RESEARCH ARTICLE

SABRAO Journal of Breeding and Genetics
57 (4) 1556-1563, 2025
http://doi.org/10.54910/sabrao2025.57.4.21
http://sabraojournal.org/
pISSN 1029-7073; eISSN 2224-8978

GENE ACTION ANALYSIS IN THE HALF-DIALLEL CROSSES OF BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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SUMMARY

The assessment of gene action in 10 × 10 half-diallel crosses in bread wheat (*Triticum aestivum* L.) was this study's focus, carried out during 2023–2024 at the Kirkuk Governorate, Iraq. The experiment based on the said breeding material had a randomized complete block design layout with three replications. The genetic analysis revealed that the t^2 values were nonsignificant for all traits, and the additive genetic variance (D) was significant for all studied traits. Dominant gene variations (H1 and H2) were higher than the additive gene variance for all traits, with H1 values exceeding H2. The average degree of dominance was greater than one, indicating a predominance of dominant gene action. The ratio of dominant to recessive alleles (KD/RR) exceeded one, reflecting unequal distribution of alleles among the genetic structures.

Keywords: Bread wheat (*T. aestivum* L.), gene action, genetic parameters, additive and dominance genetic variances, average degree of dominance

Key findings: In the bread wheat (*T. aestivum* L.), the genetic analysis revealed that t^2 values were not significant for most traits, except spike count. The dominance genetic variances were higher than the additive genetic variance for all traits, indicating a greater influence of dominant genes.

Communicating Editor: Prof. Naqib Ullah Khan

Manuscript received: January 20, 2025; Accepted: March 04, 2025

Citation: Hasan SA, Abdullah RM, Jaber HA (2025). Gene action analysis in the half-diallel crosses of bread wheat (*Triticum aestivum* L.). *SABRAO J. Breed. Genet.* 57(4): 1556-1563. http://doi.org/10.54910/sabrao2025.57.4.21.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most important staple food crop grown globally. Wheat is the chief source of protein and carbohydrates in the human diet (Mangl *et al.,* 2010). In addition to being a major source of starch and energy, wheat also provides substantial amounts of several components that are essential for health, notably protein, vitamins (specifically B vitamins), dietary fibers, and phytochemicals (Noor *et al*., 2014).

The cultivated area of wheat in Iraq for 2024 covered about 817,700 hectares, with a production of 5.234 million tons. It has an increase of 23.2% over the production of 2023, which amounted to 4.248 million tons (CBS, 2024). The food security of any country depends upon its efficiency in wheat cultivation, production, and storage. Therefore, the situation remains complex, as the current policies fail to consider the environmental impact of human efforts to feed themselves due to the direct human consumption pressure (Mangl *et al.,* 2010).

The scientifically sound approach, followed in all the developed agricultural countries, is the continuous introduction and development of new improved cultivars to replace local varieties deteriorating after several seasons of cultivation (Hasan and Abdullah, 2023). Non-superior plant genetic resources retention can be beneficial from their genetic reservoir for traits other than high yield, and in such cases, these genotypes can succeed incorporation into hybridization programs. One such breeding program is the diallel mating design, including the half-diallel (Al-Adhari, 1987), used to develop new cross combinations that apply hybrid vigor and identify the genetic action controlling key traits, such as grain yield and its components. Additionally, it assists in achieving early maturity, improving protein content, and enhancing the disease and insect resistance, as well as other quality traits.

Estimating the gene action for various primary traits and their components is essential in breeding programs because their correlations indicate how a trait will respond to selection based on the interaction between genetic and environmental factors (Hasan and Abdullah, 2023; Swain *et al*., 2022). Moreover, increased yield per unit area is the primary goal of breeding programs involved in wheat and other cereals worldwide. However, wheat remains the leading crop among the cereals in its response to genetic improvement and yield increase by developing high-yielding genotypes. Yield increase is the foremost goal of breeding programs in all crops because it is vital in evaluating genetic compositions, especially in wheat crops.

The said success has gotten support from wheat's self-pollination by nature, which has enabled breeders to produce varieties and hybrids significantly outperforming those previously dominating the world (Hasan and Abdullah, 2023). This success mainly refers to the discovery and clarity of various cross-combination hybrid wheat, which relies primarily on the genetic distance among the parental genotypes of various crops (Al-Jubouri, 2011). Based on the above discussion, the presented study aimed to estimate the effect of gene action using Jenks and Hyman genetic analysis in bread wheat.

