Full Length Research Paper

Genetics of yield and related traits in bread wheat over different planting dates using diallel analysis

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An 8x8 diallel experiment was conducted on bread wheat (*Triticum aestivum* L.) to ascertain the genetic mechanism of yield and its related traits. The observations were recorded on days to heading, productive tillers plant^{-1}, number of grains spike^{-1}, grain yield plant^{-1} and 1000-grain weight. The experiment was planted in randomized complete block design in three replicates. F-test declared significantly different means for all traits. Analysis of genetic components revealed significant additive (D) and dominant (H) genetic variations for days to heading, productive tillers plant^{-1}, number of grains spike^{-1}, grain yield plant^{-1} and 1000-grain weight under all three environments. Under normal planting both additive (D) and dominant (H) components were significant for productive tillers plant^{-1} and grain yield plant^{-1}, while under late planting significant additive (D) and dominant (H) components were found for number of grains spike^{-1}. Graphical analysis revealed additive gene action with partial dominance for days to heading and 1000-grain weight under early and normal planting. Negative intercepts of regression lines indicated non-additive gene action with over dominance for days to heading and 1000-grain weight under late planting, for productive tillers plant^{-1} and grain yield plant^{-1} under normal planting and for grains spike^{-1} under late planting. Genetic analyses of traits confirm the involvement of additive and non-additive gene effects in governing the inheritance of these traits.

Key words: Diallel analysis, genetic analysis, breed wheat, yield components of wheat.

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is the most important cereal crop. Due to its high adaptation and multiple uses, high nutritive value associated with high crop production it is used as staple food for more than one third of the world population. Being the main source of starch and protein in Pakistan, wheat occupies central position in the agricultural policies of the country. In Pakistan the average wheat production is 2534 kg/ha which is far more less than its potential (Anon, 2005). Genetic improvements in wheat have been taking place, both by slow processes of nature and by the selective processes of man since the earliest time of wheat cultivation. The

increase in yield potential has always been of extreme importance in wheat breeding programme. Information regarding nature and magnitude of genetic effects prevailing in the breeding material is necessary to decide the kind of breeding procedure to be chosen for better exploitation of the genetic potential of different plant traits in a crop.

Diallel mating design has been a useful tool for genetic analysis and used extensively by plant breeders to analyze mating system in which a set of varieties are intercrossed in all possible combinations. The techniques include diallel analysis of variance, computation of genetic components of variations, Wr,Vr (covariance, variance) graphs. Diallel analysis of variance and analysis of genetic components throw light on the presence or absence and magnitude (if present) of additive, dominant, non-allelic, maternal and

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Table 1. Analysis of variance for the characters studied under early, normal and late plantings (Mean squares).

Characters	Early			Normal			Late		
	Reps. (df = 2)	Genotypes (df = 63)	Error (df = 126)	Reps. (df = 2)	Genotypes (df=63)	Error (df = 126)	Reps. (df = 2)	Genotypes (df = 63)	Error (df = 126)
Days to heading	1.94*	20.03**	1.10	7.90**	12.03**	1.18	6.94*	3.97**	1.24
Productive tillers plant[-1]	10.41*	56.06**	3.11	3.77	12.43**	1.98	2.95**	10.11**	0.70
Grains spike[-1]	31.83	305.76**	23.68	21.29	271.16**	18.83	12.11	113.02**	11.97
Grain yield plant[-1]	5.32	592.72**	20.72	4.81	109.89	12.52	31.01**	77.32**	4.76
1000-grain weight	46.84*	61.41**	11.53	19.45	68.30**	12.18	371.85**	79.11**	19.79

** P ≤0.01.

reciprocal gene effects. An estimate of gene action is important in launching a successful breeding program. Diallel analysis developed by Hayman (1954) provides a fairly reliable mechanism to properly understand the nature of gene action involved in the development of complex genetic characters having economic values. Singh et al. (2003) and Choudhry et al. (1994) reported additive gene effects for days to heading. Dhayal and Sastry (2003) reported non-additive gene effects for productive tillers plant[-1], grain yield plant[-1] and 1000-grain weight, while Jag et al. (2003) reported non-additive gene effects for grain spike[-1]. The present study was conducted to estimate possible gene action and components of genetic variance for yield and other important agronomic traits of breed wheat.

