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Genetic Architecture of Some Agronomic Traits in Diallel Cross of Bread Wheat

Abdul Wajid Nazeer, Muhammad Safeer-ul-Hassan and Zahid Akram
University of Arid Agriculture, Rawalpind, Pakistan

Abstract: In the present study gene action was studied in diallel cross of wheat cultivars; Potowar 93, Parwaz 94, Chakwal 97, Shahkar 97, Pak 81 and Margalla 99 for plant height, number of tiller per plant, days to heading, days to maturity, grain filling period and flag leaf area. The analysis of variance was highly significant for all the traits studied. The tests of adequacy of additive dominance model suggested that these were completely adequate for plant height, number of tiller per plant, days to heading and flag leaf area whereas partially adequate for days to maturity and grain filling period. Additive type gene action was noticed in all the traits and over dominance was observed in plant height and number of tiller per plant while for other partial dominance was observed. Margalla 99 proved to be best cultivar.

Key words: Spring wheat, diallel cross, agronomic traits, gene action

INTRODUCTION

Wheat has always been remained subject of intensive research pertaining to genetic improvement. So in all breeding programmes, understanding of genetic mechanism controlling the yield relating components are helpful in development of superior genotypes.

Gene action can be studied through different methods, but in the present research the technique developed by Hayman, is followed which is still considered as an efficient tool to get the basis of genetic control for certain characters. Over dominance has been reported by Mishra *et al.*^[1], Mishra *et al.*^[2] and Sabour *et al.*^[3]. While Iqbal *et al.*^[4] and Patil *et al.*^[5] reported partial dominance with additive type gene action.

The present studies were, therefore, conducted for better and comprehensive understanding of the genetic architecture of agronomic traits and to select the parent, which combine good characters.

MATERIALS AND METHODS

Six wheat genotypes namely, Potowar 93, Parwaz 94, Chakwal 97, Shahkar 97, Pak 81 and Margalla 99 were crossed in all possible combination during 2000-2001. The F_1 's including the reciprocals and parents were sown in the three replications following randomize complete block design at the research farm of Department of Plant Breeding and Genetics, University of Arid Agriculture, Rawalpindi. Each experimental plot consisted a single 5 m

long row with inter-plant and inter-row distance of 25 and 30 cm, respectively. All agronomic and plant protection treatments were kept normal and equal for the entire experiment. At maturity, ten plants were randomly selected from each genotype of each replication. Data were recorded on plant height, number of tiller per plant, days to heading, days to maturity, grain filling period and flag leaf area. The data collected were analyzed statistically using Fisher's Analysis of Variance technique^[6] where the means were significant, data was further subjected to diallel analysis techniques advocated by Hayman^[7] and Jinks^[8].

RESULTS AND DISCUSSION

The data for yield and its related characters were subjected to analysis of variance, which indicated the presence of highly significant differences among the genotypes for all the traits (Table 1).

Plant height: The relationship of the W_r and V_r indicated over dominance as the regression line intersected the W_r -axis below the origin (Fig.1). Over dominance for plant height has also been reported by Mishra *et al.*^[1], Mishra *et al.*^[2] and Sabour *et al.*^[3]. Whereas Iqbal *et al.*^[4], Patil *et al.*^[5] and Dhonde *et al.*^[9] reported partial dominance for this trait. The difference in the results was due to different genetic material and different environment.

Table 1: Mean square values for various plant traits in a 6x6 diallel cross of wheat

Source of variation	Degree of freedom	Plant height	Number of tillers per plant	Days to heading	Days to maturity	Grain filling period	Flag leaf area
Genotypes	2	75.75**	2.46**	62.44**	95.17**	156.77**	64.76**
Replications	35	174.89	0.65	21.19	69.67	18.17	26.57
Error	70	27.84	0.38	27.40	47.81	81.54	14.00

