

*Full Length Research Paper*

# Genetic analysis for yield and its components in doubled haploid wheat

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**The inheritance of grain yield and its components (number of spikelets per spike, number of tillers, number of grains per spike, plant height) has been studied through a full diallel cross of eight doubled haploid bread wheat. Generation mean and variance analysis was carried out on P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generation of two crosses to complement the genetic information from the diallel analysis. Regression analysis, average of dominance and narrow sense heritability in both experiments revealed additive type of gene action for number of grains per spike and plant height and over dominant type of gene effects for the rest of traits. Although different types of epistasis interaction were found for different trait and cross combination, duplicate dominant epistasis only observed for number of spikelets per spike, number of tillers and grain yield per plant. Correlation analysis of dominant genes with the phenotype of the parents revealed recessive gene control for number of tillers, while dominant gene control proved to account for the rest of the traits studied.**

**Key words:** Doubled haploid wheat, gene effects, yield components, diallel, generation mean analysis.

## INTRODUCTION

Cereal crops belong to the family Gramineae which is a large family and constituted by outstanding group of food plants, where from, a majority of humanity meets its dietetic needs; amounting to an estimated 60% of calories and 50% of protein. Wheat (*Triticum aestivum* L.) is foremost among cereals and indeed among all food crops, as direct source of food and energy for human beings. The developments of improved varieties of wheat have always remained a focal point for wheat breeders all over the world (Edwards, 2001).

Yield is a polygenic trait and is greatly influenced by the environmental changes. Any improvement in yield and its related characteristics like plant height, number of spikelets per spike, number of grain per spike and number of tillers through selection and breeding would help to improve unit area production. Several studies in the recent past had identified QTLs for yield and its components in wheat. Gupta et al. (2007) reported three QTLs on chromosomes 3A, 7A and 7B for number of tillers in cross PH132×WL711 (bread wheat).

They also reported four QTLs on chromosomes 2A, 4B

and 7A for number of grains per spike and three QTLs on chromosomes 2B, 4A and 6A for number of spikelets per spike. Maccaferri et al. (2008) have identified 3 QTLs on chromosomes 1B, 3A and 7A for plant height. Also Kuchel et al. (2007) reported several QTLs on chromosomes 1B, 4D, and 7D for grain yield in bread wheat. But bread wheat genomes is very large and consist of three set of chromosomes and in most cases QTLs analysis special for traits such as yield and its components which control with several genes and alleles will be not efficient. This analyzes mostly useful for investigation of resistance to pathogens for this crop.

The choice of selection and breeding procedures for genetic improvement of wheat or any other crop is largely depends on the knowledge of type and relative amount of genetic component and the presence of non-allelic interaction for different characters in the plant materials under investigations. Diallel cross technique is the one used most commonly to estimate inheritance and behaviour of quantitative characters. Application of Hayman (1954), Jinks (1954) and Griffing (1956) models in F<sub>1</sub> generation provides information regarding nature and magnitude of the gene-action involved in the inheritance of a character. This information would be useful to plant breeders for two reasons viz. types of genetic variation in the traits for which selection is intended and rapid evaluation of yielding

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**Table 1.** Pedigree of parents.

1-TEG/GANFRENCH/6/CMH79A.955/4/AGA/3/4*...
2-CMH80.638/CMH75A.411//...
3-CMH76.1084/2*CMH72A.429//ELVIRA/6/...
4-CMH81.794/4/CHEN/AEGILOPS (TAUS)...
5-VEE/CMH77A.917//VEE/3/ELVIRA/6/CMH79A...
6-CMH79A.955/CMH74A.487//CMH81A.744/3/...
7-STDS10/CIRCUS/6/CMH79A.955/4/AGA/...
8-CMH83.2578/GANFRENCH/6/CMH79A955/...

capacity by identifying crosses which will produce superior genotypes.

Generation mean analysis also is a simple but useful technique for estimating gene effects for a polygenic trait, its greatest merit lying in the ability to estimate epistatic gene effects such as additive  $\times$  additive [i], additive  $\times$  dominance [j] and dominance  $\times$  dominance [l] effects (Singh and Singh, 1992).

Thus in the present investigations, the inheritance of yield and its components has been studied through diallel cross and generation mean analyzing design to choose an efficient breeding method for the improvement of grain yield and its components.

## MATERIALS AND METHODS

Diallel analysis: The experimental material was composed of eight lines of doubled haploid wheat from CIMMYT (Table 1). The crosses were attempted in a diallel fashion including direct crosses and their reciprocals during crop season 2006-2007. The parents and  $F_{1s}$  were sown in November 2007 in a randomized complete block design with three replications in Moghan region, Iran. The entries were assigned randomly to experimental units in each block having plant to plant and row to row distance 15 and 30 cm, respectively. At maturity, ten competitive plants were randomly selected to record data for number of spikelets per spike, number of tillers, number of grains per spike, plant height and grain yield per plant. The data were subjected to graphical and component analyses according to Hayman (1954, 1957) and Jinks and Hayman (1953). Analysis of parental measurement (Yr) and  $Wr+Vr$  values (the standard deviation graph) was done following Jonson and Askel (1959).

The  $t^2$  test and the analysis of regression coefficient test, which tests to overall assumption of diallel was performed according of the model with respect to non-allelic interaction.

