RESEARCH PAPER

Estimate of gene action for yield and polygenic yield related traits in bread wheat (*T. aestivum* L.) by using Hayman approach

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Abstract

Information about gene action involved in the inheritance of a character pays a key importance in any breeding program. Present study was carried out to determine the mode of gene action of polygenic yield related attribute in 5 x 5 diallel cross involving five wheat varieties namely Uqab 2000, Chenab 2002, Seher 2006, Millat-11 and Galaxy-13. The characters under studied were spike length, number of spikelets per spike, number of grains per spike, 100-grain weight, grain weight per spike and grain yield per plant. Highly significant differences were observed among genotypes for all the traits under consideration. It revealed that numbers of spikelet per spike and grain weight per spike were ruled by partial dominance with additive type of gene action therefore selection for improvement of these traits can be performed in early segregating populations. Over-dominance type of gene action was observed for number of grains per spike, 100-grain weight and grain yield per plant while non-allelic interaction was found to be present for spike length. Therefore selections for superior genotypes for these traits should be delayed until later filial generations.

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Introduction

Wheat is the most widely grown crop in the world and provides 20% of the daily protein and food calories for 4.5 billion people. It is the second most important food crop in the developing world after rice. With a prediction world population of 9 billion in 2050, the demand for wheat is expected to increase by 60%. To meet this demand, annual wheat yield increases must rise from the current level of below 1% to at least 1.6%.So breeders should try to develop new wheat varieties which are suitable to grow in different agro-climatic zones.

Hybridization between carefully selected parents has become dominant in the breeding of self-pollinated species. The object of hybridization is to combine desirable genes found in two different genotypes and to produce pure-breeding progeny superior in many respects to the parental types. The genetic improvement of crop plants through selection and breeding depends, mainly on the existence of variation within the species and the knowledge about the genetic basis of the variation and the nature of gene action involved in the manifestation of characters of interest. A large number of research workers have practiced different biometrical techniques but diallel analysis developed by Hayman (1954) and Jinks (1954) has most commonly been used to collect information about the type of gene action involved in the expression of various morphogenetic characters and to forecast the performance of the progenies in the segregating generations. Over-dominance type of gene action for spike length was observed by Chowdhry *et al.* (2001), Bakhsh *et al.* (2003) and Inamullah *et al.* (2006).Chowdhry*et al.* (2002), Kashif and Khaliq (2003), Kashif *et al.*(2003), Bakhsh *et al.* (2004), Heidhari *et al.* (2006) and Gurmani *et al.*(2007) found partial dominance with additive type of gene action for number of spikelets per spike. While Khaliq and Chowdhry (2001), Chowdhry *et al.* (2002) and Bakhsh *et al.* (2003) observed over-dominance type of gene action for number of grains per spike. Over-dominance controlling 100-grain weight was reported by Hussain *et al.* (2004).Khan and Habib (2003)

reported partial dominance for grain weight per spike. Whileover-dominance type of gene action for grain yield per plant was determined by Chowdhry *et al.* (2001), Khaliq and Chowdhry (2001), Chowdhry *et al.* (2002), Arshad and Chowdhry (2003), Kashif *et al.* (2003), Saleem *et al.* (2005), Heidari *et al.* (2006), Inamullah *et al.* (2006), Gurmani *et al.* (2007) and Nazan (2008). It has been reported by manyauthorsthatpresence of non-allelic interaction makes the data unfit for computing components of genetic variation (Rehman *et al.* 2009, Rehman *et al.* 2010, Farooq *et al.* 2011 and Ajmal *et al.* 2011).

The predent study was carried out to Under stand the genetic nature of some polygenictraits in diallel cross. Information obtained from this experiment will be help full to develop appropriatestrategy for geneticimprovement in grain yield and some important yield traits of wheat.

Materials and methods

Experimental conditions

The present research on gene action for various plant morphological traits was carried out in the experimental area of Department of wheat research institute, AARI, Faisalabad. The experimental material comprised of five wheat varieties/lines of spring wheat (*Triticumaestivum*L.) *viz.*, Uqab 2000, Seher 2006, Chenab 2002, Millat-11 and Galaxy-13. These varieties/lines were planted in the field during Rabi season 2015-16 and crossed in a diallel fashion including reciprocals. The hybrid seeds including reciprocals and parents were sown in the field on November 20, 2015.Using the randomized complete block design with three replications. Each replication had 20 crosses and 5 parent lines, each line of 5 meter length. The plant-to-plant and row-to-row distance was 15 and 30 cm, respectively. The sowing was done by using a dibble. Two seeds per hole were sown which were thinned to single seedling per site after germination to ensure good plant stand. At the time of maturity 10 guarded plants from each line were taken at random.

