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Research Article

Genetic analysis of grain yield and its contributing traits in four bread wheat (*Triticum aestivum* L.) crosses using six parameter model

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Abstract

In order to create a successful and efficient breeding programme, it is highly helpful to analyse the gene action governing the expression of different traits. The objective of the present study was to use generation mean analysis to ascertain the kind and extent of gene action in bread wheat utilizing six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the four crosses, cross I (HD 2967 x PBW 752), cross II (RSP 561 x PBW 779), cross III (RSP 561 x PBW 780), and cross IV (JAUW 584 x WH 1184). These crosses included elite stripe rust resistant wheat genotypes in addition to locally adapted cultivars. The results showed that all the traits in all crosses had highly significant estimated mean effects (m), showing the quantitative inheritance of the selected traits. For grain yield and most of the selected characters, it was found that additive gene effects was shown to be less significance than dominance type gene effects. Among the different characters studied 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 significance. In wheat breeding, it was found that selection for the improvement of grain yield and its contributing traits must be postponed until later generations because additive x dominant gene effects was of lesser significance.

Keywords: wheat; grain yield; additive; dominance; epistatic gene effects

INTRODUCTION

Generation mean analysis (GMA) is a useful tool for dissecting the genetic architecture of quantitative traits in crop plants, including wheat. GMA involves the analysis of variation within and between generations of crosses between different parental genotypes. According to Falconer and Mackay (1996), the GMA is a powerful statistical tool that helps to estimate the genetic correlation. It is based on the principles of quantitative genetics and the Mendelian inheritance of genes. Grain yield in wheat is a polygenic trait that is effected by different components and can be refined by indirect selection based on yield attributes. A single component's addition may have a favourable or negative impact on the other attributes (Chandra *et al.,* 2004). Generation mean test is commonly used by geneticists and plant breeders to learn more about the genes affecting the useful traits of wheat (Khaled *et al.,* 2007; Farag *et al.,* 2009). Studies such as those by Kumar *et al.* (2014) demonstrate the utility of GMA for identifying genetic effects and interactions, as well as gene networks, that underlie important traits in

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wheat. Although increasing grain yield is the foremost goal of wheat breeding, yield is a quantitative trait that is influenced by a variety of important variables. Improvement of agronomic characters that influence grain yield is required to enhance yield, but in order to do so, more knowledge of these traits' inheritance patterns is required (Singh *et al.,*1986). Estimating the genetic influences of polygenic traits can be done simply and effectively using generation mean analysis (Singh and Singh, 1992). Genetic data collected from several generations is more accurate than data collected from just one. The present investigation was conducted to determine the nature of gene action involved in the inheritance of grain yield and some agronomic traits of four wheat crosses.

MATERIALS AND METHODS

The current research was conducted during the *Rabi* 2017–18 growing season at the Research Field of the Division of Plant Breeding and Genetics, Faculty of Agriculture, Sher-e-Kashmir University of Agriculture Sciences and Technology, using Randomized block design with three replications. For genetic analysis of quantitative traits, four crosses from seven diversified elite lines of wheat (*Triticum aestivum* L.) was employed. The generations used were F_1, F_2, BC_1 and BC_2 along with parents, P1, P2. Each cross's six populations was grown in 36 rows, with 2 rows for P_1, P_2, and F_1 & ten rows for BC_1, BC_2 & F_2. 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, spike length (cm), number of grains per spike, test weight (gm), grain yield per plant (gm).

Hayman and Mather (1955) scaling tests was utilized for studying the efficiency of additive dominance model for distinctive attributes in each cross. If any of the 4 scaling tests is significant, it shows occurrence of non-allelic gene actions and the insufficiency the additive dominance model. Equations given below were used to calculate the values for the A, B, C, and D tests.

$$A = 2\overline{B_1} - \overline{P_1} - \overline{F_1}$$

$$B = 2\overline{B_2} - \overline{P_2} - \overline{F_2}$$

$$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2}$$

$$D = 2\overline{F_2} - \overline{B_1} - \overline{B}$$

The variances of the estimates were computed using following formulae:

$$V_A = 4V(\overline{B_1}) + V(\overline{P_1}) + V(\overline{F_1})$$

$$V_B = 4V(\overline{B_2}) + V(\overline{P_2}) + V(\overline{F_1})$$

$$V_C = 16V(\overline{F_2}) + 4V(\overline{F_1}) + V(\overline{P_1}) + V(\overline{P_2})$$

$$V_D = 4V(\overline{F_2}) + V(\overline{B_1}) + V(\overline{B_2})$$

RESULTS AND DISCUSSION

Findings obtained from mean sum of squares data showed significant variances between the generations for all the four crosses for all characters. This showed a substantial amount of variability among the material used for study. According to Mahpara *et al.* (2017) and Ijaz *et al.* (2017), significant genetic diversity was also found in wheat for a number of quantitative attributes (2017). **Table 1** provides ANOVA for all the four bread wheat crosses and their six generations.