Generation mean and variance analysis: Generation mean analysis was carried out on  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  generations of two crosses (Cross I: Parent 7  $\times$  Parent 5 and Cross II: Parent 8  $\times$  Parent 4) to complement the genetic information from the diallel analysis. We used the parents of the respective crosses as the male parent and the  $F_1$  generation as the female parent and effected back crosses to produce the  $BC_1$  ( $F_1$  back crossed to  $P_1$ ) and  $BC_2$  ( $F_1$  back crossed to  $P_2$ ) generation and the  $F_1$  hybrids were selfed to obtain  $F_2$  seeds. All these generation were produced during two cropping seasons and, as such, all the six generations had to be grown together in a randomized block design in three replications at the Moghan region in November 2007. The plots were 2 m long with a between-row spacing of 30 cm and a within-row spacing of 15 cm. The number of rows per plot and the number

of analyzed plants per plot varied depending on the generation (three rows for the  $P_1$ ,  $P_2$  and  $F_1$ , 10 rows for the  $F_2$  and 7 rows for the  $BC_1$  and  $BC_2$  generations and 10 plants for the  $P_1$ ,  $P_2$  and  $F_1$ , 70-75 plants for the  $F_2$  and 15 plants in the  $BC_1$  and  $BC_2$  generations, respectively). The genetic model that best fit the data was found by the mean of joint scaling test (Mather and Jinks, 1982), and the accuracy of the models was verified by chi-square test. Components within each model were evaluated for significance by t-test. The type of epistasis was determined only when dominance [h] and dominance  $\times$  dominance [l] effects were significant, when these effects had the same sign, the effects were complementary while different signs indicated duplicate epistasis (Kearsey and Pooni, 1996).

Broad-sense ( $h_b^2$ ) and narrow-sense ( $h_n^2$ ) heritabilities were estimated using the variance component method (Wright, 1968) and variance of  $F_2$  and back cross generations (Warner, 1952), respectively, as:

$$h_b^2 = \{VF_2 - [(VP_1 + VP_2 + 2VF_1)/4]\} / VF_2$$

$$h_n^2 = [VF_2 - (VBC_1 + VBC_2)/2] / VF_2$$

Variance components (additive, dominance and environment) were estimated as described by Kearsey and Pooni (1996) and Farshadfar (1998), using the following equations:

Environment variance:

$$V_E = 1/4 (VP_1 + VP_2 + 2VF_1)$$

Additive variance:

$$V_{[d]} = (2VF_2 - VBC_1 - VBC_2)$$

Dominance variance:

$$V_{[h]} = 4 (VF_2 - 1/2V_{[d]} - E)$$

Average degree of dominance:

$$(H/D)^{1/2} = (V_{[h]}/V_{[d]})^{1/2}$$

Response to selection was estimated with 5% selection intensity (i) (selection differential,  $K=2.06$ ) as:

$$R = i \times h_n^2 \times \sqrt{VF_2}$$

## RESULT AND DISCUSSION

### Diallel analysis

The mean value (parents and  $F_{1s}$ ) for the analyzed traits have shown in Table 2. The analysis of variance of means (parents and  $F_1$  families) revealed highly significant difference for all of the traits under study (data not shown).

The estimates of genetics of variation in grain yield and its component are given in Table 3. Although D,  $H_1$  and  $H_2$  items were positive and signification for number of spikelets per spike, number of tillers and grain yield per plant, the greater magnitude of  $H_1$  and  $H_2$  than that of D revealed that genes with non additive effects were

**Table 2.** Mean of parents and F<sub>1</sub>s for different traits in 8×8 diallel cross.

<b>Genotypes</b>	<b>P.H</b>	<b>N.S.S</b>	<b>N.T</b>	<b>N.G.S</b>	<b>G.Y.P</b>
1	81.12	14.9	5.28	71.74	12.54
2	70.55	15.3	6.06	92.9	19.23
3	80.36	14.6	5.51	72.61	19.43
4	84.14	16.7	5.71	72.37	21.07
5	84.89	14.1	6.1	79.53	20.12
6	84.84	14.8	4.7	88.65	20.11
7	72.58	13.6	5.7	95.03	23.12
8	80.71	14.5	5.51	84.8	18.96
1×2	85.24	15.4	6.12	80.4	13.88
1×3	82.75	17.3	4.79	74.58	17.99
1×4	83.62	16.2	6.1	67.18	22.19
1×5	84.37	14.7	4.4	83.86	23.98
1×6	86	14.7	6.6	82.29	17.42
1×7	84.31	16.9	3.67	83.23	20.7
1×8	80.83	16.6	5.19	79.1	14
2×1	80.9	14.5	5.9	77.24	19.43
2×3	79.84	17	4.73	86.38	19.82
2×4	78.1	15.6	4.85	85.2	23.15
2×5	81.23	15.5	6.55	90.78	21.78
2×6	77.4	15	6.19	90.22	20.05
2×7	75.1	14.8	5.46	85.59	14.62
2×8	76.77	14.3	5.9	83.85	23.15
3×1	84.42	15.1	5.36	81.1	22.32
3×2	81.7	15.4	4.42	84.4	20.4
3×4	80.19	16.9	4.72	79.13	16.5
3×5	91.98	16.9	5.55	72.92	20.37
3×6	83.97	13.9	5.12	74.2	20.67
3×7	77.29	14.7	6.24	86.3	14.58
3×8	82.92	15.8	4.4	81.42	13.62
4×1	90.29	16	4.72	79.77	19.33
4×2	79.55	14.6	5.06	75.35	22.81
4×3	86.05	16.9	5.82	81.8	17.93
4×5	90.11	16.9	6.51	93.53	21.23
4×6	80.53	14.6	5.76	85.9	25.71
4×7	80.13	16.3	5.38	103.44	23.13
4×8	83.4	16.4	5.1	90.93	24
5×1	89.42	15.7	5.1	90.93	22.53
5×2	83.9	15.1	5.1	84.64	23.81
5×3	82.97	15.7	6.1	82.2	19.07
5×4	88.1	16.8	5.85	73.87	16.83
5×6	86.28	14.7	4.41	86.77	18.58
5×7	81.53	15.1	5.1	80.16	16.17
5×8	86.95	14.6	4.45	79.45	19.52
6×1	91.28	16.3	4.49	79.6	25.52
6×2	80.25	14.5	4.36	93.85	20.4
6×3	84.19	15.7	5.33	99.12	19.92
6×4	81.7	15.1	4.77	87.48	19.58
6×5	85.47	14.7	4.33	91.96	17.64
6×7	82.05	15.7	4.94	92.2	17.28
6×8	82.62	14.8	5.88	84.32	25.04

Table 2. Contd.

