JSAES
Journal of Sustainable Agricultural and Environmental Sciences

Print ISSN : 2735-4377
Online ISSN : 2785-9878
Homepage: https://jsaes.journals.ekb.eg/

Research Article

Genetic Analysis of Yield and its Components in Some Bread Wheat Crosses (*Triticum aestivum* L.)

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Article info: -
- **Received:** 14 July 2025
- **Revised:** 5 August 2025
- **Accepted:** 6 August 2025
- **Published:** 24 August 2025

Keywords:
Wheat; Triple Test Cross; Additive; Dominance; Epistasis.

Abstract:

To identify epistasis and evaluate genetic variance components in two bread wheat varieties namely (Misr 4 and Giza 171) and their F1 progeny (Male tester: L1, and L2, plus L3), had crossed with fifteen different bread wheat genotypes using the triple test cross procedure This study was carried out over three growth seasons (2020/2021 through 2022/2023. Exceptions of days to heading, 1000 kernel weight, grain filling duration, and all attributes examined showed considerable epistasis. Additive × additive interaction was significantly greater than the additive × dominance and dominance × dominance interactions. The tow genetic components (dominant and additive) had a significant impact on the inheritance of all traits. For all characteristics except plant height and spike length, the D component was significantly greater than the H one, resulting in (H/D)0.5 being less, suggesting partial dominance. Meanwhile, (H/D)0.5 were more than unity for plant height and spike length, exhibiting the importance effects of dominant gene of genetic control to such traits.

1. Introduction

Insufficient knowledge gene action governs of the inheritance of the various aspects of quantitative in question is one of the main factors limiting a genotype's low yielding capacity. This knowledge decides which breeding procedures are most efficient for improving genotypes to increase production capacity. Most strategies for calculating the components of variance for metrical features using second degree statistics encounter three unwelcome difficulties. Firstly, it is are no non-allelic interactions exist (epistasis). This being true for some characteristics but not for others. This may be true for some characters but not for others, and numerous scientists have reported epistasis in wheat (Esmail, 2007; Hendawy et al., 2007; Morad, 2012). Second, the standard errors of dominance component estimations are frequently much greater than those of the corresponding additive components. Third, linkage and correlated gene distribution in parents have distinct effects on additive and dominant genetic components. A good genetic model provides the breeder with unbiased and precise estimates of each genetic variation component. Kearsey and Jinks (1968) developed a strategy to overcome these three main obstacles. Ghanem (2008) and Kandil et al. (2023) reported that triple test cross (TTC) offers a clear test for epistasis as well as effective assessments of the additive and dominant components of genetic variation. This research aims to: 1) investigate the role of epistasis and other genetic variation components in the inheritance of grain yield and its components using triple test crosses, and 2) determine the most effective breeding practices to be used for their improvement, with the goal of obtaining genotypes with higher yielding capacity. 2) Detecting and estimating genetic variation's additive (D) and dominant (H) components.

2. Materials and Methods

The study was carried out at Egypt's EL-Gemmeiza Agriculture Research Station Experimental Farm for three consecutive growing seasons in 2020/2021, 2021/2022, and 2022/2023. Misr 4 and Giza 171, two bread wheat genotypes with different agronomic traits, were crossed in the first season (2020/2021) to produce their F1 progeny, Misr 4 × Giza 171, which were utilized as three testers, P1, P2, and F1. Table 1 exhibits the bread wheat genotypes' pedigree.

In 2021/2022 growing season, 45 crosses i.e. 15 L 1i, 15 L 2i, and 15 L 3i progeny families, were developed through the crossing of 15 distinct wheat varieties to the testers Misr 4 (P1), Giza171 (P2), and their F_1 (Misr 4× Giza171), namely Gemmeiza 12, Sakha 94, Sakha 95, Sids 14, Misr 1, Misr 2, Shandweel 2, Nubaria2, Bonsu, Sokol, Baj#1, Mucuy, Atlas, PBW343, and Kingbird #1 each. In 2022/2023. Randomized complete block design experiment with 3 replicates was conducted to establish all plant materials, including the 45 families (crosses), their 15 parents, and the 3 testers. Each progeny family was planted in two rows, long rows3-meter, separated 30 cm and within rows 10 cm.

