

Genetic Studies for Yield and Yield Related Parameters in Bread Wheat

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Abstract: Information about gene action play key role in any breeding program to manipulate a genotype. The present study was conducted to evaluate six wheat genotypes in complete diallel cross and to analyze the gene action for the yield related traits. Highly significant differences were found among the genotypes for all the parameters under study. The graphical revelation of the traits indicated that the plant height, number of tillers per plant, awn length, days to heading and grain yield per plant is controlled by additive genes and partial dominance while the traits as days to maturity, 1000-grain weight were governed by over dominance type of gene action. The non allelic interaction was absent for all the traits. The distribution of dominant and recessive genes for yield parameters was also observed and noted that Lasani-2008 contains maximum dominant genes for yield. The traits controlled by additive genes and partial dominance should be selected in early segregating generation. While, the traits governed by over dominance type of gene action may cause problem for selection in early generations, so the delayed selection would be preferred for parents.

Key words: Gene action • Diallel crosses • Yield parameters • Bread Wheat • Hayman approach

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most important cereal of the world which belongs to poaceae family. It provides about 60 % of the calories and 50 % of the proteins to human race. The best quality wheat is produced in areas with cold winter as compare to warm spring or summer with moderate rainfall. It is a long day plant, shorter days stimulate tillering and delay flowering.

It plays a remarkable role in meeting the food requirements and economic stability of the country. The stupendous studies have been made for last 2-3 decades to increase the wheat production and to improve the dubious and tottering situation of food. Globally the demand of wheat is increasing at the rate of 2 % per year. To meet the demands in an appropriate way, we not only require sufficient resources as well as the new varieties with an attractive yield potential. The increase in yield and yield potential is always an ultimate goal for any breeding program.

Grain yield is basically a complex trait being the consequence of several genes and their interaction in a particular environment. The main effort of wheat breeder

is the detection of genes and to merge them in a particular genotype using most suitable combination. As the wheat is predominantly a self-pollinated crop and due to its autogamous nature it attains homozygosity at many loci [1]. So it is necessary to introduce different genes which are known to be yield contributor. The study of inheritance pattern and analysis of gene action is very important to make decision about selection of suitable parents.

The application of different models in F₁ generation may provide the information about the inheritance pattern and gene action [2]. The diallel cross is a technique developed by Hayman [3,4] provides information on genetic mechanism specially for quantitative traits involved in early generations and particularly suit to autogamous crops like wheat. The major objective of the present study was to obtain information on nature of gene action and magnitude of contribution to various characters like grain yield and its components in 6×6 diallel crosses. The information so drive would be effectively exploited to develop an appropriate breeding strategy for continued genetic improvement of this vital cereal crop, aimed at evolving new varieties with desirable yield potential.

MATERIALS AND METHODS

The research was conducted in the experimental area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad in 2010-2011. The randomized complete block design was laid out to perform the experiment in three replications for six varieties/lines of spring wheat viz., LU26S, Lasani-2008, 9381, 9407, Chakwal-50 and Chakwal-86. The genotypes were crossed in all possible combinations according to diallel fashion.

The 15 direct crosses, their 15 reciprocal F_1 's and 6 parents were sown in the field according to normal sowing time as on November 25, 2010, according to randomized complete block design with three replications. The sowing was done by using a dibbler at the rate of two seeds per hole and thinned after germination. Inter row and inter plant distances were kept 15 and 30 cm respectively. All other standard agronomic practices were adopted normally and uniformly for all treatments.

At maturity 10 guarded plants from each line in each replication were selected at random and. The data was recorded at proper stage on individual plant basis for the traits namely plant height, number of tillers per plant, awn length, peduncle length, days to heading, flag leaf area, days to maturity, 1000-grain weight and grain yield per plant.

The collected data was subjected to analysis of variance as suggested by Steel *et al.* [5] to evaluate the significance of genetic differences among the mean performance for the traits estimated in different wheat genotypes. Statistical significance was assumed at 5% and 1% levels of probability. The traits showed significant difference in genetic variances were subjected to the diallel analysis advocated by Hayman [3, 4] and Jinks [6] to evaluate the genotypes for genetic information.