Finding out whether epistatic gene effect is present/ absent, or which model is better for study, requires scaling test analysis utilising generation means. The four scaling tests were recommended by Mather and Jinks (1982). According to the findings, all four tests (A, B, C, and D) in cross I (HD 2967 x PBW 752) were significant for all traits except grain yield, where scaling test A was observed non-significant. In cross II (RSP 561 x PBW 779) all scaling tests, i.e., A, B, C, and D, were significant for plant height, days to maturity, number of tillers per plant, number of grains per spike, 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, scaling test A, B, C, and D were found to be 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 spike length (cm). In cross IV (JAUW 584 x WH 1184) scaling test A, B, C, and D were significant for plant height, days to maturity, number of tillers/plant, spike length (cm), 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. Comparable findings were revealed by studies carried by Mahpara *et al.* (2017) and Ijaz *et al.* (2017).

The generation mean for all the characters under study in the four crosses exhibited significant variations over all six generations, revealing that these traits' have high genetic variability, suggesting that they were inherited quantitatively. **Table 2** shows the estimates for the six variables, which are additive (d), dominance (h), additive x additive (I) additive x dominance (j), and dominance x dominance (l), as well as means (m). Days to maturity were not significant for crosses I (HD 2967 x PBW 752) and II (RSP 561 x PBW 779) while negative and highly significant results were observed for crosses III (RSP 561 x PBW 780) and IV. For all four crossings, the additive gene effect was highly positive and show significance for days to heading, plant height, number of tillers per plant, and grain yield (JAUW 584 x WH 1184). Among all four crosses the dominance (h) gene effect was shown to be extremely significant and positive for the number of tillers per plant, spike length (cm), test weight (gm), and grain yield per plant (gm). Days until heading, plant height (cm), spike length (cm), test weight (mg), and grain

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Table 1. Analysis of variance for four 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 effectivetillers per plant	Spike length (cm)	Number of Grainsper spike	Test weight (gm)	Grain yield perplant (gm)
Cross I (HD 2967 x PBW 752)									
Replication	2	1.45	8.69	1.40	3.27*	0.59	2.07	0.30	0.33*
Generation	5	73.58**	122.59**	92.09**	6.26*	6.05**	175.02**	27.99**	5113.74**
Error	10	1.25	3.57	1.41	0.60**	0.45	5.82	1.17	0.06
Cross II (RSP 561 x PBW 779)									
Replication	2	1.95	9.49	1.77	0.53	0.92	0.06	1.54	0.30
Generation	5	36.99*	71.78**	39.37**	6.95**	7.07**	30.95**	20.54**	1726.33**
Error	10	3.61	6.27	0.51	0.59	0.69	0.76	0.86	0.63
Cross III (RSP 561 x PBW 780)									
Replication	2	1.95	9.49	1.77	0.53	0.59	3.48	1.89	0.53
Generation	5	36.99*	71.78**	39.37**	6.95**	6.05**	71.52**	16.69**	2173.46**
Error	10	3.61	6.27	0.51	0.59	0.45	4.96	0.40	0.29
Cross IV (JAUW 584 x WH1184)									
Replication	2	1.22	1.08	1.77	0.63	0.98	26.27*	2.07	1.37
generation	5	22.91	53.02**	39.37**	12.59**	7.18**	28.62**	175.02**	11.17**
error	10	7.92	0.89	0.51	1.16	0.69	3.62	5.82	0.99

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

yield per plant were all shown to have positive and highly significant additive x additive I gene effects (gm). The number of tillers per plant in cross I (HD 2967 x PBW 752), the number of grains per spike in cross II (RSP 561 x PBW 779) and cross III, the test weight in cross II (RSP 561 x PBW 779), and the grain yield per plant in cross I (HD 2967 x PBW 752) and cross IV were all found to be significantly influenced by the additive x dominance (j) gene (JAUW 584 x WH 1184). In all four crosses, dominance x dominance (l), gene impact, was shown to be extremely important for days to heading, whereas cross I (HD 2967 x PBW 752), cross III (RSP 561 x PBW 780), and cross IV were significant for plant height and days to maturity.

