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Estimation of genetic components for yield and quality characters in five diverse wheat (*Triticum aestivum* L.) crosses by six parameter model

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Abstract
The aim of this research was to examine the gene action that controls the expression of various traits in bread wheat by using generation mean analysis. Six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of five crosses, cross I (HI 8627 x HI 8498), cross II (DBW 17 x JW 3211), cross III (HD 2993 x HD 4758), cross IV (MP 3269 x HI 1500) and cross V (HW 1900 x UP 2847), were used for this purpose. The results revealed that the estimated mean effects (m) of all the traits in all crosses were highly significant, indicating the quantitative inheritance of the traits. The epistatic interaction was present for all the eight traits in the crosses. Generally, the value of dominance effect (h) was higher than additive effect (d) in all the traits. Digenic interaction suggested that the inheritance was complex and involved non-additive gene action. The selection in early generation could be beneficial. For grain yield and most of the traits, the dominance type gene effects were more significant than additive gene effects. In the five crosses, the different traits showed a large and negative dominance x dominance degree, while the additive x additive gene actions were high and positive. In wheat breeding, the selection for enhancing grain yield and its related traits should be delayed until later generations because additive x dominant gene effects were less significant.

Keywords: Gene effects, epistasis, additive, dominance, six generation model

Introduction
Generation mean analysis is a quantitative biometric approach that utilizes phenotypic data from as many plants as possible across fundamental breeding generations, such as parental, filial, backcross, and segregating populations. Kearsey and Pooni (1996) [7] highlighted its value in plant breeding for calculating primary gene effects additive and dominance as well as two-gene interactions (additive x additive, additive x dominance, and dominance x dominance) that govern the inheritance of quantitative traits. This method sheds light on the performance of parent plants in hybridizations and the potential of these hybrids for either heterosis exploitation or pedigree selection, as noted by Sharma *et al*. (2002) [12].

Grain yield in wheat is a multifaceted polygenic trait influenced by various inherent traits and environmental factors. Enhancing wheat grain yield can be achieved through indirect selection based on yield components. A thorough comprehension of the inheritance patterns of quantitative traits, along with data on the heritability of grain yield and its components, is crucial for devising an effective breeding strategy.

Given that grain yield and bread wheat quality are complex traits of paramount importance, and their enhancement is a primary objective of global wheat breeding programs, the selection of parental lines in this study aimed to meet these criteria. Genetic data derived from multiple generations tend to be more reliable than those from a single generation. According to A, B, C, and D scaling tests, additive, dominance, and epistatic effects play significant roles in determining yield and its component traits. Research on generation mean analysis, including the work of Sharma *et al*. (2002) [12], has shown that additive and dominance genetic factors are vital for most wheat plant traits. Cavalli (1952) [1] observed that the precision of gene effect estimates improves with an increased number of segregating generations and observational plants.

In addition to gene effects, breeders are interested in the proportion of genetic variation in a crop and the degree to which this variation is heritable, as the effectiveness of selection

largely hinges on additive genetic variance and environmental influences. Analyzing gene effects not only clarifies the relative significance of different gene effects in trait control but also elucidates the mechanisms behind heterosis. Understanding the levels of heterosis and inbreeding depression is critical for selecting an appropriate breeding methodology. The exploitation of heterosis is deemed a remarkable success in plant breeding. For self-pollinating crops like wheat, the feasibility of harnessing heterosis largely depends on its direction and magnitude. This study was undertaken to assess the degree of heterosis, inbreeding depression, and the nature of gene action in the inheritance of grain yield and select agronomic characteristics in five wheat crosses.