RESULTS AND DISCUSSION

The analysis of variance showed the highly significant variation among genotypes for all the traits while replication was non-significant (Table 1).

Wr/Vr graph for plant height indicates the partial dominance type of gene action as regression line intercepted the co-variance (Wr) axis above the origin (Fig. 1). As the regression line does not deviate from unit slope it indicates the absence of epistasis. Similar results have been reported by Ullah *et al.* [1], Farooq *et al.* [7], Kashif *et al.* [8] and Khan *et al.* [9]. The genotype 9407 contains maximum dominant genes while the genotype Chakwal-86 has maximum recessive genes as their position is nearest and farthest from origin respectively.

The graphical presentation of genotypes provided the evidence that inheritance of number of tillers per plant was controlled by partial dominance along with additive type of gene action as the regression line intersected the Y-axis above origin as it has been established in various research activities; Ullah *et al.* [1], Farooq *et al.* [7], Mahpara [10], Khan *et al.* [9]. The non-allelic interactions was absent as the unit slope remained within the limits of parabola and just similar to the unit slope. Hence the line 9381 had maximum dominant genes for development of number of tillers while the line 9407 contained maximum recessive genes for this purpose.

The investigation through Wr/Vr graph shows the partial dominance type of gene action along with additive effects in the absence of epistasis is controlling the awn length as regression line intercept the Y-axis above origin and within the range of parabola. The distribution of array points reveals that the genotype Chakwal-86 contains maximum number of dominant gene while on the other hand Chakwal-50 carries maximum recessive genes to control this trait.

For days to heading in wheat Wr/Vr graph presents the partial dominance type of gene action among the genotypes under consideration for this trait. Similar type of results has been studied by Subhani and Chowdhary [11], Nazeer *et al.* [12], While Ahmad *et al.* [13], Siddique *et al.* [14] and Sultan *et al.* [15] observed the additive type of gene action for days to heading. The Wr/Vr graph also mentions the genotype with maximum recessive genes as Chakwal-50, while the genotype LU26S contains maximum dominant genes for this trait.

Table 1: Mean squares of yield traits from the analysis of variance in 6 x 6 diallel cross

Source of variation	DF	Plant height	No. of Tillers per Plant	Awn Length	Days to Heading	Days to Maturity	1000-Grain Weight	Grain Yield per Plant
Replication	2	8.27 ^{ns}	4.39 ^{ns}	0.39 ^{ns}	6.56 ^{ns}	3.40 ^{ns}	65.33 ^{ns}	2.13 ^{ns}
Genotype	35	137.82 ^{**}	18.59 ^{**}	3.19 ^{**}	28.59 ^{**}	56.12 ^{**}	257.58 ^{**}	91.15 ^{**}
Error	70	30.98	3.67	0.29	3.36	2.99	24.97	4.69

