GENETIC EVALUATION OF SOME YIELD AND YIELD RELATED TRAITS IN WHEAT

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A 5×5 complete diallel experiment was conducted involving five spring wheat varieties/lines viz., Waton, Uqab, Inqlab-96, Inqlab-91 and Bhakkar-2000 to evaluate genetic nature of various polygenic characters. The characters under studied were plant height, number of tillers, spike length, number of spikelets per spike, grains per spike, 1000 grain weight, and grain yield per plant. The analysis of variance showed highly significant differences among the genotypes for all the characters studied. The graphic representation of variance (Vr) and covariance (Wr) depicted that spike length, number of spikelets per spike and grains per spike were under the control of additive type of gene action with partial dominance. While all other characters under study, were governed by over-dominance type of gene action. Epistasis was found to be absent in the entire traits under study.

Keywords: Wheat, diallel, yield, variance

INTRODUCTION

Wheat is the leading food grain crop of Pakistan occupying the largest area (8.5 million hectares). About twenty percent of the total wheat acreage is planted under rainfed conditions. Wheat production in Pakistan can be divided into three distinct periods: 1947-65, prior to the release of semi-dwarf wheats; 1966-76, the so-called "Green Revolution" period when High Yielding Varieties (HYVs) were rapidly adopted on about two third of total wheat area; and 1976 to date, post green revolution period when HYVs continued to spread to cover the major wheat area. Wheat production in the country was increased by 480 % between1948 to 2004, whereas increase in the area was 114%. A worth of Rs.202 billion wheat is produced in the country and one percent loss in wheat production would be equivalent to rupees 2.2 billion. To keep pace with the increasing population (2.09% per year) and due to changing food habits of rural and urban population, it is necessary to further increase the current productivity level (19.5 million metric tones) to meet the requirement of 165 million peoples. Since there is no scope for horizontal expansion, the projected demand will have to be met by increasing the productivity.

The existing yield gap in different parts of the country has to be reduced to achieve the increasing demand through diversification of wheat breeding programmes by developing new varieties suitable to grow in different agro-climatic zones. Further improvement in the yield of this important crop requires adequate information regarding the nature of combining ability of the parents used in the hybridization programme and also the nature of gene actions involved in the expression of quantitative traits of economic importance.

The present study was planned to understand the genetic nature of some polygenic characters in diallel cross. Knowledge obtained from present study will be helpful to develop appropriate strategy for genetic improvement in grain yield and some important yield components of wheat.

MATERIALS AND METHOD

Five genotypes of hexaploid wheat (*Triticum aestivum* L.), namely; Waton, Uqab, Inqlab-96, Inqlab-91 and Bhakkar-2000 were selected on the basis of their differences in parentage, adaptability and morpho-physiological characters. In the present investigation all possible crosses among the selected varieties were made. F_1 was planted in the field to develop F_2 seed of the crosses. The five parents along with twenty F_2 hybrids were planted next year in triplicate following randomized completely block design as described by Steel and Torrie (1980) at Research Station of Gomal University, D.I. Khan under canal irrigated condition. Fifty competitive plants per replication were selected randomly for recording observations on these following characters: plant height, number of tillers per plant, number of spikelets per spike, number of grains per spike, 1000 grain weight (g) and grain weight per plant. The data was analysed for genetic studies and gene action was determined following Hayaman approach (1954).

RESULTS AND DISCUSSION

Plant Height

Highly significant differences were observed among genotypes for plant height as indicated in array means and analysis of variance (Table-1&2). Perusal of Vr/Wr graph (Fig. 1) reveals that regression line intercepted the co-variance (Wr) just below the point of origin indicating that the plant height was governed by the over dominance type of gene action. Epistasis was absent as the unit line does not deviate significantly form unit slop. These results have also been reported by Chowdhry *et al.* (2001) while Rehman *et al.* (2003) indicated additive type of gene action with partial dominance. However Khan (1999) reported dominant type of gene action.

Table 1. Analysis of variance for various characters of wheat genotypes

Characters	MS
Plant height (cm)	31.45**
Tillers per plant	1.41**
Spike length (cm)	5.71**
Spiklets per spike	2.25**
grains per spike	9.75**
1000 grains weight(g)	3.01**
Grain weight per plant (g)	3.12**

The distribution of varietal array points on regression line revealed that variety Uqab contains maximum dominant genes for Plant height, as it was closest to the origin while Inqlab-96 possessed most recessive genes, being farthest from the origin. In view of over dominance type of gene action, selection would be effective in later generations.

tillers per plant (Table 1&2) showed highly significant differences among the genotypes.

