

Genetic Analysis for Yield and Some Yield Traits in Spring Wheat

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Abstract A 5x5 diallel cross involving five wheat varieties/lines (Kohistan-97, Chakwal-86, 6529-11, 6544-6 and 7086-1) was conducted. Twenty hybrids along with five parents were planted in randomized complete block design with three replications in order to find out the gene action controlling some vital polygenic yield related attributes like plant height, spike length, peduncle length, number of tillers per plant and grain yield per plant. Highly significant differences among genotypes were observed for all traits. Plant height has only significant differences. The graphical presentation demonstrated that number of tillers per plant was ruled by partial dominance with additive type of gene action. While over-dominance was observed in plant height, spike length, peduncle length and grain yield per plant. It showed the potential for the availability of transgressive segregates in later filial generations. The prevalence of partial dominance type of gene action for number of tillers per plant showed that it can be gradually improved by selection.

Keywords *Triticum Aestivum*, Cultivars, Agronomic Characters, Pakistan

for the control of traits. Over-dominance type of gene action has been reported for plant height also observed by Kashif *et al.*, [16], Akram *et al.*, [1], Iqbal ., [13], Hafeez., [6], Haidari *et al.*, [9], Saleem *et al.*, [22], Nazeer., [20], Uma and Sharma., [25], Gurmani *et al.*, [5] and Nazan ., [19], Over-dominance type of gene action for spike length was reported by Bakash *et al.*, [3], Munis., [18] ,Farooq., [4], Nazeer., [20] and Inamullah *et al.*, [12] ,Over-dominance type of gene action for number of tillers per plant was observed by Khaliq and Chowdary ., [17], Akram *et al.*, [1], Hafeez., [6], Ullah *et al.* ., [24], Bakhsh., [3], Farooq., [4], Nazeer., [20], Inamullah *et al.*, [11], Inamullah *et al.*, [12] and Gurmani *et al.*, [5] and for grain yield was observed by Khaliq and Chowdary., [17], Bakash *et al.*, [3], Kashif *et al.*, [16], Munis ., [18], Akram *et al.*, [1], Saleem *et al.*, [22], Gurmani *et al.*, [5], Iqbal ., [13], Farooq., [4], Inamullah *et al.*, [11], Hafeez., [6], Haidari *et al.*, [9], Omara *et al.*, [22], Inamullah *et al.*, [12] and Nazan., [19]. Others studies reported partial dominance with additive type of gene action for peduncle length that was also observed by Munis., [18] , Ullah *et al.*, [24], Uma and Sharma., [25], Hafeez., [6] and Farooq., [4]. The present study was conducted to draw information about genetic mechanism controlling some important characters which could help devise future breeding strategy to evolve high yielding wheat genotypes.

1. Introduction

Wheat (*Triticum aestivum* L.) is the world's most widely adapted crop, supplying one third of the world population with more than half of their calories and nearly half of their protein. Pakistan's economy primarily depends on agriculture sector where wheat plays a pivotal role. This crop has always been a focus of research for genetic improvement but there has been a little improvement in genetics potential for yield improvement since green revolution. Yield is one of the most complex and economically important characters. So the information on genetic control of yield and yield components is more helpful for future breeding programme. The gene action can be studied through the diallel crossing technique developed by earlier scientists Hayman., [7], [8] and Jinks., [13], [14]. This breeding methodology is still considered as an important tool to work out the genetic basis

2. Materials and Methods

This study was conducted during the year 2010. The material comprised five varieties/lines of spring wheat viz. Kohistan-97, Chakwal-86, 6529-11, 6544-6 and 7086-1. This material was planted in the field on 18th November, 2009 in a twin row of 5 meter length. The crosses were attempted in a diallel fashion including reciprocals. The hybrid seeds including reciprocals and parents were sown in RCBD with three replications. All the entries (20 crosses and 5 parent lines) were randomly assigned to 25 plots of each replication. Each plot consisted of single row of 5 meter length. The plant-to-plant and row-to-row distance was 15 and 30 cm, respectively. Two seeds per hole were sown and after germination these were thinned to single seedling per site to

ensure good plant stand. At the time of maturity, ten guarded plants from each line were taken at random and data were recorded on plant height, number of tillers per plant, peduncle length, spike length and grain yield per plant.

The data were subjected to analysis of variance and gene action was worked out for the characters showing significant differences among the genotypes

3. Results and Discussion

Analysis of variance Steel *et al.*, [23] showed highly significant differences among genotypes for all the traits except plant height for which only significant differences were noted (Table 1).

Plant Height

Plant height is an important trait of wheat. Wheat cultivars genetically vary in plant height from short stature to medium and tall. Tall cultivars are more vulnerable to lodging than medium or short stature cultivars. So in breeding, wheat plant height should also consider as an important trait. Phenotypic expression of any trait is the out-come of the genotype × environment interaction. The five parents

included in this study varied from medium to tall stature.