MATERIALS AND METHODS

The potential study comprised the assessment of gene action in 10 × 10 half-diallel crosses in bread wheat (*Triticum aestivum* L.), carried out during 2023–2024 at the Kirkuk Governorate, Iraq (Table 1). For hybridization based on half-diallel crosses as explained by Griffing (1956), in the second method of combining ability, the seeds of 10 parental genotypes of wheat reached planting in the crossing block during the crop season of 2022–2023, with two different sowing times to ensure the largest possible number of crosses (Poehlman, 1983). The total obtained genetic compositions were 55, consisting of the 45 F_1 hybrids and 10 parental genotypes. For studying their genetic potential during 2023–2024, the sowing of seeds of all genotypes was in a randomized complete block design (RCBD) with three replications, with each genotype grown with four rows in the experimental units. Given the importance of the topic in cereal crops,

Table 1. Wheat strains with their sources used in the study.

No.	Strain name	Composition ratios
1	Site Mall	Research Center / Sulaymaniyah
2	Kauz	Kauz 2 \ yaco \\ Kauz \ 3 \ Ousis
3	Abu Ghraib	Ajeeba* Lian 12 * Mexico 24
4	Florica	Research Center / Sulaymaniyah
5	Oasis	Ousis\ Kauz \\ 4 BUC
6	Clack	Research Center / Sulaymaniyah
7	Milan	Research Center / Sulaymaniyah
8	Sham 6	Plo - Ruft GTOS - RHel (M12904)/ IM/SM/14/OSK/GAP
9	Abaa 99	Ures/ Rows/ 3/ Jup/ B/ S/ Ures
10	Hadab	Research Center / Sulaymaniyah

Table 2. The t^2 test (Vr-Wr) for regularity of the studied traits.

Traits	Number of spikelets	Grains spike^{-1}	Spikes plant^{-1}	100-grain weight	Grain yield plant^{-1}	Biological yield	Harvest index	Yield efficiency
t^2	0.51	0.16	**9.53	0.008	0.077	1.43	0.001	1.99

especially wheat, it played a role in identifying superior genes through hybridization and evaluating the parents. This could lead us to crucial results through the improvement of genetic traits and the wheat yield characteristics.

Genetic analysis

The analysis of half-diallel hybrids depends on seven assumptions, i.e., the parents are purebred, the isolation is bilateral, there are no differences among the hybrids, no interaction between the parental genotypes and the environment, no interaction among the genes, no multiple alleles, and no link between the genes (Jinks and Hayman, 1953; Jinks, 1954), with further testing using the regularity of Vr and Wr (Shekh and Aziz, 2021; Singh and Chaudhary, 2007). Moreover, the use of equations proposed by Ferreira (1988) served to achieve the last hypothesis. Scaling tests progressed through arrays of analysis of variance (Wr+Vr and Wr-Vr) and t^2-tests (Table 2). Afterward, the components of genetic variance and the rate of dominance and heritability estimates were as follows:

D = Additive genetic variance (D = Volo-E [Volo = Variance of the Parents]).

H1 = Dominance variance (H1 = Volo-4Wolo1+V1L1-[3n-2]E/n [Wolo = Mean covariance between the parents and the arrays]).

H2 = H1 (1-[u-v]2), where u and v are the proportions of positive and negative genes, in the parents.

F = Mean of Fr values over arrays = 2Volo-4Wolo1-2(n-2)E/n, where Fr is the covariance of additive and dominance effects in a single array. F is positive where dominant genes are more frequent than recessive.

h^2 = (ML1-MLo)2-4(n-1)E/n2; Dominance effect (as algebraic sum over all loci in heterozygous phase in all crosses). When frequency of dominant and recessive alleles is equal, then H1 = H2 = h2. Significance of h2 confirms that dominance is unidirectional.

E = Expected environmental component of variation.

The average degree of dominance for multiple genes: ā = $\sqrt{H1/D}$

Where: ā = 0 (No dominance), 1 = ā (Complete dominance), 1 < ā (Partial dominance), and 1 > ā (Super dominance).

The frequency of dominant to recessive alleles showing the dominance, as calculated, was:

$$(0.25)\ \frac{1}{2}=p=q\ \frac{H2}{\overline{pq}4H1}$$

$\frac{KD}{KR}$ = total number of dominant to recessive genes in all parents.

The narrow sense heritability (h^2) computation in the F1 generation for each character was according to Mather and Jinks (1982). The adopted values of heritability (narrow sense) used the following: low (<20%), medium (20%–50%), and high (>50%) (Al-Adhari, 1987).

RESULTS AND DISCUSSION

Genetic variance components

In the recorded data, the components of genetic variance, as estimated, followed the methodology explained in past studies (Jinks and Hayman, 1953; Hasan *et al.,* 2023) and the equations proposed by Ferreira (1988). The said analysis depended on the seven different assumptions as discussed earlier. The first four assumptions discussed had their achievements tested through genetic analysis. As for the last three hypotheses, conducting a regularity analysis (Vr and Wr), as mentioned in past studies (Alatawi *et al.,* 2024; Griffing, 1956; Hayman, 1954; Singh and Chaudhary, 2007), tested their validity.