MATERIALS AND METHODS

Eight cultivars of bread wheat, namely: Wafaq-2001, Takbeer, Tatara, Iqbal-2000, Margalla-99, Ghaznavi-98, Khattakwal and Inqilab-91 were crossed in an 8 x 8 diallel fashion during 2002 to 2003. Eight parental cultivars and their resulting 56 F_1s were grown in a randomized complete block design with three replications under early, (E_1-October 17, 2003), normal (E_2-November 10, 2003) and late (E_3-December 4, 2003) sown at the experimental farm of Department of Plant Breeding and Genetics, NWFP, Agricultural University, Peshawar during 2003 to 2004. Plant to plant and row to row spacing were kept 15 and 30 cm, respectively. One healthy seed was planted per site. Each treatment comprised a single row of three meters length having 20 healthy plants. Five plants from each treatment were randomly selected for recording data on five traits viz., days to heading, productive tillers plant[-1], grains spike[-1], grain yield plant[-1] and 1000-grain weight under each environment. Mean of each treatment was used for statistical analysis. Data were analyzed statistically using analysis of variance technique (Steel and Torrie, 1984) and significant differences among the genotypes were further analyzed using diallel analysis techniques (Hayman, 1954a, b; Mather and Jinks, 1982).

Information about gene action was inferred by plotting the covariance (Wr) of each array against its variance (Vr). The slope and position of the regression line fitted to the array points within the limiting parabola indicated the degree of dominance and the presence or absence of gene interaction. The points for limiting parabola (Wr$_i$) were obtained as under:

$$Wr_i = \sqrt{V_p x V r_i}$$

Where: Vp = parental variance, and Vr$_i$ = array variance

Array variances and covariances were used to draw a regression line within the limiting parabola. The distance between the origin and the point where the regression line cut the Wr-axis provides a measure of average degree of dominance are:

(i) Partial dominance: when the intercept is positive,
(ii) Complete dominance: when the line passed through the origin,
(iii) Over dominance: when the intercept is negative, and
(iv) No dominance: when the regression line touched parabola limits.

The order of array points represented the distribution of dominant and recessive genes among the parent cultivars. The parent cultivars with most dominant genes had their points nearest to the origin while the parent cultivars with most recessive genes fall farthest from the origin, and the parent cultivars with equal frequencies of dominant and recessive genes had their points in the middle.
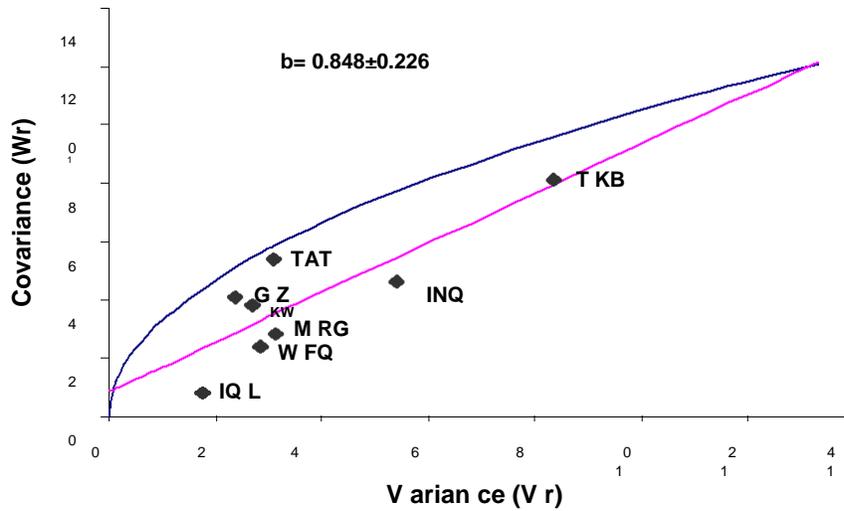
Figure 1. Wr/Vr graphs under early planting for days to heading.
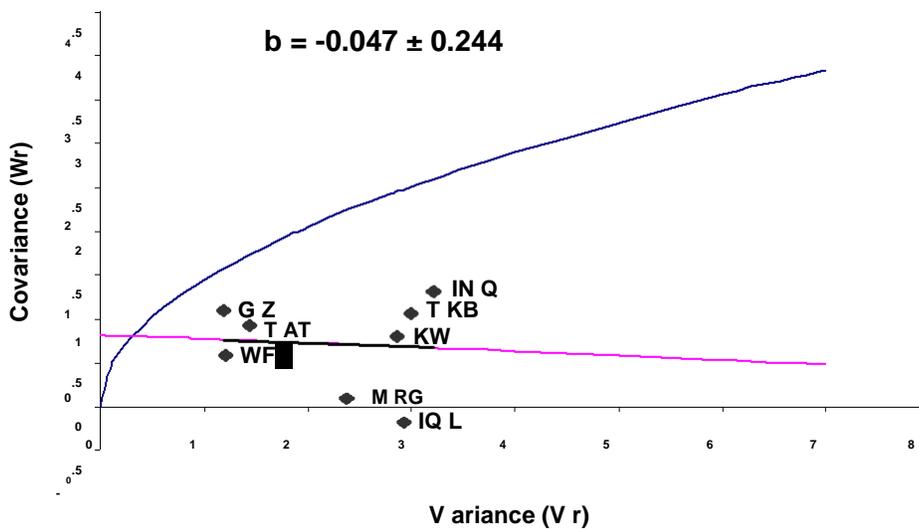