7×1	82.16	15.1	5.57	79.6	18.17
7×2	79.02	15.3	5.21	91.63	17.03
7×3	80.71	15.7	5.39	84.17	21.68
7×4	80.6	13.9	6	88.89	19.98
7×5	81.18	14.3	5.91	86.68	17.57
7×6	81.18	14.7	4.79	92.9	15.34
7×8	78.1	13.9	47.9	93.76	20.65
8×1	83.9	15.7	4.12	79.92	14.93
8×2	73.69	14.5	4.82	83.7	14.31
8×3	81.58	15.1	5.79	78.62	17.5
8×4	82.51	16.9	5.1	79.37	20.19
8×5	85.59	15.7	5.67	90.7	14.95
8×6	82.45	14.8	5.6	90.93	21.88
8×7	79.31	14.2	4.36	79.37	22.89
Mean	82.29	15.34	5.29	84.13	19.5
Mean parents	79.9	14.81	5.57	82.2	19.32
Mean F1	82.64	15.41	5.25	84.41	19.55
CV (%)	4.18	6.96	11.34	5.86	16.61
LSD <sub>5%</sub>	5.51	1.71	0.96	7.88	5.18

P.H: Plant height, N.S.S: Number of spikelet per spike, N.T: Number of tillers, N.G.P: Number of grains per spike, G.Y.P: Grain yield per plant

Table 3. Components of diallel variance and their estimates for different traits in doubled haploid wheat.

Components	N.S.S	N.T	N.G.S	P.H	G.Y.P
$\hat{D}$	0.437**± 0.611	0.929** ± 0.053	75.37** ± 6.73	25.04** ± 1.66	5.39** ± 1.94
$\hat{F}$	0.0315 <sup>n.s</sup> ± 0.27	1.48** ± 0.125	38.05 <sup>n.s</sup> ± 15.91	2.62 <sup>n.s</sup> ± 3.93	8.1 <sup>n.s</sup> ± 4.6
$\hat{H}_1$	0.799**± 0.26	2.117**± 0.122	28.4 <sup>n.s</sup> ± 15.48	13.88**± 3.82	21.97**± 4.48
$\hat{H}_2$	0.634**± 0.23	1.351**± 0.106	22.3 <sup>n.s</sup> ± 13.47	5.15 <sup>n.s</sup> ± 3.32	17.73**± 3.89
$\hat{h}^2$	0.92 <sup>n.s</sup> ± 0.15	0.192**± 0.071	8.31 <sup>n.s</sup> ± 9.03	20.75**± 2.23	- 1.56 <sup>n.s</sup> ± 2.61
$\hat{E}$	0.41**± 0.035	1.13**± 0.018	15.03**± 2.24	5.05**± 0.55	3.88**± 0.649
<b>Proportion of components of variance</b>					
$(H_1/D)^{1/2}$	1.352	2.278	0.614	0.744	2.02
$H_2/4H_1$	0.189	0.159	0.196	0.093	0.202
$[(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F]$	1.07	3.23	2.39	1.15	2.185
$r(W_r + V_r, Y_r)$	- 0.265	0.602	- 0.335	- 0.691	- 0.651
$h_b^2$	0.519	0.647	0.645	0.769	0.572
$h_n^2$	0.334	0.154	0.513	0.711	0.084

\*\* , \* : significant, at P = 0.01 and P = 0.05 respectively. D: additive variance, H<sub>1</sub> and H<sub>2</sub>: dominance genetic variance and corrected dominance genetic variance, F: product of additive by dominance, h<sup>2</sup>: square of difference P vs All, E: environmental variance, whole, (H<sub>1</sub>/D)<sup>1/2</sup>: average of degree dominance, H<sub>2</sub>/4H<sub>1</sub>: Proportion of genes with positive and negative effects in parents, [(4DH<sub>1</sub>)<sup>1/2</sup> + F / (4DH<sub>1</sub>)<sup>1/2</sup> - F]: Proportion of dominant and recessive genes in parents, R (W<sub>r</sub> + V<sub>r</sub>, Y<sub>r</sub>): correlation between parental measurement (Y<sub>r</sub>) and W<sub>r</sub>+V<sub>r</sub> values, h<sub>b</sub><sup>2</sup>: Heritability for diallel in a broad sense, h<sub>n</sub><sup>2</sup>: Heritability for diallel in a narrow sense

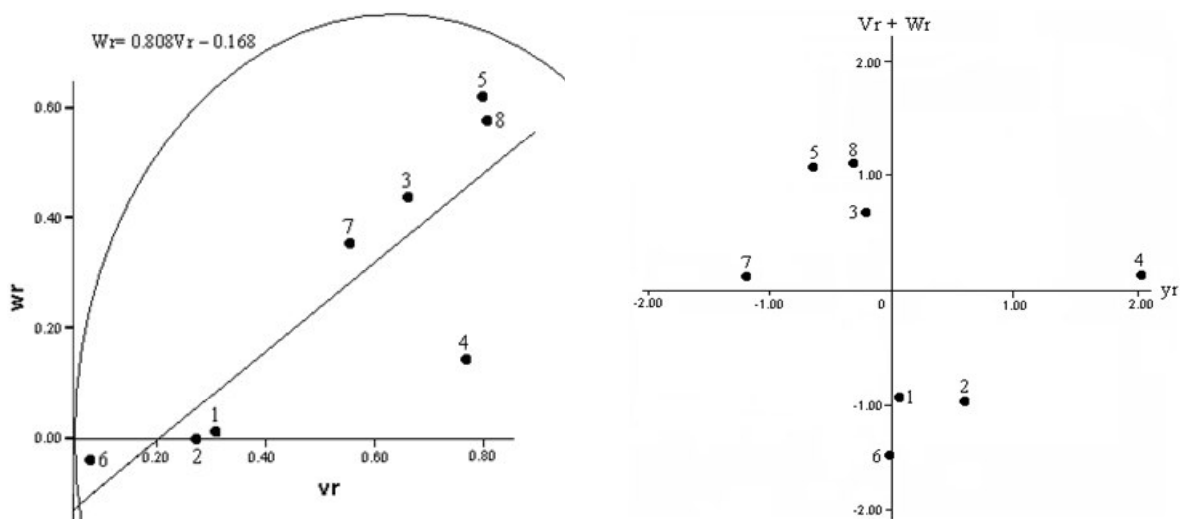


Figure 1.  $W_r/V_r$  and standard deviation graph of number of spikelets per spike.

