Pak. J. Bot., **43(2): 1141-1156, 2011.**

GENE ACTION IN SOME YIELD ATTRIBUTES OF BREAD WHEAT UNDER TWO WATER REGIMES

GHULAM RABBANI[1*], ABID MAHMOOD[1], GHULAM SHABBIR[2]
KAUSAR NAWAZ SHAH[3] AND NAEEM-UD-DIN[1]

[1]Barani Agricultural Research Institute, Chakwal, Pakistan
[2]Department of Plant Breeding and Genetics, Arid Agriculture University, Rawalpindi, Pakistan
[3]COMSAT Institute of Information Technology, Islamabad, Pakistan.

Abstract

Breeders are always interested in the task of developing new varieties for changing environments. Thus, they have to deal with new crosses to select desired combinations. Grain yield is a complex character that is influenced by the fluctuating behavior of the environment. To overcome this situation, it is necessary to breed wheat varieties which perform better than existing ones under diverse conditions. A complete diallel cross was prepared from eight parental wheat accessions with a range of tolerance to drought. F_1 hybrids and parents were grown at Barani Agricultural Research Institute, Chakwal. At maturity peduncle length, number of spikelets per spike, number of grains per spike, dry weight per plant at maturity and harvest index were recorded.

Over-dominance genetic effects were important for the expression of number of spikelets per spike, number of grains per spike, dry weight per plant at maturity and harvest index under irrigated and rainfed conditions while additive type of gene action were important for the expression of peduncle length under irrigated and rainfed conditions. Average degree of dominance for peduncle length is 0.683 and 0.829 under irrigated and rainfed conditions respectively. Average degree of dominance for peduncle length was less than unity showing partial dominance and greater than unity showing over dominance in all characters under both irrigated and rainfed conditions.

Introduction

Shortage of water is a worldwide problem and about 43% of the world land is affected to various degrees by it. Almost 15 million hectares of cultivated land in Pakistan is affected by this syndrome (Mujtaba & Alam, 2002). Agricultural production in these areas is primarily dependent on physical factors of climate and soil. These factors collectively determine the land potential, cropping pattern and crop production (Mujtaba & Alam, 2002).

Wheat (*Triticum aestivum* L. em Thell.) is one of the most widely adapted food crop in the world including Pakistan and ranks first among all the cereals. By 2020, world demand for wheat is expected to be 40% higher than that of its level in the later half of the 1990s (Rosegrant, 1997). It is grown on a large area under rainfed conditions and about 37% of the area of the developing countries consists of semiarid environments in which available moisture constitutes a primary constraint on wheat production. Rajaram (2001) reported that selection of wheat cultivars with better adaptation to water stress should increase the production in rainfed areas. Wheat contributes 13.8% to the value added in agriculture and 3.2% to GDP. In Pakistan the average wheat production is 2534kg/hectare which is far more less than its potential (Anon., 2005). Its production can be enhanced through the development of improved genotypes capable of producing better yield under various agro-climatic conditions and stresses.

---

[*]Corresponding author E-mail: rabanibari@yahoo.com

Consistency in yield has always been a problem in crop production due to the strong influence of environmental effects during the various stages of crop growth (Bull *et al.*, 1992). Genotypes x environment interactions are therefore, of major concern to plant breeders for developing commercial varieties. Many research workers from their study on genotype x environment interaction concluded that mean yields are not a satisfactory basis and emphasis should therefore be given on the evaluation of genotypes which could perform better irrespective of environmental fluctuations (Golmirzaie *et al.*, 1990; Qari *et al.*, 1990).

It has been estimated that about one-third of the world's potentially viable land suffers from an inadequate supply of water, and on most of the remaining areas, crop yields are periodically reduced by drought (Kramer, 1980). The rainfed crop production thus depends strongly on both the amount and distribution of rain. Strategies for improving drought tolerance include selection in low-stress environment, high-stress environments and a combination of stress and non-stress environments (Byrne *et al.*, 1995). Kirigwi *et al.*, 2004 indicated that alternating selection between high and low yielding environments is the most effective way to develop wheat germplasm adapted to environments where intermittent drought occurs.

