Asian Journal of Plant Sciences

ISSN 1682-3974

science alert

ANSInet
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Asian Journal of Plant Sciences 2 (17-24): 1153-1155, 2003
ISSN 1682-3974

Genetic Model of Some Economic Traits in Bread Wheat (*Triticum aestivum* L.)

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Abstract: A 5 × 5 diallel cross experiment involving five wheat varieties/lines viz., SARC-1, Tobari-66, 4072, 4943 and 4770 revealed that the traits like flag leaf area, spike length and spikelets per spike were controlled by over dominance type gene action, suggesting delayed selection to fairly good improvement in these traits. While number of grains per spike and grain yield per plant were governed by partial dominance type of gene action, determining fruitful selection in the early generation for these traits. Epistasis was absent in all the traits involved.

Key words: Bread wheat, diallel cross, over-dominance, partial dominance

INTRODUCTION

We human beings practically attain all our food directly from plants. *Gramineae* family is no doubt the most diverse and important family of plant kingdom. The cereal crops belonging to *Gramineae* family producing large edible grains and provides about one half of man's food calories and large part of his nutrients requirements. Wheat (*Triticum aestivum* L.) is foremost among cereals and indeed among all food crops, as direct source of food and energy for human beings.

Proper understanding of genetic mechanisms involving in expression of important yield related characters helps in planning effective breeding strategies. Diallel cross technique developed and illustrated by Hayman (1954 and 1958) and Jinks (1954 and 1955) provide information on genetic mechanism involved in early generations and are particularly suited to autogamous crops like wheat.

In most of the studies on wheat, over dominance type of gene action was revealed for flag leaf area, spike length and spikelets per spike (Riaz and Chowdhry, 2003; Rahman *et al.,* 2003 and Chowdhry *et al.,* 2001). Partial gene effects were found to be important for number of grains per spike and grain yield per plant (Rahman *et al*., 2003 and Chowdhry *et al*., 1999).

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. The crosses were attempted in a diallel fashion including direct crosses and their reciprocals during crop season 2001-2002.

Seeds of F_1s including parents were planted in November 2002, in the field using 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 SARC-1, Tobari-66, 4072, 4943 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 and 1958) and Jinks (1954 and 1955).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among all the wheat genotypes for all the traits under study (Table 1).

Flag leaf area: The Vr/Wr graph (Fig.1) reveals that the flag leaf area was governed by over-dominance type of gene action as the regression line intercept the Wr-axis below origin. The estimated regression line was not deviated significantly from the unit slope. This suggests the absence of non allelic interaction. Riaz and Chowdhry (2003) also reported similar results. The array points showed that the genotype SARC-1 was nearest to the origin so it contained the maximum dominant genes and line 4072 being farthest from the origin contained most recessive genes. As over-dominance type of gene action was present so selection, based on this trait would be difficult in early generation. Genotype SARC-1 possessed