Materials and Methods

The present study was carried out during the Rabi 2022- 23 cropping season at the Research field of AICRP Wheat and Barley, JNKVV, College of Agriculture Tikamgarh, Madhya Pradesh, India, using Randomized block design with three replications. For genetic analysis of quantitative traits, five crosses from eight diverse elite lines of wheat (*Triticum aestivum* L.) was used. Eight homozygous and genetically diverse wheat varieties HI 8627, HI 8498, DBW 17, JW 3211, HD 2993, HD 4758, MP 3269, HI 1500, HW 1900 and UP 2847 were selected for developing the experimental materials. The experimental material used for the current investigation consisted of the parents (P_1 and P_2), the F_1 's, F_2 's and the back crosses with both the parents (B_1 and B_2) of each of the three crosses viz., JW 3288 x HD 8864 (cross 1), MP 3269 x GW 173 (cross 2) and JW 3020 x GW 366 (cross 3). The above mentioned diverse wheat varieties were planted in crossing nursery for making desired cross combinations (F_1's) were made. Harvested seeds of each diverse parent and their F_1's were stored separately for sowing during next year. During rabi the hybrid seeds (F_1's) of five cross combinations were grown to make the back crosses (BC_1, BC_2) and F_2. In addition, fresh F_1·s were also made to make 6 generations for analysis. All the F_1 populations were planted in two rows, F_2 's in six rows and BC_1 and BC_2 in 4 rows of 3 meter length spaced 25 cm apart. The experimental set was planted under black soil having pH of 7.5-7.8 in a Compact Family Block Design in three replications. Five randomly selected plants from parents and F_1 generation, and 20 each from back crosses and F_2 generations in replications were marked before flowering. Ten plants for non-segregating populations and 30 plants for the segregating populations were randomly selected for recording of data on eight traits, namely: days to 50% flowering, number of tillers per plant, plant height (cm), days to maturity, Protein content (%), Amylose content (%), test weight (gm), grain yield per plant (gm). The data were first subjected to analysis of variance separately at Regional Agricultural Research Station Sagar Madhya Pradesh, India. Genetic analysis was done by using a six-parameter model (Hayman, 1958) [4] after applying the scaling test suggested by Hayman and Mather (1955) [15]. If any of the 4 scaling tests is significant, it indicates occurrence of non-allelic gene actions and the insufficiency the additive dominance model.

Results and Discussion

The mean sum of squares data showed significant differences between the generations for all the five crosses for all traits. This indicated a considerable amount of variation among the material used for study. Table 1 shows ANOVA for all the four bread wheat crosses and their six generations. To determine whether epistatic gene effect is present/ absent, or which model is better for study, scaling test analysis using generation means is required. Analysis of generation means having scaling test is very important to find out either nonallelic gene action is present or not and which model is suitable for this analysis. Four kinds of scaling tests were suggested by Mather and Jinks (1982) [9]. Based on the findings, all four tests (A, B, C, and D) in cross I (JW 3288 x HD 8864) were significant for all traits except grain yield, where scaling test A was nonsignificant. In cross II (MP 3269 x GW 173) all scaling tests, i.e., A, B, C, and D, were significant for plant height, days to maturity, number of tillers per plant, Amylose content (%), test weight (gm), and grain yield (gm), but B, C, and D tests were significant for days to heading, and C and D for spike length. In cross III (JW 3020 x GW 366), scaling test A, B, C, and D were significant for days to heading, plant height (cm), days to maturity, test weight (gm), and grain yield (gm), however B, C, and D tests were significant for number of tillers per plant and A, B, and C tests for Protein content (%). In cross IV (MP 3269 x HI 1500) scaling test A, B, C, and D were significant for plant height, days to maturity, number of tillers/plant, Protein content (%), and grain yield (gm). However, scaling test C and D were significant for days to heading, and B, C, and D tests for number of grains/ spike. In cross V (HW 1900 x UP 2847) all scaling tests, i.e., A, B, C, and D, were significant for plant height, days to maturity, number of tillers per plant, Amylose content (%), test weight (gm), and grain yield (gm), but B, C, and D tests were significant for days to heading, and C and D for spike length. Similar results were reported by studies conducted by Mahpara *et al*. (2017) [18]. The generation mean for all the traits under study in the five crosses showed significant variations over all six generations, indicating that these traits' have high genetic variation, suggesting that they were inherited quantitatively. Similar results were reported by Mahpara *et al*. (2017) [18] when worked on wheat., also found significant genetic variation in wheat for a number of quantitative traits.