** Highly significant at 5% level

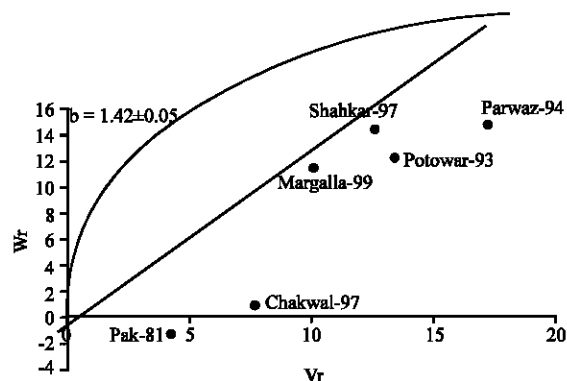


Fig. 1: W_r/V_r graph for plant height

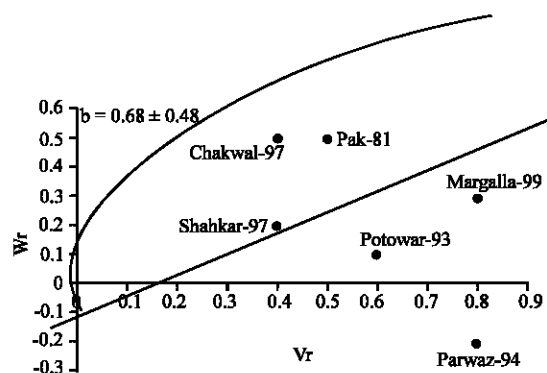


Fig. 2: W_r/V_r graph for no. of tillers per plant

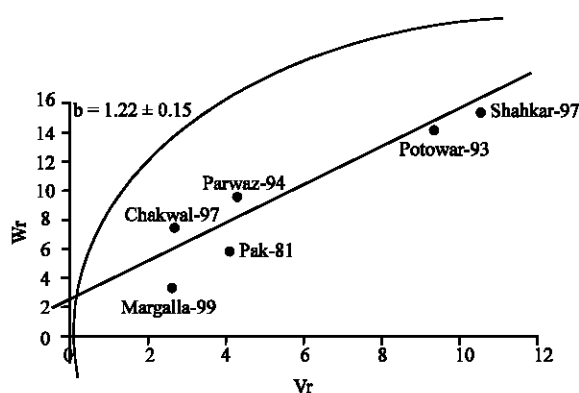


Fig. 3: W_r/V_r graph for days to heading

The distribution of array points on the regression line indicated that maximum dominant genes were present in Pak-81, as it was located nearest to origin. The variety

Parwaz-94 possessed maximum recessive genes for this trait. The other four genotypes i.e. Potowar-93, Chakwal-97, Shahkar-97 and Margalla-99 also had relatively high frequency of recessive genes for plant height.

Number of tillers per plant: Results indicated over dominance as the regression line intersected the W_r -axis below the origin (Fig. 2). Over dominance for plant height has also been reported by Mishra *et al.*^[1], Mishra *et al.*^[2] and Sabour *et al.*^[3]. The distribution of array point on the regression line indicated that maximum dominant genes for number of tillers plant⁻¹ were present in the genotype Shahkar-97 as it was nearest to the origin whereas the most recessive genes were present in the variety Margalla-99, located farthest from the origin (Fig. 2).

Days to heading: Figure 3 indicated that partial dominance was responsible for the expression of days to heading. Results of the same trait are reported by Iqbal *et al.*^[4] and Patil *et al.*^[5] which agree with the results of this study, whereas Mishra *et al.*^[2], Sabour *et al.*^[3] and Yang *et al.*^[10] reported different gene action for days to heading. This disagreement is due to the fact that this trait behaves differently for different set of genotypes and in different environments.

The distribution of array point on the regression line indicated that most dominant genes were present in Margalla-99 for days to heading as it was located nearest to origin while Shahkar-97 had maximum recessive gene for this trait. Careful selection in the early segregating generation is suggested to make maximum out of additive component of genetic variation for days to heading.

