GENETIC ANALYSIS FOR YIELD AND SOME YIELD TRAITS IN BREAD WHEAT (*T. AESTIVUM* L.)

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ABSTRACT

A study was conducted in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan during the year 2008 involving five wheat varieties/lines (Uqab-2000, Chenab-2000, Seher-2006, 9189 and 9244). Crosses were attempted in complete diallel fashion including reciprocals to find out the gene action of some vital polygenic yield related attributes like plant height, spike length, peduncle length, number of tillers per plant, flag leaf area and grain yield per plant. Highly significant differences among genotypes were observed for all traits except number of tillers per plant which showed significant differences only. Genetic analysis revealed that peduncle length was controlled by partial dominance with additive type of gene action. The characters like plant height, flag leaf area, spike length, number of tillers per plant and grain yield per plant were controlled by over-dominance type of gene action. It showed the potential for the availability of transgressive segregates in later filial generations. The prevalence of partial dominance type of gene action for peduncle length showed that it can be gradually improved by selection.

KEYWORDS: *Triticum aestivum*; cultivars; crossbreeding; agronomic characters; Pakistan.

INTRODUCTION

Wheat (*Triticum aestivum* L.) being the most valuable staple food, is considered as king of cereals. Wheat occupies the maximum cultivated area on global basis (4) i.e 22.5 billion hectares followed by rice (16.14 b.ha) and maize (15.95 b.ha). Pakistan’s economy primarily depends on agriculture sector where wheat plays a pivotal role. This crop has always been a focus of research scientists for genetic improvement. Yield is one of the most complex and economically important character. 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.

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developed by earlier scientists (12, 15). This breeding methodology is still considered as an important tool to work out the genetic basis for the control of traits. Over-dominance type of gene has been reported for plant height (8, 11, 13, 16, 21, 24) and flag leaf area (6, 10, 23). Over-dominance for number of tillers per plant (14, 17, 18, 19, 22) and spike length (7, 9) has also been reported. Some studies (5, 20) report partial dominance with additive type of gene action for peduncle length.

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.

**MATERIALS AND METHODS**

This study was conducted in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the year 2008. The material comprised five varieties/lines of spring wheat viz. Uqab-2000, Seher-2006, Chenab-2000, 9189 and 9244. This material was planted in the field on 15th November, 2008 in a twin row of 4 meter length. The crosses were attempted in a diallel fashion including reciprocals. The hybrid seeds including reciprocals and parents were sown in the field on November 20, 2008, using RCBD with three replications. All the entries (20 crosses and 5 parent lines) were randomly assigned to 20 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, flag leaf area, spike length and grain yield per plant.

The data were subjected to analysis of variance (25) and gene action was worked out for the characters showing significant differences among the genotypes (12, 15).

**RESULTS AND DISCUSSION**

Analysis of variance showed highly significant differences among genotypes for all the traits except number of tillers per plant for which only significant differences were noted (Table 1).
Table 1. Analysis of variance mean square for polygenic traits.

<table>
<thead>
<tr>
<th>SOV</th>
<th>d.f</th>
<th>Plant height</th>
<th>Peduncle length</th>
<th>Flag leaf area</th>
<th>No. of tillers/plant</th>
<th>Spike length</th>
<th>Grain yield/plant</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replication</td>
<td>2</td>
<td>82.29**</td>
<td>6.03**</td>
<td>10.87**</td>
<td>0.27**</td>
<td>3.67**</td>
<td>15.48**</td>
</tr>
<tr>
<td>Genotypes</td>
<td>24</td>
<td>73.06**</td>
<td>14.64**</td>
<td>26.35**</td>
<td>1.50*</td>
<td>2.19**</td>
<td>36.58**</td>
</tr>
<tr>
<td>Error</td>
<td>48</td>
<td>6.49</td>
<td>1.02</td>
<td>3.17</td>
<td>0.82</td>
<td>0.48</td>
<td>6.31</td>
</tr>
</tbody>
</table>

NS = Non-significant, *Significant, **Highly significant.