The estimates for the six parameters, which are additive (d), dominance (h), additive x additive (I) additive x dominance (j), and dominance x dominance (l), as well as means (m) are shown in Table 2. Days to maturity were not significant for crosses I (JW 3288 x HD 8864) and II (MP 3269 x GW 173) while negative and highly significant results were found for crosses III (JW 3020 x GW 366), cross IV (HW 1900 x UP 2847) and cross V (HW 1900 x UP 2847). For all five crossings, the additive gene effect was highly positive and significant for days to heading, plant height, number of tillers per plant, and grain yield (HW 1900 x UP 2847). Among all five crosses the dominance (h) gene effect was very significant and positive for the number of tillers per plant, Protein content (%), test weight (g), and grain yield per plant (g). Dominance gene effects were significant in yield and yield components while insignificant for additive gene effects (Sharma *et al*. 2002) [12]. Hasabnis and Kulkarni (2004) [3] mentioned that the estimate of additive gene effects and dominance gene effects were highly significant. Days to heading, plant height (cm), Protein content (%), test weight (g), and grain yield per plant had positive and highly significant additive x additive I gene effects. The number of

tillers per plant in cross I (JW 3288 x HD 8864), the Amylose content (%) in cross II (MP 3269 x GW 173) and cross III (JW 3020 x GW 366), the test weight in cross II (MP 3269 x GW 173), and the grain yield per plant in cross I (JW 3288 x HD 8864), cross IV(HW 1900 x UP 2847) and cross V (HW 1900 x UP 2847) were all significantly affected by the additive x dominance (j) gene (HW 1900 x UP 2847). In all five crosses, dominance x dominance (l), gene effect, was very important for days to heading, while cross I (JW 3288 x HD 8864), cross III (JW 3020 x GW 366), and cross IV (HW 1900 x UP 2847) were significant for plant height and days to maturity. In the current study, most of the traits showed lower magnitude of additive gene actions than that of dominance actions, indicating that the pedigree method of selection is the most effective strategy for improving these populations. For almost all of the traits studied in all four crosses, the magnitude of the dominant gene effect were higher than that of the additive gene effect, indicating a key role for the dominant component of gene action in the inheritance of these traits. Therefore, selection for these traits should be delayed until later generation when the dominant effect is reduced. The dominance gene effect was higher than additive gene effect for all the studied traits in the three crosses indicating predominant role of dominant component of gene action in inheritance of these traits, so the selection for these traits should be delayed to later generation when dominant effect is diminished. Similar conclusion was given by Novoselovic *et al*. (2004) [11]. Menon and Sharma (1995) [10] earlier reported that both additive and nonadditive gene effects are important for the inheritance of these traits. Estimates of additive effects can be small due to a high degree of dispersion of increasing alleles between parents and dominance can be small due to its bidirectional nature (Snape 1987) [14]. The magnitude of additive x additive gene effects was high and positive whereas dominance x dominance was negative (Hasabnis and Kulkarni 2004) [3]. Epistasis was significant for most of the additive x additive traits, highlighting the importance of this component. Studies conducted by Raikwar R.S. 2019 [17], Singh and Singh (1992) [18] and Novoselovic *et al*. (2004) [11] also confirmed the importance of epistasis. Although it varied by trait, the variation in the generation means fit a digenic epistatic model in most of the cases. This implies that modifying the traits studied would be more difficult than when an additive-dominance model provided the appropriate fit. These results are consistent with those reported by other authors Pawar *et al*., 1988 [16]; Singh and Singh, 1992) [18].

The opposite signs of h and l cancel out the effect of each other, resulting in less heterosis, according to Kumar *et al*. (2010) [21]. However, complementary non-allelic gene action was also observed for cross II ((MP 3269 x GW 173)) and cross IV (HW 1900 x UP 2847) for plant height (cm), where h and l values were 6.14 and 1.02 and 2.06 and 4.56, respectively. Days to maturity showed complementary non-allelic gene interaction in cross-III with values of h and l of 14.35 and 1.24, respectively. On the other hand, the Amylose content (%) and test wt. traits exhibited complimentary gene interaction in cross-IV (HW 1900 x UP 2847). In Cross I (JW 3288 x HD 8864), the values of h and l for grain yield/plant (g) were 14.56 and 6.35, respectively. According to the complementary gene effects, there is a high possibility of high heterosis in the crosses where it occurs. The complementary type suggested the possibility of considerable amount of heterosis for these two traits in this particular cross. Duplicate type of non-allelic gene interaction for most of studied traits with few exceptions further confirms the prevalence of dominance effects. Presence of duplicate epistasis indicates that variability in segregating generations may be reduced which hinder the selection process. The generation mean analysis of the data revealed that these traits exhibited all type of epistatic gene interactions (additive, dominance and epistatic) and suggested that complex additive effects are important in controlling these traits (Hussain *et al*. 2011) [5]. Fethi and Mohamed (2010) [2] reported that dominance effects and dominance x dominance epistasis were more important than additive effects and other epistatic components for grain per spike. Kaur and Singh (2004) [6] stated that the nature and magnitude of gene effect vary within the different crosses for different characters; necessitating specific breeding strategies need to be adopted for particular crosses to obtain improvement.

