



Designate the gene dose for yield related indices in spring wheat

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Abstract

Yield is economically most important and most complex polygenic trait. To meet the today's challenges new genotypes of wheat are being evaluated by continued genetic recombination. Present study was carried out using 5×5 full diallel to designate the gene action responded to yield related indices like plant height, tillers per plant, spikelets per spike, grains per spike, 1000-grain weight, and grain weight per spike. Significant genotypic differences were observed for all the observed traits. Regression line indicate that , Punjab-11 has maximum dominant genes for plant height, and grain weight per spike while Millat-11 has maximum dominant genes only for number of tillers per plant and maximum recessive genes for grains per spike and grain weight per spike. 9466 has maximum number of dominant genes for spikelets per spike, grains per spike and 1000-grain weight. Higher number of recessive genes for plant height, spikelets per spike, spike length and 1000-grain weight was the characteristics of parent 9469. While 9459-1 got maximum dominant genes only for 1000-grain weight. The W_r/V_r graphical analysis indicated that the partial dominance along with additive genetic effects was observed for all studied traits except spikelets per spike, so for desirable improvement and selection in early segregating generations may be fruitful. While existence of over dominance for spikelets per spike make difficulties for selection. Non-allelic interactions were absent for all the traits under study.

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Introduction

One third population of the world gets more than half of their calories and proteins only from wheat. It is very good source of energy and gives 72% of calories and proteins by consuming the wheat products like breads, cakes, biscuits, chapattis, nans, pasteries (Heyne, 1987). In Pakistan, wheat is grown on almost 70% of farmland and it shares 37% of total cultureable land. About 60% of Pakistani people earn their livelihood from this sector and some of its related fields. Majority of farmers (about 80%) grow wheat and it is single largest source of earning for farmers. The role of wheat crop in food safety is very important. Because wheat is basic food grain in many countries, it is necessary to produce a rich harvest every year to meet the demand of our population for food. Many agricultural scientists have done a lot of research on wheat in order to improve the grain yield per unit area. Regardless there remained an open field for wheat breeders to continue their efforts for improvement in genetic architecture of wheat plant to meet the feeding requirements of population. Proper choice of parents needs utmost care because they should not only manifest the mandatory traits but should also capable of producing hybrids with superior performance when crossed with other parents. Information so derived would be efficiently exploited to design suitable strategies for sustained genetic improvement of this essential food crop. Objective of this study to using our limited resources to gain maximum genetic gain, there is a need to identify the superior genotypes and they should be improved to get the maximum yield per unit area. So understand the genetic mechanism of yield related indices is very important and then selection of better parents for a successful wheat breeding program to develop high yielding wheat genotypes.

Materials and methods

The present research work on gene action studies for various plant morphological traits which were linked with yield related indices was carried out in the experimental area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad.

Plant material

The experimental material comprised of five wheat varieties/lines of spring wheat (*Triticum aestivum* L.) viz., Punjab-11, Millat-11, 9466, 9469 and 9459-1 and their F₁ crosses. These varieties/lines were planted in the field during Rabi season 2012-13 and crossed in a diallel fashion including reciprocals as follows: The hybrid seeds including reciprocals and parents were sown in the field on November 15, 2013, using the randomized complete block design with three replications. Each replication had 20 crosses and 5 parent lines, each line of 3 meter length. The plant to plant and row to row distance was 15 and 30 cm respectively. The sowing was done using a dibbler. Three seeds per hole were sown which were thinned to single seedling per site after germination to ensure good plant stand.

Observation of yield related indices

At the time of maturity, ten guarded plants from each line were taken at random and data were recorded for yield related indices like plant height, tillers per plant, spikelet per spike, grain per spike 1000 grain weight and grain weight per spike.

Statistical analysis

Data which were recorded was subjected to analysis of variance (ANOVA) technique proposed by Steel *et al.* (1997) to evaluate the differences among the genotypes. Investigation of gene action responsible for inheritance yield related traits in spring wheat using diallel analysis technique developed by Hayman (1954 a b) and Jinks (1955).

Result and discussions

Analysis of variance (Table 1) showed significant differences among all the genotypes and their hybrids for all studied characters.

Plant height (cm)

The graphical representation (Fig. 1) of plant height indicated the presence of partial dominance with additive type of gene action because the regression line cuts the covariance (Wr) line above the origin (positive intercept). The assumption of absence of

non-allelic interaction seemed to satisfy as the regression line did not deviate from unit slope. These results are in agreement with the findings of Farooq *et al.* (2010), Ojaghi and Akhundova (2010) and Irshad *et al.* (2012). The distribution of array points along the regression line indicated that the genotype Punjab-11 contain most of dominant genes as being

nearest to the point of origin whereas genotype 9469 carry maximum recessive genes as being far away from the origin. Due to the additive type of gene action with partial dominance was operative for this trait suggesting that the desired plant height can be fixed by gradual selection in early generations.