ns: non-significant, *: Significant **: Highly significant

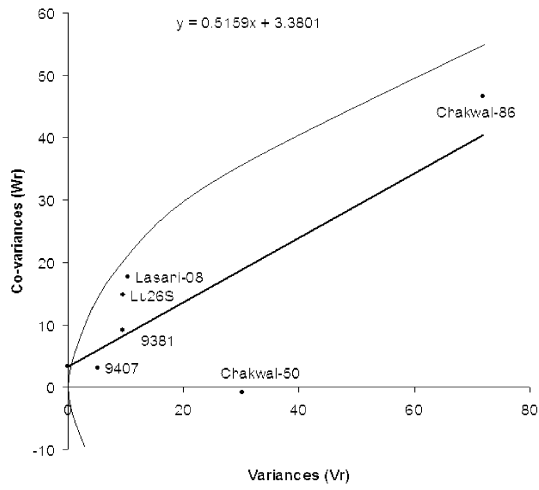


Fig. 1: W_r/V_r graph for plant beight

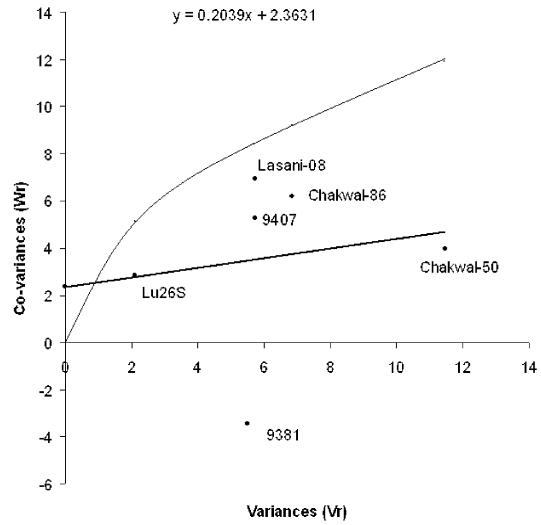


Fig. 4: W_r/V_r graph for day to heading

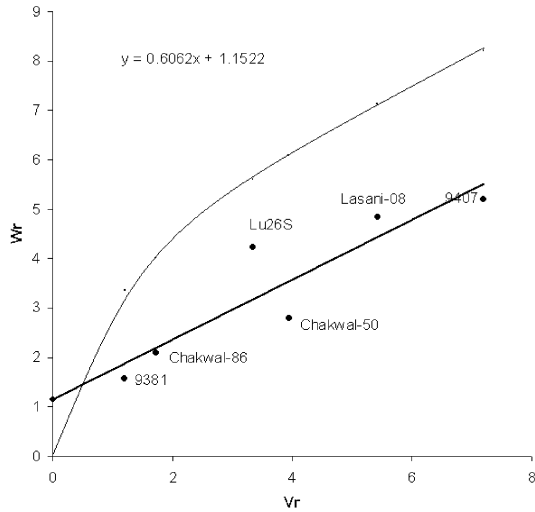


Fig. 2: W_r/V_r graph for No. Of Tillers

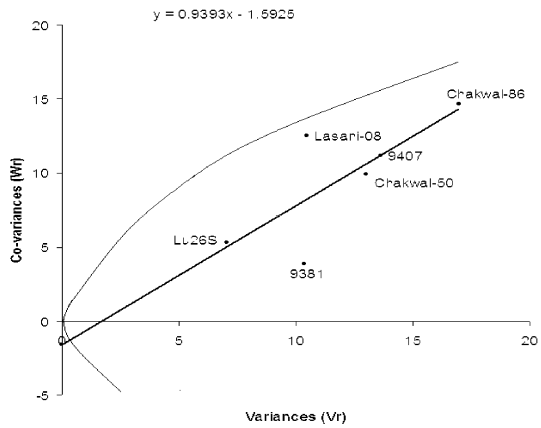


Fig. 5: W_r/V_r graph for day to maturity

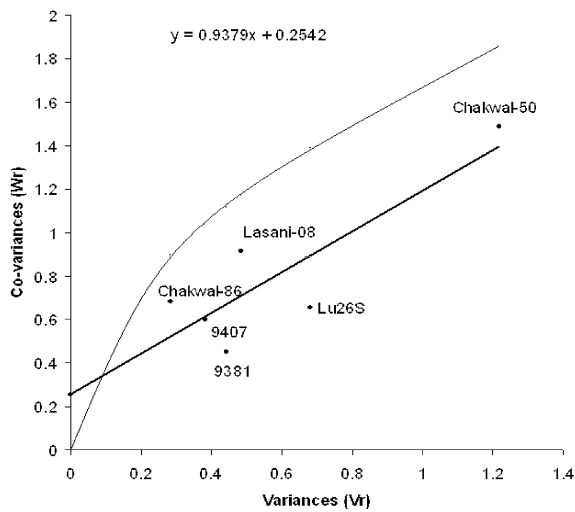


Fig. 3: W_r/V_r graph for awn length

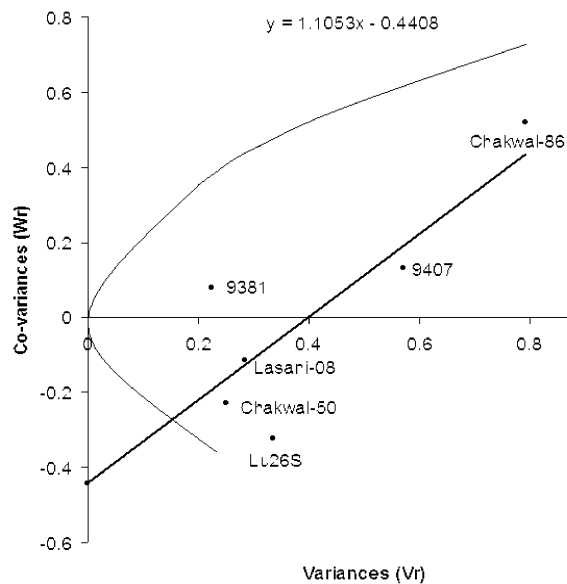


Fig. 6: W_r/V_r graph for 1000-grain weight

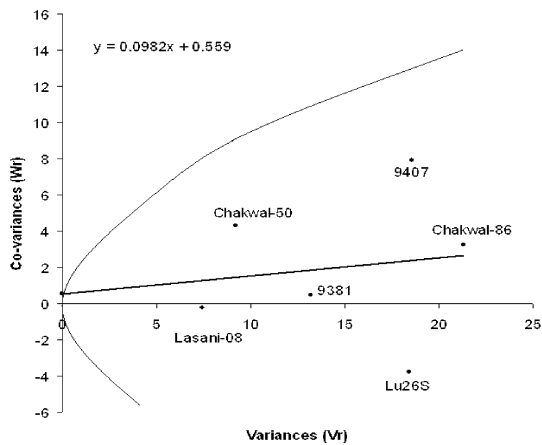


Fig. 7: Wr/Vr graph for grain yield per plant.

The Wr/Vr graph for days to maturity develops an understanding about gene as the regression line intersected the Vr-axis below origin which means over dominance type of gene action. This result is conflicting to the observation of Chandra *et al.* [16] and Sultan *et al.* [15] who observe the additive type of gene action for days to maturity while Rahman *et al.* [17], Siddique *et al.* [14], Nazeer *et al.* [13] found partial dominance along with additive gene action. It is also clear from graph that the genotype LU26S possesses maximum dominant and genotype Chakwal-86 maximum recessive genes for this character.