Measurement of morpological parameters

 Data were recorded for the following parameters like spike length, number of spikelets per spike, number of grains per spike, 100-grain weight, grain weight per spike and grain yield per plant.

Statistical analysis

The data collected for all the characters were subjected to analysis of variance technique (Steel *et al.,* 1997) to calculate the differences among the genotypes by using software MSTATC.

The analysis of gene action for the diallel crossing system was done for the characters showing significant differences using the diallel technique as developed by Hayman (1954) and Jinks (1954). All the crosses were arranged in to arrays. Two statistics, the variance (Vr) of the family means with in an array

and the covariance of these means with the non-recurrent parental value were calculated from each diallel table. The information on gene action was obtained by plotting the co-variance (Wr) of each array against the variance (Vr). The slope and position of the regression fit to the array points with in a limiting parabola (Wr²= V$_{P.*}$Vr) and indicated the degree of dominance and presence or absence of gene interaction.

Results and discussion

All the characters under study were subjected to analysis of variance and it depicted significance difference between all the genotypes (Table 1). The data were then subjected to genetic analysis to work out the gene action for all the characters which is discussedcharacter wise as below:

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

SOV	d.f	Spike length	No. of spikelets/ spike	No. of grains/ spike	100-grain weight	Grain weight/ Spike	Grain yield / plant
Replication	2	3.67**	1.60[N.S]	5.02[N.S]	2.34**	0.000457[N.S]	15.48[N.S]
Genotypes	24	2.19**	2.06*	12.19**	0.82**	0.0092**	36.58**
Error	48	0.48	0.59	2.02	0.23	0.000531	6.31

N.S = non-significant

** = highly significant

* = significant

Spike length

Genetic analysis revealed that regression line deviates significantly from unit slope indicating the presence of non-allelic interaction for this trait (Fig. 1).

As the data failed to fulfill the basic assumptions of diallel analysis therefore, further analysis was not conducted. Similar findings of spike length were observed by Chowdhry *et al.* (2001), Bakhsh *et al.* (2003) and Inamullah*et al.* (2006).Similarly Rehman *et al.,* 2001, Similarly Rehman *et al.,* 2010, Farooq *et al.* 2011 and Ajmal *et al.* 2011 also repoted that in case of presence of non-allelic interaction, the data becomes unfit for further analysis for computing component of variation.

Number of spikelets per spike

Genetic analysis indicated the presence of partial

dominance type of gene action for this trait as regression line intercepted Wr-axis above the origin. Regression line did not deviated significantly from unit slop indicating the absence of epistasis (Fig.2). Similar findings were concluded by Chowdhry *et al.* (2002), Kashif and Khaliq (2003), Kashif *et al.* (2003), Bakhsh *et al.* (2004), Heidhari *et al.* (2006) and Gurmani *et al.* (2007). While contradictory findings of over-dominance were observed by Mahmood and Chowdhry (2000) and Chowdhry *et al.* (2001).

