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Genetic Architecture of Yield Related Traits in Hexaploid Wheat

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Abstract: A 5×5 diallel cross using five wheat varieties/lines namely Saher-2006, Imdad-2006, 6500, 9242 and 9780 was carried out to examine the genetics of yield and yield related traits. All the traits studied have shown high level of significance after analysis of variance. The graphic representation demonstrated that grain yield per plant, plant height, peduncle length and number of spikelets per spike were governed by partial dominance suggesting selection in early segregating generations for good improvement in these characters while presence of overdominance for the traits like spike length, number of tillers per plant, number of grains per spike, grain weight per spike and 1000-grain weight made selection difficult in early generation. All the traits studied have shown absence of epistasis except number of tillers per plant, number of grains per spike and 1000-grain weight. [HAFIZ GHULAM MUHU-DIN AHMED, SANA E MUSTAFA, ABDUS SALAM KHAN. Genetic Architecture

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Keywords: genetic architecture, diallel, gene action, epistasis

Introduction

Wheat being the leading food grain crop and staple diet for more than one third of world population is regarded as the King of Cereals. Basic aim of wheat breeders is to develop the wheat varieties which are good responsive to a range of environments, high vielding, physiological more efficient and genetically stable than the pre-existing varieties. So a precise understanding of genetic mechanisms underlying the control and expression of various characters in focus is therefore, of obvious importance, however, selection of suitable parents is also equally important. The magnitude and type of gene action in a particular population serves as criteria for selection of parents, which after hybridization are likely to produce the best recombinants for desirable traits. Hussain et al. (2004) observed that plant height was controlled by additive genes with partial dominance while over dominance predominated for tillers per plant, number of grains per spike, and grain yield per plant. Farooq (2005) reported that yield related traits was controlled by partial dominance with additive type of gene action. However, over dominance type of gene action controlled grain yield per plant.

Heidari *et al.* (2006) reported that grain number per spike and spikelets per spike were controlled by partialdominance, while over dominance was observed for grain yield per plant, plant height and 1000-grain weight. Gurmani *et al.* (2007) showed that additive type of gene action with partial-dominance controlled spike related traits while plant height, number of tillers and grain yield per plant were governed by over dominance. Farooq *et al.* (2010) showed over dominance for number of grains per spike, while partial dominance was observed in traits like plant height, tillers per plant, 100-grains weight and grain yield per plant.

The current study was planned to understand the genetic nature of some polygenic characters of hexaploid wheat in a 5×5 diallel cross. Nine important polygenic characters viz., plant height, peduncle length, spike length, number of tillers per plant, number of spikelets per spike, number of grains per spike, grain weight per spike, 1000-grain weight and grain yield per plant were brought under consideration to generate valuable information which would be useful to determine the gene action involved in their inheritance and to examine the performance and association of F₁ hybrids and parents. Information so derived might be effectively exploited to develop appropriate strategies for continued genetic improvement of this vital food crop.

Materials and Methods

The experiment was performed in the trial zone of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan during crop season 2015-16. Five varieties/genotypes viz., Sehar-2006, Imdad-2006, 6500, 9242 and 9780 were planted in the field during the first year of experiment and were crossed in all possible combinations using diallel mating design. Seeds of all crosses alongside their parents were planted in a randomized complete block design with three repeats during the second year of experiment. Inter plant and inter row distance was kept 15 and 30 cm, respectively. Two seeds were planted per hole with the help of dibble and after germination; these were thinned to single seedling per hole. After maturity, the data was recorded for the characters like plant height, peduncle length, tillers per plant, spike length, spikelets per spike, grain weight per spike, grains per spike, 1000-grain weight and grain yield per plant. The figures obtained were subjected to analysis of variance technique (Steel et al., 1997). Characters that were genotypically significant were subjected to diallel analysis technique as delineated by Hayman (1954a,b) and Jinks (1955) to evaluate the genetics of vield and vield related traits.