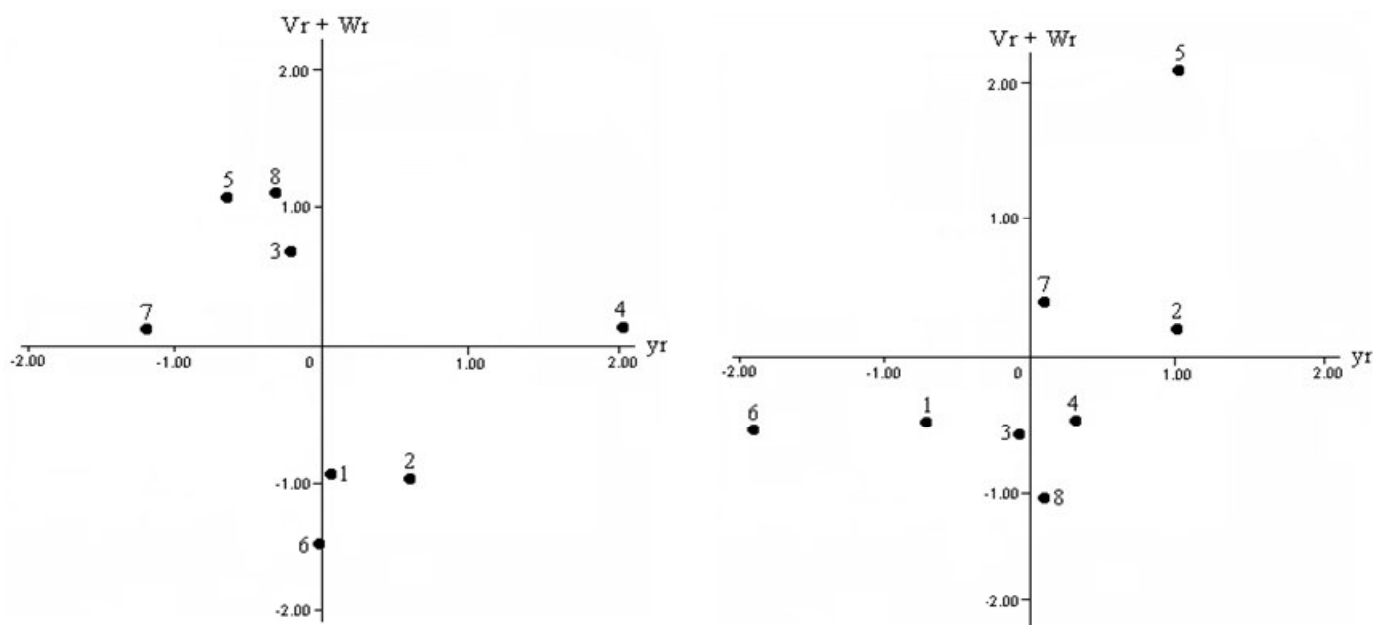


Figure 2.  $W_r/V_r$  and standard deviation graph of number of tillers.

important. The  $W_r/V_r$  graphs showed that regression line intercepts the  $W_r$ -axis below the point of origin for these traits (Figures 1, 2 and 3). Also the ratio of  $(H_1/D)^{1/2}$  was greater than unity. These results indicated that number of spikelets per spike, number of tillers and grain yield per plant were governed by over dominance gene action. Narrow sense heritability of number of tillers (0.154) and grain yield per plant (0.084) is very low while in number of spikelets per spike almost is medium enough (Table 3). Similar nature of gene action for grain yield has been reported by Chowdhry et al. (2002), Dere and Yildirim

(2006). But Khan et al. (2000), Habib and Khan (2003) reported partial dominance for this trait. Also these results are in agreement with the works of Chowdhry et al. (2001), Rahman et al. (2003), Habib and Khan (2003) that found over dominant type of inheritance for number of spikelets per spike. Although Kashif et al. (2003), Khan and Habib (2003) reported similar finding for number of tillers, additive effects for this trait have been reported by Awan et al. (2005). As the magnitude of  $H_1$  is greater than  $H_2$  therefore distribution of negative and positive alleles were unequally distributed in the parents and