These differences may be due to the use of different material and different environmental conditions. Jana (1975) and Rehman *et al.* (2010) have reported that gene action can change due to change in environmental conditions and use of different experimental material.
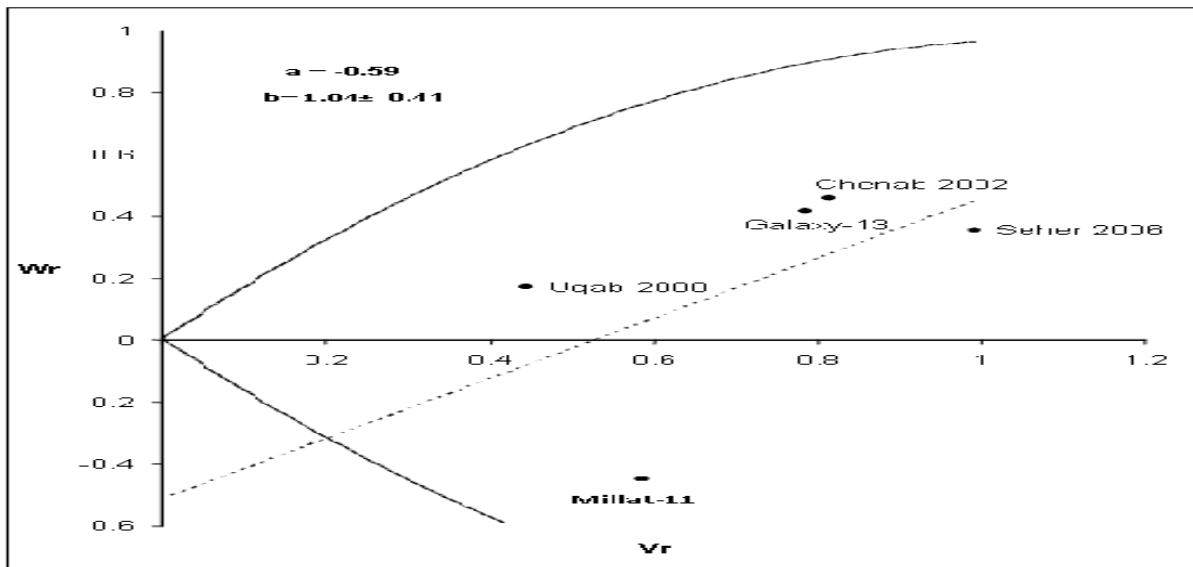
Fig. 1. Wr/Vr graph for spike length.

The distribution of genotypic array point revealedthat line Chenab 2002 having maximum dominant genes being closest to the origin followed by Millat-11.

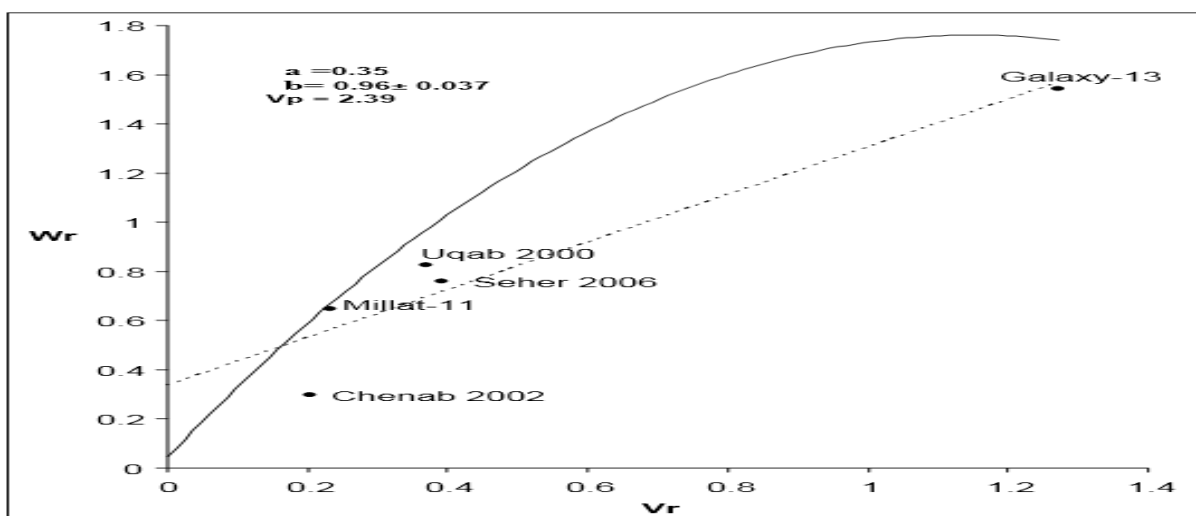Whereas, the galaxy-13 had maximum recessive alleles being the farthest from the origin.

Fig. 2. Wr/Vr graph for number of spikelets per spike.

Additive type of gene action with partial dominance suggested the possibility of better genetic gains by selection and even the selection can be done in early segregating populations and pedigree selection method can be usedsuccessfully.(Rehman *et al.,* 2010; Farooq *et al.,* 2011).

Number of grains per spike
The graphical representation of variance (Vr) and covariance (Wr) indicated over-dominance type of gene action for number of grains per spike as

regression line intercepted Wr-axis below the origin (Fig.3). As the regression line is of unit slope hence non allelic interaction was absent.