Analysis of variance indicated the significant differences among the genotype. It is evidenced from graphical analysis that plant height is controlled by over-dominance type of gene action as regression line intercepted the W_r -axis below the point of origin see Fig 1, Non-allelic interactions were absent as regression line did not deviate from the unit slope. From array mean variety Chakwal-86 was indicated the best general combiners having array mean value of 109.30 cm while genotype 6529-11 was poorest performer with an array mean value of 107.07 cm

Current results are in accordance with the findings of Kashif *et al.*, [16], Akram *et al.*, [1], Iqbal ., [13], Hafeez., [6], Haidari *et al.*, [9], Saleem *et al.*, [22], Nazeer., [20], Uma and Sharma., [25], Gurmani *et al.*, [5] and Nazan ., [19].

Distribution of array points indicates that variety Chakwal-86 contained maximum dominant genes for plant height as being nearest to the origin while genotype 7086-1 was present farthest from the origin indicating maximum recessive genes for plant height.

Because over-dominance type of gene action controlled this trait so selection in early generations for plant height would be difficult.

Table 1. Analysis of variance mean square for polygenic traits.

SOV	Df	PH	PL	T/P	SL	GY/P
Replication	2	10.10 ^{n.s}	11.48*	1.53 ^{n.s}	0.78 ^{n.s}	29.29 ^{n.s}
Genotypes	24	32.02*	5.63**	1.32*	1.37**	28.60**
Error	48	17.48	2.47	0.59	0.54	9.77

n.s = Non-significant, *Significant, **Highly significant.

PH = Plant height, PL= Peduncle length, T/P = Number of tillers per plant, SL = Spike length, GY/P = Grain yield

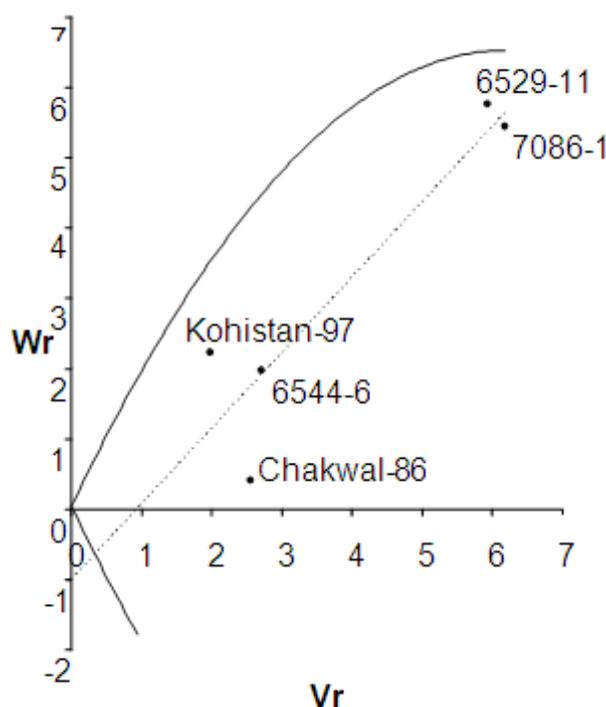


Figure 1. W_r/V_r graph for plant height

Spike Length

Spike length is an important yield related trait of wheat. It directly contributes to the yield. More spike length produces more spikelets per spike that ultimately produce more grains per spike thus leading to yield increase. So in wheat breeding importance should be given to this trait and spikes with more spike length should be selected.

Analysis of variance for spike length revealed highly significant differences among genotypes under study. From array mean, genotype 6529-11 was indicated the best general combiners having array means value of 13.79 cm while genotype 6544-6 was poorest performer with array mean value of 13.04 cm.

Graphical presentation indicated the presence of over-dominance type of gene action for this trait as regression line intercepted W_r -axis below the origin, see Fig. 2. Epistasis is absent as regression line followed the unit slope.

Similar results have also been reported by Bakash *et al.*, [3], Munis., [18], Farooq., [4], Nazeer., [20] and Inamullah *et al.*, [12].

So it can be concluded from present study that selection in early segregating generations will not be possible.

Peduncle Length

Peduncle length is also an important trait in wheat. It plays an important role in plant yield during heading stage. It varies from genotype to genotype. Analysis of variance of the data showed highly significant differences among genotypes for this trait. Pursual of array means revealed that genotype 6529-11 was good general combiner having an array mean value of 18.47 cm while variety Chakwal-86 showed poor performance having an array mean value of 17.17 cm.

Over-dominance type of gene action is observed from graphical analysis as regression line intercepted the W_r -axis below the point of origin, see Fig. 3. Due to over-dominance type of gene action, selection for this trait in early generations is difficult. Epistasis is not present because regression line did not deviate from unit slope.