Figure 2. Wr/Vr graphs under normal planting for days to heading.

RESULTS AND DISCUSSION

The analysis of variance of means showed highly significant differences among genotypes for days to heading, productive tillers plant[-1], number of grains spike[-1], grain yield plant[-1] and 1000-grain weight studied (Table 1).

Days to heading

Regression analysis for days to heading revealed that positive intercepts of Wr/Vr regression lines supported an additive gene action with partial dominance under early and normal planting (Figures 1 and 2). Additive gene action for this trait has also been reported by Singh et al. (2003) and Dhayal and Sastry (2003) reported the importance of both additive and non-additive gene actions for days to heading. The array points allocation under early planting showed that variety Iqbal possessed maximum dominant genes being nearest to the origin, while Takbeer possessed maximum recessive genes being farthest from the origin. It means that genotype Iqbal is efficient for taking minimum time to reach the heading stage during early sowing when used in hybrid condition whereas, Takbeer variety with more
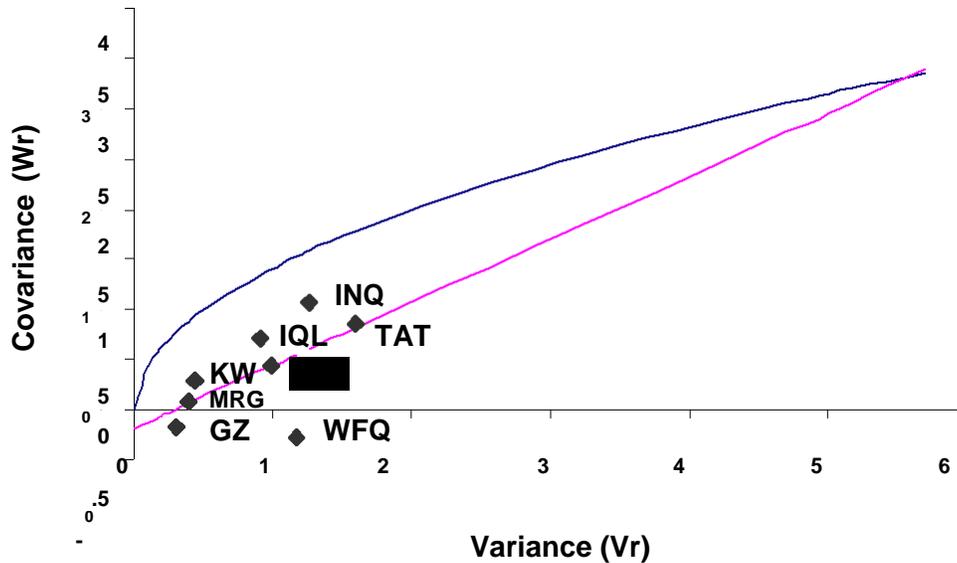
Figure 3. Wr/Vr graph for days to heading under late planting.