It is a general agreement that germplasm diversity and genetic relatedness among elite breeding material is the fundamental element in plant breeding (Mukhtar *et al.*, 2002). Hence breeding wheat genotypes with diverse genetic base is needed to achieve self-efficiency and sustainability. Enhancement in yield in most situations is more effectively fulfilled on the basis of performance of yield components, which are closely associated with grain yield (Ashfaq *et al.*, 2003).

Average per hectare yield in Pakistan was 2716 kg from irrigated areas and 1142 kg from rainfed areas during 2007. This shows a big yield gap between the two production situations. Seventy percent of its agricultural land (22.05 million hectares) is canal irrigated and the rest is rainfed, where annual rainfall ranges between 350-500 mm (Anon., 2007). Annual rainfall is uneven with erratic distribution. The present study was, therefore, planned to screen genotypes for stress tolerance and to study inheritance mechanism of drought adaptive traits under irrigated and rainfed conditions, in terms of the types of gene action. It will help to feed the ever-increasing population and make the country self-sufficient.

Materials and Methods

Eight wheat genotypes viz., Inqlab-91, MAW-1, 2KC033, Saleem-2000, No.2495, 3C061, 3C062 and 3C066 were planted during 2005-06 at Barani Agricultural Research Institute (BARI), Chakwal. Crosses were made among these selected genotypes in all possible combinations. Necessary precautions were taken during the crossing operations to avoid contamination of the genetic materials used. The female parents were hand emasculated and pollinated to produce enough seed for all the crosses.

Seeds of the crosses were planted under irrigated as well as under rainfed conditions during 2006-07. The parents along with 56 F_1's including reciprocals were space planted in Randomized Complete Block Design with three replications. F_1's, their reciprocals and the 8 parents were sown in 4 meter long single row. Two seeds per hill were sown, and later on thinned to one plant per hill by maintaining a distance of 30 centimetres between rows. Extra non-experimental lines were also raised at the start and ends of each replication to eliminate border effects.

For the two treatments, the field was irrigated before seed bed preparation. After planting of experimental population, four irrigations were applied to irrigated treatment during the active growing period (tillering, booting, anthesis and grain formation). Whereas the other treatment entirely depended on natural precipitation and no surface irrigation was applied to rainfed experiment for maintaining moisture stress conditions. Normal agronomic practices like fertilizer application and weed control were applied. The amount of rainfall received during the experimental period (October to April, 2006-07) was 393.6 mm. Data on peduncle length, number of spikelets per spike, number of grains per spike, dry weight per plant (g) at maturity and harvest index were recorded from ten randomly selected guarded plants from each entry and each replication.

Statistical analysis: The analysis of variance was carried out for all the characters (irrigated and rainfed conditions) according to method of Steel & Torrie (1980). If significant results were obtained then genetic analysis tests were carried out. According to Mather & Jinks (1982). There are two phases of analysis of the diallel cross. First phase is the formal genetic analysis of variance of the data is done which indicates whether there are significant additive and/or non-additive genetic differences among the genotypes. The main items for differences among the same set of genotypes and so, in the absence of complications such as maternal effects, should yield estimates of the same genetic component of variation, which will indicate the additive variation (*D*).

The second phase of diallel analysis is the graphic representation of the variance (*Vr*) of all components of the rth array and the covariance (*Wr*) of all the offspring's in each parental arrays with the non-recurring parents. The information of gene action was inferred by plotting the covariance (*Wr*) of each array against its variance (*Vr*). The slope and the position of regression line fitted to the array points within the limiting parabola ($Wr^2=Vp \times Vr$) and from zero origin showed the degree of dominance and the presence or absence of gene interaction. The corresponding values of Wr for all observed Vr values were calculated as $(Vp \times Vr)^{0.5}$ where *Vp* = variance of the parents. The different arrays (cultivars) were fitted within the limits for the parabola using the individual variance and covariance as their limiting points. Parent array points nearest to the origin possessed most recessive genes, and intermediate position signified the presence of both dominant and recessive genes in the array and farthest most points dominant genes. The validity of the additive- dominance model to the data set and hence fulfillment of assumptions for the model can be determined with the help of the above two tests. Failure of those assumptions makes the model inadequate. For the additive-dominance model to be adequate and hence the fulfillment of the assumptions is provided by regression analysis of *Wr* and *Vr*. According to Mather & Jinks (1982) the regression coefficient is expected to be significantly different from zero but not significantly different from unity if all the assumptions are fulfilled. Failure of this test means that either genes show non-allelic interaction i.e., are not independent in their action, or show non-random association among the parents i.e., are non-independent in their distribution.

