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# Mechanism of Genetic Control of Some Quantitative Traits in Bread Wheat

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**Abstract:** A  $5 \times 5$  diallel cross of spring wheat (*Triticum aestivum* L.) was conducted to estimate the gene action for some polygenic traits like plant height, flag leaf area, fertile tillers per plant, spike length, spikelets per spike, grains per spike, 1000-grain weight and grain yield per plant. Additive type of gene action with partial dominance was observed for flag leaf area, fertile tillers per plant, spike length, spikelets per spike and grains per spike, suggesting early selection for fairly good improvement in these traits. While over dominance for plant height, 1000-grain weight and grain yield per plant indicated fruitful selection in the later segregating generations. Epistasis was absent for all the traits studied.

Key words: Wheat, diallel cross, polygenic traits, gene action, Pakistan

### INTRODUCTION

Wheat (Triticum aestivum L.) being the most valuable staple food is highly esteemed in the world. It is the leading grain crop of the temperate climates of the world, just like rice in the tropics. It is a dietary mainstay for millions of people. Wheat constitutes a major staple food for the rapidly increasing population of Pakistan and plays a most significant role in critical areas of food security and economic stability of the country. Studies have been made to boost up the production of wheat. Its production can be enhanced through the development of improved cultivars having wider genetic base capable of producing better yield under various agro-climatic conditions. The diallel cross method developed and advocated by Hayman (1954 and 1958) and Jinks (1954) provide fairly reliable mechanism especially in self fertilized crops like wheat to assess the genetic system and gene action involved in the expression of important plant attributes right in the F<sub>1</sub> generation.

Petrovic and Cermin (1994) reported additive gene action for spikelets per spike, grains per spike and 1000-grain weight. Over dominance was observed for plant height while number of grains per spike indicated an incomplete dominance. Mann and Sharma (1995) observed partial dominance for grains per spike. Aziz and Chowdhry (1999) studied 5 × 5 diallel cross on spring wheat and observed that spike length and number of grains per spike were controlled by additive type of gene action with partial dominance and 1000-grain weight was controlled by over dominance type of gene action. Epistasis was absent for all the characters. Over dominance type of gene action for economic yield per plant in the absence of non-allelic interactions was reported by Asif *et al.* (1999).

Chowdhry et al. (2002) investigated from a  $5 \times 5$  diallel cross in wheat that plant height, number of tillers per plant, number of grains per spike, 1000-grain weight and grain yield per plant were controlled by over dominance type of gene action. Number of grains per spike was under the control of partial dominance while spike length was governed by partial dominance with additive type of gene action. Riaz and Chowdhry (2003) found additive gene action for plant height, tillers per plant, grains per spike, 1000-grain weight and grain yield per plant. While they observed over dominance for flag leaf area.

## MATERIALS AND METHODS

The studies were carried out at the University of Agriculture, Faisalabad. The experimental material comprising five wheat varieties viz., Inqalab 91, Uqab 2000, Punjab 96, MH. 97 and Fsd. 85 were crossed in a full diallel fashion during crop season 2001-02.

Seeds of F<sub>1</sub> crosses along with their parents were planted in the field on November 8, 2002 following randomized complete block design with three replications keeping inter-plant and inter-row distances at 15 and 30 cm, respectively. A single row of 5m length served as an experimental unit. All agronomic and plant protection practices were kept normal and equal for entire experiment.

At maturity, 10 guarded plants were taken randomly from each treatment and data were recorded for traits like plant height (cm), flag leaf area (cm²), number of fertile tillers per plant, spike length (cm), number of spikelets per spike, number of grains per spike, 1000-grain weight (g) and grain yield per plant (g). The data thus collected were subjected to analysis of variance technique (Steel and Torrie, 1980). Plant traits which showed significant

differences among genotypes were further analysed by using diallel technique developed by Hayman (1954 and 1958) and Jinks (1954).

### RESULTS AND DISCUSSION

The analysis of variance revealed that the differences among genotypes for all characters under study were highly significant ( $P \le 0.01$ ). Parental mean values for some polygenic traits are presented in Table 1.