recessive genes took maximum days to heading when sown earlier. Rest of the parent cultivars possessed equal proportion of dominant and recessive genes. Under normal planting (Figure 2) genotypes Wafaq, Margalla and Iqbal possessed maximum dominant genes being nearest to the origin. These genotypes produced heads earlier as compare to other varieties like Inqilab, Takbeer and Khattakwal which had most recessive genes being farthest from the origin. Negative intercept of Wr/Vr regression line under late planting indicated over-dominance (Figure 3). On the basis of array points allocation Ghazanvi, Margalla and Khattakwal possessed maximum dominant genes being nearest to the origin, which showed that these varieties reached earlier to heading stage under late sowing condition in contrast to normal sowing in which Khattakwal variety possessed more recessive genes. The rest of cultivars possessed equal proportion of dominant and recessive genes under late sowing.

Productive tillers plant[-1]

Negative intercept of regression line under normal planting indicated an over-dominant gene action for this trait (Figure 4). It means that the genotypes are efficient for producing more tillers in hybrid condition. Similar findings have been reported by (Sheikh et al., 2000). Placement of array points as displayed by position of the parent cultivars along the regression line showed that under normal planting Margalla and Tatara being nearest to the origin, had maximum dominant genes, whereas Khattakwal and Inqilab located farthest from the origin had maximum

recessive genes. Under normal planting Khattakwal and Inqilab produced less tillers/plants and will showed few tillers when used in hybrid condition. Rest of parent cultivars possessed equal proportion of dominant and recessive genes.

Number of grains spike[-1]

Negative intercept of regression line indicated non-additive gene action with partial dominance for number of grains per spike for all eight wheat genotypes under late planting (Figure 5), which showed that selection for number of grains per spike in the early segregating generation would be difficult. Similar findings have been reported by Adnan and Bhutta (1994), Tahir et al. (1995) and Hall and Van Sanford (2003). The allocation of array points along the regression line indicated that Tatara and Khattakwal had most dominant genes being nearest to the origin, while Iqbal and Wafaq possessed maximum recessive genes being farthest from the origin. The rest of the parent cultivars were intermediary in position having equal proportion of dominant and recessive genes.

Grain yield plant[-1]