The variety Uqab being closer to the origin possess maximum dominant genes while the Galaxy-13 have maximum recessive genes. Khaliq and Chowdhry (2001), Chowdhry *et al.* (2002) and Bakhsh *et al.* (2003) observed similar results for number of grains per spike. Incomplete dominance was observed by Petrovic and Cermin 1994 while Partial dominance

was observed by Husa and Walton 1969. These differences may be due different material and environmental conditions. In the presence of over dominance type of gene action selection in early segregating populations will not be useful(Rehman *et al.*, 2009;Rehman *et al.*, 2010;Farooq *et al.*,2011; Ajmal *et al.*, 2011).

Genetic analysis for this character revealed over-dominance mode of inheritance as the regression line intercepted Wr-axis below the origin. Regression line followed unit slop showing the absence of non-allelic interaction (Fig.4). Maximum dominant genes were possessed by Chenab 2002 while maximum recessive genes were present in the Galaxy-13 as indicated by the positionof array points on the regression line.
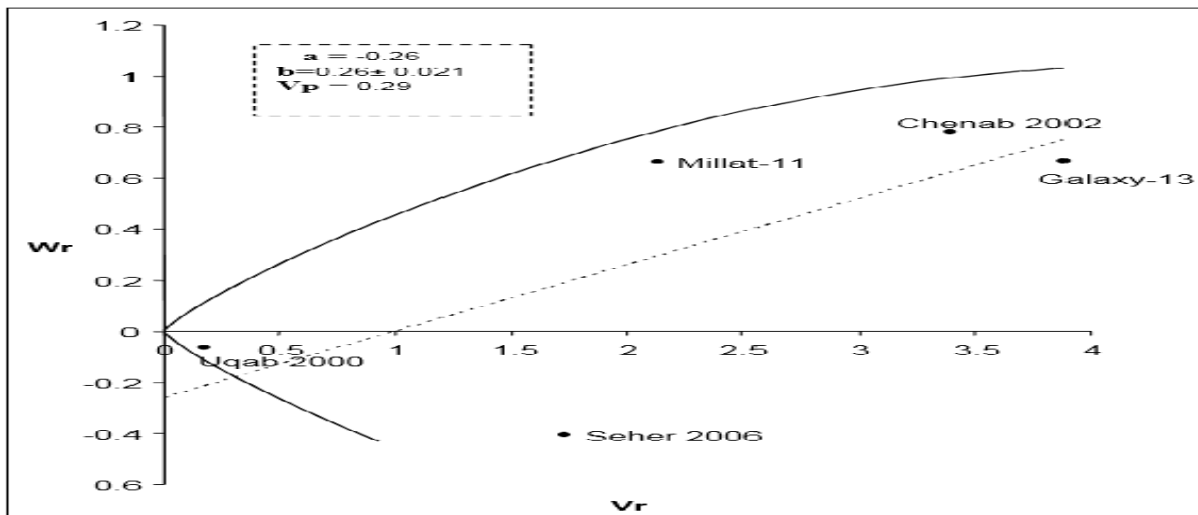
100-grain weight

Fig. 3. Wr/Vr graph for number of grains per spike.

In the view of over-dominance type of gene action, it can be suggested that selection in early segregating generations will not be fruitful.Similar findings have been reported by Hussain *et al.* (2004) and Singh *et al.* (1969) while Khaliq *et al.* (1991) reported partial