The second test of adequacy of this additive-dominance model is that of *Wr* + *Vr* and *Wr* –*Vr*. If dominance (or for that matter certain types of non-allelic interaction) is present *Wr*+*Vr* must change from array to array and at the same time if there is non-allelic interaction between the alleles, *Wr* – *Vr* will vary between arrays. Although if dominance is present, *Wr* – *Vr* will not vary more than expected from error variation. If data fulfill both tests, the additive dominance model is completely adequate for further analysis. However if one of them fails to fulfill assumptions, the additive-dominance model is partially adequate.

Genetic analysis: Diallel cross analysis method developed by Hayman (1954), Jinks (1954) and applied by Mather & Jinks (1982) was used for genetic analysis.

Parameters used in this experiment were: D, variation attributed to additive genetics effects: H_1, variation due to dominance genetics effects: H_2, variation due to dominance genetics effects corrected for gene distribution: F determine the relative frequency of dominant to recessive alleles in the parental populations and the variation level over loci, which is positive displaying the important role of the frequency of dominant genes: h^2 indicated the dominance effects due to heterozygous loci: The value of $(H_1/D)^{1/2}$ is the measure of average degree of dominance, which is equal to one when the dominance is complete and E, is expected environmental component of variation.

Results and Discussion

Results of the analyses revealed that genotypic differences were highly significant for all the characters under both conditions Table 1 and 2. This exhibited the presence of sufficient variability in the material grown under irrigated and rainfed conditions. Results of diallel analysis for various traits are discussed as below. The additive-dominance model was found to be fully adequate for peduncle length, number of spikelets per spike, dry weight at maturity and harvest index under both irrigated and rainfed conditions. The additive-dominance model was found to be partially adequate, to explain the type of gene action governing the expression of number of grains per spike under both irrigated rainfed conditions (Tables 3 and 4).

Peduncle length: The estimates of components of variation are presented in (Tables 5 and 6). D component was found significant, which indicated the importance of additive variation in the heridity of peduncle length under irrigated conditions. H_1 and H_2 were also found significant showing their important role in the expression of peduncle length. Component F and h^2 was significant displaying their important role of dominant genes. Expected environmental component of variation (E) was found non-significant under irrigated conditions. The value of $H_1/D^{1/2}$ is the measure of Average degree of dominance (0.683) indicating that dominance for increased peduncle length was almost incomplete. Narrow sense heritability was estimated to be 81%. D component, the variance due to additive effects of genes was found significant, which indicated the importance of additive variation in the heridity of peduncle length under rainfed conditions. Significant values of variance for D and H_1 showed that both additive and dominance effects were involved in the expression of peduncle length. H_1 and H_2 were also found significant showing their important role in the expression of peduncle length. H_1 and H_2 are noted to be unequal, indicating unequal number of positive and negative alleles for peduncle length. In the presence of unequal gene frequencies the sign and magnitude of F determine the relative frequency of dominance to recessive alleles in the parental population and the variation level over loci. Component F was significant displaying their important role of dominant genes. The non-significant effect obtained for h^2 revealed an unimportant contribution of dominant genes toward determining peduncle length under rainfed conditions. Expected environmental component of variation (E) was found significant under rainfed conditions. The value of $(H_1/D)^{1/2}$ is the measure of Average degree of dominance (0.829) indicated partial dominance for peduncle length. Narrow sense heritability was estimated to be 40%. Average degree of dominance (0.683) and graphical analysis of the results (Fig. 1a) depicted partial dominance along with

Table 1. Analysis of variance of eight bread wheat genotypes and their possible F_1 hybrids under irrigated conditions.