The dominant effects' predominance was further confirmed by the duplicate type of gene effects with few exceptions, which was observed for most of the traits studied. It is not appropriate to use them in breeding programmes because the presence of duplicate type of epistasis indicated, diversity in segregating generations had reduced, and impedes the process of selection. Among different traits recorded in the four crosses, the degree of dominance x dominance was large and negatively significant, whereas additive x additive gene actions were high and positively significant. Raikwar R.S. (2019) [17] also reported high degree of dominance x dominance and additive x additive gene actions with negative and positive significance respectively. In wheat breeding, it was found that selection for the enhancement of grain yield and contributing traits should be delayed until later generations because additive x dominant gene effects were of less importance. It was seen that additive x dominance effects in gene was of lesser significance, thus, suggesting that in wheat breeding, selection for the improvement of grain yield and its contributing traits should be delayed for advanced generations. The complementary gene action was observed in cross II, IV and V for plant height (cm), cross-III for days to maturity, cross-IV for no. of grains per spike and test weight (g) and cross-I for grain yield per plant and that can be used for gene fixation through conventional breeding methods. The duplicate type of gene action was recorded for, majority of the traits under study where (h) and (l) effect had opposite signs. Thus it indicated that non-fixable gene effects are expressing that particular traits i.e., greater role of non-additive gene effects in such cases.

The gene effects estimation results reveal important information about the genetic control of key agronomic traits in bread wheat. The gene actions and effect sizes varied across the crosses, reflecting the complex genetic structure of these traits. Knowing the genetic basis of days to heading, plant height, yield-related traits, and test weight is crucial for breeding programs aiming to develop high-yielding and resilient bread wheat varieties. Further research identifying specific genes and their interactions could improve our understanding of the genetic mechanisms regulating these traits and enable targeted breeding efforts for better bread wheat varieties.

Table 1: Analysis of variance for five crosses and their six generations in bread wheat

Source	df	Mean Sum of Square							
		Days to heading	Plant height (cm)	Days to maturity	Number of effective tillers per plant	Protein content (%)	Amylose content (%)	Test weight (g)	Grain yield per plant (g)
HI 8627 x HI 8498									
Replication	2	1.65	7.58	1.65	3.78	0.53	2.63	0.80	0.45
Generation	5	72.45**	125.45**	96.14**	6.74**	6.25**	165.12**	30.35**	5255.64**
Error	10	1.15	3.67	1.48	0.50	0.45	4.65	1.12	0.08
DBW 17 x JW 3211									
Replication	2	1.89	9.56	1.64	0.64	0.78	0.07	1.65	0.42
Generation	5	36.89*	78.95**	39.89**	6.78**	7.23**	32.96**	20.64**	2895.63**
Error	10	2.47	6.65	0.53	0.65	0.58	0.87	0.87	0.98
HD 2993 x HD 4758									
Replication	2	1.69	9.65	1.79	0.65	0.65	3.56	1.98	0.87
Generation	5	42.36**	78.74**	39.78**	6.78**	6.13**	75.62**	16.63**	3245.96**
Error	10	2.75	6.89	0.56	0.63	0.45	2.65	0.48	0.45
MP 3269 x HI 1500									
Replication	2	1.32	1.05	2.13	1.21	0.96	27.12	2.12	1.45
Generation	5	32.25**	58.03**	42.32**	14.23**	8.14**	27.26**	187.13**	2324.52**
Error	10	5.63	0.79	0.74	1.08	0.34	2.56	3.72	1.02
HW 1900 x UP 2847									
Replication	2	1.08	2.12	1.89	0.54	1.02	28.69	2.32	1.45
Generation	5	30.25**	85.13**	48.65**	10.24**	5.68**	32.24**	198.65**	1454.32**
Error	10	4.63	0.65	0.52	0.98	0.69	1.56	2.65	0.45

Table 2: The results of scaling tests and estimates of gene effects in the five crosses of bread wheat

