

## DIALLEL ANALYSIS OF THE INHERITANCE PATTERN OF AGRONOMIC TRAITS OF BREAD WHEAT

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### Abstract

Studies were carried out on the inheritance pattern of the important yield parameters viz., tillers per plant, spike length, grains per spike, 1000 grains weight, harvest index and yield per plant of 8 bread wheat varieties. The component analysis indicated that the additive component was significant for all the traits except tillers per plant and yield per plant. The dominance component was significant for spike length, tillers per plant and yield per plant. Regression analysis revealed additive type of gene action for grains per spike, 1000 grains weight and harvest index and over dominant type of gene action for rest of the traits. Correlation analysis of dominant genes with the phenotype of the parents revealed recessive gene control for tillers per plant and spike length, while dominant gene control was indicated for rest of the traits studied.

### 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. It contributes 13.8% to the value added in agriculture and 3.2% to GDP. In Pakistan the average wheat production is 2534kg/hectar which is far more less than its potential (Anon., 2005). Its production can be enhanced through the development of improved genotypes capable of producing better yield under various agroclimatic conditions and stresses.

During the recent past, concerted efforts have resulted in the development of improved geneotypes by exploiting Borlaug's wheat improvement programme, which resulted in lack of genetic diversity (Tillman, 1998). It is a general agreement that germplasm diversity and genetic relatedness among elite breeding material is the fundamental element in plant breeding (Mukhtar *et al.*, 2002). Hence breeding wheat genotypes with diverse genetic base is needed to achieve self-sufficiency and sustainability.

The amelioration of varietal yield potential is of primary importance in increased crop production programmes. Genetic analysis of wheat yield has shown that grain yield is a highly complex character determined by component traits (Adams, 1976; Blum 1988), also the analysis showed that genes for yield per se do not exist (Grafius, 1959). The increase in wheat production remains always an issue for sustainability of supply to the increasing population.

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The diallel analysis studies developed by Hayman (1954) and Jinks (1955), provides a fairly reliable mechanism to properly understand the nature of gene action involved in the development of complex genetic characters of economic value. Diallel analysis was thus employed to determine the pattern of gene action for yield potential.

### Materials and Methods

Eight varieties of wheat (*Triticum aestivum* L.) viz., Ghaznavi-98, Fakhre Sarhad, Tatar, Takbeer, SQ-92, SARC-3, ICP-3 and Dera-98 were crossed in all possible combinations. Seeds of 56 F<sub>1</sub>s along with their parents were sown in the field during November 2003 in a randomized complete block design with three replications. Plant to plant and row-to-row spacing kept were 15 and 30 cm, respectively. Each treatment was of two rows of 2.5-meter length. The data were recorded on tillers per plant, spike length, grains per spike, 1000 grains weight, harvest index and yield per plant. The data were analyzed statistically using analysis of variance method of Steel & Torrie (1984). Significant differences among the genotypes were further subjected to regression and correlation analysis using diallel analyses technique. The research was carried out at the Department of Plant Breeding and Genetics, NWFP Agricultural University, Peshawar during the year's 2001 to 2003.

### Results and Discussion

Analysis of variance of means showed highly significant differences among genotypes with respect to tillers per plant, spike length, grains per spike, 1000 grains weight, harvest index and yield per plant.

Regression analysis revealed over dominant type of gene action for tillers per plant (Fig. 1a). 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 genotypes along the regression line shows that ICP-3 had the maximum dominant genes for tillers per plant being closest to the origin, where as Dera-98 had the least dominant gene effect for tillering being farthest from the origin (Fig. 1a). Correlation analysis of the genotypes showed recessive gene control ( $r = 0.583$ ) for tillers per plant (Fig. 1b). The result showed that tillers per plant is over dominant with respect to regression while correlation analysis showed recessive gene control for tillers per plant.

The regression analysis revealed over dominant type of gene action for spike length (Fig. 1c). It means that the genotypes are more efficient for producing increased spike length in hybrid condition. Similar findings can be observed in literature like Gouis *et al.*, 2002 and Altinbas & Bilgen (1996). Both the tests suggested the adequacy of the additive-dominance model for spike length. The genotype Takbeer possessed the most dominant genes being closest to the origin while Dera-98 possessed the most recessive genes being located farthest from the origin (Fig. 1c). Hence selection for spike length in the early segregating generation would be difficult. Correlation analysis of the genotypes (Fig. 1d) showed recessive gene control ( $r = 0.022$ ) for spike length.

