

## INHERITANCE MECHANISM OF SOME YIELD COMPONENTS IN BREAD WHEAT

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**ABSTRACT:** A set of 8x8 diallel cross comprising promising genotypes was studied to analyze the inheritance pattern of yield components in bread wheat. The different yield related traits estimated were spike length, number of spikelets spike<sup>-1</sup>, number of grains spike<sup>-1</sup>, 1000 grain weight and grain yield plant<sup>-1</sup>. The analysis of variance depicted that 56 F<sub>1</sub> and their parents were significantly different for all the parameters. Uniformity of Wr-Vr over arrays as well as significant deviation of regression coefficient (b) from unity confirmed the suitability of additive-dominance model to account for the data analysis. The estimates of genetic component of variation in all the traits exhibited the preponderance of over dominance gene action. The estimates of average degree of dominance for spike length (1.139), 1000 grain weight (1.421), number of spikelets spike<sup>-1</sup> (2.293), number of grains spike<sup>-1</sup> (1.631) and grain yield plant<sup>-1</sup> (1.111) evidenced the prevalence of non additive gene action controlling these traits. The present results, therefore, revealed that selection for these traits in early generation may not be useful and it has to be delayed till segregating generations.

*Key Words: Bread Wheat; Diallel; Yield Components; Gene Action; Pakistan.*

### INTRODUCTION

Wheat (*Triticum aestivum*) is the staple diet of most of the countries including Pakistan. Wheat has contributed significantly to the overall production in the country as well as giving economic returns to the farming community. In spite of high yield potential, Pakistan is lagging behind the world's average and maximum potential is yet to be exploited. This indicates that there is a good scope of increasing wheat production in the country.

Grain yield is a complex phenomenon that results from the interaction of various yield contributing characteristics. It cannot be improved by mere phenotypic selection of desirable plants, rather study of inheritance mechanism governing various components of yield need to be ascertained. A first prerequisite is knowledge of its genetic make up and the nature of gene action. Diallel analysis technique as developed by Hayman (1954a,b) provides opportunity on the nature and type of gene action in early generation and helps the breeders

to make his choice of selection for desired objectives.

Hussain et al. (1986) reported that additive type of gene action was operative with partial dominance for number of spikelets spike<sup>-1</sup> while for number of grains spike<sup>-1</sup> and grain yield plant<sup>-1</sup>, over dominance type of gene action was present. Khan et al. (1992) found additive type of gene action with some degree of partial dominance for spike length. Altinbas and Bilgen (1996) and Chowdhry et al. (1997) have reported partial dominance with additive type of gene action for most of yield components in wheat. However researchers like Chowdhry et al. (2002), Riaz and Chowdhry (2003), Kashif and Khaliq (2003), Suleyman and Akguni (2007 and Akbar et al. (2009) have observed the prevalence of over dominance for number of grains spike<sup>-1</sup>, 1000 grain weight and grain yield plant<sup>-1</sup>.

During the present study the F<sub>1</sub> data on yield parameters obtained by crossing eight parents of bread wheat were analyzed to determine the inheritance mechanism

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of these traits following additive dominance model (Hayman, 1954 a, b).

## MATERIALS AND METHODS

The experimental material used in the present study was developed by crossing eight local wheat genotypes viz. Pak-81, Pothowar 93, Parwaz 94, Shahkar 95, Suleiman 96, Chakwal 97, Kohistan 97 and MH 97 which were quite distinguishable for the traits studied. Sowing was done during November, 2000 with two sowing dates November 5 and 20 to facilitate hybridization. Crossing of the varieties was performed according to diallel fashion, during February-March 2001, whereas, the parent varieties were self-pollinated to maintain the true to type seed.

The seeds of 28 direct crosses and 28 reciprocal crosses along with their parents were sown in the field on November 3, 2001. Randomized complete block design was followed in the experiment having three replications. Each treatment comprised a single 5 m long row in each replication. Inter row and interplant distances were kept at 30 cm and 20 cm, respectively. Basal fertilizer dose of NPK was applied @ 100-40-0 kg ha<sup>-1</sup> to meet the nutritional requirements of the crop.

