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Gene Action in a Five Parent Diallel Cross of Spring Wheat (*Triticum aestivum* L.)

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Abstract: In the present study graphic analysis was made for 5×5 diallel cross involving wheat varieties/lines viz., Tobari-66, SARC-1, 4943, 4072 and 4770 to determine genetic mechanism controlling some important yield components during crop season 2001-2002. Number of tillers per plant and grain weight per spike were governed by over-dominance type of gene action while plant height and peduncle length were controlled by partial dominance with additive type of gene action. Whereas, 1000-grain weight exhibited partial dominance type of gene action. Genotype Tobari-66 possessed maximum dominant genes for plant height and peduncle length and SARC-1 for number of tillers per plant. While genotype 4072 had maximum dominant genes for traits like grain weight per spike and 1000-grain weight. Epistasis was absent for all the above mentioned traits. For the traits like plant height, peduncle length and 1000-grain weight, selection in early generation will be fruitful whereas delayed selection should be preferred for the traits like number of tillers per plant and grain weight per spike.

Key words: Spring wheat, diallel cross, over-dominance, gene action, partial dominance

INTRODUCTION

Wheat (*Triticum aestivum* L.) being the most valuable staple food is highly regarded in the world as King of cereals. Being an Agricultural country, Pakistan's economy primarily depends on this sector and wheat no doubt is the mainstay of agriculture in our country. Among all wheat traits, yield is one of the most complex and economically important character. Identification and improvement of superior genotypes can only be possible through exploiting latest plant breeding techniques.

The evolution of new genotypes by continued genetic recombination is the need of the day. In order to achieve the maximum genetic gain with minimum resources and in minimum time, the gene action studies are of great importance in executing an efficient breeding programme, and attaining useful information regarding the selection of hybrids in terms of performance of their parents.

The diallel cross technique developed and illustrated by Hayman (1954) and Jinks (1954 and 1955) provides information on genetic mechanism involved in early generation.

In most of the studies on wheat, plant height and peduncle length were governed by partial dominance with additive type of gene action (Subhani and Chowdhry, 2000; Chaudhry *et al.*, 2001 and Khan *et al.*, 2000). Kashif *et al.* (2003) in an experiment involving six Durum wheat varieties and Seitkozhaev *et al.* (1990) observed over-dominance type of gene action for number of tillers per plant and grain weight per spike, respectively. Whereas Ali *et al.* (1999) and Rahman *et al.* (2003) in their studies

on bread wheat indicated partial dominance type of gene action for 1000-grain weight.

The central objective of present studies was to obtain information on nature of gene action and magnitude of contribution to various characters like grain yield, and its components in a 5×5 diallel cross. These informations would be of great value in selection of desirable parents to develop an affective breeding programme to evolve new varieties with desirable economic yield.

MATERIALS AND METHODS

The proposed studies for the estimation of gene action were carried out in the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The experimental material was composed of five wheat varieties/lines viz., SARC-1, Tobari-66, 4072, 4943 and 4770. These genotypes were crossed in a diallel fashion including direct crosses and their reciprocals during crop season 2001-2002.

Seeds of F₁s including parents were planted on 8th of November 2003, in the field in a triplicated Randomized Complete Block Design. 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. Two seeds per hole were sown with the help of a dibble and later thinned to one seedling per site after germination.

At maturity, 10 guarded plants were randomly selected from each genotype in each replication. The data thus recorded for Tobari-66, SARC-1, 4943, 4072 and 4770 was subjected to analysis of variance techniques (Steel

and Torrie, 1980). The characters showing significant differences among genotypes were further analyzed by using diallel technique unreduced by Hayman (1954, 1958) and Jinks (1955).

RESULTS AND DISCUSSION

The differences among the genotypes were highly significant for all the traits. Array means for various traits are given in Table 1 and variance and co variance graphs are given in Fig. 1 to 5.

Plant height (cm): The value of Vr/Wr graph (Fig. 1) indicated that plant height was governed by additive type of gene action with partial dominance, as the regression line intercepted the Wr-axis well above the point of origin. The estimated regression line was not deviated significantly from the unit slope. This suggests the absence of non allelic interaction. Subhani and Chowdhry (2000) and Chaudhry *et al.* (2001) also showed similar results while studying this trait. The distribution of array point on regression line revealed that the variety Tobari-66 possessed maximum dominant genes being closest to the point of origin whereas the variety SARC-1 had maximum recessive genes being farther from the origin. Additive gene action with partial dominance is very useful for selection in early generations.

