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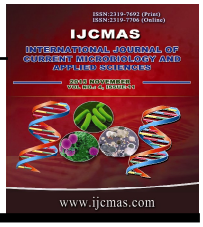

Original Research Article

Using Triple Test Cross Analysis to Estimates Genetic Components, Prediction and Genetic Correlation in Bread Wheat

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Keywords

Wheat, Triple test cross analysis, Epistasis, additive, Dominance, Prediction and genetic correlation

A B S T R A C T

Studies were conducted in 2011/12, 2012/13 and 2013/14 to detect epistasis, additive and dominance genetic effects for eight quantitative traits using triple test cross analysis and predicted a new recombinant lines and genetic correlation between this traits. Significant epistasis is presented in most traits studied. Additive × additive epistatic type was found to be much larger in magnitude than additive × dominance and dominance × dominance (J + L) epistatic types for all traits studied. Both additive (D) and dominance (H) genetic components play an important role in the inheritance of all traits studied except number of kernels per spike and grain yield per plant. The average degree of dominance $(H/D)^{1/2}$ was in the range of partial dominance for all traits studied. Predicting revealed that it could be possible to derive reasonable proportion of new recombinants which are falling out side parental range for grain yield per plant, no. of kernels per spike, no. of spikes per plant, 1000-kernels weight and spike yield. Genetic correlation revealed that additive and epistasis genetic correlations among some traits suggesting common genetic pool. Thus, selection based on additive genetic correlation indicated that indirect selection via, spike yield, 1000-kernels weight and grain yield per plant would be effective.

Introduction

Triple test cross is one of the best design for detecting and estimating genetic components of variation for quantitative traits. So many wheat breeders have been used T.T.C analysis in wheat that proposed by Kearsey and Jinks (1968). Information of the type of gene action involved in the inheritance of traits is helpful in deciding the breeding procedures to be followed for plant improvement and is necessary for efficient utilization of available germplasm in a plant breeding programe. Therefore, the presence of epistasis (additive × additive, additive × dominance, dominance × dominance) should be studied precisely before deciding any breeding programe. T.T.C is considered one of 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 Youns, 1986).

The aim of many selfing breeding 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 triple test cross (Pooni and Jinks, 1979).

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 T.T.C makes computed correlations from them more reliable. In wheat, the correlation of components of genetic variance was computed using T.T.C analysis by Eissa (1994c), Al-Kaddoussi (1997), Menshawy (2008), Morad (2012) and Dawwam *et al.* (2015).

The objectives of this study were: 1) Existence of epistasis and to determine the additive (D) and dominance (H) variances of quantitative traits in wheat. 2) To make prediction for traits studied 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 the Experimental Farm, Faculty of Agriculture, Minufiya University at Shebin El-Kom, Egypt during the three successive seasons of 2011/2012, 2012/2013 and 2013/2014. In the first season (2011/2012), two genotypes of bread wheat, differ in most of their agronomic traits namely Gemmeiza11 and Masr 1, were crossed to obtain their F1 progeny (Gemmeiza11 × Masr 1) to be used as three testers. The pedigree of bread wheat genotypes are illustrated in table 1.

Fifteen wheat varieties, namely Gemmeiza 9, Gemmeiza 10, Sahel, Shandaweel 1, Giza 167, Giza 168, Sakha 8, Sakha 61, Sakha 69, Sakha 94, Sids 4, Sids 6, Sids 8, Sids 9 and Sids 12 each was crossed to the three testers Gemmeiza 11 (P1), Masr 1 (P2) and their F1 (Gemmeiza 11 × Masr 1) to generate 45 crosses i.e. 15 L1i, 15 L2i and L3i progeny families of a triple test cross design in 2012/2013 winter growing season. All plant materials, the forty five families (crosses), their fifteen parents and the three testers were grown in a randomized complete block design with three replicates in 2013/2014 winter growing season. Each progeny family was growing in 3m long row. The spacing between (row to row distance) and within (plant to plant distance) rows were maintained at 30 and 10 cm, respectively. All the normal agronomic practices were followed as usual in the ordinary wheat field in the area of study. Data were scored on ten guarded plants from each row in each replications for the eight characters, heading date (days), plant height (cm), no. of spikes per plant, spike length (cm), no. of kernels per spike, spike yield (g), 1000-kernels weight (g) and grain yield per plant (g).