Data regarding spike length (cm), number of spikelets spike<sup>-1</sup>, number of grains spike<sup>-1</sup>, 1000 grain weight (g), and grain yield plant<sup>-1</sup>(g) were recorded during the cropping season and after harvest. Before analyzing the data set for diallel technique, the data were subjected to analysis of variance technique following Steel and Torrie (1980) to ascertain the significant differences among mean values of genotypes.

Additive-dominance model of Hayman (1954 a,b) is widely used technique to study the basis of genetic variation in early generations like F<sub>1</sub> and it also provides the nature and magnitude of the genetic behaviour. In this technique, the total sum of squares is partitioned into various components, namely, a (additive), b (non-additive, which is further subdivided into b<sub>1</sub>, b<sub>2</sub> and b<sub>3</sub>), c (maternal) and d (reciprocal dif-

ferences other than c).

Significance of test of item 'a' suggests the significance of additive effects of genes and of item 'b', the dominance effects. Significance of 'b<sub>1</sub>' indicates that the dominance is unidirectional. Asymmetry of gene distribution is indicated by the item 'b<sub>2</sub>', whereas item 'b<sub>3</sub>' tests that part of dominance deviation which are not attributable to 'b<sub>1</sub>' and 'b<sub>2</sub>'. Item 'c' tests the presence of maternal effects whereas item 'd' tests the reciprocal differences other than 'c'. Further analysis of data using Vr, Wr approach of Hayman (1954 a) is valid only when 'b' item is significant.

## Testing the Validity of the Hypothesis

Two scaling tests i.e., uniformity of Wr, Vr and joint regression analysis were conducted to ascertain the data sets for adequacy of the additive-dominance model. Wr-Vr is expected to be constant over arrays, if all assumptions of the analysis are fulfilled. Heterogeneity of Wr-Vr arrays indicates that one or more of the assumptions are not fulfilled for that character. The Wr-Vr values were calculated for each of eight arrays and their homogeneity was tested through the value of t<sup>2</sup>.

In joint regression analysis, the regression coefficient (b) of covariance (Wr) on variance (Vr) for each character is expected to be significantly different from zero, but not significantly different from unity, if all assumptions hold true (Jinks and Hayman, 1953).

## Genetic Parameters

The genetic parameters i.e., E (environmental variance from ANOVA), D (estimate of additive and some portions of additive x additive genetic variance), F (estimate of relative frequencies of dominant and recessive alleles in the parents), H<sub>1</sub> and H<sub>2</sub> (estimate of dominance and dominance x dominance interactions, respectively), h<sup>2</sup> (overall dominance effect), H<sub>2</sub>/4H<sub>1</sub> (the proportion of genes with positive and negative effects in the parents), (H<sub>1</sub>/D)<sup>1/2</sup> as the mean degree of dominance, KD/KR (the

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proportion of dominant and recessive genes in the parents) and heritability estimates in narrow sense were computed according to Mather and Jinks (1982).

### RESULTS AND DISCUSSION

This approach is based on the estimation of components of variation. It was initially developed by Jinks and Hayman (1953). Diallel analysis has been extensively used in both self and cross pollinated crops to understand the nature of gene action involved in the expression of quantitative traits.

The mean squares of the analysis showed that genotypic differences for all the characters were highly significant ( $P=0.01$ ) (Table 1). Therefore, the data were arranged in diallel tables for formal analysis of variance. Hayman's analysis of variance was conducted for each character under study and is discussed as under:

#### Spike Length

The results of two scaling tests (Table 2) i.e. uniformity of  $W_r$  and  $V_r$  ( $t^2$  test) and regression analysis indicated that assumptions were completely fulfilled. Therefore, simple additive dominance model was ad-

equated to determine genetic component of variation in spike length.

The non-significant 'a' item revealed the absence of additive genetic effects (Table 3). The non-significant 'b<sub>1</sub>' item showed the absence of directional dominance effects. Both 'b<sub>2</sub>' and 'b<sub>3</sub>' items were found to be significant indicating that genes for spike length were distributed asymmetrically among the parents and specific gene effects were also present. The significant ( $P=0.01$ ) 'b' item suggested the presence of dominance gene effects. Due to non-significant 'c' and 'd' items, maternal and reciprocal effects were not present.