As explained earlier, in the event of not achieving these three hypotheses assumptions, it is possible to continue estimating the components of genetic variance. Additionally, to achieve the special hypothesis about the absence of a link between genes, the equations proposed by Ferreira (1988) were successful. The values of the components of genetic variance, as estimated after calculating the values of the statistical constants, appear in Table 3. From these constants, using the proposed equations of Ferreira (1988), estimated the genetic parameters D, H1, H2, and F (Table 4), while their further comparison applied the method by Singh and Chaudhary (2007).

Table 3. Values of statistical constants according to the Jinks-Hayman analysis.

Statistical constants	Number of spikelets	Grains spike^{-1}	Spikes plant^{-1}	100-grain weight	Grain yield plant^{-1}	Biological yield	Harvest index	Yield efficiency
Vp	5207.77	25147.11	8543.53	14631.36	17703.38	188208.99	1.376833	0.010329
Vr	3.24	36.272	66.726	16.26	64.60	521.24	0.002297	0.00017
Wr	0.82	-0.010	4.591	0.58	7.42	19.74	0.000369	0.00000073
Vr	0.40	4.051	3.302	1.81	7.27	48.20	0.000184	0.0000113
$(ML - Mp)^2$	0.006	0.044	0.072	0.008	0.017	2.53	0.00000623	0.000000041

Table 4. Genetic parameters of the studied traits.

Traits	Statistical constants (Mean±S.E.)	F (Mean±S.E.)	H1 (Mean±S.E.)	H2 (Mean±S.E.)
Number of spikelets	2.93±369.20	3.14±2.19	11.73±1.98	10.19±1.66
Grains spike^{-1}	25.26±3408.00	53.98±20.27	153.20±18.27	111.61±15.36
Spikes plant^{-1}	30.83±6586.13	50.34±39.17	256.95±35.31	228.15±29.69
100-grain weight (g)	10.80±1214.80	19.98±7.22	71.34±6.51	55.87±5.47
Grain yield plant^{-1} (g)	38.28±4967.00	56.97±29.54	234.18±26.63	192.86±22.39
Biological yield (g)	507.27±47401.09	992.40±281.94	2279.50±254.18	1645.28±213.67
Harvest index	0.00242±0.28	0.00366±0.00170	0.009529±0.001536	0.007698±0.001291
Yield efficiency	0.0000565±0.018801	0.0000998±0.000112	0.000647±0.000101	0.00057±0.0000848

The results revealed that additive genetic variance (D) was significant for all traits under study. Additive genetic variance refers to the differences attributed to the effects of additive genes, with direct inheritance from parental genotypes to offspring. However, when the additive genetic variance is significantly different from zero, it indicates an apparent influence of individual genes contributing to managing the studied traits (Abdullah and Hasan, 2021). The significance of additive genetic variance in wheat reflects the presence of considerable genetic potential for further exploration to improve productivity and quality traits. These findings underscore the importance of studying genetic variance and leveraging it in breeding programs to improve field crops and sustainably enhance their productivity (Hasan and Abdullah, 2020). The presented results were also greatly analogous to past findings based on genetic analysis in bread wheat and other field crops (Hasan and Abdullah, 2021; Hasan *et al.,* 2022a, b; Younis *et al*., 2022).

Estimation of genetic features and heritability

On the genetic features and heritability, the results revealed the average degree of dominance ($\sqrt{H1/D}$) was greater than one for all traits (Table 5). However, when the average degree of dominance is greater than one, it indicates the presence of overdominance in controlling the studied traits in wheat. Overdominance means that hybrids exhibited better performance than parental genotypes for the traits under investigation. This type of dominance often has associations with increased growth and development, productivity, and tolerance to environmental stresses (Hasan *et al.,* 2023). The considerable significance of these results reflects the relevance of genetics in achieving significant improvement in wheat productivity.

When the degree of dominance is high, breeders can explore the heterosis to enhance the crucial traits, such as grains and grain weight per spike and resistance to environmental stress conditions (Hayman, 1954). Moreover, the presence of a degree of dominance greater than one emphasizes the importance of hybridization programs among the different wheat strains to boost productivity and stability (Jinks, 1954). The results may also indicate the existence of broad genetic variation, supporting the success of selection efforts to improve targeted traits. Such phenomena demonstrate remarkable potential for developing crops capable of adapting to climate changes and meeting food security demands (Hasan and Abdullah, 2020, 2021; Hasan *et al.,* 2023).