Table 1. Analysis of variance (ANOVA) for yield related indices in spring wheat.

Mean Squares	d.f	Plant Height	Tillers per Plant	Spikelet per Spike	Grain per Spike	1000 weight	Grain /spike	weight
Rep	2	20.29	3.35	1.19	51.41	71.57	0.13	
Genotypes	24	107.13*	3.61*	2.16*	82.79*	199.63*	0.24*	
Error	48	11.22	1.50	0.63	25.64	27.25	0.04	
Total	74							

Level of significance = 0.5%,

Significance=*

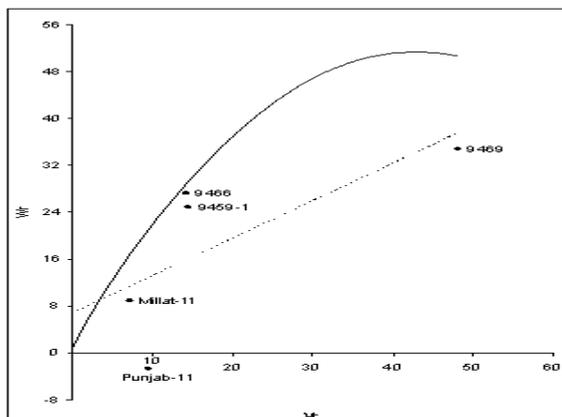


Fig. 1. W_r/V_r graph for Plant height.

Tillers per plant

The graphical analysis (Fig. 2) revealed that the intercept of regression line on the covariance axis being over the origin, showing a clear cut case of partial dominance type of gene action with additive effects. The assumption of the absence of non-allelic interaction appears to be satisfied as the regression line following the unit slope. Current results are in accordance with the observation of Inamullah *et al.* (2006), Gurmani *et al.* (2007), Rabbani *et al.* (2009), Nazeer *et al.* (2010) and Ajmal *et al.* (2011). The pattern of distribution of varieties/lines along the regression line indicates that Millat-11 has maximum number of dominant genes while 9466 has maximum number of recessive genes for this character. So it can be concluded from the present study that improvement of this trait is possible through selection

in early generations because this is the only variance which respond to selection.

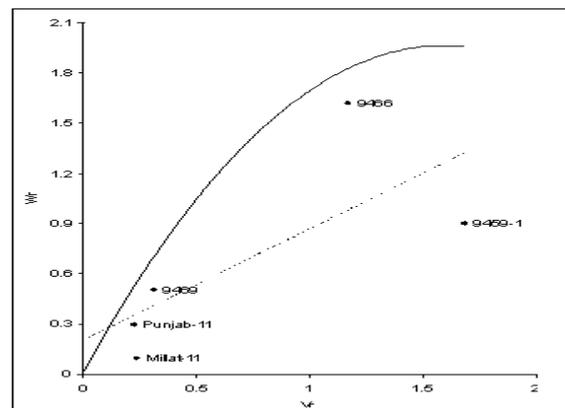


Fig. 2. W_r/V_r graph for tillers per plant.

Spikelet per spike

By viewing the W_r/V_r graphical description (Fig. 3) for the number of spikelets per spike it is clear that the intercept of the regression line on the covariance axis is on the negative side i.e. below the point of origin indicates the involvement of over-dominance type of gene action. As the regression coefficient did not differ significantly from unity, hence the non-allelic interactions were absent. The information so derived, seemed to be compatible with the findings of Habib and Khan (2003), Ojaghi *et al.* (2010), Rabbani *et al.* (2011) and Irshad *et al.* (2012). The scattered array varietal points along the regression line showed that maximum dominant genes were observed in 9466 as nearer to the point of origin and

9469 receives maximum recessive genes being distant from the origin. Prevalence of over dominance type of gene action indicated that fruitful selection in early generations is not possible and it must delay till later generations.

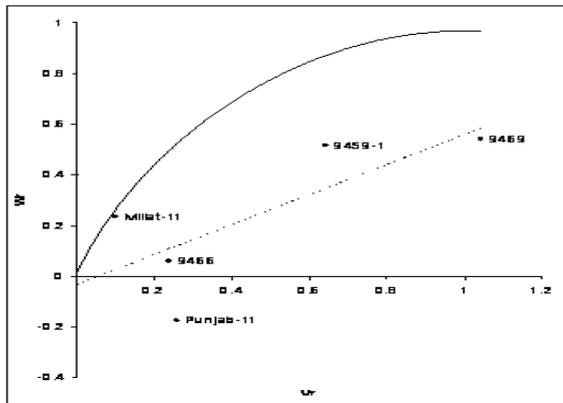


Fig. 3. W_r/V_r graph for Spikelet per spike.