dominance type of gene action. According to Farooq *et al.*, 2011 and Ajmal *et al.*, 2011, the selection in late filial generation (F5-F6) will be effective for the traits showing over dominant type of gene action.
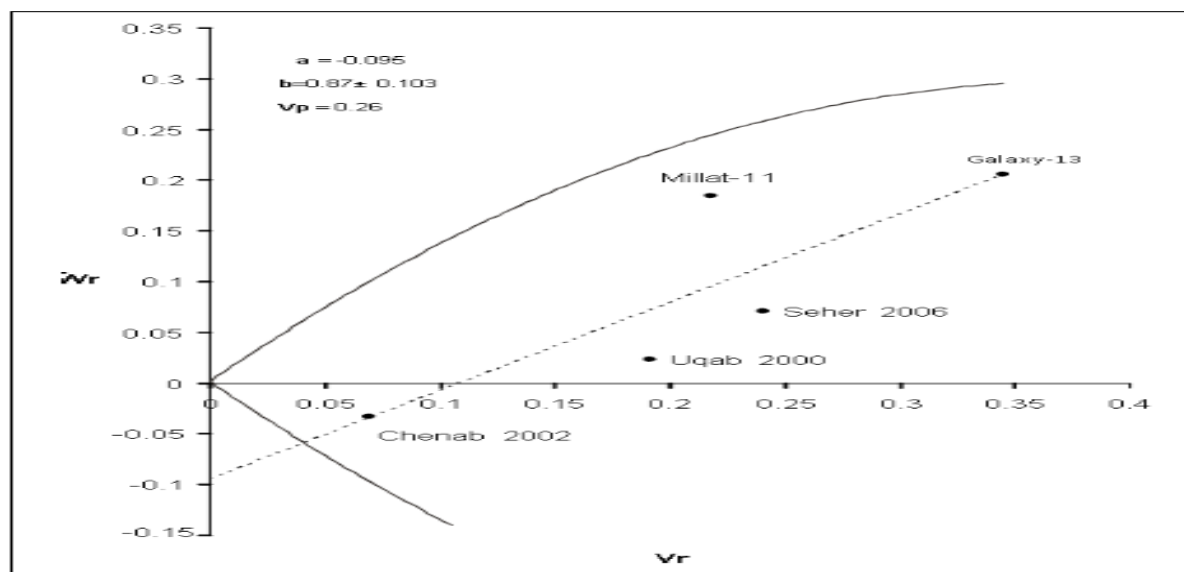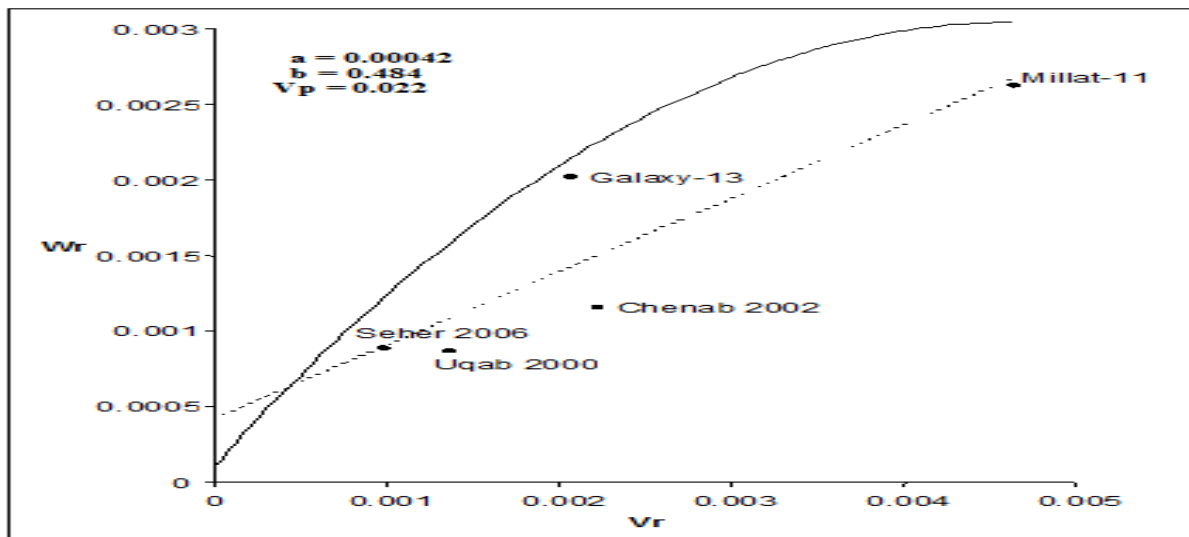

Fig. 4. Wr/Vr graph for 100-grain weight.

Grain weight per spike

The genetic analysis revealed that regression line intercepted Wr-axis above the origin to indicate the partial mode of inheritance for grain weight per spike. Regression line followed unit slop showing the absence of non-allelic interaction (Fig. 5). Seher-06 possessed maximum dominant genes due to the closest position of array points to the origin whereas the Millat-11 have maximum recessive genes being far from the origin.In the view of this it can be suggested that selection in early segregating generations will be fruitful. Results of present study are in agreement with earlier findings of Khan and Habib (2003). While additive type of gene action controlling grain weight per spike was reported by Goldringer*et al.* (1997).