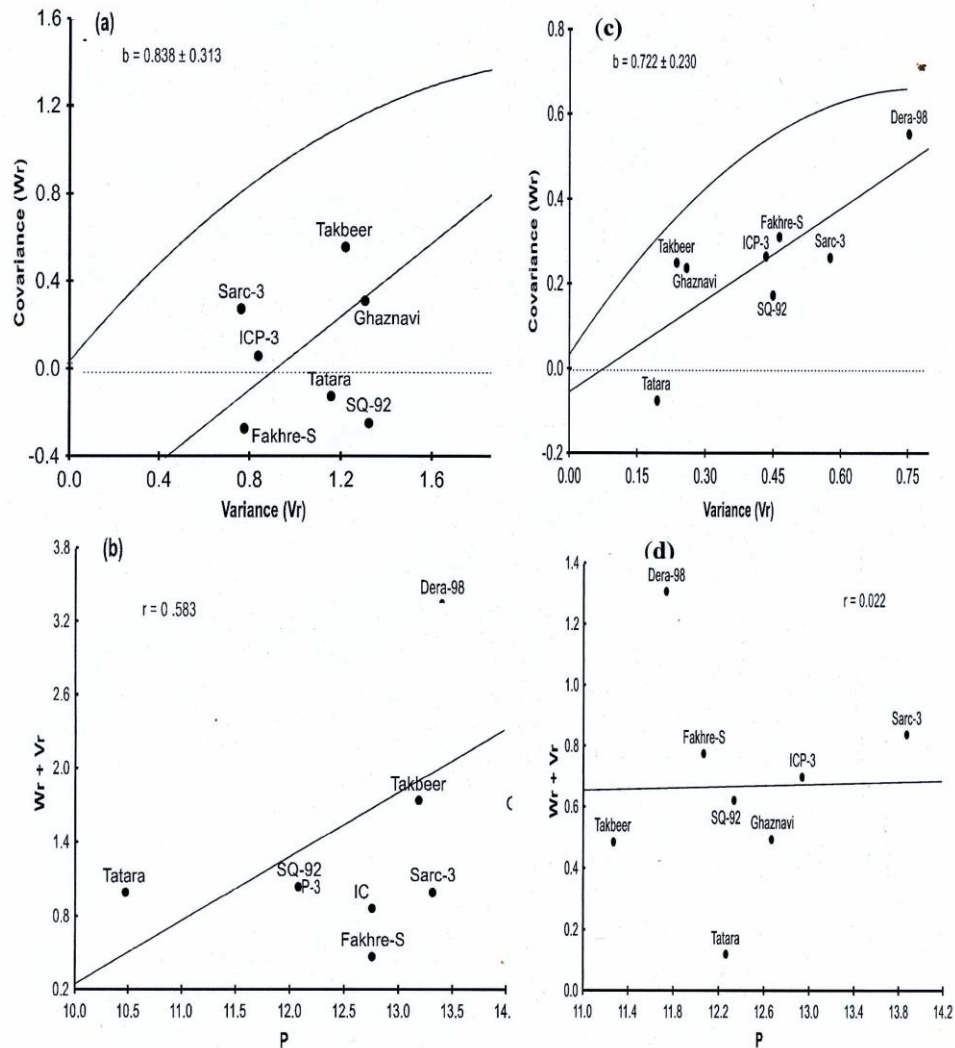


Fig. 1. Regression and correlation studies of gene action through diallel analysis: (a) Showing over dominant gene action for tillers per plant. (b) Correlation of variance and covariance with the parents for tillers per plant. (c) Showing over dominant gene action for spike length. (d) Correlation of variance and covariance with the parents for spike length.

The regression analysis for grains per spike revealed additive genetic control (Fig. 2a). It means that due to the presence of additive variance selection for this trait can be practiced in early generations. Unit slope of the regression line confirms the absence of epistasis for this trait. Similar findings have been reported by Adnan & Bhutta (1994), Tahir *et al.*, (1995) and Hall and Van Sanford (2003). The position of the array points along the regression line revealed that Fakhre Sarhad had the most dominant genes while Sarc-3 had the most recessive genes for this trait being farthest from the origin. Correlation analysis of the genotypes showed dominant gene control ( $r = -0.325$ ) for grains per spike (Fig. 2b).