Statistical analysis

The detection of epistasis was done according to the method outlined by Kearsey and Jinks (1968) and is based on genetic model;

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

Where,

L_{ijk} = Phenotypic value of cross between tester i and line j in k replication.

M = Overall mean of all single and three way crosses.
G_{ij} = Genotypic value of cross between tester i and line j.
R_k = Effect of k^{th} replication.
E_{ijk} = Error.

The mean squares for deviations $L_{1i} + L_{2i} - 2L_{3i}$ 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 $L_{1i} + L_{2i}$ and differences $L_{1i} - L_{2i}$ were obtained to detect the direction of dominance, according to Jinks and Perkins (1970). The degree of dominance was calculated as $(H/D)^{1/2}$.

The proportion of superior inbreds, that outperform their parental range, is equal to the normal probability integral corresponding to the value $[d]/\sqrt{D}$ while, the range of inbred lines is $m \pm 2\sqrt{D}$ wherem = $\overline{L_3}$ 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.

Additive (Ra), dominance (Rd) and epistasis (Ri) correlation coefficients were computed from $(\overline{L_{1i}} + \overline{L_{2i}} + \overline{L_{3i}})$, $(\overline{L_{1i}} - \overline{L_{2i}})$and $(\overline{L_{1i}} + \overline{L_{2i}} - 2\overline{L_{3i}})$, respectively.

Results and Discussion

The analysis of variance for all traits studied is presented in table 2. Genotypes, hybrids and parents mean square estimates were found to be highly significant for all traits studied, indicating the presence of variability among hybrids and their parents.

Testers mean squares were found to be highly significant for all traits except no. of kernels per spike. The mean performance of the two parents Gemmeiza11 and Masr 1 (P1 vs P2) were significantly different from each other in all traits except no. of kernels per spike. The unbiased estimates of additive and dominance gene action and unambiguous test of epistasis would only be achieved when the testers are different from each other. However, when this condition of difference between two parents is not met, the estimates are biased to an unknown extent (Kearsey and Jinks, 1968; Jinks *et al.*, 1969).

Test for epistasis

The analysis of variance for testing the presence of epistasis in the inheritance of all traits studied is presented in table 3. The mean square for the deviations $L_{1i} + L_{2i} - 2L_{3i}$ revealed the presence of significant epistasis for all traits studied except plant height.

Partitioning of the total epistatic effect revealed the presence of highly significant additive × additive (i) type of epistasis for all traits studied. Also, estimates of additive × dominance and dominance × dominance, J + L types of epistasis mean square were highly significant for all traits studied except plant height and no. of kernels per spike. The additive × additive epistatic type (i) was found to be much larger in magnitude than additive × dominance and dominance × dominance (J + L) epistatic types for all traits studied, indicating that fixable components of epistasis were more important than non-fixable one in the inheritance of these traits. The same results were reported by Eissa (1994a,b), El-Nahas (2005), Esmail (2007) and Morad (2012).

Detection of genetic variance components

Analysis of variance for sums ($L_{1i} + L_{2i}$) and difference ($L_{1i} - L_{2i}$) are presented in table 4. The mean square due to sums were found to be highly significant for all traits studied, indicating the presence of additive genetic variance for these traits. The mean square due to difference were also found to be highly significant for all traits studied except no. of kernels per spike and grain yield per plant, indicating the importance of dominance genetic variance for these traits.