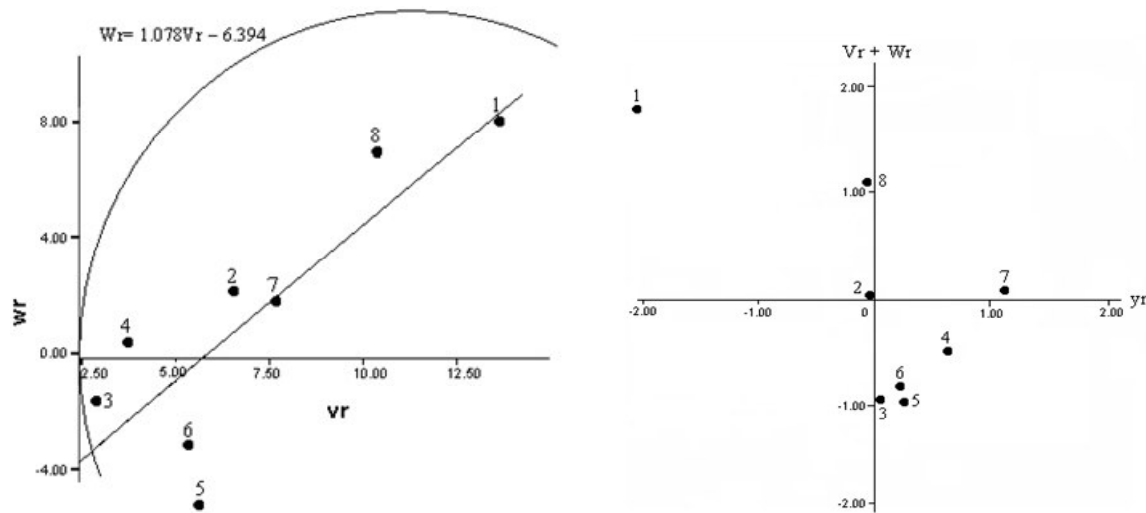


Figure 3.  $W_r/V_r$  and standard deviation graph of grain yield per plant

further proof of this unequal distribution of alleles over loci is provided by the ratio  $H_2/4H_1$ , which is lesser than its maximum value 0.25 (Table 3). Positive value of  $F$  in number of spikelets per spike, number of tillers and grain yield per plant suggested that dominant alleles were more abundant than the recessive alleles in the parents, and its claim was supported by the ratio of  $[(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F]$  which is more than one in these traits. The study of  $W_r/V_r$  graph in Figure 1 shows that parent 6 had maximum number of dominant genes and parents 5 and 8 being away from origin carried maximum number of recessive genes for number of spikelets per spike.

Figure 2 showed that parent 8 had maximum number of dominant genes and parent 5 carried maximum number of recessive genes for number of tillers. Also the regression line and standard deviation graph revealed that parents 5, 3 and 6 had the most dominant genes while parents 1 and 8 had the most recessive genes for grain yield per plant being located farthest from the origin (Figure 3). Correlation analysis of the genotypes showed recessive gene control for number of tillers. However, this analysis showed dominant gene control for number of spikelets per spike and grain yield per plant (Table 3).

The genetic components of variation for number of grains per spike and plant height revealed that genes with additive properties influenced the inheritance of these characters (Table 3). Although in number of grains per spike only value of additive component ( $D$ ) was significant, in plant height both of  $D$  and  $H_1$  were significant, but  $D$  value was more than  $H_1$ . The lesser ratio of  $(H_1/D)^{1/2}$  from unity indicated partial dominance occurring in the inheritance of number of grains per spike and plant height. The estimate of narrow sense heritability is 0.513 and 0.711 for number of grain per spike and plant height, respectively. Chowdhry et al. (2001), Khan and Habib (2003) showed similar results while studying plant height.

Also Rahman et al. (2003), Habib and Khan (2003) reported similar finding for number of grains per spike. The difference  $H_1-H_2$  indicated the unequal distribution of genes for number of grains per spike and plant height and this claim is strengthened by the ratio of  $H_2/4H_1$  which is lesser than 0.25 (Table 3). Ratio of  $[(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F]$  more than unity for number of grains per spike indicated that dominant genes were more frequent. But in plant height this ratio was near unity and showed that frequency of dominance and recessive genes was equal. The relative distribution of array points along the regression line indicated that for number of grains per spike, parents 8 and 5 had the most dominant genes, while parent 4 had the most recessive genes being farthest from origin (Figure 4). The parental order of dominance for plant height was almost similar to  $W_r/V_r$  and standard deviation graph. Parental orders of dominance are in order of parents 1, 5, 3, 6, 4, 7, 8 and 2 (Figure 5).

Correlation analysis of the genotypes showed dominant gene control, for number of grains per spike and plant height (Table 3).

### Generation mean analysis

Analysis of variance for all the traits in two crosses showed significant difference among generations (data not shown). We were therefore, allowed to go ahead to study heredity and to analyze generation means. The mean value and their standard errors for the analyzed traits are presented in Table 4.

Parents 1 and 3 out performed parents 2 and 4 with respect to plant height, number of grains per spike and grain yield per plant, but performed almost similar to parents 2 and 4 for number of tillers and number of

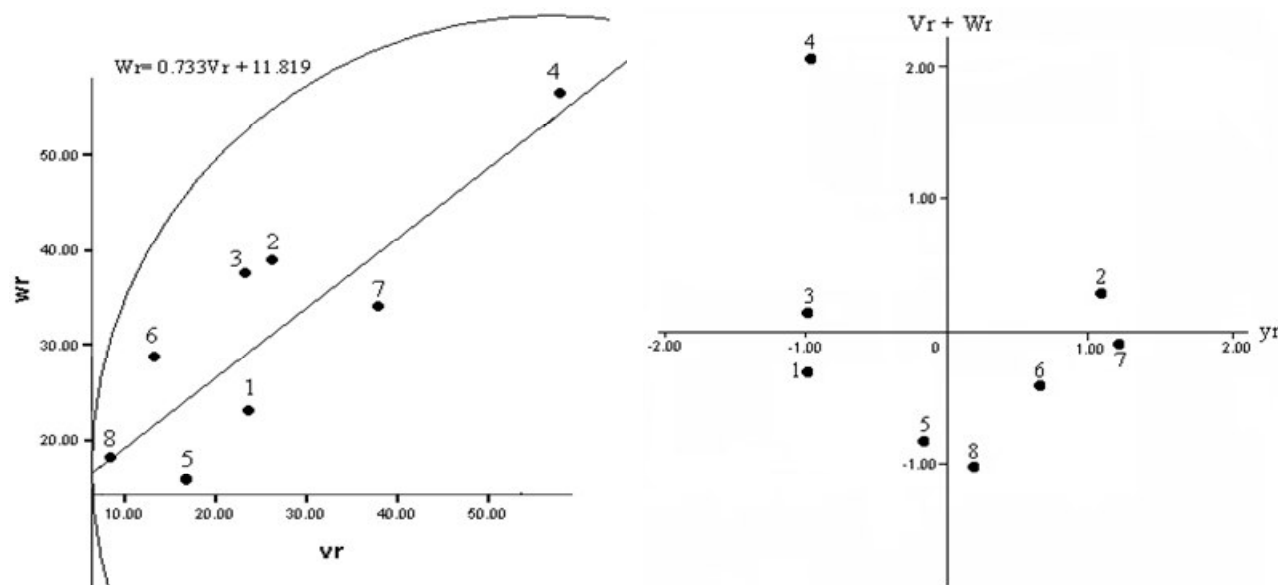


Figure 4.  $W_r/V_r$  and standard deviation graph of number of grains per spike.

Table 4. Mean comparison between sub-main plots (genotypes) for various traits of the cross I and II.