In the present study, most of the traits showed lesser magnitude of additive gene actions than that of dominance actions, indicating that the pedigree technique of selection is the most effective strategy for enhancing these populations. Similarly, Prasad and Virk (2015) found lesser magnitude of additive gene actions as compare to dominance. For almost all of the studied traits in all four crosses, the extent of the dominant gene effect were greater than that of the additive gene effect, indicating a crucial role for the dominant component of gene action in the inheritance of these traits. As a result, selection for these traits must be postponed until afterward generation when the dominant effect is concise. Epistasis was significant for the majority of additive x additive characteristics, underlining the importance of this component. Studies conducted by Singh and Singh (1992) and Novoselovic *et al.* (2004) also confirmed the importance of epistasis. Although it varied by trait, the variation in the generation means fit a digenic epistatic model in the majority of cases. This suggests that changing the investigated traits would be more challenging than when an additive-dominance model provided the suitable fit. These results line up with those presented by other authors (Pawar *et al.,* 1988; Singh and Singh, 1992).

According to Kumar *et al.* (2010), the opposite signs of h and l neutralise the effect of each other, resulting in less heterosis. However, complementary non-allelic gene action was also seen for cross II (RSP 561 x PBW 779) and cross IV (JAUW 584 x WH 1184) for plant height (cm), where h and l values were respectively 5.17 and 1.93 and 0.43 and 3.60. Days to maturity exhibited complementary non-allelic gene interaction in cross-III with values of h and l of 10.18 and 1.17, respectively. In contrast, the number of grains per spike and test wt. traits showed complimentary gene interaction in cross-IV (JAUW 584 x WH 1184). In Cross I (HD 2967 x PBW 752), the values of h and l for grain yield/plant (gm) were 13.85 and 5.23, respectively. According to the complementary gene effects, there is a high likelihood of abundant heterosis in the crosses where it occurs (Punia *et al.,* 2011). The majority of

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

Cross	Scaling tests				Three parameter model			Chi ²	Six parameter model						Gene Actions
	A	B	C	D	M	D	H	χ^2	m	d	h	i	j	L	
							Days to heading								
I	3.03**	-1.27**	-31.30**	-16.53**	98.27**	5.16**	4.59*	248.97**	65.62**	4.32**	72.72**	33.07**	2.15	-34.83**	D
II	-0.37	-13.17**	-15.73**	-1.10**	100.35**	4.49**	4.01**	6.57*	100.57**	1.90**	-6.27**	2.20**	6.40	11.33**	D
III	13.13**	1.23**	-39.37**	-26.87**	90.66**	14.86**	-6.13**	2162.62**	38.48**	12.45**	115.82**	53.73**	5.95	-68.10**	D
IV	2.25**	0.57	-10.39**	-6.60**	91.01**	2.97**	3.74**	6.54*	77.75**	2.83**	32.71**	13.21**	0.83	-16..03**	D
							Plant height (cm)								
I	-3.30**	5.17**	-11.47**	-6.67**	90.27**	9.02**	-5.78**	108.49**	-6.67**	77.23**	9.10**	23.60**	13.33	-4.23**	D
II	-7.60**	-8.47**	-31.53**	-7.73**	87.72**	5.05**	-3.35**	0.10	-7.73**	75.03**	5.17**	15.63**	15.47	0.43	C
III	12.40**	-13.03**	-6.17**	-2.77**	86.72**	2.64**	1.47**	79.04**	-2.77**	82.55*	-2.75**	10.55**	5.53	12.72**	D
IV	11.67**	-9.27**	-1.20**	-1.80**	83.73**	4.36**	0.88**	94.07**	-1.80**	79.80**	1.93**	11.67**	-6.00	3.60**	C
							Days to Maturity								
I	-5.40**	-12.92**	-39.00**	-10.34**	134.92**	5.09**	0.79**	8.74**	116.85**	4.43*	28.34**	20.68**	3.76**	-2.36**	D
II	-1.83**	-15.67**	-24.57**	-3.53**	131.76**	5.51**	10.36**	0.95	133.12**	-1.65**	-0.05**	7.07**	6.92**	10.43**	D
III	4.30**	-13.93**	-18.10**	-4.23**	138.46**	1.15**	-0.48**	4.14	130.62**	-0.55**	10.18**	8.47*	9.12	1.17	C
IV	0.90**	-18.30**	-18.73**	-0.67**	141.58**	2.78**	-6.32**	35.22**	140.37**	-2.40**	-13.03**	1.33**	9.60	16.07**	D
							Number of tillers/Plant								
I	2.63**	-1.44**	-7.57**	-4.38**	12.63**	1.16**	0.88**	239.72**	3.16**	0.85**	20.06**	8.77**	2.04**	-9.95**	D
II	2.23**	-1.17**	-7.70**	-4.38**	11.23**	1.79**	1.59**	131.27**	3.16**	1.18**	19.99**	8.77**	1.70	-9.82**	D
III	0.23	-1.60**	-2.90**	-0.77**	12.24**	0.99**	1.98**	0.09	10.85**	0.72**	4.12**	1.53	0.92	-0.17	D
IV	3.20**	-3.37**	-3.23**	-1.53**	13.36**	2.27**	3.00**	23.19**	10.52**	1.52**	8.55**	3.07**	3.28	-2.90**	D
							Spike length (cm)								
I	2.63**	-1.44**	-7.56**	-4.38**	11.63**	1.16**	0.88**	138.25**	3.16**	0.85	20.06**	8.77**	2.04	-9.95	D
II	-0.38	-3.27	-9.71**	-3.03**	12.11	1.61	-0.36	20.33	6.38**	1.33**	9.22**	6.06**	1.44	-2.410**	D
III	2.63**	-1.44**	-7.56**	-4.38	13.13**	1.16**	0.88**	300.85**	4.15**	0.85**	20.06**	8.76**	2.03	-9.953**	D
IV	-0.43*	-3.28**	-9.76**	-3.02**	12.09**	1.65**	-0.27**	19.18**	6.44**	1.35**	9.11**	6.05**	1.42	-2.34**	D