From the Vr/Wr graph (Fig. 2) for number of tillers per plant, it was evident that regression line cut the y-axis just below the point of origin revealing over dominance type of gene action. Epistasis was absent as the regression line did not deviate significantly from the unit slop. The results are in conformity with the findings of Munir (1997) and Shekhawat *et al.* (2000), while Subhani and Chowdhry (2000) and Chawdhry *et al.* (2001) reported additive type of gene action for this trait. The position of array points on regression line indicated that genotype Inqlab-96 has maximum dominant genes being closest to the origin followed by variety Uqab and Bhakhar-2000, whereas genotype Waton, which is away from the origin had maximum recessive genes.

Spike length (cm)

This particular character hold great importance for plant breeders as it contributes a lot to the wheat yield. The analysis of variance and array means tables (Table 1&2) revealed that differences for spike length among the genotypes were highly significant.

The Vr/Wr graph shows that regression line cut the Wr-axis above the origin indicating additive type of gene action with partial dominance (Fig. 3). The deviation of regression line was not significant from unit slop, thus indicating the absence of non allelic interactions. Chowdhry *et al.* (1999) observed the similar results but on the other hand, Ali *et al.* (1999) found non-additive type of gene action with over dominance for this trait. From the graphical representation (Fig. 3) it was clear that genotype Inqlab-96 had maximum dominant genes, which was nearest to the origin while Inqlab-91 had most of the recessive genes being farthest from the origin. Besides Inqlab-96, Uqab and Waton also

Table 2. Array means for various characters of wheat genotypes

Characters	Waton	Uqab	Inqlab-91	Bhakkar-2000	Inqlab-91
Plant height (cm)	104.36	103.27	106.33	104.20	103.63
Tillers per plant	11.67	11.87	11.57	11.27	11.92
Spike length (cm)	12.22	12.10	12.42	11.93	11.19
Spiklets per spike	18.48	19.14	19.35	18.87	18.67
Grains per spike	62.66	67.33	67.80	66.90	65.66
1000 grains weight(g)	43.03	44.57	43.86	43.45	43.86
Grain weight per plant (g)	23.06	23.36	23.39	24.05	24.49

Number of tillers per plant

Number of tillers per plant is an important yield component. Analysis of variance for the number of