Source of variance	d.f.	Mean square				
		Peduncle length	Number of spikelets per spike	Number of grains per spike	Dry weight per plant (g) at maturity	Harvest index
Replications	2	4.291	1.021	1.127	26.313	2.229
Genotypes	63	155.859**	14.130**	17.924**	232.701**	152.545**
Errors	126	1.794	1.328	0.371	20.403	8.544
CV %		4.13	5.29	1.39	5.47	10.83

** Significant at 1 percent probability level

Table 2. Analysis of variance of eight bread wheat genotypes and their possible F_1 hybrids under rainfed conditions.

Source of variance	d.f.	Mean square				
		Peduncle length	Number of spikelets per spike	Number of grains per spike	Dry weight per plant (g) at maturity	Harvest index
Replications	2	2.673	1.234	0.244	1.617	9.255
Genotypes	63	38.382**	7.279**	26.392**	61.704**	75.567**
Errors	126	14.783	1.002	0.406	10.666	7.562
CV %		16.4	5.82	1.69	5.85	13.37

** Significant at 1 percent probability level

Table 3. Regression analysis and analysis of *wr* and *vr* for various plant traits in 8 x 8 diallel cross of wheat under irrigated conditions grown at BARI, Chakwal during 2006-07.

S. No.	Traits	Regression analysis (*t* value of *b*)		Analysis of variance of arrays	
		b_0	b_1	*Wr+Vr*	*Wr-Vr*
1.	Peduncle length	7.863**	0.974	26.820**	10.765**
2.	Number of spikelets per spike	4.660**	0.446	5.225**	1.058
3.	Number of grains per spike	4.082**	0.635	24.704**	5.215**
4.	Dry weight at maturity	3.677*	0.591	7.483**	1.114
5.	Harvest index	3.537*	1.287	5.203**	1.634

Table 4. Regression analysis and analysis of *wr* and *vr* for various plant traits in 8 x 8 diallel cross of wheat under rainfed conditions grown at BARI, Chakwal during 2006-07.

S. No.	Traits	Regression analysis (*t* value of *b*)		Analysis of variance of arrays	
		b_0	b_1	*Wr+Vr*	*Wr-Vr*
1.	Peduncle length	5.364**	0.215	1.241	2.341
2.	Number of spikelets per spike	3.511*	1.312	8.510**	1.774
3.	Number of grains per spike	9.021**	-1.326	26.553**	19.382**
4.	Dry weight at maturity	2.661*	1.768	4.100**	0.901
5.	Harvest index	2.652*	1.41	4.184**	2.091

additive type of gene action controlling the inheritance of peduncle length with a line of unit slope and positive intercept of the regression line under irrigated conditions. It was observed that the 2KC033 had the maximum dominant genes among the genotypes studied followed by 3C062 for peduncle length while the genotype containing the most recessive and the least dominant genes was 3C066 followed by Saleem-2000 under irrigated conditions. Rest of the genotypes had intermediary gene constitution. Graphical analysis of the results (Fig. 1b) depicted partial dominance along with additive type of gene action controlling the inheritance of peduncle length with a line of unit slope and positive intercept of the regression line under rainfed conditions. It was observed that the MAW-1 had the maximum dominant genes among the genotypes studied followed by No. 2495 for peduncle length while the genotype containing the most recessive and the least dominant genes was 3C062 followed by 2KC033 under rainfed conditions. These findings also corroborated the results of Gill *et al*., (1983).

Number of spikelets per spike: The estimates of components of variation are presented in Tables 5 and 6. *D*, the additive component was significant. H_1 and H_2 were also found significant showing their important role in the expression of number of spikelets per spike under irrigated conditions. Component *F* was non-significant displaying their unimportant role of dominant genes. The non-significant effect obtained for h^2 revealed an unimportant contribution of dominant genes toward determining this trait under irrigated conditions. Expected environmental component of variation (*E*) was found non-significant under irrigated conditions. The value of $(H_1/D)^{1/2}$ is the measure of average degree of dominance (1.992) indicated over-dominance for increased number of spikelets per spike. Narrow sense heritability was estimated to be 21%. *D* component was found significant under rainfed conditions, which indicated the importance of additive variation in the heridity of number of spikelets per spike. H_1 and H_2 were also found significant showing their important role in the expression of number of spikelets per spike. Component *F* was non-significant displaying their unimportant role of dominant genes.