The graphical study of 1000-grain weight revealed the over dominance type of gene action. Similar results were reported by Sultan *et al.* [15] and Hussain [8]. But Mahpara [10], Gurmani *et al.* [18], Kashif *et al.* [8]. The genotypes LU26S and 9381 showed more dominant gene, on the other hand Chakwal-86 is presenting more recessive genes for this trait.

The partial dominance type of gene action is shown by the graphical presentation of genotypes for yield per plant. This result corroborates the research of Inamullah *et al.* [19], Dere and Yildirim [20] and Hussain [21]. The genotype Lasani-08 contains maximum dominant genes as it is nearest to the origin while the genotype 9407 possesses maximum recessive genes for this trait.

CONCLUSION

The analysis of data has shown the significant differences among genotypes. The genetic analysis with Wr/Vr graphs indicated that all the traits except days to maturity and 1000-grain weight are governing by additive

type of gene action with partial dominance which advocates the selection of genotypes in early stages for the crop improvement. The days to maturity and 1000-grain weight are governing by over dominance type of gene action, so delayed selection in segregation generations should be preferred for mentioned traits. The evaluation of six genotypes also reveals that the genotype Chakwal-86 act as best yield contributor, the line 9407 may use to develop a short stature variety while, LU26S can improve the earliness in next crosses.

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