Traits	Genotypes					
	$P_1$	$P_2$	$F_1$	$F_2$	$BC_1$	$BC_2$
<b>Cross I</b>						
Number of spikelets / spike	15.25c	14.8d	16.27a	16b	16.38a	15.8b
Number of tillers	5.5b	5.2c	5.3bc	6.2a	6.4a	6.2a
Number of grains / spike	91.4b	75.2e	93.3a	81.5d	81.4d	84.2c
Plant height	73.2d	84.2a	80.3b	79.5b	80.1b	77.2c
Grain yield / plant	21.11bc	15.28d	20.45c	21.9b	21.4bc	23.2a
<b>Cross II</b>						
Number of spikelets / spike	16.1c	15.1d	16.2bc	16.1c	16.5a	16.3b
Number of tillers	5.6c	5.1d	5.2d	6.4ab	6.6a	6.3b
Number of grains / spike	88.7c	76.2d	90.3b	89.1bc	92.4a	90.1bc
Plant height	78.22d	86.74a	83.61b	80.9c	80.1c	81.4c
Grain yield / plant	19.47b	15.52c	20.54a	19.7b	20.21a	19.83b

spikelets per spike. For plant height all the generation means were between parental means, in both crosses. In cross I, all the generation means except  $F_1$  for number of grains per spike were between parental means and  $F_1$  mean was greater than the top parent ( $P_1$ ). Whereas in cross II for this trait all the generation means were greater than the top parent.  $F_1$  means were almost between parental means for number of tillers in both crosses, but  $F_2$ ,  $BC_1$  and  $BC_2$  means were greater than the top parents for this trait. Also, all the generation means for number of spikelets per spike and grain yield per plant were close or greater than the top parent ( $P_1$ ) in both crosses.

Different 3 to 5 parameter models showed the best fit to

generation means of different traits and cross combination (Table 5). Additive effects were significant for all traits in both crosses. As is shown in Table 5, additive effects for plant height were negative in both crosses. The negative and positive signs for additive effects depend on which parent is chosen as  $P_1$  (Cukadar-Olmedo and Miller, 1997; Edwards et al., 1975). Generation variance analysis (Table 6) indicated additive variance was larger than dominance for plant height and number of grains per spike in both crosses. Also the average degree of dominance was less than unity showed that partial dominance gene action for these traits. These results are in accordance with Awaad (1996), Akhtar and Chowdhry (2006) who reported that additive gene effects

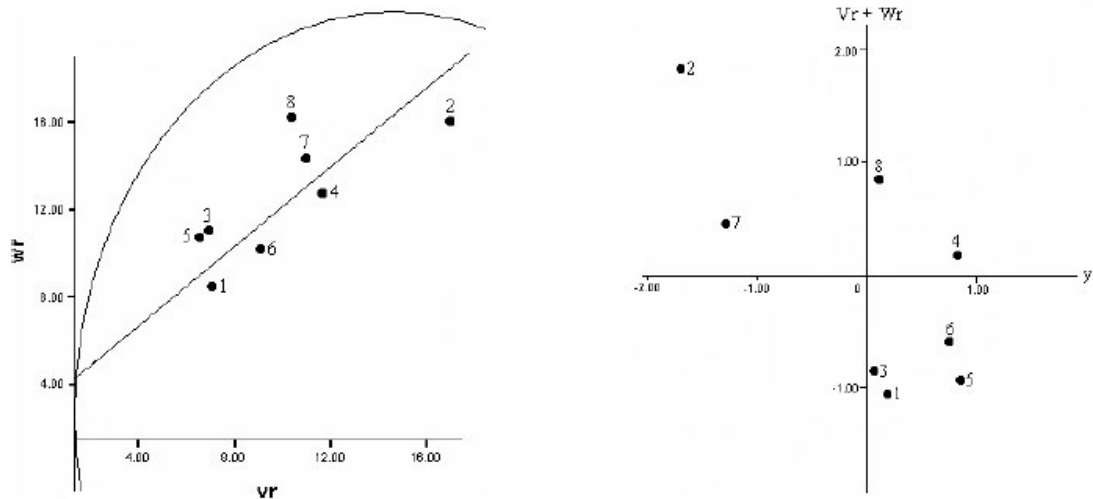


Figure 5.  $W_r/V_r$  and standard deviation graph of plant height.

**Table 5.** Best model fit estimates for generation mean parameters by weighted least squares analysis of various quantitative traits of the cross I and II.

Traits	m	[d]	[h]	[i]	[j]	[l]	$\chi^2$
<b>Cross I</b>							
Number of spikelets/spike	14.11±0.88**	0.24±0.09**	3.63±0.755**	-	-	-2.34±1.1*	0.49 (2)
Number of tillers	4.65±0.70**	0.16±0.07*	4.45±0.72**	-	-	-4.4±1.1**	0.1 (2)
Number of grains / spike	77.1±13.12**	8.2±0.95**	-	-	21.7±4.23**	-	3.9 (3)
Plant height	80.1±10.94**	-5.6±0.62**	-	-	16.5±3.1**	-	2.5 (3)
Grain yield / plant	16.4±3.28**	2.86±0.334**	17.26±8.11*	-	-9.23±2.1**	-13.11±4.43**	0.08 (1)
<b>Cross II</b>							
Number of spikelets/spike	14.1±2.3**	0.53±0.19**	5.7±2.38*	-	-	-	4.5 (3)
Number of tillers	5.35±0.85**	0.25±0.1*	4.75±2.2*	-	-	-4.7±1.14**	1.14 (2)
Number of grains / spike	70.15±11.6**	6.1±0.71**	-	-	-7.6±3.21*	-27.1±12.29*	2.8 (2)
Plant height	81.01±7.28**	-4.16±0.29**	-	-	5.82±1.71**	-	0.98 (3)
Grain yield / plant	15.71±4.27**	1.77±0.41**	18.91±9.38*	-	-	-	3.7 (3)

\*, \*\* : Significant at 5% and 1% level of probability, respectively

were predominant for plant height in wheat. Also Awaad (1996) reported similar finding for number of grains per spike. However, Akhtar and Chowdhry (2006) reported dominance effects were important in cross Chakwal-86 × V-8060 for number of grains per spike.