Non-additive genetic variances play significant role in the expression of this character as indicated by the value of non-additive variance (Table 4). Positive F value expressed that dominant alleles were more frequent than the recessive one. The  $(H_1/D)^{1/2}$  value also revealed the presence of over dominance gene action. As the  $h^2/4H_1$  did not deviate from its expected value 0.25, therefore the gene distribution was symmetrical. The ratio of KD/KR revealed that more dominant alleles were present in the parents for the trait. The researchers like Patil et al. (1995) and Hassan et al. (1996) also reported over dominance for spike

**Table 1. Analysis of variance for some yield contributing traits in bread wheat**

Parameter	Genotypic mean squares	Replication mean squares	Error mean squares
Spike length	2.18*	2.24	1.44
Number of spikelets spike <sup>-1</sup>	15.59**	8.89	3.55
Number of grains spike <sup>-1</sup>	50.73**	92.45	8.26
1000 grain weight	25.62**	33.40	16.91
Grain yield plant <sup>-1</sup>	3506.10**	3173.80	448.10

\*\* , \* = Significant at 1% and 5% probability level, respectively.

**Table 2. Validity of hypothesis through two scaling tests**

Parameter	Analysis of uniformity of $W_r$ - $V_r$ ( $t^2$ )	Joint Regression Analysis		
		Regression coefficient $\pm$ Standard error	H <sub>i</sub> : b = 0	H <sub>i</sub> : b = 1
Spike length	0.81	b = 0.72 $\pm$ 0.20	2.69*	1.15
No. of spikelets spike <sup>-1</sup>	1.57	b = 0.62 $\pm$ 0.17	3.51*	4.20**
No. of grains spike <sup>-1</sup>	0.63	b = 0.61 $\pm$ 0.22	2.77*	3.79**
1000 grain weight	0.14	b = 0.85 $\pm$ 0.25	3.36*	2.69*
Grain yield plant <sup>-1</sup>	1.00	b = 0.95 $\pm$ 0.07	3.69*	3.40*

\*\* , \* = Significant at 1% and 5% probability level, respectively.

**Table 3. Formal analysis for some yield contributing traits in an 8 x 8 diallel cross of wheat**

Source of variation	Spike length		No. of spikelets spike <sup>-1</sup>		No. of grains spike <sup>-1</sup>		1000 grain weight		Grain yield plant <sup>-1</sup>	
	D.F.	M.S.	D.F.	M.S.	D.F.	M.S.	D.F.	M.S.	D.F.	M.S.
a	7	1.66	7	21.12*	7	200.52**	7	20.14	7	19171.60*
b <sub>1</sub>	1	45.80	1	88.07	1	106.54*	1	14.88*	1	2266.10
b <sub>2</sub>	7	6.12**	7	15.28	7	11.54**	7	21.02	7	7609.60
b <sub>3</sub>	20	3.56*	20	8.45	20	52.65**	20	17.86	20	5642.90**
b	28	5.70**	28	13.00*	28	44.30**	28	18.54*	28	6014.00*
c	7	1.79	7	17.50*	7	65.56**	7	8.83	7	426.40
d	21	2.38	21	6.60	21	48.28**	21	9.55	21	2235.10
Blocks	63	3.71*	63	12.27*	63	65.35**	63	14.64	63	5595.40**
B x a	14	3.66	14	7.28	14	4.95	14	19.94	14	5941.70
B x b <sub>1</sub>	2	4.17	2	10.70	2	3.70	2	0.19	2	1051.90
B x b <sub>2</sub>	14	1.08	14	7.19	14	1.71	14	13.96	14	6909.70
B x b <sub>3</sub>	40	1.96	2	7.60	40	5.56	40	10.07	40	2185.40
B x b	56	1.82	56	7.61	56	4.53	56	10.69	56	3326.00
B x c	14	2.75	14	5.49	14	1.02	14	32.81	14	2676.40
B x d	42	3.21	42	10.84	42	2.92	42	11.55	42	3031.30
Block	126	2.59	126	8.41	126	3.65	126	14.46	126	3446.20

interaction

\*\* , \* = Significant at 1% and 5% probability level, respectively.