Plant height

Graphical analysis of the data on plant height revealed over-dominance type of gene action as the regression line intercepted Wr-axis below the point of origin (Fig.1). Regression line did not deviate significantly from unit slope showing that epistasis was absent, thus the data was fit for genetic analysis. Similar results were obtained earlier (8, 11, 13, 16, 21, 22, 24). The results further indicated that line 9189, by virtue of its closest position to the origin, contained maximum dominant genes followed by Seher-2006, while genotype 9244 possessed maximum recessive genes for plant height being farthest from the origin. The presence of over-dominance type of gene action showed that transgressive segregates should be searched out in later filial generations.

Peduncle length

The Wr/Vr graph (Fig. 2) indicated additive effects with partial dominance for peduncle length as regression line cuts Wr-axis above the origin. Absence of epistasis was indicated as regression line did not deviate significantly from the unit slope. Partial dominance with additive type of gene action for peduncle length was also found by earlier scientists (5, 6, 19, 20). Distribution of array points depicted that the variety Seher-2006 contained maximum dominant genes while 9244 being farthest from the origin had maximum recessive genes for peduncle length. Therefore, it can be concluded that selection in early generation for this attribute would be worthwhile.

Flag leaf area (cm²)

Over-dominance type of gene action was observed for flag leaf area as regression line intercepted Wr-axis below the origin (Fig.3). Similar results have been reported for flag leaf area in the past (2, 6, 10, 23). Array points distribution of the regression line pointed out that Seher-2006 owing to its closeness to origin, possessed maximum dominant genes while Uqab-2000
Fig. 1 Wr/Vr graph of plant height.

Fig. 2 Wr/Vr graph of peduncle length.

Fig. 3 Wr/Vr graph of flag leaf area.

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being away from origin had maximum number of recessive genes. Due to over-dominance, the character seems difficult to fix in early generation and progress in selection will be low.

**Number of tillers per plant**

Graphical analysis (Fig.4) revealed that regression line intercepted Wr-axis below the point of origin indicating over-dominance expression for number of tillers per plant. As the regression line deviated from unit slope, non-allelic interaction was found to be present. Array points distribution of the regression line shows that Uqab-2000 owing to its closeness to origin, possessed maximum dominant genes while line-9244 being away from origin had maximum number of recessive genes. Many workers have reported similar results for number of tillers per plant (6, 11, 14, 17, 18, 19, 22).

**Spike length**

Regression analysis indicated the presence of over-dominance type of gene action for this trait as regression line intercepted Wr-axis below the origin (Fig. 5). Similar findings about spike length were observed by other scientists (7, 9, 14). The distribution of genotypic array points on regression line revealed that Uqab-2000 had maximum dominant genes being closest to origin. Seher-2006 being farthest from the origin had maximum recessive genes. So it can be concluded that selection in early segregating generations will not be fruitful for spike length.

**Grain yield per plant**

The differences among genotypes for grain yield per plant were highly significant. This trait was controlled by over-dominance type of gene action as shown by the graphical analysis where regression line intercepted the Wr-axis below the origin (Fig.6). These conclusions suggest that selection will not be effective in early segregating generations due to presence of over-dominance type of gene action as has been previously reported (1). The graphical distribution of array points showed that line 9244 had maximum dominant genes due to its closeness to point of origin and maximum recessive genes were observed in Chenab-2002 being farthest from the origin. Over-dominance type of gene action for grain yield per plant was also observed by previous scientists (3, 7, 8, 9, 11, 14, 17, 18, 21, 24).
Fig. 4 Wr/Vr graph of number of tillers per plant.

Fig. 5 Wr/Vr graph of spike length.

Fig. 6 Wr/Vr graph of grain yield per plant.
CONCLUSION

The present study revealed the presence of over-dominance type of gene action for plant height, spike length, number of tillers per plant, flag leaf area and grain yield per plant whereas, additive type of gene action with partial dominance was found for peduncle length. Transgressive segregates can be found for plant height, flag leaf area, spike length, number of tillers per plant and grain yield per plant in later segregating generations. However, desirable peduncle length can be fixed by gradual selection in segregating populations.

REFERENCES