



Full Length Article

Gene Action Analysis of Yield and Yield Related Traits in Spring Wheat (*Triticum aestivum*)

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ABSTRACT

Present study was carried out to determine the mode of gene action in a 6 x 6 diallel cross involving six wheat varieties namely Sehar 06, Pb 96, GA 2002 Barani 83, Kohistan 97 and Chakwal 86. Analysis of variance showed highly significant differences among genotypes for all the traits studied. Data was collected for different morphological traits associated with yield. Additive type of gene action with partial dominance was observed for plant height, number of tillers per plant, spike length, number of spikelets per spike and grain yield per plant, while over-dominance was observed for peduncle length. Non-allelic interaction was absent for all the traits studied. © 2010 Friends Science Publishers

Key Words: Gene action; Diallel; Morphological traits; Wheat

INTRODUCTION

Human beings practically attain all food directly from plants. Poaceae family is no doubt most diverse and important family of plant kingdom. 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. It is cheapest source of energy and supplies 72% of calories and protein in the average diet and related products (Heyne, 1987).

Demand of wheat is also increasing with increasing population. Thus efficient management of the available resources including breeder's efforts to breed varieties of wheat with high production even in water stress conditions is required. Wheat is predominantly self pollinated crop and because of autogamous reproductive behavior, wheat population after hybridization rapidly attains state of homozygosity. There is a dire need to develop genotypes having better yield potential per unit area. This could be achieved by exploring maximum genetic potential from available germplasm of wheat. The varying nature of drought and the complexity of the genetic control of plant responses determine the difficulties in developing high yielding cultivars under water-limited environments (Sadiq *et al.*, 1994).

Yield has prime importance in any breeding program. Ultimate goal of breeder is to increase yield. But it is a much complicated traits. Habib and Khan (2003), Mahmood *et al.* (2003) and Riaz and Chowdhry (2003) describe additive type of gene action with partial dominance controlling this trait. On the other hand Inamullah *et al.* (2005), Dere and Yildirim (2006) and Hassan *et al.* (2008)

showed that over dominance type of gene action controls this parameter.

Main objective of the study was to investigate the mode of gene action operative for different yield related traits in wheat. Gene action and inheritance studies by diallel technique developed by Hayman (1954 a, b) and Jinks (1955) provide valuable information regarding nature and magnitude of the gene action involved in the inheritance of characters.

MATERIALS AND METHODS

The experiment was conducted in experimental field of department of Plant Breeding and Genetics, University of Agriculture Faisalabad during 2008-2009. Six varieties of wheat (*Triticum aestivum* L.) i.e., Sehar-06, Pb-96, GA-2002 Barani-83, Kohistan-97 and Chakwal-86 were crossed in a full diallel fashion. The experimental field was thoroughly prepared. F1 seeds along with their parents were space planted in the field using randomized complete block design with three replications. Inter-row and inter-plant spacings were kept 30 and 15 cm, respectively. Seeds were sown in holes made with the help of dibble at the rate of 2 seeds per hole, which were later thinned to single healthy seedling per hole after germination. The data was recorded for plant height, number of tillers per plant, days to maturity, spike length, peduncle length, number of spikelets per spike and grain yield per plant. An ordinary analysis of variance (Steel & Torrie, 1984) was performed to determine whether the genotypic differences were significant for the characters under consideration or not. Traits showing significant genotypic differences were further analyzed using diallel

analysis technique described by Hayman (1954 a, b) and Jinks (1955).

RESULTS AND DISCUSSION

Analyses of variance showed significant differences among the genotypes for all the traits studied (Table I). Wr/Vr showed that plant height is controlled by additive type of gene action as regression line cut the Wr axis above the point of origin (Fig. 1). As regression line followed unit slope so epistasis was absent as has been established in various studies (Arshad & Chowdhry, 2003; Kashif *et al.*, 2003; Rahman *et al.*, 2003; Riaz & Chowdhry, 2003; Gorjanovic & Balalic, 2005; Inamullah *et al.*, 2005). Distribution of array points indicated that genotype Pb-96 has maximum dominant genes for plant height as it is nearest to the origin, while Kohistan-97 is present farthest from the origin indicating its maximum recessive genes for plant height.