The additive genetic variance (D) was found to be much larger in magnitudes than the dominance variance (H) for all traits studied. Consequently, it could be concluded that selection procedures based on accumulation of additive effects would be successful in improving all traits studied. However, to maximize selection advance, procedures which are known to be effective in shifting gene frequency when both additive and non-additive genetic variance are involved would be preferred. Similar results were previously obtained by Esmail (2007), El Massry (2009), Koumber (2011), Morad (2012) and Dawwam *et al.* (2015). The degree of dominance $(H/D)^{1/2}$ was less than unity for all traits studied suggesting the role of partial dominance in the inheritance of these traits and as certain the fact that in self pollination crops, most genes are homozygous and the over-dominance is rare. Further, the correlation coefficient between the sums ($L_{1i} + L_{2i}$) and difference ($L_{1i} - L_{2i}$) were found to be positive and significant for no. of spikes per plant indicating that dominance seemed to be acting in one direction. However, the correlation coefficient for the remaining traits was insignificant indicating the genes with positive and negative effects were equally distributed among the genotypes including in this study.

Prediction of superior recombinants:

Triple test cross is the useful sources for such information to make prediction of new recombinants line. These informations will allow predictions of the proportion of inbreds which as good as or superior to better parent of F1 hybrid. Prediction results given in table 5, revealed that it could be feasible to predict as early as possible for transgressive segregates and the highest proportions of recombinants which outperform parental range for grain yield per plant (49.20%), no. of kernels per spike (48.40%), no. of spikes per plant and 1000-kernels weight (47.60%), spike yield (47.21%), spike length (43.64%), plant height (43.63%) and heading date (41.29%).

For traits studied, the range of inbred likely to exceed parental range was nearly 40%. The obtained high proportion could be explained that the studied wheat cultivars 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. 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. In this respect, a reasonable proportion of new recombinants could be predicted for yield and its components in wheat by Eissa (1994c), Al-Kaddoussi (1997), Menshawy (2008) and Dawwam *et al.* (2015).

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

additive, dominance and epistasis genetic correlation illustrated in table 6. The results obtained provide evidence for positive and significant correlation between additive gene effects controlling between plant height and heading date, between no. of spikes per plant and heading date, between no. of kernels per spike, between spike yield and each of spike length and no. of kernels per spike, between 1000-kernels weight with those of spike length, no. of kernels per spike and spike yield, between grain yield per plant with those of no. of kernels per spike, spike yield and 1000-kernels weight.

Table.1 The origin and pedigree of the studied parental bread wheat varieties

Pedigree	Origin	Name	No.
		lines	
Ald"S"/Huac"S"//CMH74A.630/5X CGM4583-5GM-1GM-0GM	Egypt	Gemmeiza 9	1
MAYA74"S"/ON//1160-147/3/BB/GLL/4/CHAT"S"/5/CROW"S".	Egypt	Gemmeiza 10	2
NS.732/PIMA// Vee"S". SD 735-4SD-1SD-1SD-0SD	Egypt	Sahel	3
SITE//MO/4/NAC/TH.AC//3*PVN/3/MIRLQ/BUC.CMSS93B00567 S-72Y-010M-010Y-010M-OHTY-OSH	Egypt	Shandaweel 1	4
Au/UP301//G11/SX/Pew"S"/4/Mai"S"/May"S"//Pew"S"CM67245-C-1M-2Y-1M-7Y-1M-0Y	Egypt	Giza 167	5
M1L/BUC//SeriCM93046-8M-0Y-0M-2Y-0B	Egypt	Giza 168	6
INDUS 66 / NORTENO "S". PK 3418-6S-1 SW-0S	Egypt	Sakha 8	7
Inia/RL4220//7C/Yr"S"CM15430-25-55-0S-0S	Egypt	Sakha 61	8
Inia/RL4220//7C/Yr"S"CM15430-25-65-0S-0S	Egypt	Sakha 69	9
OPATA/RAYON//KAUZ.CMBW90Y 3180-0TOM-3Y-010M-010Y-10M-015Y-0Y-0AP-0S.	Egypt	Sakha 94	10
Maya"S"/Mon"S"/ CMH74.A.592/3/CHZa157*	Egypt	Sids 4	11
Maya"S"/Mon"S"/CMH74.A592/3/Sakha8*2SD10002-4sd-3sd-1sd-0sd	Egypt	Sids 6	12
Maya"S"/Mon"S"/CMH74.A592/3/Sakha8*2SD10002-14sd-3sd-1sd-0sd	Egypt	Sids 8	13
Maya"S"/Mon"S"/4/CMH47-428/MRC//Jup/3/CMH47A-582/5/Giza-157*2	Egypt	Sids 9	14
BUC//7C/ALD/5/MAYA74/ON//1160.147/3/BB/GLL/4/CHAT"S"/6/ MAYA/VUL//CMH74A.630/4*SX. SD7096-4SD-1SD-1SD-0SD.	Egypt	Sids 12	15
		testers	
BOW"S"/KVZ"S"//7C/SER182/3/GIZA168/SAKHA61 GM7892-2GM-1GM-2GM-1GM-0GM (P_1)	Egypt	Gemmeiza 11	1
OASIS/KAUZ//4*BCN/3/2*PASTOR. CMSS00Y01881T-050M-030Y-030M-030WGY-00M-0Y-0S (P_2)	Egypt	Masr 1	2
($P_1 \times P_2$)	Egypt	F_1	3