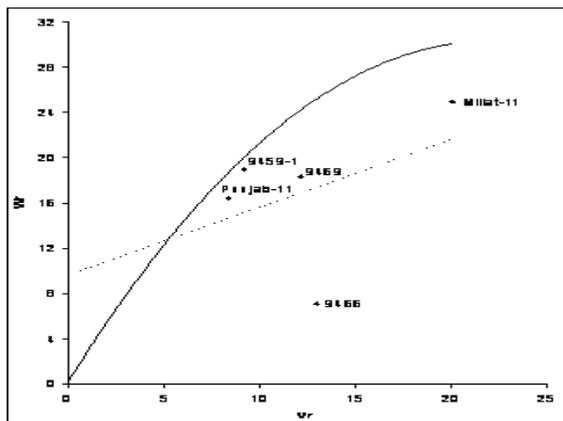


Fig. 4. W_r/V_r graph for grain weight/spike.

Grains per spike

The W_r/V_r graphical analysis (Fig. 4) indicated that the intercept of the regression line on the covariance axis being above the origin (positive intercept), shows a clear cut case of partial dominance with additive type of gene action. The regression line did not deviate from unit slope, which reveals absence of epistasis. These results are in agreement with the findings of Kamboj *et al.* (2000), Riaz and Chowdhry (2003), Chowdhry *et al.* (2007) and Kumar and Sharma (2008). The distribution of array varietal points on the regression line indicated that 9466 carry most dominant genes for number of grains per spike while Millat-11 carries most recessive genes for the trait under study. Due to the presence of partial dominance selection in early generations would be

fruitful for the improvement of trait under consideration.

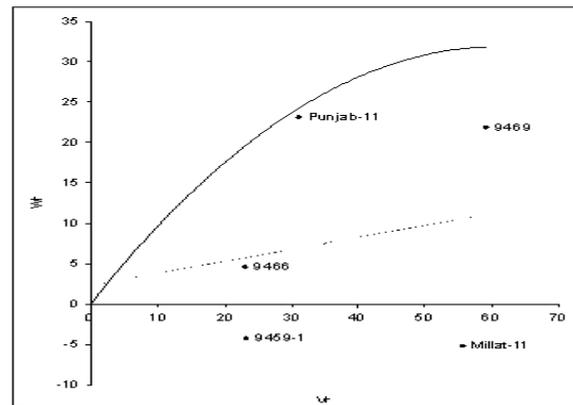


Fig. 5. W_r/V_r graph for 1000-grain weight.

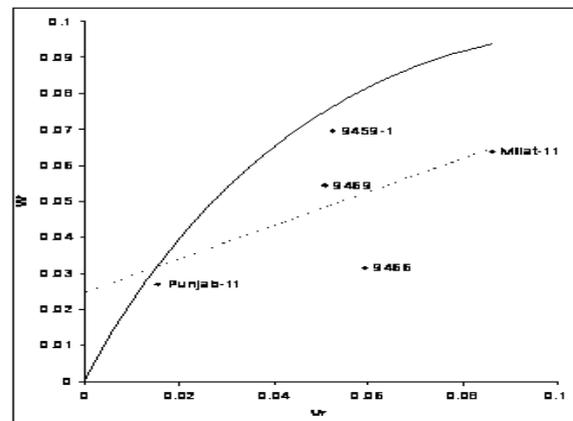


Fig. 6. W_r/V_r graph for grain weight/spike.

1000-grain weight (g)

One of the significant yield related parameter is 1000-grain weight. By the study of graphical representation (Fig. 5) it was evident that the inheritance of 1000-grain weight in the selected genotypes was governed by partial dominance with additive type of gene action as the regression line intersected the covariance axis above the point of origin (positive intercept). Epistasis was absent for above said trait as the regression line did not deviate from unit slope. The current observation are in conformity with the findings of Sheikh *et al.* (2000): Nazeer *et al.* (2010). The scattered array points along the regression line indicate the diversity among parents. The parents 9466 and 9459-1 carry maximum dominant genes as both are in the vicinity of origin while genotype 9469 contains most of recessive genes being far away from the origin. As 1000-grain weight is inherited by partial dominance so selection must be done in early

generations to fix this character.

Grain weight per spike (g)

By examining the graphical representation (Fig. 6) it is apparent that the regression line cuts the covariance axis above the point of origin (positive intercept) that indicated the involvement of partial dominance with additive type of gene action. The assumption of the absence of non allelic interaction seems to be satisfied as the regression coefficient does not differ significantly from unity. The present research work has harmony with the findings of Khaliq *et al.* (1991); Lonc and Zalewski (1996) while opposing results of over dominant type of gene action were observed by Khan and Habib (2003). The scattered array varietal points along the regression line indicate the diversity among parents. The parent Punjab-11 contains an excess of dominant genes being in the vicinity of origin whereas the parent Millat-11 carries most of the recessive genes as it is distant from the origin. As the trait is governed by partial dominance so selection in early generations would be fruitful.

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