Cross	Scaling test				Tree parameter model			Chi^2	Six parameter model						Gene Actions
	A	B	C	D	M	D	H	X^2	m	d	h	i	j	l	
Days to heading															
I	3.65**	-1.29**	-36.45**	-17.65**	99.54**	6.32**	5.36**	325.63**	67.89**	5.12**	78.45**	36.11**	3.12	-36.12**	D
II	-1.36	-14.32**	-17.21**	-1.32**	114.25**	5.63**	5.23**	7.45**	102.65**	1.65**	-7.35**	3.12**	7.32	12.31**	D
III	15.23**	1.45**	-42.12**	-29.31**	95.35**	16.32**	-7.96**	2231.45**	45.32**	13.64**	119.68**	59.65**	6.23	-70.14**	D
IV	3.14**	0.85	-12.32**	-7.35**	90.12**	3.87**	4.63**	7.32**	87.69**	2.87**	36.21**	14.36**	1.02	-15.36**	D
V	3.65**	1.25**	-14.36**	-6.23**	95.12**	4.36**	5.32**	8.69**	88.32*	3.12**	37.54**	15.32**	2.34	-16.35**	D
Plant height (cm)															
I	-4.65**	6.32**	-14.12**	-7.32**	92.31**	10.01**	-7.45**	110.14**	-8.64**	79.023**	8.02**	32.12**	15.13	-3.25	D
II	-6.32**	-9.45**	-36.45**	-8.13**	98.32**	6.23**	-4.36**	1.02	-8.23**	79.32**	6.14**	16.32**	16.78	1.02	C
III	14.23**	-14.63**	-7.12**	-2.88**	87.15**	3.12**	2.34**	78.01**	-3.12**	98.45**	-3.12**	12.14**	5.45	14.32	D
IV	12.31**	-10.12**	-1.02**	-1.79**	87.73**	3.65**	1.02**	96.01**	-2.08**	80.12**	2.06**	15.12**	7.64	4.56	C
V	13.24**	12.35**	3.24**	2.08**	87.23**	4.02**	2.31**	96.01**	-3.02**	87.12**	3.02**	16.32**	8.32	5.63	C
Days to maturity															
I	-5.32**	-13.21**	-41.02**	-12.32**	145.63**	6.13**	0.89	9.35**	125.32**	6.14**	30.12**	25.63**	4.65**	-3.24**	D
II	-1.68**	-17.65**	-28.68**	-4.35**	138.74**	6.45**	12.34**	1.08	145.13**	-1.23**	-0.12	8.96****	7.96**	12.32**	D
III	5.63**	-14.63**	-19.23**	-5.12**	142.56**	1.25**	-0.48	5.63	140.69**	-0.48	14.35**	10.12**	10.12	1.24	C
IV	1.02**	-19.31**	-20.12**	-1.02**	156.63**	3.87**	-5.68**	39.45**	148.96**	-3.12**	-14.35**	1.45**	10.23	18.96**	D
V	3.62**	-12.36**	-22.31**	-2.12**	169.23**	4.56**	6.32**	40.25**	156.32**	4.21**	-15.63**	2.31**	12.34**	19.34**	D
Number of effective tillers per plant															
I	3.02**	-1.58**	-8.69**	-5.36**	13.21**	1.56**	1.05**	245.47**	4.32**	1.02**	22.01**	9.23**	2.31**	-10.08**	D
II	3.12**	-1.27**	-8.45**	-5.36**	12.35**	1.78**	2.08**	138.34**	4.65**	1.68**	20.23**	9.78**	1.89	-10.02**	D
III	1.02	-1.89**	-3.21**	-1.21**	14.21**	1.32**	2.01**	0.25	12.45**	1.02**	4.35**	2.08	1.02	-0.25**	D
IV	3.15**	-4.36**	-3.14**	-1.32**	14.63**	3.45**	3.08**	28.14**	11.65**	2.65**	9.65**	4.01**	4.23**	-3.08**	D
V	2.36**	-5.63**	-2.13**	-2.12**	15.32**	1.24**	2.08**	27.12**	13.21**	3.08**	10.12**	5.63**	3.21**	-4.01**	D
Protein content (%)															
I	3.21**	-1.78**	-8.36**	5.45**	12.08**	1.23**	0.89**	148.35**	4.36**	1.01**	11.23**	9.32**	3.01**	-10.13**	D
II	-1.02**	4.35**	-10.45**	-4.01**	13.45**	1.45**	-0.45	25.36**	7.98**	1.39**	10.32**	7.45**	2.08**	-3.34**	D
III	3.28**	-2.32**	-8.64**	5.32**	15.12**	1.54**	0.79**	328.97**	5.69**	1.56**	14.12**	9.35**	3.01**	-10.35**	D
IV	-1.02*	4.65**	-10.45**	-4.12**	13.89**	1.89**	0.98**	20.14**	7.96**	1.78**	10.01**	7.06**	1.45	-3.45**	D
V	2.31**	-3.12**	-9.87**	-3.12**	14.31**	1.65**	-0.36	18.32**	6.39**	1.56**	9.35**	6.58**	2.34**	-5.61**	D
Amylose content (%)															
I	4.18**	-18.89**	30.89**	-8.96**	40.25**	3.65**	2.04**	12.38**	28.96**	3.12**	8.36**	7.56**	4.12**	-3.12**	D
II	4.23**	-10.98**	-24.36**	2.65**	45.63**	4.65**	4.16**	125.87**	47.68**	2.65**	-9.32**	-3.36**	7.96**	9.12	D
III	3.36**	-14.35**	40.23**	-18.36**	42.35**	4.63**	2.08**	135.24**	13.24**	1.45	6.21**	5.34**	8.36**	-4.36**	D
IV	4.36**	-6.48**	-28.63**	10.45**	48.69**	2.08	1.98	1.65	69.74**	3.21**	9.12**	7.48**	4.14**	-7.80**	C
V	4.78**	10.23**	32.89**	12.45**	40.24**	4.65**	4.89**	2.34**	59.36**	2.45**	-7.23**	-6.34**	-3.12	-6.89**	C
Test weight (g)															
I	6.78**	-7.39**	-14.56**	6.34**	36.47**	5.63**	4.36**	3.08.21**	28.12**	1.89**	32.45**	12.32**	7.36	-12.32**	D