Results and Discussion

It is evident from the analysis of variance as indicated in table 1 that the difference among the genotypes for all the characters studied was highly significant. Graphical analysis revealed that partial dominance type of gene action controlled the traits like plant height (Fig 1), peduncle length (Fig 2), spikelets per spike (Fig 5), grain yield per plant (Fig 9) as regression line intercepted the Wr-axis above the point of origin. Nonallelic interactions were absent as regression line did not depart from the unit slope. Graphical presentation showed that over dominance controlled spike length (Fig 3), tillers per plant (Fig 4), grains per spike (Fig 6), grain weight per spike (Fig 7) and 1000-grain weight (Fig 8) as regression line intercepted Wr-axis below the point of origin. Epistasis was absent as the assessed regression line diverged considerably from the unity.

Plant height: Tall cultivars are more susceptible to lodging than medium or short stature cultivars. So in breeding program of wheat, plant height should also be considered as an important trait. From array means (Table 2), variety 9780 was indicated the best general combiner having array mean value of 108.95 cm while genotype Saher-2006 was poorest performer with an array mean value of 101.78 cm. Cross combination 9780×9780 proved to be the best specific combiner with an array value of 116.37 cm while cross combination Imdad-2006 × Saher-2006 and Saher- $2006 \times$ Imdad-2006 proved to be the poorest specific combiners with an array value of 97.73 cm. Distribution of array points indicates that genotype 9242 possessed maximum dominant genes for plant height as being nearest to the origin while genotype 9780 was away from the origin indicating maximum recessive genes for plant height. Results of gene action with partial dominance were similar to the findings of Farooq (2005) and Inamullah *et al.* (2006).

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 produces more grains per spike thus leading to yield increase. From array means table (Table 2), genotype 9242 was indicated the best general combiners having array means value of 14.96 cm while variety Imdad-2006 was poorest performer with array mean value of 13.96 cm. Cross combination 9242×9242 proved to be the best specific combiner with an array value of 15.64 cm while Imdad-2006 \times 9780 and 9780 \times Imdad-2006 were the poor specific combiners with an array value of 13.54 cm. Distribution of array points along the regression line (Fig 3) revealed that variety Imdad-2006 contained maximum dominant genes for spike length as it is situated more nearer to point of origin whereas genotype 9242 lied most apart from the origin so it contained most recessive genes for spike length. Similar results of partial dominance have also been reported by Farooq (2005) and Inamullah et al. (2006).

Number of tillers per plant: Tillers per plant is a vital vield trait. Greater number of tillers per plant ensure higher grain yield. From array mean table (Table 2), it is revealed that genotype 9242 was good general combiner having an array mean value of 12.88 cm while variety Saher-2006 had poorest performance with an array mean value of 11.05 cm. The best specific combiner was 9780×9780 with an array value of 15.13 cm while the poor specific combiners were Imdad-2006 \times 9780 and 9780 \times Imdad-2006 having an array value of 9.33 cm. Distribution of array points along the regression line (Fig 4) showed that variety Saher-2006 contained maximum dominant genes for this character being the nearest to the origin and genotype 9780 contained maximum recessive genes being away from the origin. The results of over dominance were also confirmed by Kashif et al. (2003) and Khan and Habib (2003).

Spikelets per spike: Spikelets per spike is also an important yield related trait because more spikelets per spike produce more grains per spike so this trait should be given due consideration while selecting genotypes for high yield. From array means (Table 2), genotype 6500 was the best general combiner having array mean of 24.82 cm, while variety Imdad-2006 was poorest performer with array mean of 22.76 cm. However, the best specific combiner was 9242×9242 with an array value of 26.2 cm while the poor specific combiners were $9242 \times$ Imdad-2006 and Imdad-2006 \times 9242 with an array points along the regression line (Fig. 5) showed that among parents, variety Saher-2006 contained maximum dominant genes as their difference from origin is

minimum. Genotype 9242 possessed minimum dominant genes as is present away from the origin. Gurmani *et al.* (2007) and Nazan (2008) observed additive type of gene action with partial-dominance.

Grains per spike: It was indicated from table 2 that genotype 6500 performed as best general combiner having highest array mean of 65.95 cm while genotype 9780 as poorest performer having array mean of 61.47 cm. Cross combinations Saher-2006 \times 6500 and 6500 \times Saher-2006 proved to be the best specific combiners with an array value of 73.2 cm while cross combination Imdad-2006 \times Imdad-2006 proved to be the poor specific combiner with an array value of 58.4 cm. Distribution of array points along the regression line (Fig. 6) showed that genotype 9780 had maximum dominant genes for grain yield per plant as it was closest to the point of origin. However, variety Sehar-2006 had minimum dominant genes as it was farthest from the point of origin. Chowdhry et al. (2002) and Farooq et al. (2010) also reported over dominance type of gene action.