Plant height: The Vr/Wr graph (Fig.1) showed that the regression line intercepted the Wr-axis on the negative side below the point of origin indicating that plant height was governed by over dominance type of gene action. Epistasis was found absent as the regression line did not deviate significantly from unit slope. Similar results have been reported by Petrovic and Cermin (1994). The distribution of array points along the regression line revealed that Inqalab 91 contained the maximum dominant genes being located closest to the origin while MH. 97 which was located farthest from the origin possessed the most recessive genes for plant height. Selection would be difficult in early generations for plant height due to over dominance type of gene action.

Flag leaf area: Partial dominance with additive type of gene action was the inheritance pattern for flag leaf area, as regression line intercepted the Wr-axis above the origin (Fig. 2). Absence of non-allelic interactions was confirmed from the regression line which did not deviate significantly from unit slope. These results are in accordance with those of Srivastava and Nema (1993). The variety Inqalab 91 being in proximity to the point of origin, possessed maximum number of dominant genes for flag leaf area, whereas MH. 97 exhibited maximum recessive genes for being distant from the origin. Absence of epistasis and presence of partial dominance with additive gene action suggest that selection in early generations would be helpful.

**Fertile tillers per plant:** The graphical representation of data indicated an additive type of gene action with partial dominance in the absence of epistasis as Wr-axis was intercepted above the point of origin by the regression

line (Fig. 3). The results are in agreement with the findings of Khan *et al.* (2000) and Riaz and Chowdhry (2003). The relative position of array points along the regression line depicted that genotype Inqalab 91 had maximum dominant genes being closest to origin whereas genotype MH. 97 being farthest from the origin possessed maximum recessive genes. Additive gene action with partial dominance in the absence of epistasis implies the possibility of obtaining transgressive segregates for this character and selection will be effective in early segregating generations.

Spike length: This trait was controlled by additive gene action as shown by the Vr/Wr graph where regression line intercepted the Wr-axis above the point of origin (Fig. 4). Similar conclusions were illustrated by Asif *et al.* (1999). The graphical distribution of array points showed that the variety Inqalab 91 contained the maximum dominant genes being closest to the origin. Varieties Uqab 2000, Punjab 96 and MH. 97 were also in close proximity and contained higher dominant genes as compared to Fsd. 85 which being farthest from the origin possessed maximum recessive genes. Additive gene control and absence of epistasis for spike length suggested that effective selection may be practiced during early generations without going for further progeny testing.

Spikelets per spike: The illustration of Vr/Wr graph (Fig. 5) showed that inheritance pattern for number of spikelets per spike appeared to be additive with partial dominance type of gene action, as the regression line intercepted the Wr-axis above the point of origin. Epistasis was found absent, as the regression line did not deviate significantly from the unit slope. These results are in agreement with the findings of Asif et al. (1999) and Chowdhry et al. (2002). A perusal of Vr/Wr graph indicated that Uqab 2000 was the repository of the most dominant genes for spikelets per spike closely followed by Inqalab 91 and MH. 97. The farthest position of Fsd. 85 displayed that it possessed the least dominant genes. While the midway position of Punjab 96 indicated an intermediate gene constitution in this genotype. In view of the partial dominance with allelic interactions, effective selection may be possible for number of spikelets per spike in early generations.

 $\underline{\textbf{Table 1: Mean values for some polygenic traits of spring wheat varieties used in a 5 \times 5 diallel cross}$ 

	Plant	Flag leaf	Fertile tillers	Spike	Spikelets	Grains	1000-grain	Grain yield
Varieties	height (cm)	area (cm²)	per plant	length (cm)	per spike	per spike	weight (g)	per plant (g)
Inqalab 91	103.63	49.27	12.70	15.06	21.60	71.30	35.97	22.40
Uqab 2000	109.37	56.49	12.60	15.34	22.90	87.33	35.23	26.41
Punjab 96	97.06	51.05	11.47	14.16	21.30	66.33	34.37	21.23
MH. 97	98.56	40.32	18.10	12.04	19.90	64.50	29.13	19.65
Fsd. 85	106.70	58.54	13.80	12.55	21.37	62.10	37.93	22.55