The negative intercept of regression line in Wr/Vr graph under normal planting indicated over-dominance gene action for grain yield per plant (Figure 6). Therefore selection in early generations for grain yield is not suggested. Similar observations for different genotypic
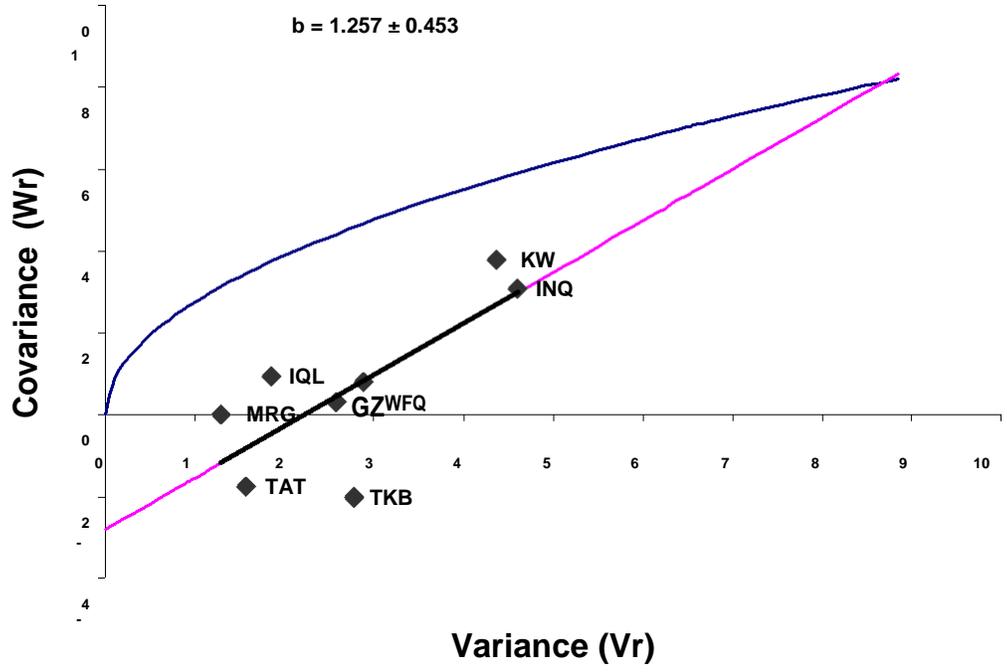
Figure 4. Wr/Vr graph for productive tillers plant^{-1} under normal planting.
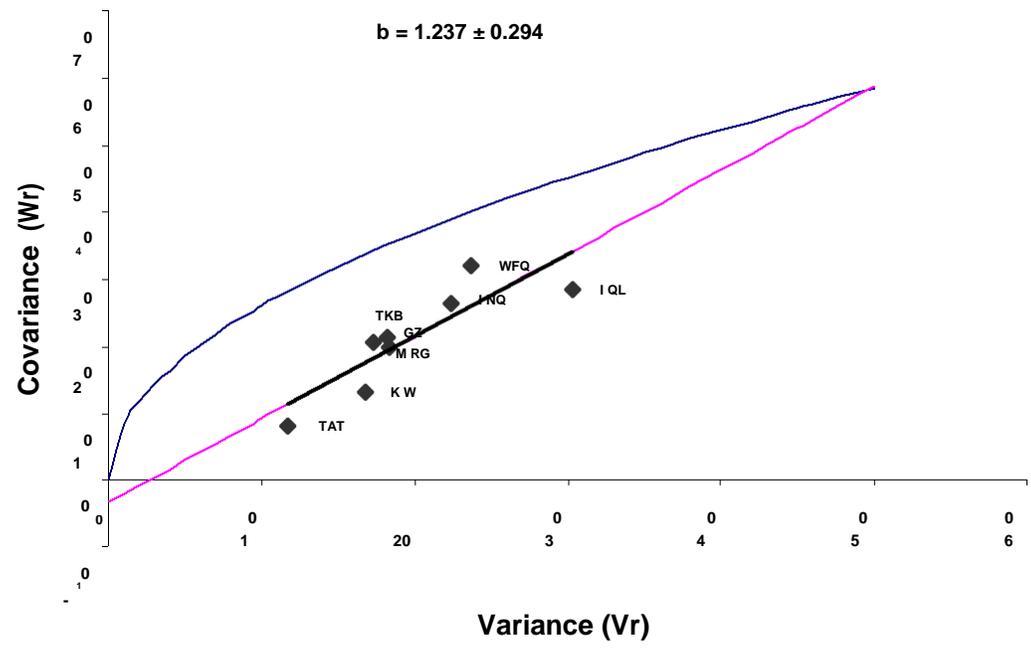

Figure 5. Wr/Vr graph for number of grains spike^{-1} under late planting.