Grain weight: Grain weight is the most important trait directly contributing in yield. From array mean table (Table 2), it was indicated that variety Saher-2006 performed as best general combiner having highest array mean of 2.78 g while genotype 6500 was the poorest performer having array mean of 2.67 g. Cross combination Saher-2006 × Saher-2006 was the good specific combiner having an array value of 3.13 g while cross combinations 9242×6500 and 6500×9242 were the poor specific combiners having an array value of 2.13 g. Distribution of array points along the regression line (Fig 7) revealed that variety Imdad-2006 contained maximum dominant genes for grain weight per spike being closest to the point of origin. However, genotype 9242 had minimum dominant genes as being farthest from the point of origin. The results of over dominace were similar to the findings of Nazeer (2005) and Heidari et al. (2006).

1000-grain weight: 1000-grain weight is a vital yield component and is more or less stable character of wheat cultivars. From array means table (Table 2), it was indicated that genotype 9780 performed as best general combiner having highest array mean of 42.92 g while genotype 6500 was the poorest performer having array mean of 40.49 g. The best specific combiners were the cross combinations $9780 \times \text{Saher-}2006$ and Saher-2006 \times 9780 with an array value of 45.65 g while the poorest specific combiners were the cross combinations Saher-2006 × Imdad-2006 and Imdad- $2006 \times$ Saher-2006 with an array value of 36.606 g. Distribution of array points along the regression line (Fig 8) showed that genotype 6500 contained maximum dominant genes for this trait being nearest to the origin while variety Saher-2006 had maximum recessive genes being away from the origin. These

results of over dominance type of gene action were also confirmed by findings of Singh *et al.* (1969) and Hussain *et al.* (2004).

Grain yield per plant: Ultimate goal of any wheat breeding is to get maximum vield. 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. From array mean table (Table 2), it was indicated that variety Imdad-2006 performed as best general combiner having highest array mean of 22.56 g while genotype 6500 was the poorest performer having array mean of 13.28 g. The best specific combiner was cross combination Imdad-2006 \times Imdad-2006 having highest array value of 31.603 g while poor specific cross combination was 6500×6500 having lowest array value of 8.54 g. Distribution of array points along the regression line (Fig 9) showed that genotype 6500 contained maximum dominant genes for grain yield per plant being closest to the point of origin. However, variety Imdad-2006 had minimum dominant genes as it had maximum distance from the point of origin. Khan and Habib (2003) and Ullah et al. (2010) also observed similar results of partial-dominance with additive type of gene action for grain yield per plant.

Conclusion

Hence, it is concluded that selection should be postponed at advanced generations for the improvement of traits like spike length, tillers per plant, grains per spike, grain weight per spike and 1000-grain weight. However, selection in initial generations would be fruitful for the improvement of traits like plant height, peduncle length, spikelets per spike and grain yield per plant. Epistasis was absent for all the characters studied except tillers per plant, grains per spike and 1000-grain weight. Partial dominance in the absence of non-allelic interaction for the traits like plant height, peduncle length, spikelets per spike and grain yield per plant proposed that selection in early segregating generations may lead to good improvement in these characters while presence of over-dominance made selection difficult in early generation for spike length, grain weight per spike. However, overdominance accompanied with non-allelic interaction made selection impossible in early generation for the traits like tillers per plant, grains per spike and 1000grain weight.