a (additive), b (non-additive), b<sub>1</sub> (unidirectional dominance), b<sub>2</sub> (asymmetric gene distribution), b<sub>3</sub> (tests that part of dominance deviation which are not attributable to b<sub>1</sub>' and 'b<sub>2</sub>'), c (tests the presence of maternal effects), d (tests the reciprocal differences other than c).

length. Due to involvement of over dominance, selection of this trait in early generations would be difficult.

### Number of Spikelets Spike<sup>-1</sup>

The significant 'a' and 'b' items exhibited the presence of additive and dominance genetic effects in the genetic control of number of spikelets spike<sup>-1</sup> (Table 3). The non-significant 'b<sub>1</sub>' item revealed the absence of directional dominance. Similarly 'b<sub>2</sub>' and 'b<sub>3</sub>' items were also non-significant indicating the symmetrical distribution of genes and absence of specific genetic effects in the inheritance of this character. Due to significant (P=0.05) 'c' item, the mean square of 'a' was retested against 'c' which then reduced to non-significant. It evidenced that additive genetic effects were suppressed by maternal effects for this particular character. The 'd' item was observed to be non-significant.

Hayman's analysis of variance (Table

3) suggested that the item 'b' was significant. Therefore further analysis of variance (Vr) and covariance (Wr) was conducted. To test the adequacy of the additive dominance model for the data sets two scaling tests were carried out. The analysis of data revealed that uniformity test of Vr-Vr validated the model whereas joint regression analysis partially fulfilled the assumptions (Table 2). However, further analysis of genetic components could still be carried out.

Dominance genetic variances (H<sub>1</sub>, H<sub>2</sub>, h<sup>2</sup>) to play an important role in the expression of this character as the values of non-additive genetic variances were significant (Table 4). Over dominance was suggested for this trait on the basis of (H<sub>1</sub>/D)<sup>1/2</sup> ratio. A low value (0.156) of the proportion H<sub>2</sub>/4H<sub>1</sub> indicated that positive and negative alleles were unequally distributed at the loci exhibiting dominance in the parental genotypes. The ratio of KD/KR proposed that more dominant alleles than the recessive

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**Table 4. Estimates of genetic components for some yield contributing traits in an 8 x 8 diallel cross of wheat**

Parameter	Spike length		No. of spikelets spike <sup>-1</sup>		No of grains Spike		1000 grain weight		Grain Yield plant <sup>-1</sup>	
	Estimates	Estimates	Estimates	Estimates	Estimates	Estimates	Estimates	Estimates	Estimates	Estimates
D	0.444* ± 0.179	0.784 ± 0.654	10.309* ± 20.17	2.899* ± 1.242	210.357* ± 7.725					
F	0.553 ± 0.426	1.1323 ± 1.554	-4.411 ± 4.788	1.270 ± 2.947	499.268 ± 0.247					
H <sub>1</sub>	0.581 ± 0.415	4.125* ± 1.512	27.437* ± 4.658	5.861* ± 2.867	485.730* ± 4.127					
H <sub>2</sub>	0.612 ± 0.361	2.586* ± 1.315	25.910* ± 4.053	1.058 ± 2.494	422.596* ± 4.164					
h <sup>2</sup>	0.373 ± 0.241	11.513* ± 0.880	14.743* ± 2.711	-0.011 ± 1.669	82.715 ± 0.069					
E	0.854* ± 0.060	3.041* ± 0.219	1.812 ± 0.675	4.985** ± 0.416	70.433 ± 1.770					
(H <sub>1</sub> /D) <sup>1/2</sup>	1.139	2.293	1.631	1.421	1.111					
H <sub>2</sub> /4H <sub>1</sub>	0.263	0.156	0.236	0.045	0.220					
KD/KR	3.377	2.164	0.767	1.364	1.071					
Heritability	-0.053	0.119	0.495	0.039	0.607					
(N.S.)										