The ratio of dominant to recessive alleles ($\overline{pq}$) showed dominance had no regular distribution among the parental genotypes, as also evidenced by the value not being equal to 0.25 for all studied traits. The ratio of the number of dominant to recessive genes (KD/RR) was greater than one for all traits in bread wheat. However, when the ratio of dominant genes to recessive genes (KD/RR) is greater than one, then it indicates the dominance of dominant genes in controlling the expression of these traits. The results reflected that dominant genes played a vital role in determining the phenotypic differences among the individuals compared with recessive genes (Hasan *et al.,* 2023).

Table 5. Genetic parameters and heritability ratios in the narrow sense of the studied traits.

Genetic constants ratios	Number of spikelets	Grains spike^{-1}	Spikes plant^{-1}	100-grain weight	Grain yield plant^{-1}	Biological yield	Harvest index	Yield efficiency
$\sqrt{H1/D}$	2.00	2.46	2.88	2.57	2.47	2.11	1.98	3.38
$H2 / 4H1 = \bar{p}\,\bar{q}$	0.21	0.18	0.22	0.19	0.20	0.18	0.20	0.22
KD /KR	1.73	2.53	1.78	2.12	1.86	2.71	2.23	1.70
h^2 (n.s.)	0.20	0.18	0.075	0.18	0.19	0.15	0.13	0.10

Table 6. Sequence of parental genotypes as per their average values and degree of dominance for all the traits.

Dominant>>recessive alleles	Sequence of parents according to degree of dominance (dominant>>recessive alleles)									
Number of spikelets	10	5	7	1	8	2	6	3	9	4
Grains spike^{-1}	5	7	4	10	2	8	9	6	3	1
Spikelets plant^{-1}	9	1	8	10	5	3	6	7	4	2
100-grain weight (g)	4	3	2	8	1	5	6	10	9	7
Grain yield plant^{-1} (g)	4	5	2	8	1	10	9	7	6	3
Biological yield (g)	4	8	3	7	5	6	10	2	1	9
Harvest index	4	10	5	1	7	9	2	3	8	6
Yield efficiency	3	8	2	10	9	1	5	4	7	6
Characteristics	Sequence of parents according to their average values (Highest —<<— Lowest)									
Number of spikelets	9	10	1	7	5	6	4	3	8	2
Grains spike^{-1}	2	6	4	9	3	7	10	8	5	1
Spikelets plant^{-1}	9	2	5	4	6	7	3	8	10	1
100-grain weight (g)	4	3	6	5	1	9	2	8	10	7
Grain yield plant^{-1} (g)	5	6	8	2	10	4	9	3	1	7
Biological yield (g)	4	7	6	8	2	3	10	1	5	9
Harvest index	2	4	7	1	3	9	6	5	8	10
Yield efficiency	9	3	1	10	6	8	2	4	5	7

Prominent sequence

The narrow-sense inheritance rate was low in all traits, except for the number of spikes, which was high. Low narrow-sense heritability indicates that a small proportion of the phenotypic variation in the studied traits was ascribable to the additive genetic variance that is inheritable. This suggests the influence of the environment and gene interactions (dominance and epistasis) because it highlights the significance of the genetic composition in relation to yield traits was greater than the additive gene effects. In such cases, improving traits through direct selection becomes less effective, necessitating the use of other breeding strategies, such as hybridization, and enhancing the environmental options to achieve better results (Jinks, 1954; Hasan *et al.,* 2023).

By comparing the sequence of the degree of dominance of the parental genotypes from the average values (Table 6), it was noteworthy that these genotypes were identical for containing dominant genes and the high average values of the parental genotypes Kauz and Abaa-99 in most studied traits. These results agree with past findings in the estimation of genetic components of variance in diallel crosses of crop plants (Ferreira, 1988). The outcomes further revealed that parental genotype Florica came in first place for the sequence of the degree of dominance in most studied traits. It was possible to benefit from the dominant genes to obtain better hybrid strength for the mentioned traits, and the same reached confirmation by the results about the hybrid strength in subsequent studies, and it is also possible to benefit from other strains in hybridization programs to benefit from their other traits (Muhammad *et al.*, 2021).

It is evident that a match exists, indicating that dominant genes play a key role in the studied traits, and the performance of the parents was superior in all traits of the oat crop (Hasan *et al.,* 2023). The higher average values for the father (2 and 9) reflect the dominance of these genetic structures for gene expression for most traits (Hasan *et al.,* 2023). It suggests the studied traits gained more influence from the genetic dominance of these structures, enhancing their potential use in breeding programs to improve productivity or quality. This result also supports the importance of evaluating dominant genes when selecting parents in hybridization programs. This study result is consistent with the research of Al-Adhari (1987), and Ferreira (1988).

CONCLUSIONS

Dominant genetic variances emerged greater than the additive variance for all traits in bread wheat. The average degree of dominance exceeded one, indicating the dominance of gene action. The parental genotype Florica stood out as leading for its high ranking in terms of dominance.

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