combination are available in literature (Ansari, 2003; Mann et al., 1995). Placement of array points displayed that Ghaznavi, Margalla, Wafaq and Khattakwal varieties, had the maximum dominant genes for yield per plant being closest to the origin and produced maximum grain yield under normal planting, whereas Inqilab and Iqbal
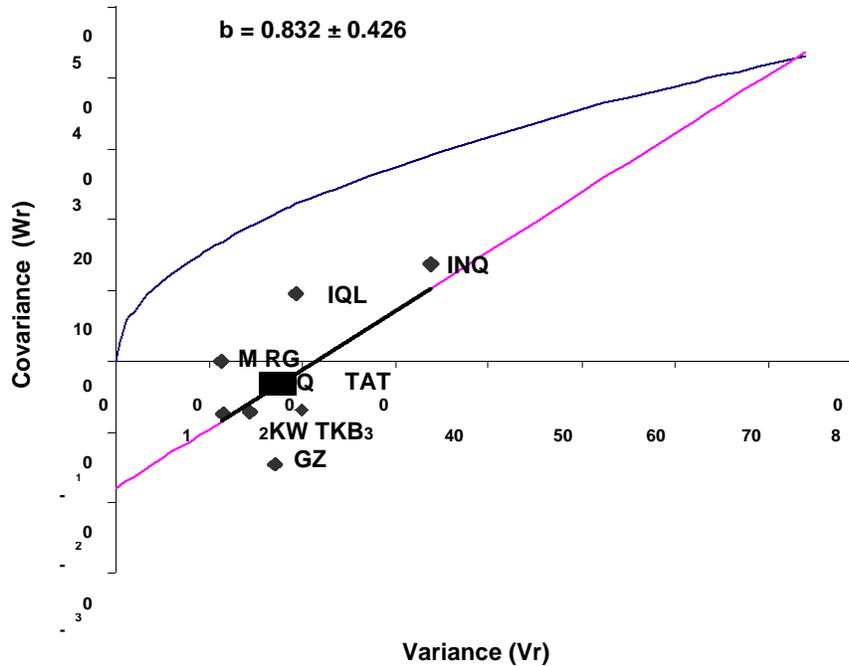
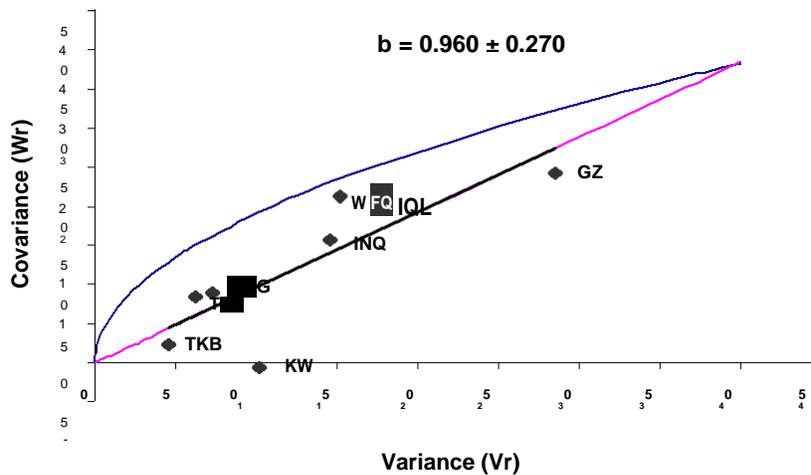**Figure 6.** Wr/Vr graph for grain yield plant^{-1} under normal planting.

Figure 7. Wr/Vr graphs under early planting for 1000-grain weight.

cultivars had the least dominant genes being farthest from the origin. These results are in accordance with those of Sangwan and Chaudhry (1999) and Dhayal and Sastry (2003) who also reported non-additive gene effects for grain yield plant^{-1}.