These results are in accordance with Munis., [18] Ullah *et al.*, [24], Uma and Sharma., [25], Hafeez., [6] and Farooq., [4]. It is clear from distribution of array point that genotype 6544-6 contained maximum dominant genes for this trait being nearest to the point of origin while variety Chakwal-86 had maximum recessive genes being farthest from the origin.

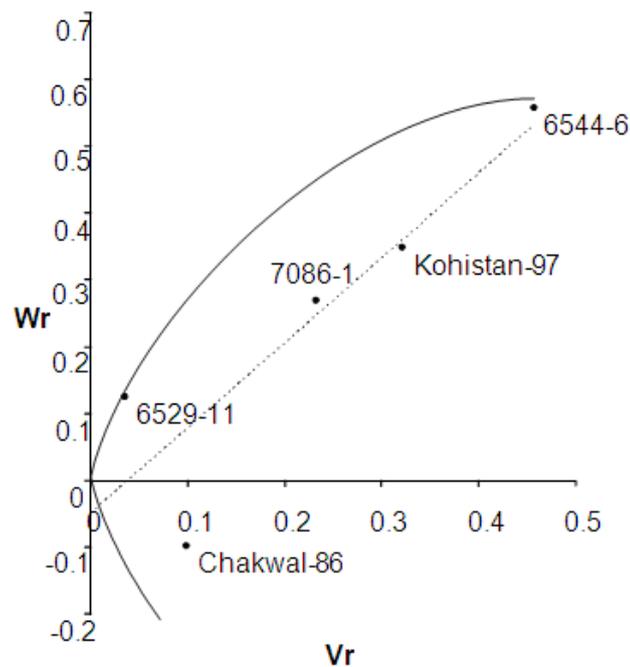


Figure 2. W_r/V_r Graph for Spike Length

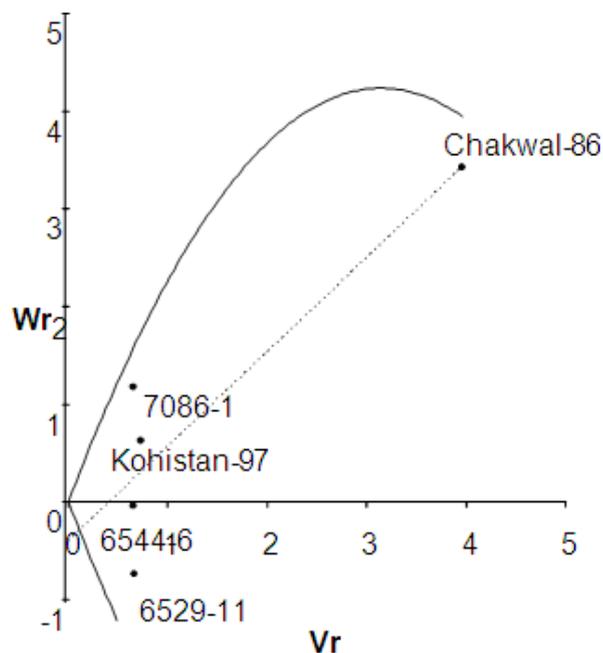


Figure 3. W_r/V_r Graph for Peduncle Length

Number of Tillers per Plant

Number of tillers per plant is a vital yield related trait. Greater number of tillers per plant ensure higher grain yield.

Analysis of variance showed highly significant differences among all genotypes. Graphical analysis for tillers per plant revealed additive types of gene action with partial dominance as W_r -axis is touched above the point of origin by the regression. As regression line follows the unit slope so epistasis is not present. It suggests early generation selection for this trait. From array mean table it is revealed that genotype 6544-6 was good general combiners having an array mean value of 11.78 cm while variety 7086-1 had poorest performance with an array mean value of 11.03 cm.

These results are also confirmed by Khaliq and Chowdary., [17], Akram *et al.*, [1], Inamullah *et al.*, [11], Hafeez., [6], Ullah *et al.*, [24], Bakhsh., [3], Farooq., [4], Nazeer., [20], Inamullah *et al.*, [12] and Gurmani *et al.*, [5]. Number of tillers per plant is a vital yield related trait. Greater number of tillers per plant ensure higher grain yield. Analysis of variance showed highly significant differences among all genotypes. Graphical analysis for tillers per plant revealed additive types of gene action with partial dominance as W_r -axis is touched above the point of origin by

the regression line, see Fig 4. As regression line follows the unit slope so epistasis is not present. It suggests early generation selection for this trait. From array mean table it is revealed that genotype 6544-6 was good general combiners having an array mean value of 11.78 cm while variety 7086-1 had poorest performance with an array mean value of 11.03 cm.