had maximum number of dominant genes being in the proximity of the origin. The present study showed the additive type of gene action for spike length so selection in early generations would be fruitful.
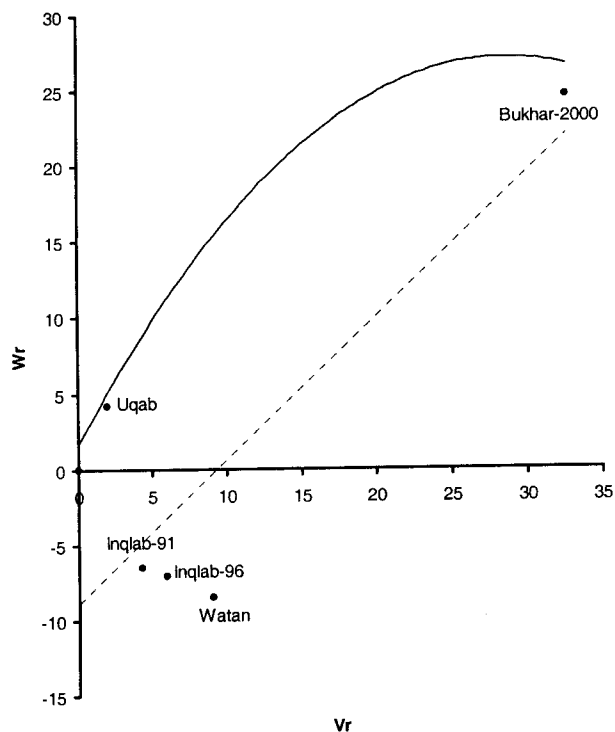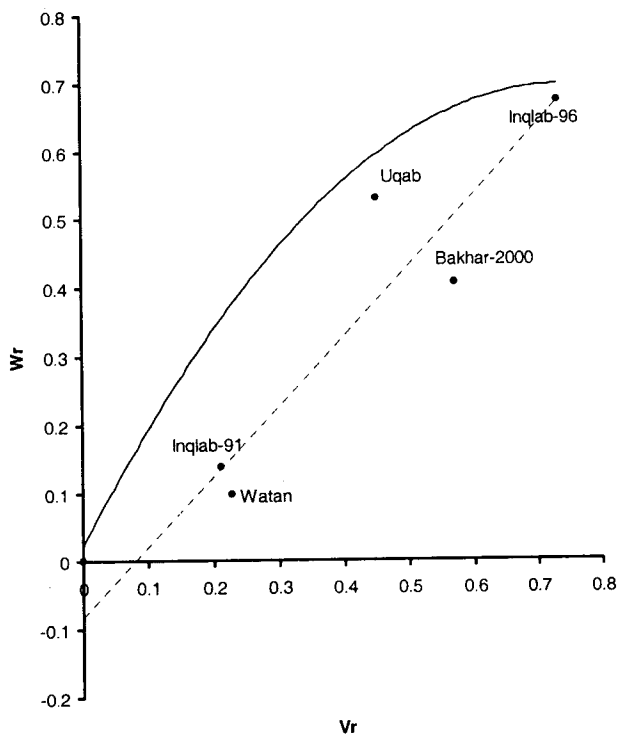
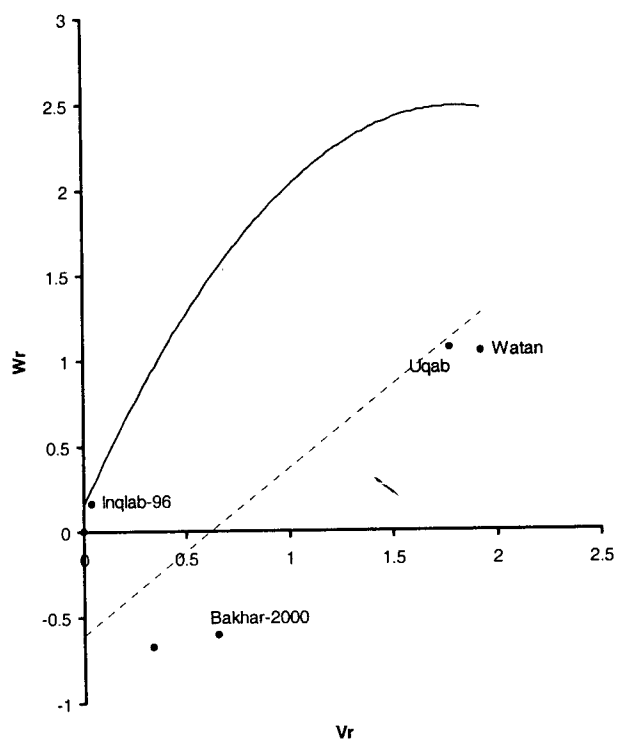Fig. 1. Vr/Wr graph for plant height

Fig. 2. Vr/Wr graph for No. of tillers
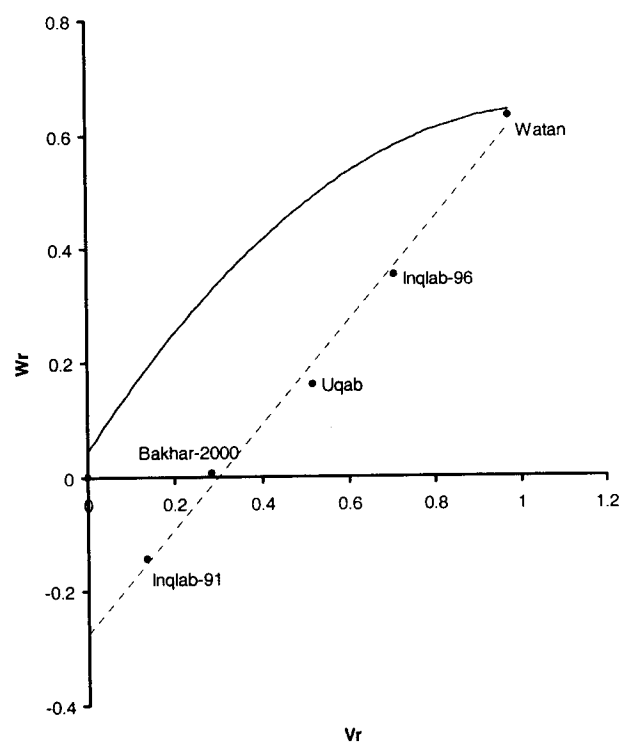

Fig, 3. Vr/Wr graph for Spike length

Fig. 4. Vr/Wr graph for No. of grains per spike

Number of grains per spike

One of the most important yield components is number of grains per spike. From the analysis of variance (Table 1) and array means table (Table 2) for the number of grains per spike showed that there were highly significant differences among the genotypes. The graphical representation indicated the partial dominance for this trait, as the regression line intercepted the Wr-axis just below the origin (Fig. 4). The estimated regression line did not deviate significantly from the unit slope suggesting the absence of epistasis. The observed results are in good agreement with the findings of Shehzad *et al.*, (1998) and Asif *et al.*, (1999), however Tahir (1995); Munir (1997) and Aziz *et al.*, (1999) reported additive type of gene action with partial dominance for the trait.