Table 5. Components of variation for various traits of bread wheat under irrigated conditions.

Components of variance	Peduncle length	Number of spikelets per spike	Number of grains per spike	Dry weight per plant (g) at maturity	Harvest index
D	108.143* ± 3.453	3.905* ± 0.665	3.757* ± 0.865	63.856* ± 14.777	39.493* ± 9.803
H1	50.447* ± 7.939	15.497* ± 1.529	17.642* ± 1.988	252.493* ± 33.970	176.852* ± 22.536
H2	37.524* ± 6.907	14.809* ± 1.330	16.693* ± 1.730	243.384* ± 29.554	166.229* ± 19.607
F	39.411* ± 8.159	2.394 ± 1.571	2.009 ± 2.043	35.823 ± 34.913	26.522 ± 23.162
h^2	18.677* ± 8.159	0.434 ± 0.892	0.097 ± 1.160	5.674 ± 19.820	0.268 ± 13.149
E	0.458 ± 1.174	0.331 ± 0.226	0.096 ± 0.294	5.12 ± 5.023	2.111 ± 3.332
(*H1/D*)1/2	0.683	1.992	2.167	1.988	2.116
Heritability (Narrow sense)	0.806	0.214	0.240	0.220	0.213

* Significant component within the limits of standard error

Table 6. Components of variation for various traits of bread wheat under rainfed conditions.

Components of variance	Peduncle length	Number of spikelets per spike	Number of grains per spike	Dry weight per plant (g) at maturity	Harvest index
D	49.595*±2.265	0.860* ±0.411	8.028* ±0.998	6.793*±3.782	13.912* ±5.977
H1	34.109*±5.207	8.605* ±0.946	34.545* ±2.294	74.029*±8.695	93.069* ±13.741
H2	18.148*±4.530	8.408* ±0.823	30.413* ±1.996	68.588*±7.564	86.887* ±11.954
F	54.702*±5.351	0.425 ±0.972	9.423* ±2.358	6.829 ±8.936	11.524 ±14.122
h^2	-0.474 ±3.038	0.392 ±0.552	8.354* ±1.339	8.765 ±5.073	5.000 ±8.017
E	3.648*±0.770	0.251 ±0.140	0.101 ±0.339	2.631*±1.286	1.897 ±2.032
(*H1/D*)1/2	0.829	3.163	2.074	3.301	2.586
Heritability (Narrow sense)	0.399	0.118	0.151	0.120	0.154

* Significant component within the limits of standard error

Non-significant effect obtained for h^2 revealed an unimportant contribution of dominant genes toward determining number of spikelets per spike. Expected environmental component of variation (*E*) was found non-significant. The value of $(H_1/D)^{1/2}$ is the measure of average degree of dominance (3.163) indicated over-dominance for number of spikelets per spike. Narrow sense heritability was estimated to be 12%. With an equal contribution additive and dominance effects to the genetic behavior of number of spikelets per spike, genetic improvement of this character with the genotype at hand should not present any serious problem. Graphical analysis of the data (Fig. 2a) showed that the cultivar MAW-1 had the maximum dominant genes for spikelets per spike followed by 3C062 under irrigated conditions while the genotype containing the most recessive and the least dominant genes was 3C061, followed by Inqlab-91. The regression line intercepted the *Wr* axis below the point of origin showing an over-dominance type of gene action. Graphical analysis of the data (Fig. 2b) disclosed that the cultivar, MAW-1 had the maximum dominant genes for number of spikelets per spike followed by 3C062 under rainfed conditions while the genotype containing the most recessive and the least dominant genes was Inqlab-91, followed by 3C061. The regression line intercepted the *Wr* axis below the point of origin showing an over-dominance type of gene action. Similar results were reported by Khan *et al*., (1992) who reported the over-dominance type of gene action for number of spikelets per spike.