\*\* , \* = Significant at 1% and 5% probability level, respectively.

E = Environmental variance, D = Estimate of additive and some portions of additive x additive genetic variance, F = Estimate of relative frequencies of dominant and recessive alleles in the parents, H<sub>1</sub> and H<sub>2</sub> = Estimate of dominance and dominance x dominance interactions, respectively, h<sup>2</sup>= Overall dominance effect, H<sub>2</sub>/4H<sub>1</sub>= Proportion of genes with positive and negative effects in the parents, (H<sub>1</sub>/D)<sup>1/2</sup>= Mean degree of dominance, KD=KR= Proportion of dominant and recessive genes in the parents.

were controlling this character. The ratio of h<sup>2</sup>/H<sub>2</sub> revealed that four groups of genes might be controlling this character. Low values of heritability were obtained due to over dominance type of gene action. Over dominance gene action was also reported by Khan et al. (1992) and Altinbas and Bilgen (1996) for number of spikelets spike<sup>-1</sup>. The over dominance type of gene action indicated that effective selection may not be possible in the early generations. The variation in the results might be due to different genetic materials and environmental conditions involved.

**Number of Grains Spike<sup>-1</sup>**

The formal analysis of variance for number of grains spike<sup>-1</sup> (Table 3) showed that all the items were highly significant (P=0.01) except 'b<sub>1</sub>' item which was significant (P=0.05). The significant 'a' and 'b' items revealed the presence of additive and dominance genes for number of grains spike<sup>-1</sup>. The significant 'b<sub>1</sub>' item (P=0.05) showed the presence of directional dominance. The parents contained differing number of dominant genes for this character, as 'b<sub>2</sub>' item was significant. The significant 'b<sub>3</sub>' item revealed the presence of specific gene action. The significant 'c' and 'd' items showed the presence of maternal and reciprocal effects in the expression of this character. As 'c' and 'd' items are significant, the values of 'a' and 'b' items are to be tested against 'c' and 'd' items, respectively, (Mather and Jinks, 1982).

After retesting 'a' and 'b' items, the situation became quiet different. The non-significant 'a' item suggested that maternal effects had masked the genes acting additively. Similarly non-significant 'b', 'b<sub>1</sub>', 'b<sub>2</sub>' and 'b<sub>3</sub>' suggested the predominant role of reciprocal effects on the development of number of grains spike<sup>-1</sup>. The analysis of variance (Vr) and covariance (Wr) was carried out, since the item 'b' was significant for number of grains spike<sup>-1</sup>. The results of the uniformity tests and joint regression analysis indicated that assumptions were completely fulfilled by uniformity test. However, for regression analysis the data par-

tially fulfilled the assumptions. The estimation of genetic parameters could still be carried out.

The estimates of components of variation i.e.  $D$ ,  $H_1$ ,  $H_2$ ,  $F$  and  $h^2$  for number of grains spike<sup>-1</sup> showed that both additive and non-additive types of gene actions were involved in the inheritance of this character as indicated by the significant additive and dominance variances (Table 4). Dominance genetic variances ( $H_1, H_2, h^2$ ) were found to play an important role in the expression of this character due to their higher magnitude.  $F$  value was negative and non-significant indicating greater frequency of recessive alleles than dominant ones. Over dominance was suggested for this trait on the basis of  $(H_1/D)^{1/2}$  ratio. The proportion of positive and negative alleles was close enough to 0.25 which indicated that both the alleles were distributed equally over the loci. Similar results were obtained by Sabour et al. (1996), Pandey et al. (1999) and Riaz and Chowdhry (2003) who reported over dominance gene action for number of grains spike<sup>-1</sup>. The character thus seems difficult to fix and the progress in selection will be inherently slow.

### 1000 Grain Weight

The analysis of variance of components of variation in 1000 grain weight (Table 3) revealed that 'a' item was non-significant showing the absence of additive genetic effects in the manifestation of this character. The significant ( $P=0.05$ ) 'b<sub>1</sub>' item showed the presence of directional dominance and 'b' item revealed the presence of dominance genes for 1000 grain weight, respectively. The genes were distributed symmetrically among the parents as the item 'b<sub>2</sub>' was non-significant. Similarly, non-significant 'b<sub>3</sub>' expressed the absence of specific gene action in the inheritance of 1000 grain weight. The maternal and reciprocal effects did not contribute in the genetic control of 1000 grain weight as 'c' and 'd' items were non-significant.