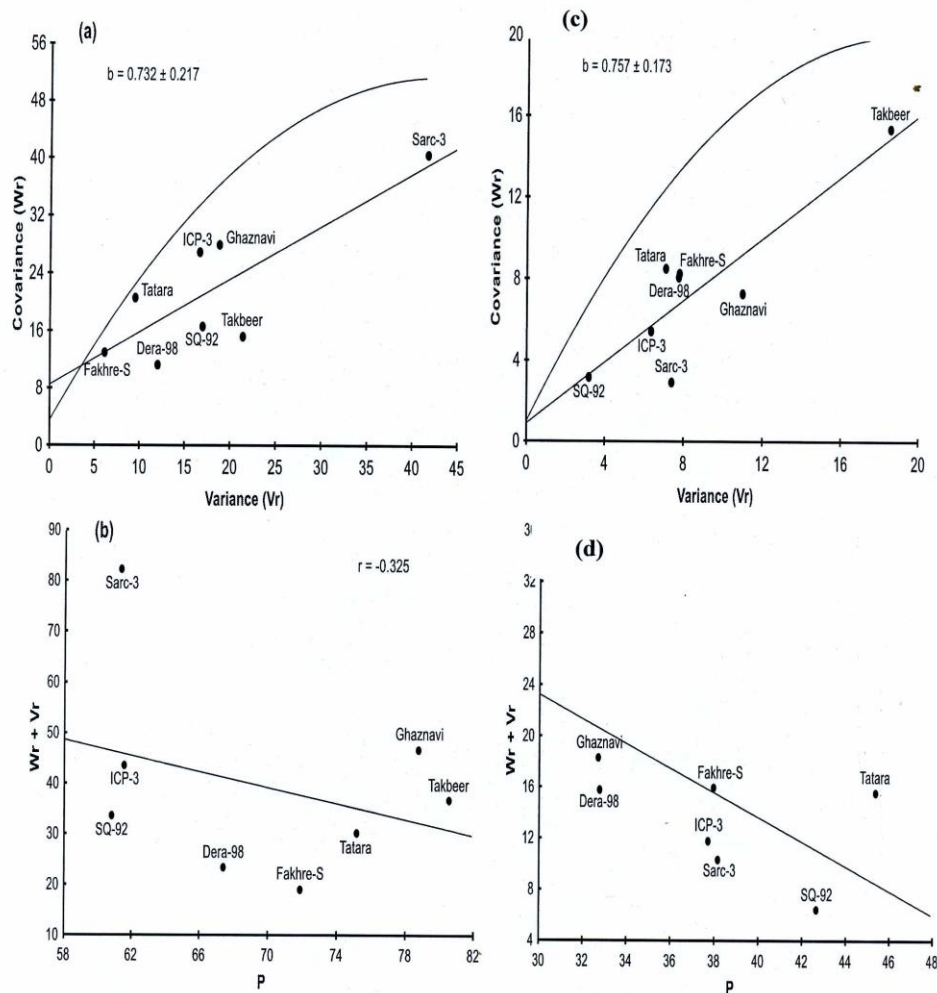


Fig. 2. Regression and correlation studies of gene action through diallel analysis: (a) Showing additive gene action for grains per spike. (b) Correlation of variance and covariance with the parents for grains per spike. (c) Showing additive gene action for 1000 grain weight. (d) Correlation of variance and covariance with the parent for 1000 grain weight.

The regression analysis revealed that 1000-grain weight is governed by partial dominance with additive gene effect (Fig. 2c). These results are in conformity to the findings of Hakizimana *et al.*, (2004) and Chaudhry *et al.*, (1992b). The relative position of array points on the regression line depicted that SQ-92 had the most dominant genes while Takbeer had the most recessive genes for 1000-grain weight. Partial dominance with additive gene action revealed that selection would be effective in early generations. Correlation analysis of the genotypes showed dominant gene control ( $r = -0.553$ ) for 1000-grains weight (Fig. 2d).