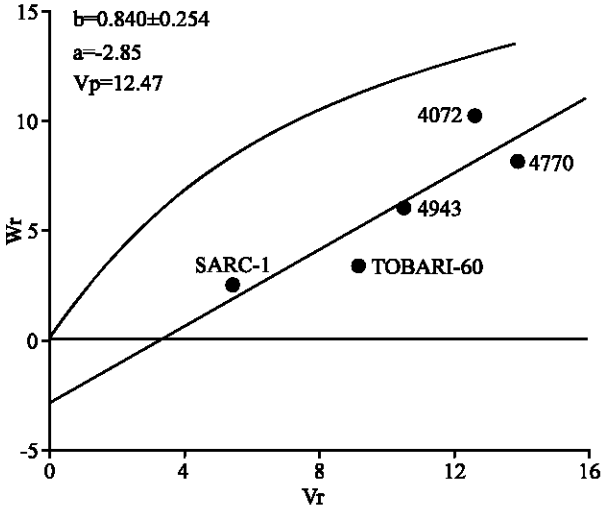

Fig. 1: Vr/Wr graph for flag leaf area

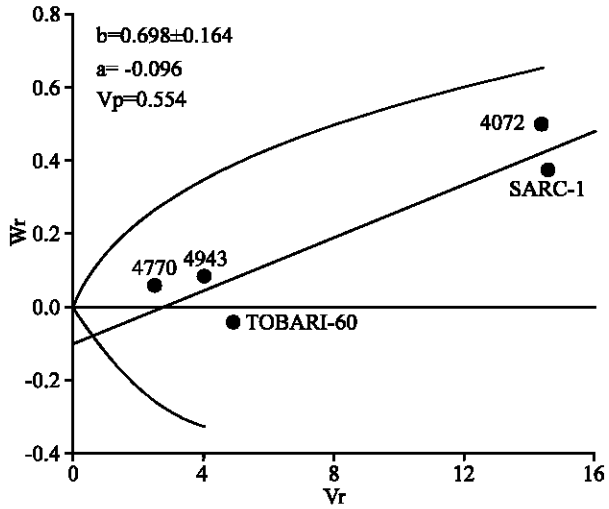

Fig. 2: Vr/Wr graph for spike length

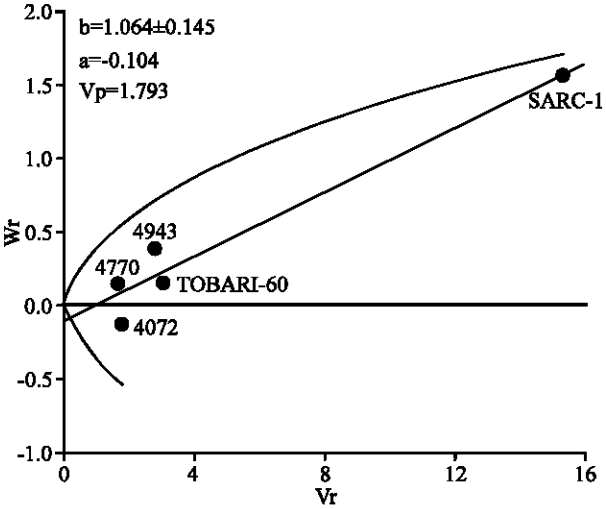

Fig. 3: Vr/Wr graph for spikelets per spike

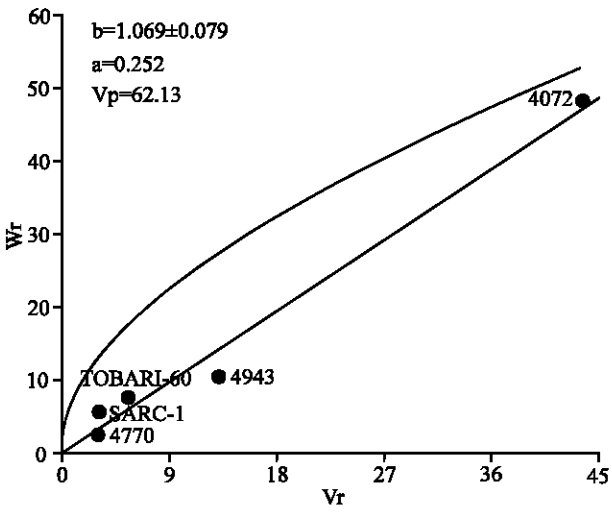

Fig. 4: Vr/Wr graph for grains per spike

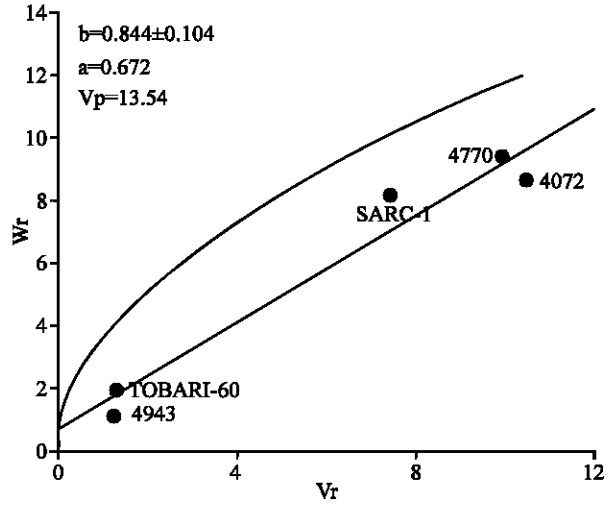

Fig. 5: Vr/Wr graph for grain yield per plant

higher array mean of 42.77 while genotype 4770 showed lowest array mean with a value of 33.71 (Table 2).