Genotype 4770 possessed higher array mean of 112.30 being good general combiner for this trait while genotype SARC-1 showed lowest array mean with a value of 86.92 (Table 1).

Number of tillers per plant: From Vr/Wr graph (Fig. 2) for number of tillers per plant, it was evident that regression line cut the Wr-axis below the origin revealing over-dominance type of gene action. Epistasis was absent as the regression line did not deviate significantly from unit slope. Kashif *et al.* (2003) reported similar type of gene action while studying this trait. SARC-1 possessed maximum dominant genes being closest to the origin (Fig. 2) whereas the line 4770 had maximum recessive genes being farther from the origin. Genotype 4943 possessed higher array mean of 13.90 while on the other hand genotype SARC-1 had the lowest array mean of 10.77 (Table 1). Due to the over-dominance shown by this trait, the selection in the early generation would be unfruitful.

Peduncle length (cm): The Vr/Wr graph showed that the regression line intercepts the Wr-axis above the point of origin (Fig. 3). This indicated that peduncle length was governed by partial dominance with additive type of gene action. The estimated regression line did not deviated

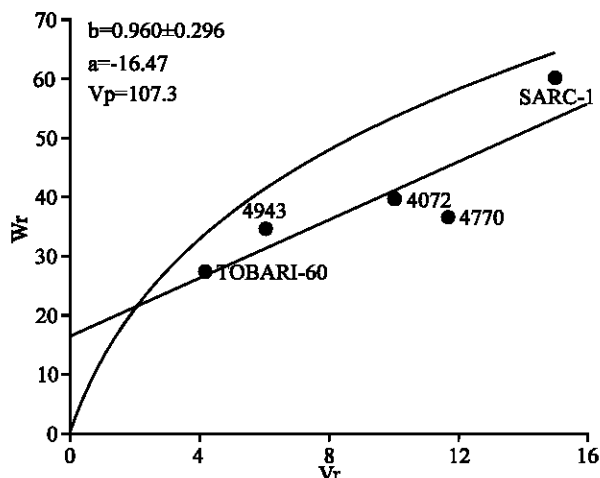


Fig. 1: Vr/Wr graph for plant height

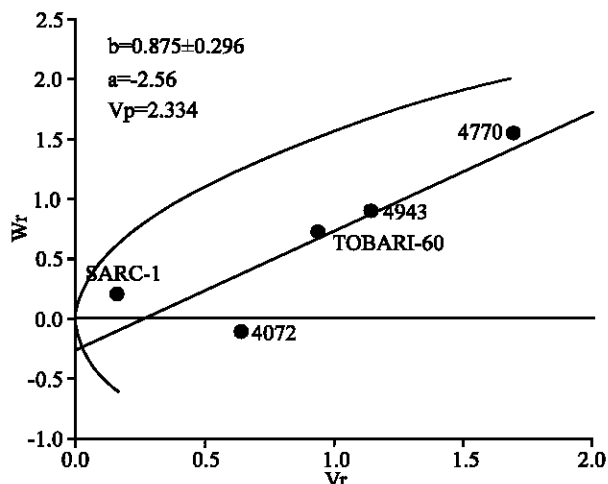


Fig. 2: Vr/Wr graph for tillers per plant

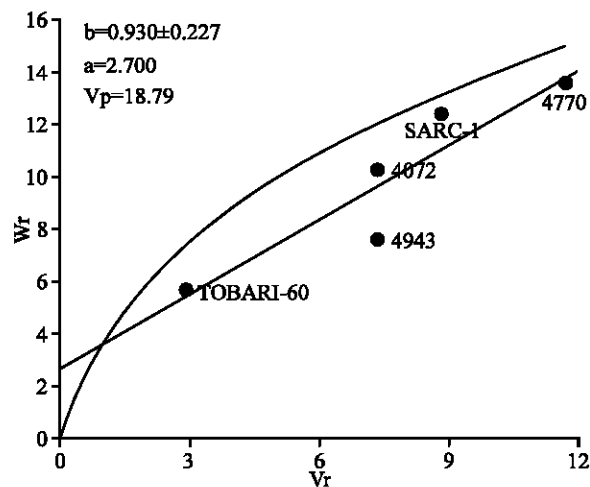


Fig. 3: Vr/Wr graph for peduncle length

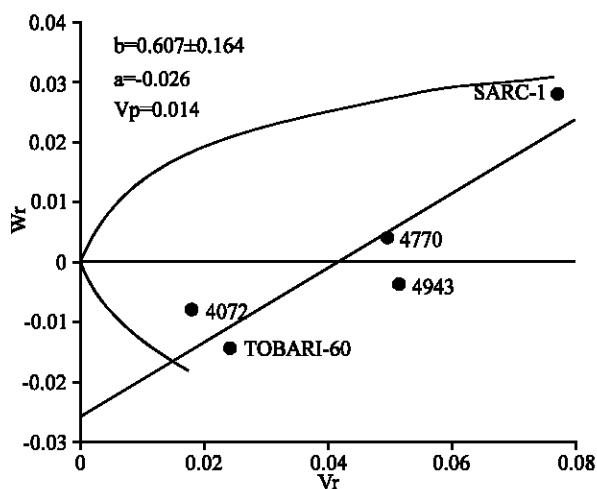


Fig. 4: Vr/Wr graph for grain weight per spike

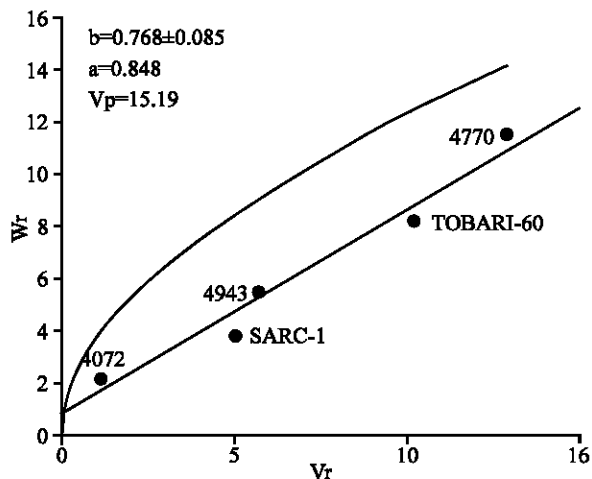


Fig. 5: Vr/Wr graph for 1000-grain weight

significantly from unit slope indicating the absence of non allelic interaction. These results are in good agreement with the work of Khan *et al.* (2000). The variety Tobari-66 was close to the origin, indicating that most of the dominant genes were present in it. Whereas line 4072 being farthest from the origin, possessed most recessive genes (Fig. 3). The genotype 4770 had higher array mean of 38.40 whereas SARC-1 showed lowest array mean of 27.57 (Table 1). Additive with partial dominance type of gene action is very helpful for selection in early generation.