Number of tillers per plant revealed additive types of gene action with partial dominance as Wr-axis is touched above the point of origin by the regression line (Fig. 2). As regression line follows the unit slope so epistasis was absent as reported by Subhani and Chowdhry (2000), Chowdhry *et al.* (2001), Kashif and Khaliq (2003), Riaz and Chowdhry (2003) and Hafeez (2006). Distribution of array points along the regression line showed that Sehar-06 had maximum dominant genes for tillering, while Pb-96 has minimum dominant genes for this trait.

Additive type of gene action with partial dominance was observed for days to maturity as regression line touched the Wr-axis above the point of origin (Fig. 3). Rahman *et al.* (2003) and Inamullah *et al.* (2005) also reported similar findings. Distribution of arrays points along the regression line showed that parent Sehar-06 had maximum dominant genes for this trait as it is present nearest to the origin, while parent Chakwal-86 and Barani-83 contained minimum dominant genes for this trait as these are present most away from the point of origin. Epistatic effects are absent as regression line follows the unit slope (Fig. 3).

Graphic presentation of data (Fig. 4) indicated the additive type of gene action with partial dominance for spike length as point of intercept on Wr-axis was positive. The epistasis is absent as regression line followed the unit slope. Similar results have also been reported by Chowdhry *et al.* (2002), Kashif and Khaliq (2003), Gorjanovic and Balalic (2005) and Gurmani *et al.* (2007). Distribution of array point along the regression line illustrate that Chakwal-

86 contains maximum dominant genes for spike length as it is situated more near to point of origin. Sehar-06 lies most apart from the origin so it contains most recessive genes for spike length.

Over dominance type of gene action is evident for peduncle length from graphical representation (Fig. 5) as regression line intercepts the Wr-axis below the point of origin. Epistasis is not present, because regression line did not deviate significantly from unit slope, which is in accordance with the findings of Umma and Sharma (1997) and Hafeez (2006). It is clear from distribution of array points that genotype Barani-83 has maximum dominant genes for this trait, while genotype Sehar-06 has maximum recessive genes.

Graphical demonstration (Fig. 6) of data for spikelets per spike indicates the additive type of gene action with partial dominance as intercept point on Wr-axis is positive. Regression line followed the unit slope, which reveals the absence of epistasis. Mahmood and Chowdhry (2000), Sener *et al.* (2000), Chowdhry *et al.* (2002), Bakhsh *et al.* (2004), Saeed *et al.* (2005), Gurmani *et al.* (2007) also reported same kind of results. Distribution of array points along the regression line showed that among parents Sehar-06 and Pb-96 contain maximum dominant genes as their distance from origin in minimum. Chakwal-86 lies at maximum difference from the origin so it contains minimum dominant genes for this trait.

Additive type of gene action with partial dominance is evident for grain yield per plant from graphical representation (Fig. 7) as intercept point on Wr-axis is positive. Non allelic differences are absent as regression line did not deviate significantly from the unit slope. These results are similar to the conclusions of Habib and Khan (2003), Mahmood *et al.* (2003) and Riaz and Chowdhry (2003). Distribution of array points along the regression line showed that Kohistan-97 has maximum dominant genes for grain yield per plant as it is nearest to the point of origin. While Barani-83 has minimum dominant genes as its distance from the point of origin is maximum.

CONCLUSION

The data indicated that all the traits showed significant genotypic differences. Genetic analysis showed that all the traits studied are controlled by additive type of gene action except peduncle length. Presence of additive gene action in traits like plant height, number of tillers per plant, days to maturity, spike length spikelets per spike and grain yield per plant suggested early selection for improvement.

Table I: Mean squares from the analysis of variance 6 x 6 diallel cross

Source of variation	df	Plant height	Number of tillers per plant	Days to maturity	Spike length	Peduncle length	Spikelets per spike	Grain yield per plant
Replication	2	45.64	1.80	8.56	1.41*	18.74	0.3811	38.84*
Genotype	35	107.90**	6.14**	17.36**	0.72**	24.74**	3.9393**	22.18**
Error	70	13.86	2.67	3.52	0.37	6.13	0.5464	9.81