Table.2 Mean squares of the analysis of variance of (L1i, L2i and L3i) triple test cross hybrids for all traits studied

Grain yield/ plant (g)	1000-kernels weight (g)	Spike yield (g)	No. of kernels/ spike	Spike length (cm)	No. of spikes/ plant	Plant height (cm)	Heading date (days)	d.f	Sours of variance
2.34	0.55	0.26	45.33	0.17	0.32	57.78	0.19	2	Replications
158.19**	186.99**	3.88**	700.38**	15.61**	27.09**	166.43**	127.90**	62	Genotypes
122.29**	201.00**	4.29**	726.15**	14.98**	25.03**	138.92**	89.52**	44	Hybrids
259.75**	126.07**	3.05**	559.29**	17.98**	29.39**	228.56**	216.13**	17	Parents
11.43**	606.50**	0.21*	1965.05**	2.71**	78.62**	320.68**	316.86**	1	Hybrids vs parents
33.36**	96.33**	3.50**	673.19**	18.46**	23.75**	233.56**	234.02**	14	Lines
10.94**	21.12**	0.78**	15.16	7.01**	6.68**	155.63**	25.23**	2	Testers
3926.82**	752.30**	1.31**	52.98*	33.30**	153.77**	304.37**	347.39**	1	Line vs tester
17.14**	36.65**	0.69**	16.30	12.44**	7.87**	243.97**	12.70**	1	P_1vs P_2
3.71	3.16	0.09	21.03	0.10	0.46	9.09	0.19	124	Error

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

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

Grain yield/ plant (g)	1000-kernels weight (g)	Spike yield (g)	No. of kernels/ spike	Spike length (cm)	No. of spikes/ plant	Plant height (cm)	Heading date (days)	d.f	Sours of variance
19.02*	43.66**	1.42**	145.50*	8.53**	6.41**	53.31	101.37**	15	Total epistasis
29.51**	418.18**	8.67**	1153.37**	86.14**	47.82**	156.98*	754.15**	1	I type epistasis
18.27*	16.91**	0.91**	73.51	2.98**	3.46**	45.91	54.74**	14	j+I type epistasis
13.31	0.87	0.045	3.64	0.13	0.03	79.44	0.08	3	I type epistasis x block
6.92	2.60	0.079	66.81	0.34	1.22	27.62	0.36	42	j+I type epistasisx block
7.35	2.48	0.077	62.60	0.32	1.14	31.08	0.34	45	Total epistasisx block

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

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

Table.4 Mean squares from analysis of variance for sums and differences and estimates of additive (D), dominance (H) and degree of dominance in triple test cross for all traits studied

Grain yield/ plant (g)	1000-kernels weight (g)	Spike yield (g)	No. of kernels/ spike	Spike length (cm)	No. of spikes/ plant	Plant height (cm)	Heading date (days)	d.f	Sours of variance
500.55**	785.81**	17.65**	3008.96**	59.51**	99.63**	285.39**	345.91**	14	Sums (L11+L21)
6.93	2.00	0.16	27.18	0.11	0.78	22.20	0.31	28	Error
7.10	8.42**	0.73**	38.66	1.18**	3.64**	45.00**	26.01**	14	Differences (L11-L21)
5.69	2.68	0.16	24.65	0.23	0.50	12.16	0.22	28	Error
658.16	1045.1	23.31	3975.70	79.19	131.80	350.92	460.81		D
1.87	7.65	0.74	18.68	1.27	4.19	43.77	34.38		H
0.05	0.08	0.18	0.06	0.12	0.17	0.35	0.27		$(H/D)^{0.5}$
-0.44	-0.23	0.17	0.25	0.15	0.56*	-0.29	0.04		r

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

r = correlation coefficients between sums (L1i + L2i) and differences (L1i - L2i).