Grain weight per spike (g): The inheritance pattern for grains weight per spike appeared to be over-dominance type as regression line cuts the Wr-axis well below the origin (Fig. 4). The results are in agreement with the findings of Seitkozhaev *et al.* (1990). The estimated

Table 1: Array means for various characters

Characters	SARC-1	Tobari-66	4072	4943	4770
Plant height (cm)	86.92	107.88	110.29	108.60	112.30
Number of tillers per plant	10.77	13.53	10.87	13.90	13.30
Peduncle length (cm)	27.57	35.48	34.18	37.83	38.40
Grain weight per spike (g)	2.08	2.39	2.29	2.22	2.16
1000-grain weight (g)	45.63	39.33	35.30	41.53	37.97

regression line did not deviated significantly from the unit slope suggested the absence of non allelic interaction. The array points revealed that line 4072 being nearest to the origin had maximum dominant genes while genotype SARC-1 being farthest from the origin possessed maximum recessive genes. Genotype Tobari-66 had the highest array mean of 2.39 whereas genotype SARC-1 had the lowest array mean value of 2.08 (Table 1). Due to over-dominance type of the inheritance pattern, selection in early generation would be difficult.

1000-grain weight (g): The inheritance pattern for 1000-grain weight appeared to be partial dominance as regression line cuts the Wr-axis above the origin (Fig. 5). The regression line did not deviated significantly from the unit slope suggesting the absence of epistasis. Similar results has been reported by Khan *et al.* (2000). The array point revealed that line 4072 being nearest to the origin had maximum number of dominant genes whereas line 4770 being farthest from the origin possessed maximum number of recessive genes. Additive gene action with partial dominance in the absence of epistasis suggests that selection will be fruitful in the early generation. The genotype SARC-1 had higher array mean of 45.63 while on the other hand genotype 4072 had lower array mean of 35.30 (Table 1).

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