The typical wheat field in the research area, all recommended agronomic processes were carried out as usual. Guarded 10 plants of each row in each replication were utilized to collect data for nine characters: Grain filling period (days), 1000-kernel weight (g), grain yield / plant (g), height of plant (cm), spikes number / plant, spike length (cm), number of kernel/ spikes, and days to heading (days), as well as days to maturity (days).

Table 1. Cultivars of bread wheat under study.

No	Name	Origin	Pedigree and selection history
Testers			
1	Misr 4	Egypt	NS732 / HER /3/ PRL / SARA // TSI / VEE 5 /6/F RET2 /5/ WHEAR / SOKOLL CM SA09Y007125-050Y- 050ZTM-0NJ-099NJ-0B-0EG
2	Giza171	Egypt	Sakha 93/Gemmeiza 9 Gz 2003-101-1Gz- 4Gz-1Gz-2Gz-0Gz
3	F_1	Egypt	(Misr 4 X Giza171)
Lines			
1	Gemmeiza12	Egypt	OTUS /3/ SARA / THB // VEE CMSS97YOO227S-5Y-010M-010Y-010M-2Y–1M-0Y-OGM
2	Sakha94	Egypt	OPATA / RAYON // KAUZ CMBW90Y3180-0TOPM-3Y-010M-010M -010Y-10M-015Y-0Y-0AP-0S
3	Sakha95	Egypt	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBLL1 CMSA01Y00158S-040P0Y-040M-030ZTM-040SY-26M-0Y-0SY-0S
4	Sids 14	Egypt	BOW "S" / VEE"S" // BOW"S" / TSI /3/ BANI SEWEF 1 SD293-1SD-2SD-4SD-0SD
5	Misr 1	Egypt	OASIS / KAUZ // 4*BCN /3/ 2*PASTOR CMSS00Y01881T-050M-030Y-030M-030WGY-33M-0Y-0S (P2)(
6	Misr 2	Egypt	SKAUZ / BAV92 CMSS96M03611S-1M-010SY-010M-010S-8M-0Y-0S
7	Line Shandweel 2	Egypt	QUAIU /5/ FRTE2*2 /4/ SNT / TRAP#1 /3/ KAUZ*2 / TRAP CMSS06B001095-0Y-099-ZTM-099NJ-099NJ-13WGY-0B-0SH
8	Line Nubaria 2	Egypt	FRTE2*2 /4/ SNI / TRAP#1 /3/ KAUZ*2 / TRAP // KAUZ*2 /5 /BOW /URES // 2*WEAVER /3 / CROC_1 / AE.SQUARROSA (213) // POG CGSS05B00144T-099TŌPY-099M-7WGY-0B-5Y-0B-NUB
9	BONSU	CIMMYT	MXI18-19\MTESTIGOSBW\12 CMSS08B00259S-099M-099NJ-30RGY-0B
10	SOKOLL	CIMMYT	MXI19-20\C8WYCYT\32 CMSS97M00316S-0P20M-0P20Y-43M-010Y
11	BAJ #1	CIMMYT	MXI19-20\C8WYCYT\121 CGSS01Y00134S-099Y-099M-099M-13Y-0B
12	MUCUY	CIMMYT	MXI19-20\M3NDCWYT\1 CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY
13	ATLAS	CIMMYT	MXI19-20\MICARDALINES\14 ICW08.50001-6AP-0AP-0AP-1TR
14	PBW343	CIMMYT	MXI18-19\MRUST&KBCHKS\3 CM85836-4Y-0M-0Y-8M-0Y-0IND
15	KINGBIRD #1	CIMMYT	MXI18-19\MRUST&KBCHKS\5 CMSS99M00216S-040M-030Y-030M-16Y-2M-0Y