Grain Yield per Plant

Ultimate goal of any wheat breeding is to get maximum yield. So it is most important trait. The plant express its potential the most when it has all its needs met in right proportions and at right time.

Analysis of variance showed highly significant differences among all parental and hybrid genotypes. It was indicated that variety Kohistan-97 performed as best general combiner having highest array mean of 25.07g while genotype 7086-1 was the poorest performer having array mean of 21.88g.

Graphical analysis indicated that regression line intercepted the W_r -axis below the point of origin, thus revealing over-dominance type of gene action, see Fig 5. Non-allelic differences are absent as regression line did not deviate from the unit slope.

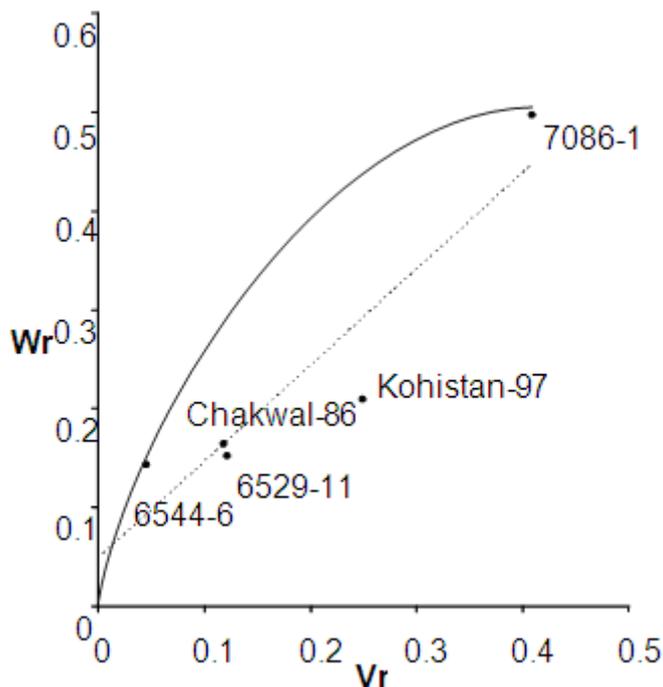


Figure 4. W_r/V_r graph for No. of tillers/P

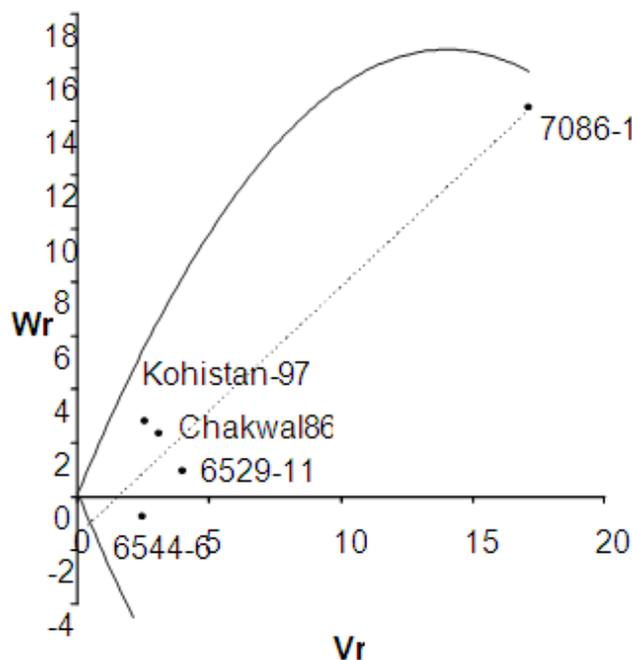


Figure 5. W_r/V_r Graph for Grain Yield Per Plant

These results are similar to the findings of Khaliq and Chowdary., [17], Bakash *et al.*, [3], Kashif *et al.*, [16], Munis ., [18], Akram *et al.*, [1], Saleem *et al.*, [22], Gurmani *et al.*, [5], Iqbal ., [13], Farooq., [4], Inamullah *et al.*, [11], Hafeez., [6], Haidari *et al.*, [9], Omara *et al.*, [22], Inamullah *et al.*, [12] and Nazan., [19]. Distribution of array points along the regression line showed that genotype 6544-6 had maximum dominant genes for grain yield per plant being nearest to the point of origin while genotype 7086-1 had minimum dominant genes as its distance from the point of

origin is maximum

4. Conclusions

The present study revealed the presence of over-dominance type of gene action for plant height, peduncle length, spike length and grain yield per plant whereas, additive type of gene action with partial dominance was found for number of tillers per plant. Transgressive

segregates can be found for plant height, spike length, number of tillers per plant in later segregating generations. However, desirable peduncle length can be fixed by gradual selection in segregating populations.

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