Number of grains per spike: The estimates of components of variation are presented in Tables 5 and 6. *D* component, the variance due to additive effects of genes was found significant under irrigated conditions, which indicated the importance of additive variation in the heridity of number of grains per spike. H_1 and H_2 were also found significant showing their important role in the expression of number of grains per spike. In the presence of unequal gene frequencies the sign and magnitude of *F* determine the relative frequency of dominance to recessive alleles in the parental population and the variation level over loci. Component *F* and h^2 was non-significant displaying their unimportant role of dominant genes. Expected environmental component of variation (*E*) was found non-significant under irrigated conditions. The value of $(H_1/D)^{1/2}$ is the measure of average degree of dominance (2.167) indicated dominance for increased number of grains per spike was complete and offered a quantification of the level of over-dominance. Narrow sense heritability was estimated to be 24%. *D* component was found significant under rainfed conditions, which indicated the importance of additive variation in the heridity of number of grains per spike. H_1 and H_2 were also found significant showing their important role in the expression of number of grains per spike. Component *F* was significant displaying their important role of dominant genes. The significant effect obtained for h^2 also revealed a substantial contribution of dominant genes toward determining number of grains per spike under rainfed conditions. The component of error variation (*E*) was recorded non-significant under rainfed conditions, indicating unimportance of the environmental factors in determining number of grains per spike. The value of $(H_1/D)^{1/2}$ was 2.074, indicating over dominance type of gene action. Narrow sense heritability was estimated to be 15%. The Vr/Wr graph (Fig. 3a) exhibited that the Maw-1 had the maximum dominant genes for number of grains per spike under irrigated conditions. It was followed by 3C062. The maximum recessive genes were exhibited by Inqlab-91 and it was followed by 2KC033. The regresssion line cut the Wr axis above the point of origin showing over-dominance type of gene action controlling number of grains per spike. The *Vr/Wr* graph (Fig. 3b) exhibited that the MAW-1 had the maximum dominant genes for number of grain per spike under rainfed conditions. It was followed by 3C062. The maximum recessive genes were exhibited by Inqlab-91 and it was followed by 2KC033. Rest of genotypes had intermediary gene constitution. The regresssion line cuts the *Wr* axis above the point of origin showing over-dominance type of gene action controlling number of grains per spike. These findings are in agreement with the findings of' Chowdhry *et al*., (1992) who also reported over-dominance genetic control of number of grains per spike. However, many other researchers like Sharma & Ahmad (1980), Bebyakin & Korobovo (1989), Lonc (1989), Alam *et al*., (1991), Khan *et al*., (1992) observed a partial dominance type of gene action for number of grains per spike while Khan *et al*., (2007) observed additive type of gene action for number of grains per spike.

Dry weight of plant at maturity: The estimates of components of variation are presented in Tables 5 and 6. As it is clear from the Table, the value of *D*, the additive component was significant under irrigated conditions. H_1 and H_2 were also found significant showing their important role in the expression of dry weight at maturity. Component *F* was recorded to be non-significant indicating the presence of dominant genes. The variance due to h^2 was found non-significant. Environmental component of variation (*E*) was found non-significant suggested that the environment played an unimportant role in the expression dry weight at maturity. The value of $(H_1/D)^{1/2}$ (1.988) was more than one indicating an over-dominance type of gene action with narrow sense heritability 21%. The significant values of *D* and H_1 components showed that expression of dry weight at maturity is conditioned by additive and dominant gene effects under rainfed conditions. H_2 was also found significant showing the important role in the expression of dry weight at maturity. H_2 component was found to be approximately equal to H_1, indicating that positive and negative alleles were present in equal proportions in the parents. Component *F* was non-significant displaying their unimportant role of dominant genes. Non-significant effect obtained for h^2 revealed an unimportant contribution of dominant genes toward determining dry weight at maturity. Expected environmental component of variation (*E*) was found significant. The value of $(H_1/D)^{1/2}$ (2.116) indicated over-dominance type of gene action with narrow sense heritability (21%) for dry weight at maturity. With an equal contribution additive and dominance effects to the genetic behavior of dry weight at maturity, genetic improvement of this character with the genotype at hand should not present any serious problem.