Biometrical analysis

Kearsey and Jinks (1968), Jinks et al. (1969), and Jinks and Perkins (1970) conducted epistasis tests and estimated the additive (D) and dominant (H) components of genetic variation. Epistasis was detected using the method suggested by Kearsey and Jinks (1968) depending on the genetic model;

$$\mathbf{Lijk = M + Gij + Rk + Eijk}$$

Where,
Lijk = Phenotypic value of cross between tester i and line j in k replication.
M = Overall mean of all single- and 3-way crosses.
Gij = Genotypic value of cross between tester i and line j.
Rk = Effect of kth replication.
Eijk = Error

A mean squares of deviations analysis was employed to test for the presence of non-additive interactions between loci L1i+L2i-2L3. Total epistasis was divided into two types based on additive x dominance and dominance x dominance gene interactions: (i) type (additive x additive), and (i + j) type. Jinks and Perkins (1970) evaluated the direction of dominance by estimating the genetic components(dominance and additive) and computing the correlation coefficient (r) between sums (L1i + L2i)and differences (L1i - L2i). The$(H/D)^{1/2}$ (dominance degree) was calculated. The variance of sums (+) and difference (-) was utilized to determine the presence of dominating (H) and additive (D) genetic components in genetic variation, respectively. The direction of dominance and the types of genes displaying dominance can be determined by computing the correlation coefficients between sums (+) and differences (-).

3. Results

ANOVA for all studied traits is present in Table 2. Parents, hybrids, and genotypes mean squares for were highly significant for all variables investigated, indicating the presence of genetic diversity between hybrids and their parents. In general, the findings were consistent with those of Morad (2012), Dawwam et al. (2015), Divya and Panwar (2016), and Kandil et al. (2023). Except for spike length, the mean squares for the two parents, Misr 4 and Giza 171 (P1 vs. P2), were very significant for all of the characters under study.

Mean square estimates of hybrids vs. parents, as well as the average heterosis for all crosses, were found to be quite significantly for each attribute examined. Also, the fifteen wheat varieties (lines) were shown to differ significantly from the 3 testers (P1, P2, and their F1) in all attributes tested. Except for grain filling duration, all of the characteristics investigated had significant tester mean square estimates. Line vs. tester mean squares were significant for all characteristic except plant height, spike length, and 1000-kernel weight. Unbiased estimates of additive (D) and dominant (H) gene activity, an unambiguous epistasis test, are achievable in cases where the testers are different. However, biased to an unknown extent if no differences were discovered between the two testers, the estimates would be (Kearsey and Jinks, 1968; Jinks et al., 1969).

3.1. Investigations for epistasis:

Data in Table 3 was employed to detect epistatic interactions influencing the inheritance of the studied traits. Variance (L1i + L2i - 2 L3i) was significant, suggesting the presence of an overall epistasis. For all characteristics examined in this study, the overall effect of epistasis was found to be statistically highly significant. These findings correspond with those published by Ghanem (2008) and Kandil et al. (2023). Total epistasis can partitioning into three interactions types, (I) type (additive × additive), (L) type (dominance × dominance) and (J) type (additive × dominance) indicated that mean squares estimates for additive × additive (I) type was highly significant for all investigated characteristics. J+L epistasis mean squares were found to be highly significant for all traits. Except for days to heading, grain filling period, and 1000 kernel weight, the epistatic type (I) (homozygote × homozygote) overcame the other two epistatic types (J) and (L) (homozygote × heterozygote and heterozygote × heterozygote) significantly.

Table 2. Triple test cross hybrids (L1i, L2i, and L3i) mean squares for all traits..