Table2. Continued..

Cross	Scaling tests				Three parameter model			Chi ²	Six parameter model						Gene Actions
	A	B	C	D	M	D	H	χ^2	m	d	h	i	j	L	
							Number of grains/ Spike								
I	3.50**	-16.80**	-29.17**	-7.93*	39.34**	2.97**	-1.69**	11.43**	25.52**	2.65**	23.98**	15.87**	10.15**	-2.57**	D
II	3.53**	-9.93**	-3.47**	1.47**	41.28**	3.58**	3.16**	111.42**	44.70**	1.60	-8.27**	-2.93**	6.73**	9.33	D
III	3.23**	-12.03**	-39.27**	-15.23**	40.86	3.96	2.84	110.51	11.43**	1.47	55.90**	30.47**	7.63**	-12.67*	D
IV	3.11	5.60**	27.68**	9.48**	45.59**	1.00**	1.26**	1.41	62.79**	2.13**	-28.38**	-6.04**	-1.88	-6.04**	C
							Test weight (gm)								
I	5.77**	-6.63**	-12.33**	-5.73**	33.57**	4.04**	3.84**	292.14**	24.00**	1.60**	24.77**	11.47**	6.20	-10.60**	D
II	5.93**	-6.17**	-15.77**	-7.77**	34.01**	0.39**	3.96**	656.03**	19.65**	-1.62**	34.35**	15.53**	6.05**	-15.30	D
III	5.70**	-8.23**	-13.47**	- 47**	34.37**	-0.49**	-1.51**	242.04**	24.13**	-1.50**	20.07**	10.93**	6.97	-8.40**	D
IV	2.48**	-25.52**	-39.50**	-8.23	38.66**	7.66**	1.04**	26.97**	24.90**	4.30**	14.85**	16.46**	14.00	6.57**	C
							Grain yield / plant (gm)								
I	2.07	-2.63**	-6.37**	-2.90**	16.24	1.71	2.61	56.11	10.55**	1.28	13.85**	5.80**	2.35**	5.23**	C
II	2.90**	-4.53**	-5.43**	-1.90**	16.29**	1.34**	2.09**	11.64**	12.78**	0.52*	7.85**	3.80**	3.72	-2.17	D
III	3.20**	-3.37**	-3.23**	-1.53**	15.36**	2.27*	3.00**	23.19**	12.51**	1.52**	8.55**	3.07**	3.28	-2.90**	D
IV	3.20**	-3.90**	-3.77**	-1.53**	15.68**	1.98**	2.51**	15.49**	12.78**	1.25**	7.75**	3.07**	3.56**	-2.37	D

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

investigated traits had duplicate type of gene effects with few anomalies, which further confirmed the dominant effects' pervasiveness (Singh and Sharma 2019). It is not suitable to use them in breeding programmes because the appearance of duplicate type of epistasis demonstrated, diversity in segregating generations had decreased, and hinders the process of selection (Kumar and Patra 2010). Among different characters 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 favourably showed significance. Similarly, Singh and Sharma (2019) revealed 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 improvement of grain yield and contributing traits must be postponed until later generations because additive x dominant gene effects were of less consequence. It was seen that additive x dominance effects in gene was of lesser significance, thus, suggesting that in wheat breeding, selection for the refinement of grain yield and its contributing traits must be postponed for advanced generations.

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