Spike length: The graph for Vr/Wr showed that the regression line intercepts the Wr-axis below the origin indicating over-dominance (Fig. 2). These results are supported by the earlier findings of Rahman *et al.* (2003). The deviation of regression line was not significant from unity. This indicates that non allelic interaction is not present or there is no epistasis. Array point (Fig. 2) showed that line 4770 being nearest to the origin had most of the dominant genes while line 4072 was the farthest from origin so it carried most of the recessive genes. Selection would be possibly ineffective in this type of gene action in early generation. Genotype 4770 being a good general combiner for this trait had the higher array mean of 13.75 while 4072 had lowest array mean of 12.02 (Table 2).

Table 1: Mean squares for various traits in wheat

Sources of variation	df	Flag leaf area (cm^2)	Spike length (cm)	Number of spikelets $spike^{-1}$	Number of grains $spike^{-1}$	Grain yield $plant^{-1}$ (g)
Mean Squares						
Replications	2	5.42^{NS}	0.03^{NS}	0.63^{NS}	1.30^{NS}	0.84^{NS}
Genotypes	24	34.80**	1.65**	1.80**	47.97**	23.39**
Error	48	1.81	0.25	0.30	5.40	2.15

N.S = Non significant ** = Highly significant

Table 2: Array means for various characters in wheat

Characters	SARC-1	Tobari-66	4072	4943	4770
Flag leaf area (cm^2)	42.77	37.23	35.06	38.81	33.71
Spike length (cm)	12.46	13.54	12.02	13.36	13.75
Number of spikelets $spike^{-1}$	16.77	19.13	19.77	20.10	19.63
Number of grains $spike^{-1}$	45.03	60.60	64.93	53.50	61.23
Grain yield $plant^{-1}$ (g)	20.03	28.82	20.96	25.01	21.13

Number of spikelets per spike: Over-dominance type of gene action for this trait was revealed by the Vr/Wr graph as the regression line cuts Wr-axis below origin (Fig. 3). Similar results have already been reported by Chowdhry *et al.* (2001) and Rahman *et al.* (2003). The estimated regression line was not deviated significantly from unit slope. This suggests the absence of non allelic interaction or epistasis. The array points (Fig. 3) showed that the line 4072 was nearest to the origin so it contained maximum dominant genes whereas genotype SARC-1 being the farthest from the origin contained most of the recessive genes. Genotype 4943 possessed higher array mean of 20.10 while on the other hand genotype SARC-1 had the lowest array mean of 16.77 (Table 2). Due to the presence of over-dominance type of gene action selection in early generation would be difficult.

Number of grains per spike: The graphical representation of Vr/Wr indicated partial dominance for this character as regression line intercepts the Wr-axis just above the point of origin (Fig. 4). Similar results were also given by Rahman *et al.* (2003). It is apparent from the graphic illustration that line 4770 being closest to the origin possessed maximum dominant genes whereas line 4072 contained maximum recessive gene being farthest from the point of origin. The regression line did not deviate significantly from unit slope suggesting the absence of epistasis. The genotype 4072 had higher array mean of 64.93 whereas SARC-1 showed lowest array mean of 45.03 (Table 2). Genotype 4072 with higher array mean can be used as one of the parent for fruitful results. Partial dominance in the absence of epistasis suggests that selection will be effective in early generation.

Grain yield per plant: The inheritance pattern for grain yield per plant appeared to be partial dominance as regression line cuts the Wr-axis above the origin (Fig. 5). Chowdhry *et al.* (1999) and Khan *et al.* (2000) also showed similar findings for this particular trait. The estimated regression line did not deviate significantly from unit slope suggested the absence of epistasis. The distribution of array points on the regression line revealed that genotype 4943 being nearest to the origin possessed maximum dominant genes while line 4770 being farthest from origin possessed most recessive genes. Due to partial dominance type of gene action in the absence of non allelic interaction, the selection in early generation would be very helpful. Genotype Tobari-66 had the highest array mean of 28.82 and appeared to be good general combiner for this trait whereas genotype SARC-1 had the lowest array mean value of 20.03 (Table 2).

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