Dominance effects were positive and significant in cross I, for number of spikelets per spike, number of tillers and grain yield per plant. In cross II, dominance effects were significant for all traits, except plant height and number of grains per spike. The average of dominance as indicated over dominance towards the better parent for number of tillers, number of spikelets per spike and grain yield per plant in both crosses. Chowdhry et al. (1999) reported additive and dominance components for genetic variance

for number of tillers per plant. However, Chowdhry et al. (1992) found non-additive type of gene action for this trait in wheat. Although Akhtar and Chowdhry (2006) showed that in order to control the number of spikelets per spike in cross V-95199×PART – 73 the share of the dominance were more than additive effects, Sharma and Ahmad (1980) and Walia et al. (1995) reported that the estimated additive genetic effects were important for spikelets per spike. Also Waial et al. (1995), Chowdhry et al. (1999), Akhtar and Chowdhry (2006) showed that dominance genetic effects were more important than additive gene action for grain yield per plant in wheat. But Kamboj et al. (2000) reported that the additive genetic effects were important for this trait.

As it is shown in Table 5 that, different types of epistasis

**Table 6.** Estimates of variance components and heritability for quantitative traits in cross I and II.

Traits	$V_{[d]}$	$V_{[h]}$	$V_E$	$(H/D)^{1/2}$	$h^2_b$	$H^2_n$	R
<b>Cross I</b>							
Number of spikelets/spike	0.011	0.035	0.013	1.78	0.47	0.21	0.43
Number of tillers	0.014	0.022	0.011	1.25	0.51	0.27	1.33
Number of grains / spike	15.34	1.57	1.74	0.32	0.82	0.78	6.1
Plant height	11.26	0.954	0.8	0.29	0.88	0.84	5.53
Grain yield / plant	0.148	0.798	0.25	2.32	0.52	0.14	0.95
<b>Cross II</b>							
Number of spikelets/spike	0.109	0.281	0.069	1.6	0.64	0.28	1.56
Number of tillers	0.015	0.042	0.022	1.67	0.45	0.19	1.21
Number of grains / spike	15.3	1.62	1.145	0.32	0.87	0.83	5.81
Plant height	6.74	0.275	0.271	0.2	0.92	0.91	4.5
Grain yield / plant	0.798	1.13	0.392	1.41	0.59	0.29	2.93

$V_{[d]}$ : Additive variance  $V_{[h]}$ : Dominance variance  $V_E$ : Environmental variance  $(H/D)^{1/2}$ : Average degree of dominance  $h^2_b$ : Broad sense heritability  $h^2_n$ : Narrow sense heritability R: Genetic advance.

sis interaction effects were found for different trait and cross combinations. No additive  $\times$  additive [i] type of interaction was present in the genetic control of the studied traits. However, additive  $\times$  dominance [j] epistasis was positive and significant for plant height in both crosses and negative and significant for grain yield per plant in cross I and number of grains per spike in both crosses. Dominance  $\times$  dominance non-allelic interaction was significant and negative for number of spikelets per spike for cross I, number of grains per spike in cross II, and number of tillers in both crosses.

The dominance [h] and dominance  $\times$  dominance [l] gene effects showed opposite signs for number of spikelets per spike and grain yield per plant in cross 1 $\times$ 2 and number of tillers in both crosses, indicating the presence of duplicate dominant epistasis in the expression of these traits, which would limit the range of variability. Since none of the signs of [h] were similar to the [l] type of epistasis, it was concluded that no complementary type of interaction was present in the genetic control of the studied traits. The presence of epistasis has important implication for any plant breeding program. Confounding epistatic effects in models suggested that inheritance of these traits is complex and polygenic. Novoselovic et al. (2004) disclosed that plant height was governed by additive  $\times$  additive [i] gene interaction. Also Akhtar and chowdhry (2006) reported different type of epistasis for number of tillers and number of spikelets per spike. Mehla et al. (2000) reported that additive  $\times$  additive [i] and dominance  $\times$  dominance [l] type of epistasis were important for grain yield per plant in wheat.

Heritability estimates in each of broad and narrow sense were generally found to be high in magnitudes in the cross II comparative to cross I, except for number of tillers (Table 6). Difference between the genetic backgrounds of the two crosses may be to explain these

ambiguous results. The highest estimates of narrow sense heritability associated with highest genetic advance for plant height and number of grains per spike in two crosses, indicated sufficient improvement of their variability traits. These results are in agreement with diallel analysis. Dabholkar (1992) stated that when additive effects are larger than the non additive, it is suggested that selection in early segregation generation would be effective. Low heritability with low genetic gain was found for number of tillers, number of spikelets per spike and grain yield per plant in both crosses. These results are conformity to the findings of diallel analysis. Straight forward selection from the segregation population of the characters does not seem to be possible, the genetic variation existed in these characters could be improved successfully following reciprocal recurrent selection. Furthermore, these characteristics in which over dominance was involved may advantageously to be utilized by the breeders to develop hybrid, as suggested by Chowdhry et al. (2002), Dere and Yildirim (2006) and Akhtar and chowdhry (2006).

## REFERENCES

- Akhtar N, Chowdhry MA (2006). Genetic analysis of yield and some other quantitative traits in bread wheat. *Intern. J. Agri. Biol.* 4: 523-527.
- Awaad HA (1996). Genetic system and prediction for yield and its attributes in four Wheat crosses (*Triticum aestivum* L.) *Ann. Agric. Sci.* 34: 69-90.
- Awan SI, Malik MFA Siddique M (2005). Combining ability analysis in intervarietal crosses for component traits in hexaploid wheat. *J. Agri. Soc. Sci.* 4: 316-317.
- Chowdhry MA, Ambreen A, Khaliq I (2002). Genetic control of some polygenic traits in *aestivum* species. *A. J. Plant. Sci.* 3: 235-237.
- Chowdhry MA, Rasool I, Khaliq I, Mahmood T, Gilani MM (1999). Genetic of some metric traits in spring wheat under normal and drought environments. *Rachis.* 18: 34-9.