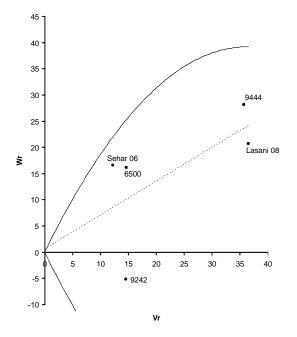
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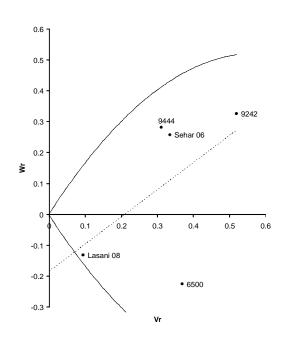
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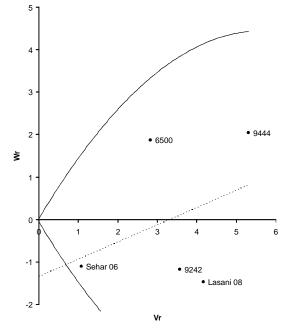
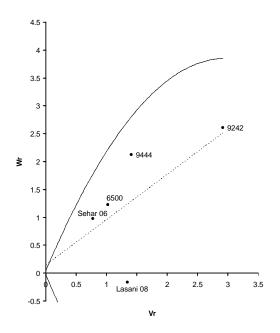


Fig.4 : Wr/Vr graph for no. of tillers per plant

Fig.3 : Wr/Vr graph for spike length





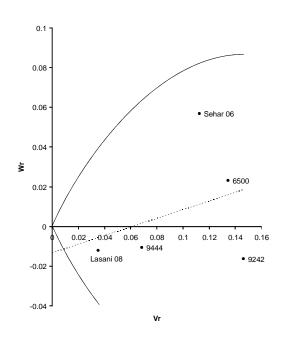


Fig.7 : Wr/Vr graph for grain weight per spike

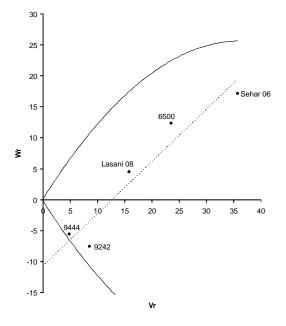


Fig.6 : Wr/Vr graph for No. of grains per spike

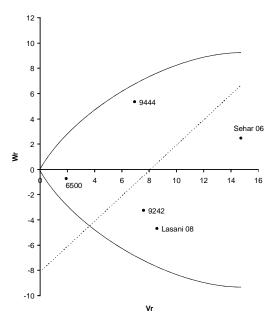


Fig.8 : Wr/Vr graph for 1000-grain weight.

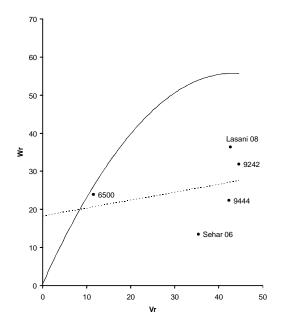


Fig.9 : Wr/Vr graph for grain yield per plant

Table 1. Mean squares for various morphological traits.

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Source of		Plant	Peduncle	Spike	No. of	Spikelets	No.of	Grain	1000-	Grain	
variation	d.f.	height	length	length	tillers	per spike	grains	weight	grain	yield per	
			-	-	per		per	per	weight	plant	
					plant		spike	spike			
Replication	2	3.20	1.52**	0.49	0.64	3.94**	3.46	0.11	1.45	0.67	
Genotype	24	153.79**	15.00**	1.55**	11.83**	13.70**	240.80**	0.11**	38.909**	181.77**	
Error	48	0.39	0.27	0.15	0.32	0.45	1.15	0.05	0.68	0.35	

****** = Highly significant

Table 2. Array means table from 5×5 diallel cross for various morphological traits.

Genotype	Plant	Peduncle	Spike	No.of	Spikelets	No.of	Grain	1000-	Grain
	height	length	length	tillers	per spike	grains	weight	grain	yield per
				per plant		per spike	per spike	weight	plant
Saher-	101.708	29.006	14.49	11.05	23.73	65.05	2.78	41.58	16.88
2006									
Imdad-	106.89	28.504	13.96	12.12	22.76	64.09	2.73	40.91	22.56
2006									
6500	103.41	27.96	14.501	12.006	24.82	65.95	2.67	40.49	13.28
9242	104.01	29.25	14.63	12.88	23.98	62.93	2.76	41.93	19.505
9780	108.95	29.3	14.46	11.21	23.58	61.47	2.69	42.92	17.88

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