Fig. 5. Wr/Vr graph for grain weight per spike.

It has been reported by previous workers (Rehman *et al.* 2009, Rehman *et al.* 2010, Farooq *et al.,* 2011 and Ajmal *et al.,* 2011) that selection for traits showing additive gene action will be fruitful I early generations (F2-F4) in case of characters with additive gene action. As grain weight in wheat depicted additive gene action head selectionfor this character can be done in early segregating population.

Use of sieves with different sized hole can be fruitful in separating bold grains from the bulked lot of early segregating population.
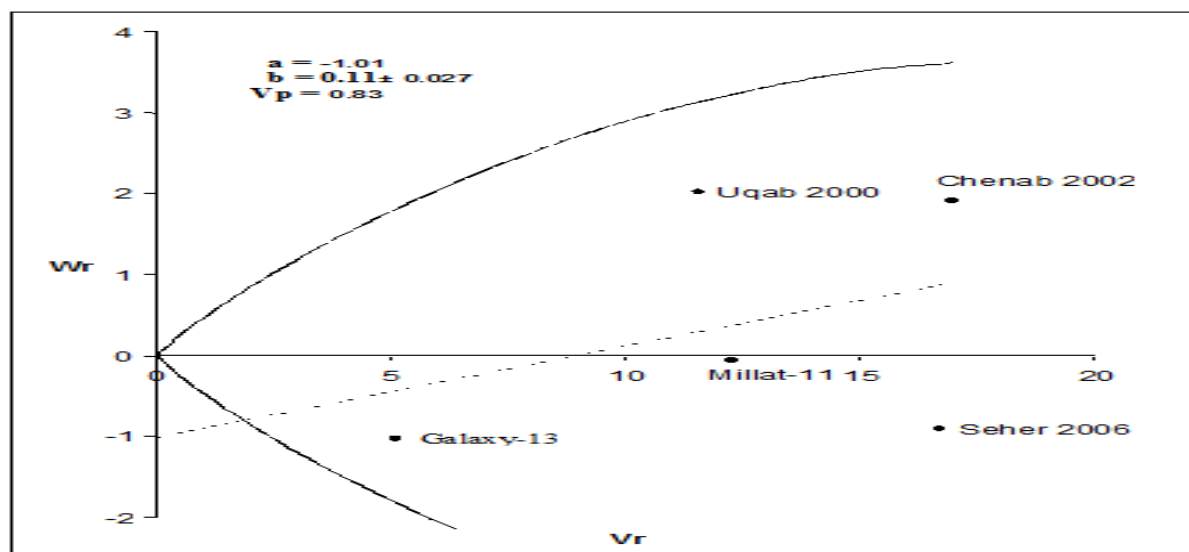
Fig. 6. Wr/Vr graph for grain yield per plant.

Grain yield per plant

Genetic analysis depicted that 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). This showed selection in early segregating generations will not be effective due to presence of over-dominance type of gene action as reported by Alam *et al.* (1991).

The graphical distribution of array points showed that line Galaxy-13 had maximum dominant genes due to its closeness to the point of origin and maximum recessive genes were observed in Chenab 2002 being farthest from the origin.Chowdhry *et al.* (2001), Khaliq and Chowdhry (2001), Chowdhry *et al.* (2002), Arshad and Chowdhry (2003), Bakhsh *et al.*(2003), Kashif *et al.* (2003), Saleem *et al.* (2005), Heidari *et al.* (2006), Inamullah *et al.* (2006), Gurmani *et al.* (2007) and Nazan (2008) showed over-dominanc type of gene action for grain yield per plant.

According to Rehman *et al.,* 2010 and Farooq *et al.,* 2011 selection in early segregating population will not be fruit full for the traits showing overdominance type of gene action. Hence the yield being a complex trait as the result of interaction of many physiological and morphological traits and being controlled by non-additive type of gene action will show much improvement if selection is practiced in later segregating populations (F5-F6).

Conclusion

The genetic analysis revealed partial dominance for number of spikelets per spike and grain weight per spike while over dominance was observed for number of grains per spike, 100 grain weight and grain yield per plant. Epistatsis (non-allelic interaction) was present for spike length only.

Hence, it is recommended that selection in early segregating population will give genetic advancement only for number of spikelets per spike and grain weight per spike. For other traits selection should be delayed until the later segregating population and the

material may be advanced by using bulk method.

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