- Chowdhry MA, Chaudhry MA, Gilani SMM, Ahsan M (2001). Genetic control of some yield attributes in bread wheat. *Pak. J. Biol.* 4: 980-982.
- Chowdhry MA, Akhtar MS, Ahmad MT (1992). Combining ability analysis for flag leaf area, yield and its component in spring wheat. *J. Agric. Res.*, 30: 17-23.
- Cukadar-Olmedo B, Miller JF (1997). Inheritance of the stay green trait in Sunflower. *Crop. Sci.* 37: 150-153.
- Dabholkar AR (1992). Elements of Biometrical Genetics. College of Agriculture Indore, India.
- Dere S, Yildirim MB (2006). Inheritance of grain yield per plant, flag leaf width, and length in an 8x8 diallel cross population of bread wheat (*T. aestivum* L.). *Turk. J. Agric. For.* 30: 339-345.
- Edwards IB (2001). Hybrid wheat. In: *The World Wheat Book: A History of wheat breeding.* (Eds.: A.P. Bonjean and W.J Angus), Lavoisier Publishers, Paris. pp.1019-1045.
- Edwards LH, Ketata H, Smith EL (1975). Gene action of heading date, plant height, and other characters in two winter wheat crosses. *Crop. Sci.* 16: 275-277.
- Farshadfar E (1998). Application of Biometrical Genetics in Plant Breeding. Razi Uni Press. Kermanshah, Iran. Vol. 1
- Griffing B (1956). Concept of general and specific combining ability in relation to diallel crossing system. *Aust. J. Biol. Sci.* 9: 463-493.
- Gupta PK, Balyan HS, Kulwal PL, Kumar N, Kumar A, Mir RR, Mohan A, Kumar J (2007). QTL analysis for some quantitative traits in bread wheat. *J. Zhejiang. Univ. Sci. B.* 8(11): 807-814.
- Habib I, Khan AS (2003). Genetic model of some economic traits in bread wheat (*Triticum aestivum* L.). *Asian. J. Pl. Sci.* 2: 1153-1155.
- Hayman BI (1954). The theory and analysis of diallel crosses. *Genetics.* 39: 789-809.
- Hayman BI (1957). Interaction heterosis and diallel crosses. *Genetics.* 42: 336-355.
- Jinks JL (1954). The analysis of continuous variation in a diallel cross of *Nicoiana rustica* varieties. *Genetics* 39: 767-788.
- Jinks JL, Hayman BI (1953). The analysis of diallel crosses. *Maize Genetics Co-op. News.* 23: 48-54.
- Johnson LPV, Askel R (1959). Inheritance of yielding capacity in a fifteen-parent diallel cross of barley. *Can. J. Genet. Cytol.* 1: 208-265.
- Kamboj MC, Subhadra NC, Yadava RK (2000). Genetic analysis of yield and its components in bread wheat (*Triticum aestivum* L.). *Ann. Agri. Bio. Res.* 5: 41-43.
- Kashif M, Ahmad J, Chowdhry MA, Perveen K (2003). Study of genetic architecture of some important agronomic traits in durum wheat (*Triticum durum* Desf.). *Asian. J. Pl. Sci.* 2: 708-712.
- Kearsey MJ, Poony HS (1996). The genetical analysis of quantitative trait. Chapman and Hall, Inc., London.
- Khan AS, Habib I (2003). Gene action in a five parent diallel cross of spring wheat (*Triticum aestivum* L.). *Pak. J. Biol. Sci.* 6(23): 1945-1948.
- Khan AS, Khan MKR, Khan TM (2000). Genetic analysis of plant height, grain yield and other traits in wheat (*Triticum aestivum* L.). *Intern. J. Agri. Bio.* 2: 129-132.
- Kuchel H, Williams KJ, Langridge P, Eagles HA, Jefferies SP (2007). Genetic dissection of grain yield in bread wheat. I. QTL analysis. *Thor Appl Genet.* 115: 1029-1041.
- Maccaferri M, Sanguineti MC, Corneti S, Ortega JLA, Salem MB, Bort J, DeAmbrogio E, Moral LFG, Demontis A, Eh-Ahmed A, Maalouf F, Machlab H, Martos V, Moragues M, Motawaj J, Nachit M, Nserallah N, Ouabbou H, Royo C, Slama A, Tuberosa R (2008). Quantitative trait loci for grain yield and adaptation of durum wheat (*Triticum durum* Desf.) across a wide range of water availability. *Genetics* 178: 489-511.
- Mather K, Jinks JL (1982). Biometrical Genetics: The study of continuous variation. Chapman and Hall, Inc., London.
- Mehla BS, Sharma SC, Hooda JS (2000). Gene action for certain quantitative traits in wheat. *Ann. of Biol.* 6: 95-100.
- Novoselovic D, Baric M, Drezner G, Gunjaca J, Lalic A (2004). Quantitative inheritance of some wheat plant traits. *Genet. Mol. Biol.* 27(1): 92-98.
- Rahman MA, Siddique NA, Alam MR, Khan ASM, Alam MS (2003). Genetic analysis of some yield contributing and quality characters in spring wheat (*Triticum aestivum* L.). *Asian. J. Pl. Sci.* 2: 277-282.
- Sharma JC, Ahmad Z (1980). Genetic architecture of some traits in spring wheat. *Indian J. Agric. Sci.*, 50: 547-61.
- Singh RP, Singh S (1992). Estimation of genetic parameters through generation mean analysis in bread wheat. *Indian. J. Genet.* 52: 369-375.
- Walia DPTD, Plaha P, Chaudhry HK (1995). Gene effect controlling grain yield and its components in bread wheat (*Triticum aestivum* L.). *Agric. Sci. Digest.* 15: 29-31.
- Warner JN (1952). A method for estimating heritability. *Agron. J.* 44: 427-430.
- Wright S (1968). Evolution and the genetics of populations. Genetic and Biometric Foundation. The University of Chicago Press, Chicago. Vol. 1.