Days to maturity: The W_r/V_r graph indicated that partial dominance was responsible for the expression of days to maturity (Fig. 4). Results of the same trait were reported by Iqbal *et al.*^[4] and Patil *et al.*^[5]. Parwaz-94 had highest dominance gene frequency for days to maturity, as it is located nearest to the origin whereas the genotype Chakwal-97 had highest recessive gene for this particular trait as it was farthest from the origin.

Grain filling period: Figure 5 indicated that partial dominance was responsible for the expression of grain

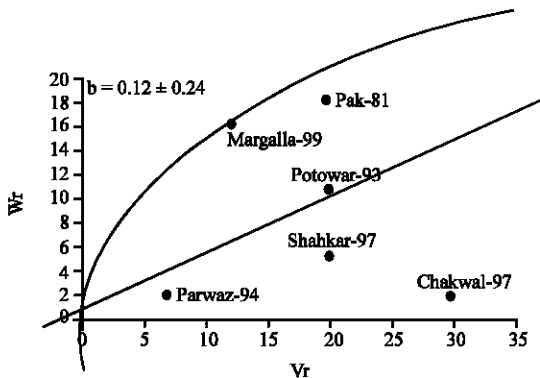


Fig. 4: Wr/Vr graph for days to maturity

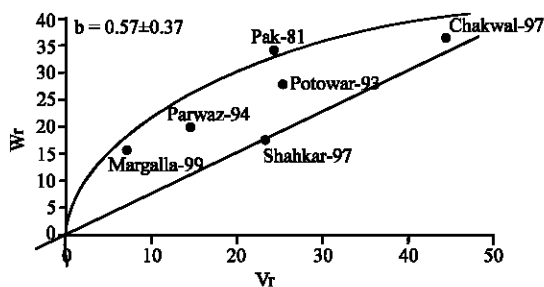


Fig. 5: Wr/Vr graph for grain filling period

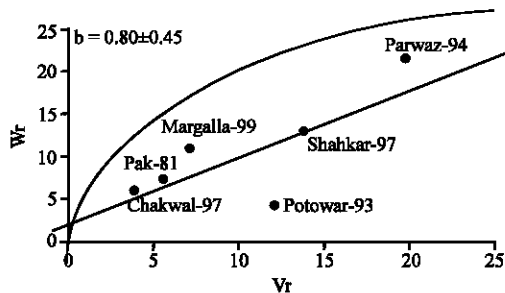


Fig. 6: Wr/Vr graph for flag leaf area

filling period. Results of the same trait are reported by Iqbal *et al.*^[4] and Patil *et al.*^[5] which agree with the results of this study, whereas Mishra *et al.*^[1], Sabour *et al.*^[3] and Yang *et al.*^[10] reported different gene action for grain filling period. This disagreement is due to the fact that this trait behaves differently for different set of genotypes and in different environments.

The distribution of array points on the regression line depicted that Margalla-99 was the genotype containing the maximum dominant gene, as it was located nearest to the origin while Chakwal-97 had maximum recessive gene for this particular trait being located farthest from the origin. Remaining varieties i.e. Parwaz-94, Pak-81, Potowar-93 and Shahkar-97 contain intermediate recessive genes for grain filling period.

Flag leaf area: The Wr/Vr graph indicated that partial dominance was responsible for the expression of flag leaf area (Fig. 6). Results of the same trait are reported by Iqbal *et al.*^[4] and Patil *et al.*^[5] which agree with the results of this study, whereas Mishra *et al.*^[1], Sabour *et al.*^[3] and Yang *et al.*^[10] reported different gene action for flag leaf area. This disagreement is due to the fact that this trait behaves differently for different set of genotypes and in different environments.

The distribution of array points on the regression line makes it clear that Chakwal-97 is the variety that possess maximum dominant genes for flag leaf area because it is located nearest to the origin while Parwaz-94 contain maximum recessive gene for this particular character. These results showed that early selection of segregating generation through simple selection technique would be suitable.

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