* = Significant, ** = Highly significant

Fig. 1: Vr/Wr graph for plant height

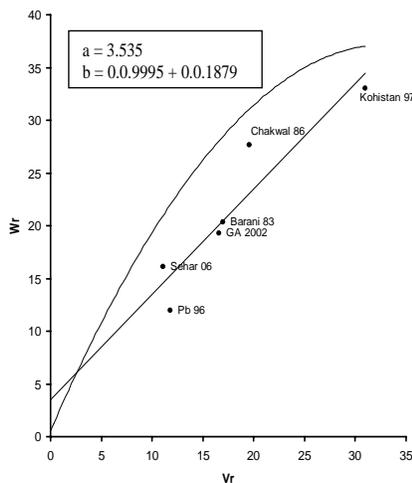


Fig. 2: Vr/Wr graph for number tillers per plant

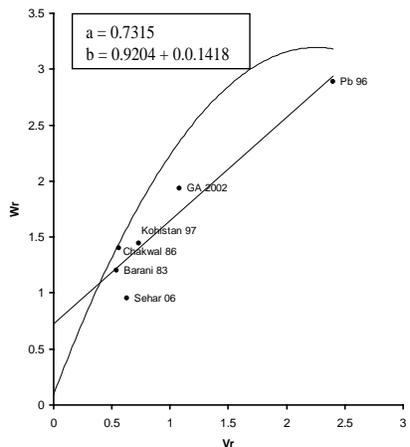


Fig. 3: Vr/Wr graph for days to maturity

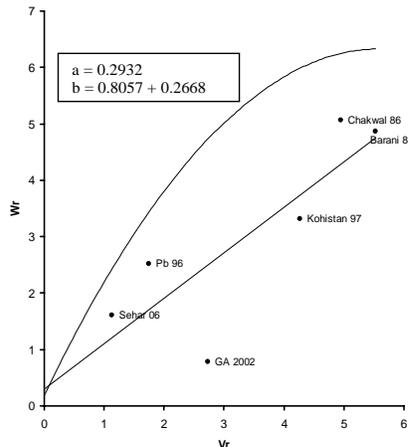


Fig. 4: Vr/Wr graph for spike length

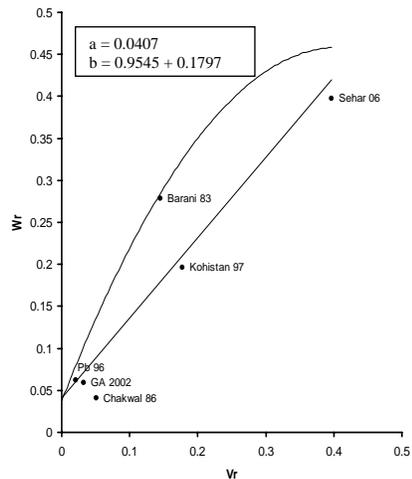


Fig. 5: Vr/Wr graph for peduncle length

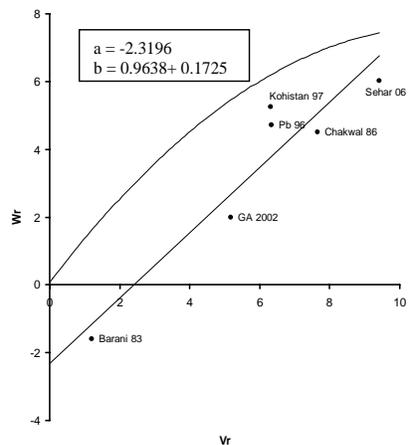


Fig. 6: Vr/Wr graph for spikelets per spike

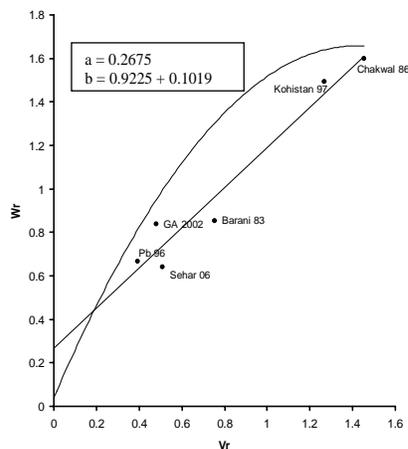
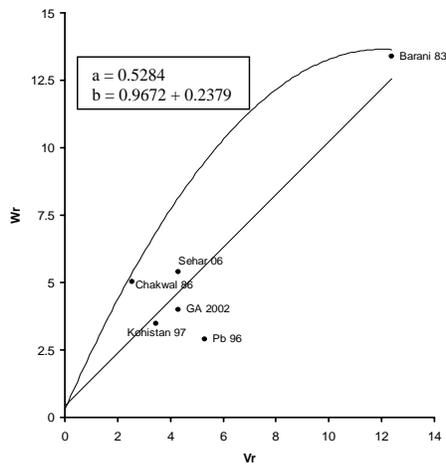


Fig. 7: Vr/Wr graph for grain yield per plant



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