**	**0.641**	**0.482**	**0.350**	**0.614**	**0.162**	**0.148**	**0.530**	**0.401**	**0.652**	**0.831**	**0.010**	**0.014**	**0.641**	**0.512**
L_1+L_2 Between (L_1+L_2) Families		**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**
Within families within replicates	**29**	**6.821**	**6.314**	**9.220**	**8.134**	**4.513**	**5.248**	**0.852**	**1.361**	**5.848**	**4.793**	**7.301**	**6.959**	**0.140**	**0.139**	**3.676**	**3.003**
Dominance	**1620**	**0.221**	**0.340**	**0.710**	**0.653**	**0.412**	**0.963**	**0.113**	**0.207**	**0.410**	**0.602**	**0.690**	**0.708**	**0.013**	**0.012**	**0.591**	**0.793**
(L_1-L_2) Between (L_1-L_2) Families		**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**
Within families within replicates	**29**	**5.656**	**3.412**	**6.991**	**4.823**	**3.517**	**4.232**	**0.791**	**0.929**	**4.656**	**3.143**	**5.008**	**4.947**	**0.111**	**0.132**	**3.050**	**3.026**
Additive (L_1+L_2+L_3) families	**1630**	**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**

Table 8: Estimates of additive (D) dominance (H) and direction of dominance (F) in two wheat crosses for the studied characters.

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)**	
Parameters	**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	**-165.23**	**-191.92**	**-144.31**	**-190.32**	**163.61**	**149.82**	**96.53**	**85.72**	**53.506**	**163.62**	**151.93**	**140.66**	**0.301**	**0.226**	**5.824**	**6.697**
r.sums/diferences	**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**

The estimates of additive (D), dominance (H) and direction of dominance (F) give in (Table, 8), indicated that the magnitude of the dominance components were larger 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 over dominance gene effects in the genetic control for these characters, However, for the remaining characters, the additive gene effects were discovered to be the predominate kind of these characters (**Eissa 1994a and Salama *et al.* (2006)**.

For 1000-grain weight in both crosses, the (F) values were positive and substantial, which explains why dominance appeared to be acting in a single direction. The F value was unimportant because the remaining characters had ambidirectional dominance.

3- Predicting recombinant lines' characteristics:

Recombinant inbread lines are intended to be produced by several selfing systems in order to be employed directly or to create F_1 hybrids of many cross hybrids. Breeding techniques can be used to extract such inbreds. These are all labor-intensive, sluggish techniques.

Table 9: 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 inbreds $m \pm 2\sqrt{D}$**		**Probability $(d)\sqrt{D}$**	**P max $m+h / \sqrt{H/D}$**	**2nd cycle of F_1-F_2 $\sqrt{\frac{1}{2}D+\frac{1}{4}H}$**	**Proportion of inbreds falling outside parental range%**
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**
Flag 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**

To solve these issues from looking at the early generations, predictions can be drawn. According to the prediction results shown in (Table, 9) it may be possible to predict as early as possible for transgressive segregants that outperform parental range for days to heading and flag leaf area in cross 1 expect to throw a reasonable proportion of recombinant lines that outperform parental range. In this respect **Eissa 1994** and **Awaad 1996** and **Al-Kaddussi (1997)**. The -highest proportion of recombinant lines in cross 2 were obtained grain yield / plant.

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