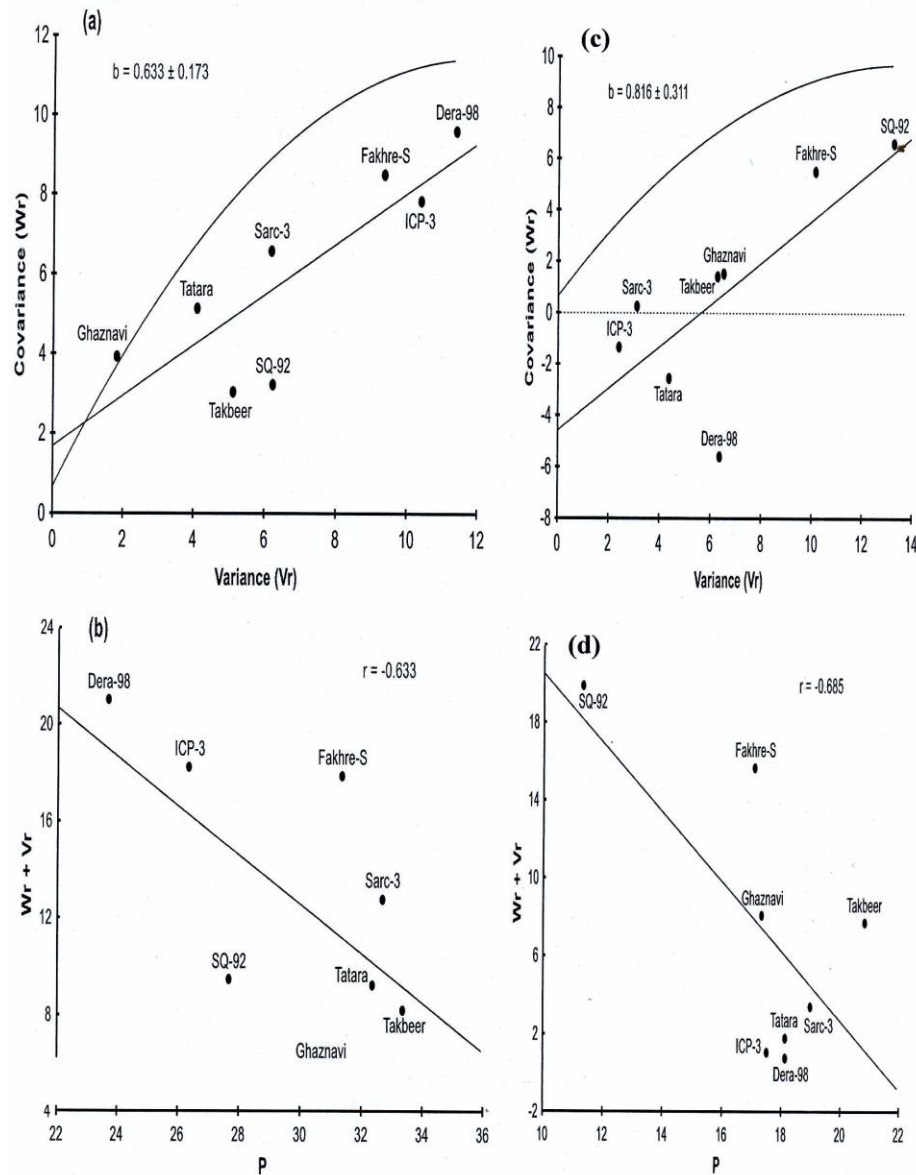


Fig. 3. Regression and correlation studies of gene action through diallel analysis: (a) Showing additive gene action for harvest index. (b) Correlation of variance and covariance with the parents for harvest index. (c) Showing over dominant gene action for yield per plant. (d) Correlation of variance and covariance with the parents for yield per plant.

The regression analysis revealed additive type of gene action for harvest index (Fig.3a). Joshi *et al.*, (2004), Farshadfor *et al.*, (2000) and Singh & Singh (1996) also reported similar type of gene interaction in their studies. The position of the parents along the regression line revealed that Ghaznavi-98 had the most dominant genes while Dera-

98 had the most recessive genes for harvest index being located farthest from the origin. Selection in early generations for harvest index is suggested. Correlation analysis showed dominant gene control ( $r = -0.633$ ) for harvest index (Fig. 3b).

Regression analysis showed over dominant type of gene action for yield per plant (Fig. 3c). Similar observations for different genotypic combination are available in literature (Ansari, 2003; Mann *et al.*, 1995). Placement of array points displayed that Sarc-3 and Takbeer had the maximum dominant genes for yield per plant being closest to the origin, whereas SQ-92 had the least being farthest from the origin. Correlation analysis showed dominant gene control ( $r = -0.685$ ) for yield per plant (Fig. 3d).

**Table 1. Analysis of variance for different yield parameters in Bread wheat.**

Traits	Mean Squares		
	Replications (df 2)	Genotypes (df 63)	Error (df 126)
Tillers per plant	17.07	6.31**	3.61
Spike length	6.81	1.93**	0.72
Grains per spike	219.64	110.85**	54.30
1000 grain weight	105.59	41.90**	24.22
Harvest index	200.38	35.51**	24.46
Yield per plant	2.42	25.60**	15.57

\*\*P  $\leq$  0.01

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