The graphical representation illustrated that the variety Inqlab-91 and Uqab being closest to the origin had the most number of dominant genes, while the variety Inqlab-96 being far away from the origin had maximum number of recessive genes for this trait. Fixation of this character would be possible in early generation because of absence of non-allelic interaction.

1000-grain weight (g)

1000-grain weight is the most important yield related characters reflecting grain size in wheat. The array means of traits and analysis of variance for 1000-grain weight showed that there are highly significant differences among the genotypes in (Table-1&2).

The graphical representation indicated the over-dominance type of gene action for this trait, as the regression line intercepted the Wr-axis just below the origin (Fig. 5). The estimated regression line did not deviate significantly from the unit slope suggesting the absence of epistasis. The graphical representation illustrated that Bhakkar-2000 being closest to the origin had more number of dominant genes followed by Inqlab-96. Waton being the farthest from the origin indicated that it has maximum number of recessive genes for 1000-grain weight. The same findings were also observed by Shekhawat *et al.*, 2000 and Kashif and Khaliq (2003).

Grain yield per plant (g)

There were highly significant differences among the genotypes as shown form the array means of traits and analysis of variance for grain yield per plant (Table-1&2). The inheritance pattern for grain yield appeared to be non additive type of gene action as the regression line intercepted the Wr-axis below the origin (Fig. 6). Deviation of the estimated regression line from the unity was not significant thus indicating the absence of non-allelic interaction. The results derived from the present study are in accordance with the findings of Shekhawat *et al.* (2000) and Kashif and Khaliq (2003), while Tahir *et al.* (1995) found complete dominance type of gene action for this trait.
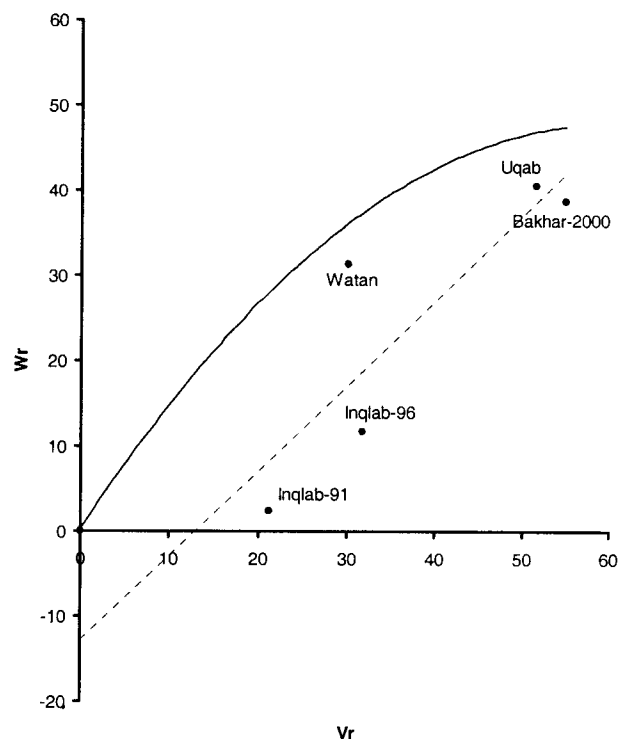