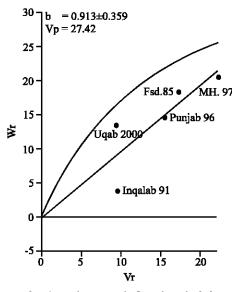


Fig. 1: Vr/Wr graph for plant height

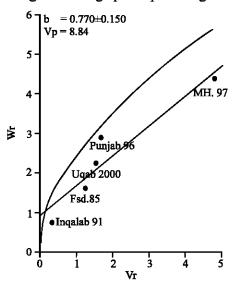


Fig. 3: Vr/Wr graph for tillers per plant

Grains per spike: The trait was found to be controlled by partial dominance with additive type of gene action as the regression line intercepted the Wr-axis above the point of origin (Fig. 6). The deviation of the regression line from unit slope was found non-significant which indicated the absence of non-allelic interactions. The results corroborated the findings of Aziz and Chowdhry (1999). Maximum dominant genes for grains per spike were present in the genotype Uqab 2000 as it was closest to the origin. However, the genotype Fsd. 85 located far from the origin holds maximum recessive genes. Presence of partial dominance and absence of epistasis indicate the possibility of useful selection for grains per spike in early segregating generations.

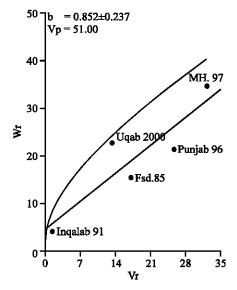


Fig. 2: Vr/Wr graph for flag leaf area

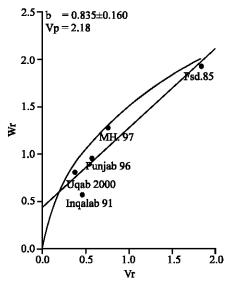


Fig. 4: Vr/Wr graph for spike length

1000-grain weight: The inheritance pattern for this trait was found to be over dominance type of gene action, as the regression line in Vr/Wr graph (Fig. 7) intercepted the Wr-axis below the point of origin. These results are in conformity with those already given by Mahdy (1988) and Chowdhry et al. (2002). The graphical representation of array points indicated maximum dominant genes in variety Fsd. 85 as being closest to the origin. While genotype MH. 97 possessed minimum dominant genes as being placed distantly away from the origin. The deviation of regression line from unit slope was not significant which indicated the absence of non-allelic interactions. Effective selection in early generations would be some what

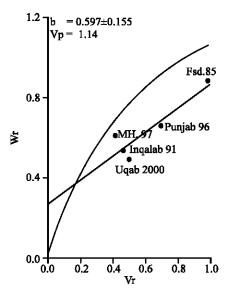


Fig. 5: Vr/Wr graph for spikelets per spike

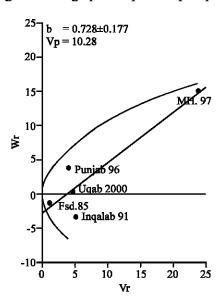


Fig. 7: Vr/Wr graph for 1000-grain weight

difficult due to the over dominance type of gene action for 1000-grain weight.

Grain yield per plant: Over dominance type of gene action was found for this trait as the Vr/Wr graph showed that regression line intercepted the Wr-axis below the point of origin (Fig. 8). There was an indication of absence of non-allelic interactions as the regression line did not deviate significantly from the unit slope. Mann and Sharma (1995) also reported similar findings. The manner in which array points are displayed in the Vr/Wr graph (Fig. 8), indicated that the genotype Uqab 2000 being closest to the origin contained the most dominant genes for this trait. While the genotype MH. 97 which was the

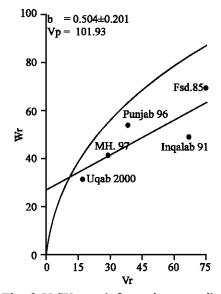


Fig. 6: Vr/Wr graph for grains per spike

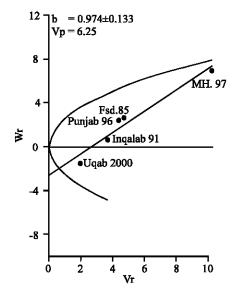


Fig. 8: Vr/Wr graph for grain yield per plant

farthest from the origin, possessed the maximum recessive genes for grain yield per plant. As this character exhibited non-additive type of gene action, the selection would be difficult in early segregating generations.

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