Table.5 Predicting the range of inbred lines and the proportion of inbreds expected to fall outside their parental range for the traits studied

Proportion of inbreds falling outside parental range%	probability	Range of inbred	(D)	(d)	(m)	parameters Traits
41.29	0.22	298.16 – 212.31	460.81	4.74	255.23	Heading date
43.63	1.71	377.82 – 302.90	350.92	32.05	340.36	Plant height
47.60	0.06	55.59 – 9.67	131.80	0.69	32.63	No. of spikes/ plant
43.64	-0.16	61.14 – 25.56	79.19	-1.49	43.35	Spike length
48.40	0.04	346.68 – 94.47	3975.70	2.56	220.58	No. of kernels/ spike
47.21	-0.07	20.99 – 1.69	23.32	-0.38	11.34	Spike yield
47.60	-0.06	195.14 – 65.84	1045.10	-2.05	130.49	1000-kernels weight
49.20	-0.02	125.52 – 22.92	658.16	-0.76	74.22	Grain yield/ plant

Table.6 Additive (Ra), dominance (Rd) and epistasis (Ri) correlation coefficients among eight traits in the triple test cross

1000-kernels weight	Spike yield	No. of kernels/ spike	Spike length	No. of spikes/ plant	Plant height	Heading date	Type	Traits
						0.617*	Ra	
						-0.122	Rd	**Plant height**
						-0.367	Ri	
					0.380	0.660**	Ra	
					-0.011	-0.224	Rd	**No. of spikes/ plant**
					-0.002	-0.190	Ri	
				-0.495	0.029	-0.517	Ra	
				-0.334	-0.015	-0.024	Rd	**Spike length**
				-0.168	0.308	-0.420	Ri	
			0.666**	-0.228	-0.138	-0.510*	Ra	
			-0.139	0.048	0.144	0.050	Rd	**No. of kernels/ spike**
			-0.042	0.168	-0.224	0.041	Ri	
		0.743**	0.873**	-0.517*	-0.058	-0.452	Ra	
		-0.093	0.178	-0.117	0.357	-0.106	Rd	**Spike yield**
		0.231	0.134	0.093	-0.389	-0.163	Ri	
	0.818**	0.915**	0.800**	-0.256	-0.150	-0.510*	Ra	
	-0.080	-0.238	0.113	0.019	-0.176	-0.019	Rd	**1000-kernels weight**
	-0.620*	-0.250	-0.003	-0.221	0.410	0.233	Ri	
0.766**	0.637*	0.721**	0.467	-0.005	-0.352	-0.452	Ra	
-0.423	-0.203	0.262	-0.069	0.328	0.264	0.236	Rd	**Grain yield/ plant**
0.230	-0.196	0.061	-0.241	0.546*	-0.098	0.278	Ri	

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

Concerning the dominance genetic correlations, the results didn't have any positive and significant additive correlation between the traits in this investigation. Regarding epistasis genetic correlation the results indicated positive and significant correlation only between grain yield per plant and no. of spike per plant. From the results of genetic correlation, most of the characters were not associated with each other and confirmed that the T.T.C matting system was useful in breaking up undesirable linkage groups to obtain new recombinant lines. In this regard, Eissa (1994c), Menshawy (2008), Morad (2012) and Dawwam *et al.* (2015) reported the efficiency of triple test cross for obtaining new recombinant lines in wheat.

These investigation was designed to use triple test cross analysis to obtain additional information about type of gene actions, genetic correlation and predicting the likely performance of new recombinants that could be derived after series of selfing generations. Thus, this study helps breeder for rightful decision about effective breeding method to be applied for improving yield and its contributing traits.

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