Source of Variance	D.f	Days to Heading (days)	Days to Maturity (days)	Plant Height (cm)	No. of spikes/plan	Spike Length (cm)	No. of kernels spike	Grain filing Period (days)	100-kernels Weight (g)	Grain Yield plant (g)
Replications	2	0.30	3.81	0.28	1.91	1.71	0.57	5.86	1.61	2.09
Genotypes	62	29.43**	61.62**	77.97**	17.97**	2.40**	160.76**	61.43**	122.79**	365.05**
Hybrids	44	17.91**	44.67**	54.44**	19.85**	2.59**	155.89**	48.54**	110.83**	370.94**
Parents	17	60.65**	98.66**	127.97**	12.60**	2.03**	182.62**	91.26**	156.29**	359.44**
Hybrids vs parents	1	53.90**	88.85**	147.71**	6.81**	2.26**	171.11**	91.69**	187.15**	328.19**
Lines	14	108.33**	17.44**	53.57**	27.52**	1.39**	327.42**	59.11**	17.45**	484.30**
Testers	2	16.67**	24.00**	2.34**	36.65**	0.76*	654.80**	0.67	2.17*	824.38**
Line vs tester	1	59.74**	398.46**	0.36	63.78**	0.01	54.14**	149.63**	1.86	547.36**
P1vs P2	1	5.40**	177.99**	263.41**	26.54**	0.16	3.29**	121.40**	79.83**	201.46**
Error	124	0.70	0.61	0.76	0.51	0.30	0.85	1.33	1.33	1.17

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

Table 3. ANOVA testing for epistatic interactions among the studied traits in a triple test cross.

Source of Variance	D.f	Days to Heading (days)	Days to Maturity (days)	Plant Height (cm)	No. of spikes /plan	Spike Length (cm)	No. of kernels spike	Grain filing Period (days)	100-kernels Weight (g)	Grain yield plant (g)
Total epistasis	15	448.089**	180.0**	14.495**	7.033**	6.272**	72.835**	1196.089**	1985.759**	1023.785**
I type epistasis	1	78.184**	276.524**	228.811**	71.884**	16.431**	732.310**	246.422**	577.790**	1031.689**
J +L type epistasis	14	102.844**	270.089**	214.523**	67.561**	15.754**	688.345**	309.733**	671.655**	1031.162**
I type epistasis x Block	3	6.326	0.533	0.302	1.241	3.436	2.561	5.437	1.923	0.061
J +I type epistasis x Block	42	2.389	1.692	3.293	1.912	1.500	2.519	4.135	4.310	3.778
Total epistasis x Block	45	2.652	1.615	3.094	1.868	1.629	2.521	4.222	4.151	3.530

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

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

In wheat, a self-pollinating crop, the significant presence of (I) epistasis—a linear, fixable form of genetic variation—is particularly valuable as it is more easily utilized by breeders than either (J) or (L) epistasis. For the majority of the traits under investigation through standard hybridization and selection procedures, and pure lines for these traits can be developed. Similar findings were reported by Eissa (1994 a,b), Esmail (2007), Ghanem (2008), Morad (2012), El-Nahas, Marwa (2015), and Kandil et al. (2023). Table 4 illustrates the variance analysis for both sums (L1i+L2i) and differences (L1i - L2i). The mean squares for sums (L1i+L2i) were highly significant for all triats, showing additive genetic variation. Also, mean squares due to differences (L1i - L2i) were highly significant for all traits, suggesting that dominant genetic variance is effective for these characteristics. The same results were achieved by Hendawy et al. (2007), Koumber (2011), and Kandil et al. (2023)

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Table 4. ANOVA mean squares for sums and differences and the resulting estimates of additive (D) and dominance (H) genetic components, including the degree of dominance, for all traits in the triple test cross.

Source of Variance	D.f	Days to Heading (days)	Days to Maturity (days)	Plant Height (cm)	No. of spikes/ plan	Spike length (cm)	No. of kernels spike	Grain filing Period (days)	1000-kernels Weight (g)	Grain yield plant (g)
Sums (L_{11}+L_{21})	14	61.87**	113.41**	71.60**	46.34**	3.20**	409.10**	117.09**	250.04**	949.15**
Error	28	1.88	1.19	0.74	0.89	0.50	1.44	2.35	2.71	1.99
Differences (L_{11}-L_{21})	14	21.08**	100.59**	185.90**	41.82**	8.47**	319.32**	97.55**	224.73**	836.26**
Error	28	1.29	1.59	1.92	1.39	0.44	1.98	3.29	2.11	2.62
D		79.987	149.63	49.474	60.598	3.6006	543.55	152.99	329.77	1262.9
H		26.387	132.01	245.31	53.907	10.701	423.11	125.68	296.82	1111.5
$(H/D)^{0.5}$		0.574	0.939	1.611	0.943	1.724	0.882	0.906	0.949	0.938
r Correlation		-0.274	-0.218	0.048	-0.108	0.119	-0.161	-0.288	0.108	-0.508