II	6.35**	-7.58**	-16.78**	-8.96**	36.12**	1.08**	4.65**	786.14**	22.35**	1.87**	36.45**	16.32**	7.68**	-18.63**	D
III	7.12**	-9.15**	-15. **31	-6.47**	39.12**	1.36**	1.25**	356.32**	29.12**	-1.65**	25.12**	12.8**7	7.96	-9.36**	D
IV	3.08**	-30.12**	-40.26**	-8.96**	40.21**	9.25**	-1.12**	32.24**	28.18**	5.63**	15.63**	18**.96	18.36**	7.65**	C
V	2.35**	-28.32**	-38. 12**	-9.45*	38.96**	1.25**	2.31**	642.12**	32.14**	6.21**	14.23**	17**.32	23.14**	6.32**	C
Grain yield per plant (g)															
I	3.02**	-3.08**	7.63**	-3.12**	15.32	2.32	3.12**	57.23	12.23**	1.30	14.56**	6.78**	3.12**	6.35**	C
II	3.06**	5.63**	6.48**	-2.65**	17.85**	2.45**	3.02**	12.14**	14.32**	1.02**	8.36**	4.78**	4.56**	-5.14**	D
III	4.23**	4.45**	-4.32**	-2.32**	16.35**	3.12**	4.01**	25.32**	13.25**	2.03**	9.23**	4.36**	4.12	-4.08**	D
IV	4.12**	4.36**	-4.66**	-2.32**	16.32**	2.35*	3.24**	16.45**	13.14**	2.12**	8.32**	4.31**	4.36	-4.05**	D
V	3.21**	-3.65**	-2.45**	-3.36**	17.14**	3.21**	2.48**	17.34**	12.31**	1.76**	11.25**	5.6**3	6.45**	-6.12**	D

*, ** Significant at 5% and 1%, respectively. D=Duplicate gene action ; C=Complementary gene action

Conclusion

In conclusion, the study reveals the intricate genetic control underlying key agronomic traits in bread wheat. Significant variation among generations underscores the importance of understanding genetic mechanisms. Dominant gene effects play a crucial role across different crosses, emphasizing the need for tailored breeding strategies. Complementary and duplicate gene interactions observed offer avenues for heterosis and gene fixation. These findings provide valuable insights for breeding programs aiming to develop high-yielding and resilient wheat varieties. Further research into specific gene interactions is essential for targeted breeding efforts and the development of superior wheat cultivars adapted to diverse agricultural conditions.

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