1000-grain weight

In regression analysis for 1000 grain weight the positive intercepts of regression lines under early and late planting (Figures 7 and 9) indicated additive gene action with partial dominance, while under normal planting negative intercept of regression line showed over-dominance (Figure 8). Therefore selection for 1000 grain weight in early generations is suggested under early and late planting and in late generations under normal planting of wheat genotypes. Dhayal and Sastry (2003) reported additive gene effects for the trait under study, while Asad et al. (1992)
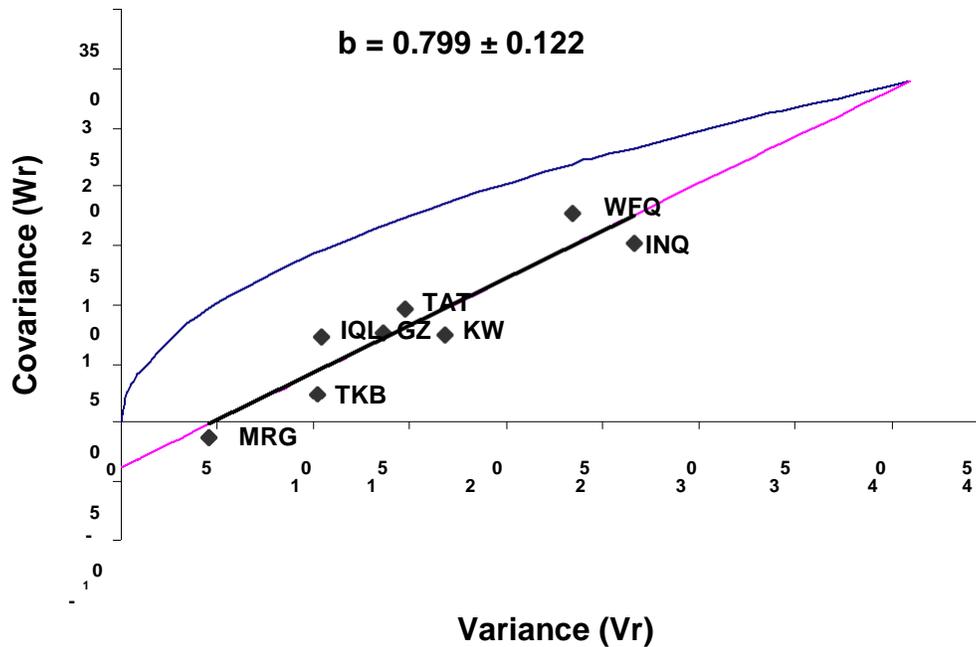
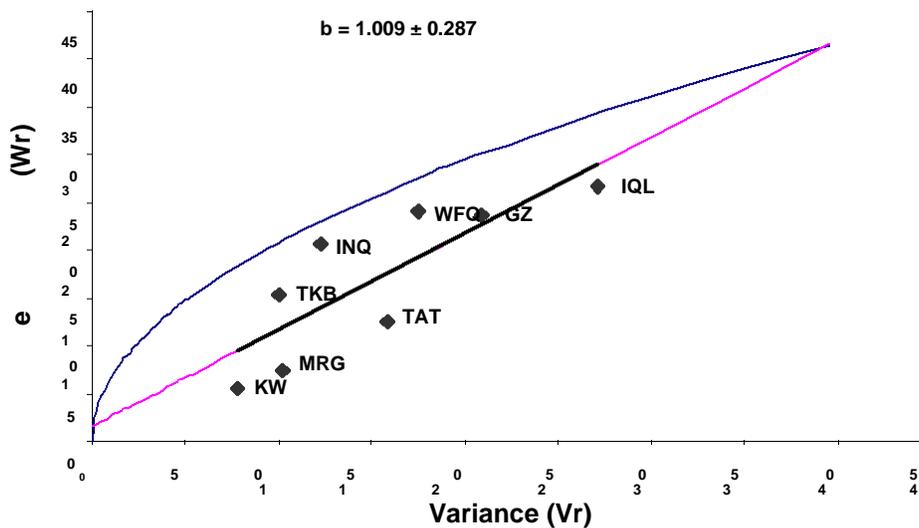**Figure 8.** Wr/Vr graphs under normal planting for 1000-grain weight.

Figure 9. Wr/Vr graph for 1000-grain weight under late planting.

reported non-additive gene action for 1000 grains weight. The arrangement of array points in Wr/Vr graph (Figure 7) under early planting revealed that Takbeer and Khattakwal possessed maximum dominant genes being nearest to the origin, while Ghaznavi, Iqbal and Wafaq had maximum recessive genes being farthest from the origin. Rest of the cultivars occupied an intermediary position having equal proportion of dominant and recessive genes.

Under normal planting (Figure 8) Margalla and Takbeer possessed maximum dominant genes, while Wafaq and Inqilab possessed most recessive genes. Similarly under late planting (Figure 9) the relative position of array points on the regression line depicted that Khattakwal and Margalla had maximum dominant genes being nearest to the origin, while Iqbal, Ghaznavi and Wafaq possessed maximum recessive genes being farthest from the origin.

Rest of the cultivars possessed equal proportion of dominant and recessive genes.

CONCLUSIONS AND RECOMMENDATIONS

Additive type of gene action for days to heading and 1000-grain weight indicated that early generation selection will be effective for these traits. Non-additive type of gene action for productive tillers plant^{-1}, grains spike^{-1} and grain yield plant^{-1} was indicated. Therefore, diallel and recurrent mating system is useful for these traits that allows for recombination and gene accumulation. Selection would be effective in later generations.

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