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

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

4. Discussion

For the majority of the traits under research, the additive genetic variance (D) was greater than the dominance variance (H), except for plant height and spike length, where dominance variance was predominant. The results obtained by Ghanem (2008), Koumber (2011), Morad (2012), Dawwam et al. (2015), and Kan-dil et al. (2023) are similar. Less than unity values were found for (H/D)0.5 (the degree of dominance), indicating the role of partial dominance in the inheritance of all characters studied, with the exception of plant height and spike length, which were more than unity, indicating that overdominance controlled the inheritance of these traits. These findings are consistent with previous studies by Esmail (2007), Ghanem (2008), EL-Nahas and Marwa (2015), Dawwam et al. (2015), and Kandil et al. (2023). By calculating The correlation coefficients between sums ($\overline{L_{1i}} + L_{2i}$) and differences ($L_{1i} - \overline{L_{2i}}$), (the dominant alleles and the nature of their dominance), a negative and significant correlation (r) suggests that one gene type is dominant, while a positive correlation indicates the dominance of the other Because the correlation coefficient was insignificant, in this study, the genotypes were equally affected by both positive and negative gene effects. For the remaining traits examined, no significant correlation coefficients were found, indicating that these traits did not provide evidence for directional dominance in wheat, i.e., ambidirectional dominance. The results obtained herein indicate that epistasis is an integral component of the genetic structure of all traits studied in this investigation. Therefore, detection, consideration, and estimation of this component is important for establishing the most efficient breeding program to improve these traits studied. If epistasis is ignored, no specific conclusion can be established about the relative importance of additive, dominance, and epistasis, because epistasis has an undetermined impact on the calculation of dominant and additive genetic components. as in the current materials (Sood and Dawa 1999). Consequently, non-allelic interactions, which are represented for all traits explored in this investigation, can be modified using recurrent selection method to improve these traits. The application of recurrent selection has been advocated for the enhancement of quantitatively inherited traits in wheat by Hendawy et al. (2007), Ghanem (2008) and Heena Attri et al. (2021). Since nearly all traits evaluated in this study had significant values for both additive and dominant gene effects, utilizing a simple selection strategy in the early generations may not be effective in considerably improving these traits. Because additive gene effects play a significant role in late generations of segregating populations, the pedigree method of selection can successfully maximize the benefits of additive genetic components in these traits. Singh (1980), Singh and Dahiya (1984), Singh et al. (1988), Eissa (1994a-b), Katiyar and Ziauddin (1996), Salama (1998), Esmail (2007), Hendawy et al. (2007), and Al-Naggar et al. (2022) all arrived to similar conclusions.

5. Conclusions

The inheritance of all studied traits was significantly influenced by both additive (D) and dominant (H) genetic effects. For most traits, the magnitude of the additive component (D) exceeded that of the dominance component (H), with an H/D ratio of less than one indicating partial dominance. In contrast, plant height and spike length were exceptions; their H/D ratios exceeded one, suggesting that non-additive, dominant gene effects play a more critical role in controlling these specific traits

Author Contributions

Ghanem design and sowing the experimental trial. Ghanem, yahya and Yassin sharing in collected data. Ghanem wrote the manuscript. Yassin reviewed the manuscript and approved the final version for publication. All authors contributed to this article and approved the submitted version.

Acknowledgments: The authors are thankful to the Wheat Research Department, FCRI, and Wheat Disease Research Department, ARC for providing plant materials, finance and technical support in addition to the experimental farm and green house facilities.

Conflicts of Interest: This research was conducted without any commercial or financial ties that could be perceived as a conflict of interest.

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