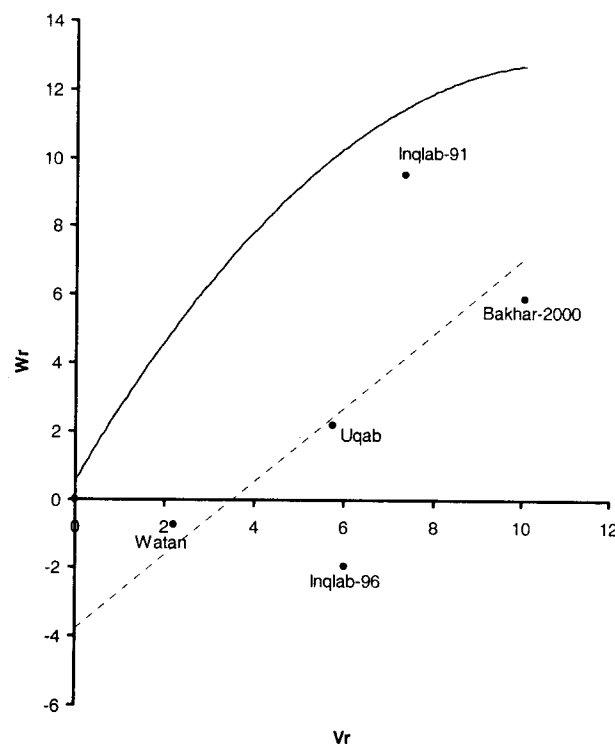
Fig. 5. Vr/Wr graph for 1000 grain weight

Fig. 6. Vr/Wr graph for grain yield per plant

Number of spikelets per spike

The analysis of variance revealed that differences among the genotypes were highly significant for number of spikelets per spike (Table 1&2). The Vr/Wr graph shows that regression line intercepted the Wr-axis above the origin indicating additive type of gene action with partial dominance (Fig. 7). From the graph, it is shown that genotype Uqab, Inqlab-91 and Waton had maximum dominant genes, while Inqlab-96 had the maximum recessive genes as it fall farther form the origin. Khan, (1995); Ali *et al.,* (1999) and Aziz *et al.,* (1999) reported the similar results but Khan, (1992) and Habib and Khan (2003) demonstrated the over dominance type of gene action for this trait. The additive with partial type of gene action indicates that the selection in early generations would be helpful.
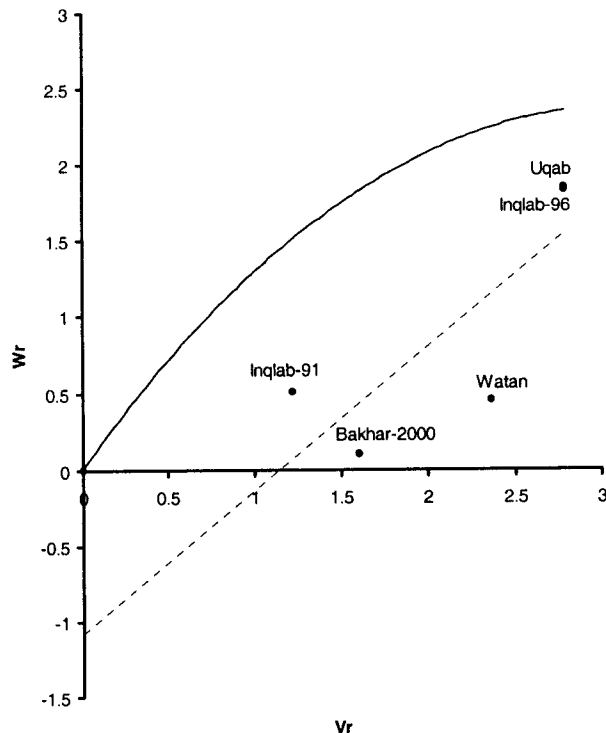

Fig. 7. Vr/Wr graph for spikelets per spike

CONCLUSION

The analysis of variance revealed that the difference among the genotypes for all the traits studied were highly significant. The graphic representation of variance (Vr) and covariance (Wr) understanding that spike length and number of spikelets per spike were under the control of additive type of gene action with partial dominance. While characters like plant height, number of tiller, number of grains per spike, 1000 grain weight and grain yield per plant were governed by over-dominance type of gene action. Epistasis was founf to be absent for all the traits under study.

Majority of the dominant genes for plant height, No. of tillers, grains per spike and grain yield per plant were observed in genotypes Uqab, Inqlab-96 and Waton. However most of the dominant genes for 1000-grain weight were found in Bhakkar-2000. For spike length and number of spikelets, genotypes Inqlab-91, Waton and Inqlab-96 contains the maximum number of recessive genes, while Waton, Inqlab-96 and Inqlab-91 were observed to possess maximum number of recessive genes for the trait like plant height, number of tillers number of grains per spike, 1000-grain weight and grain yield per plant.

Additive gene action with partial dominance in the absence of non-allelic interaction for the traits like spike length, number of grain per spike and number of spikelets per spike suggested that selection in early segregation generations may lead to fairly good improvement in these characters. Whereas, selection would be effective in the later generations for number of grains per spike and 1000-grain weight as they were controlled by over-dominance type of gene action in absence of epistasis.

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