The results divulged that the item 'b' was significant (Table 3). Therefore analysis of variance (Vr) and covariance (Wr) was

accomplished for this trait. The two scaling tests i.e. uniformity of  $Wr-Vr$  and joint regression analysis were carried out to determine the fitness of data to additive dominance model (Table 2). The uniformity test completely fulfilled the assumptions while the joint regression analysis shows the partial failure. On the basis of these results, the data can still be processed for further genetic studies.

Both additive and non-additive types of gene actions were involved in the inheritance of 1000 grain weight as is indicated by significant additive and dominance variances (Table 4). The dominance genetic effects, however seemed to be more prominent due to higher magnitude of  $H_1$  than  $D$ .  $F$  value was positive suggesting the presence of dominant genes in more frequency than recessive genes.  $(H_1/D)^{1/2}$  ratio evidenced the over dominance genetic effects. The proportion of genes with positive and negative effects ( $H_2/4H_1$ ) in the parents was less than 0.25 denoting asymmetry at the loci showing dominance. The  $KD/KR$  ratio suggested more dominant alleles in the parents for the trait. Similar results were also obtained by Hassan et al. (1996), Mishra et al. (1996), Sabour et al. (1996) and Chowdhry et al. (2002). Since the inheritance of the said trait involved over dominance therefore, early selection of this trait is highly difficult. The difference in the results might be attributed to the variation in genetic constitution of the genotypes and environmental conditions.

### Grain Yield Plant<sup>-1</sup>

The formal analysis of variance for grain yield plant<sup>-1</sup> (Table 3) showed that both 'a' and 'b' items were significant ( $P=0.05$ ) and indicated the presence of additive and dominance genetic effects controlling this character. The non-significant 'b<sub>1</sub>' and 'b<sub>2</sub>' items exhibited the absence of directional dominance and unequal distribution of genes. The significant ( $P=0.01$ ) 'b<sub>3</sub>' item reflected the presence of specific gene action. The non-significant 'c' and 'd' items showed the absence of maternal and reciprocal effects in the expression of this char-

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acter.

Hayman's analysis of variance of diallel tables showed that the item 'b' being significant for character under study, hence the analysis of variance (Vr) and Covariance (Wr) was carried out. To see the fitness of data for Hayman Jinks model of genetic analysis, two scaling tests were carried out. The uniformity tests supported the data while joint regression analysis partially fulfilled the assumptions suggesting that the simple genetic model was partially adequate to analyse the data.

The results showed that the estimates of additive (D) and non-additive ( $H_1$ ) genetic variances were significant indicating the importance of both additive and dominance types of gene actions (Table 4). However, the magnitude of non-additive gene effects ( $H_1$  and  $H_2$ ) was higher revealing the role of dominance gene effect. Over dominance genetic effects were also detected for this trait on the basis of  $(H_1/D)^{1/2}$  ratio. The proportion of genes with positive and negative effects  $H_2/4H_1$  in the parents was less than 0.25 denoting asymmetry at the loci showing dominance. The KD/KR ratio suggested more dominant alleles in the parents for this character. The findings of Hassan et al. (1996), Lonc and Zalewsky (1996), Pandey et al. (1999), Chowdhry et al. (2002), Riaz and Chowdhry (2003) and Kashif and Khaliq (2003) agreed with the present results.

It is therefore concluded that the prevalence of over dominance type of gene action controlling the yield contributing traits in bread wheat genotypes involved in this study. The selection for these traits in early generations may not be useful and it had to be delayed till segregating generations. Although there is scope for improvement of these yield traits, there exist limitations in the use of information gained because the eight parents crossed were specifically selected and did not represent a random sample of all wheat genotypes. However, the present findings may not apply to whole of wheat germplasm and

therefore needs more testing.

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