Average degree of dominance (1.988) and Graphical analysis of the data (Fig. 4a) depicted an over-dominance type of gene action controlling the inheritance of dry weight at maturity with a line of unit slope and positive intercept of the regression line. Distribution of the array points in the graph represented the genic constitution of the parental genotypes. It was observed that the genotype, MAW-1 had the maximum dominant genes, followed by 3C062 for dry weight at maturity while the genotypes containing the most recessive and the least dominant genes were Inqlab-91 and 3C061 under irrigated conditions. Graphical analysis of the data (Fig. 4b) depicted an over-dominance type of gene action controlling the inheritance of dry weight at maturity with a line of unit slope and positive intercept of the regression line. Distribution of the array points in the graph represented the genic constitution of the parental genotypes. It was observed that the genotype, 3C062 had the maximum dominant genes, followed by MAW-1 for dry weight at maturity while the genotypes containing the most recessive and the least dominant genes were 3C061 and Inqlab-91 under rainfed conditions. Rest of genotypes had intermediary gene constitution. Similar results have also been reported by Srivastava & Nema (1993) while Khan *et al*., (2007) observed additive type of gene action for number of grains per spike.

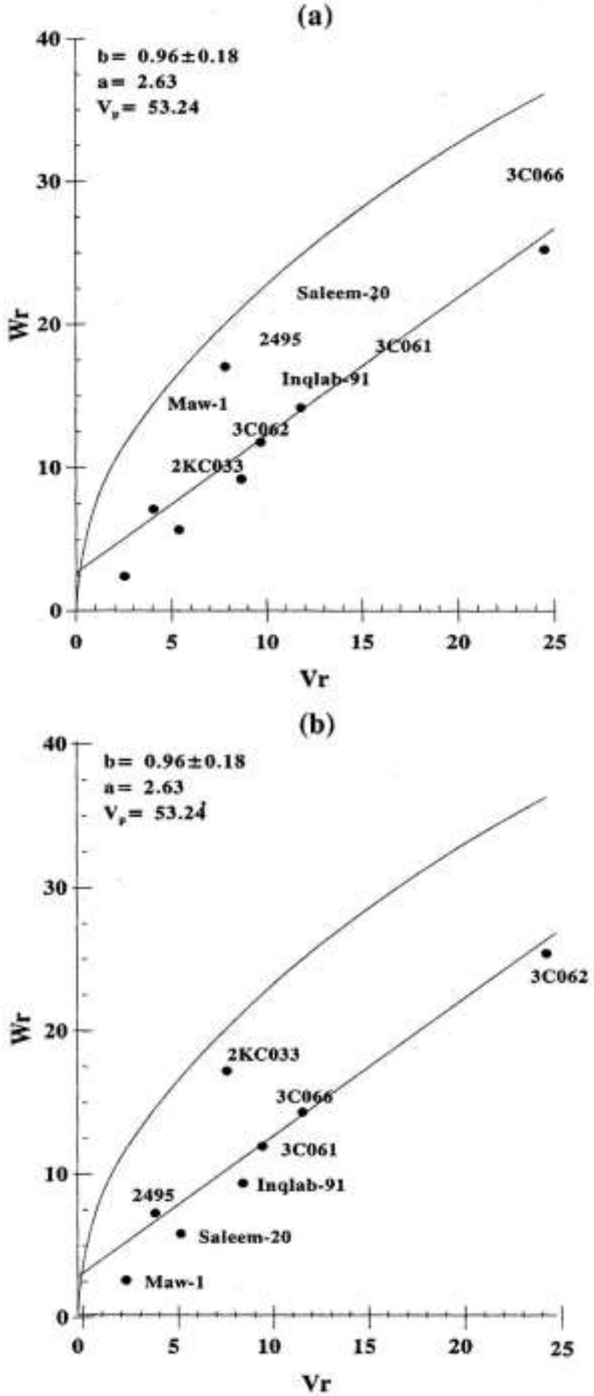

Fig. 1. Wr/Vr graph for peduncle length under (a) irrigated, and (b) rainfed conditions.

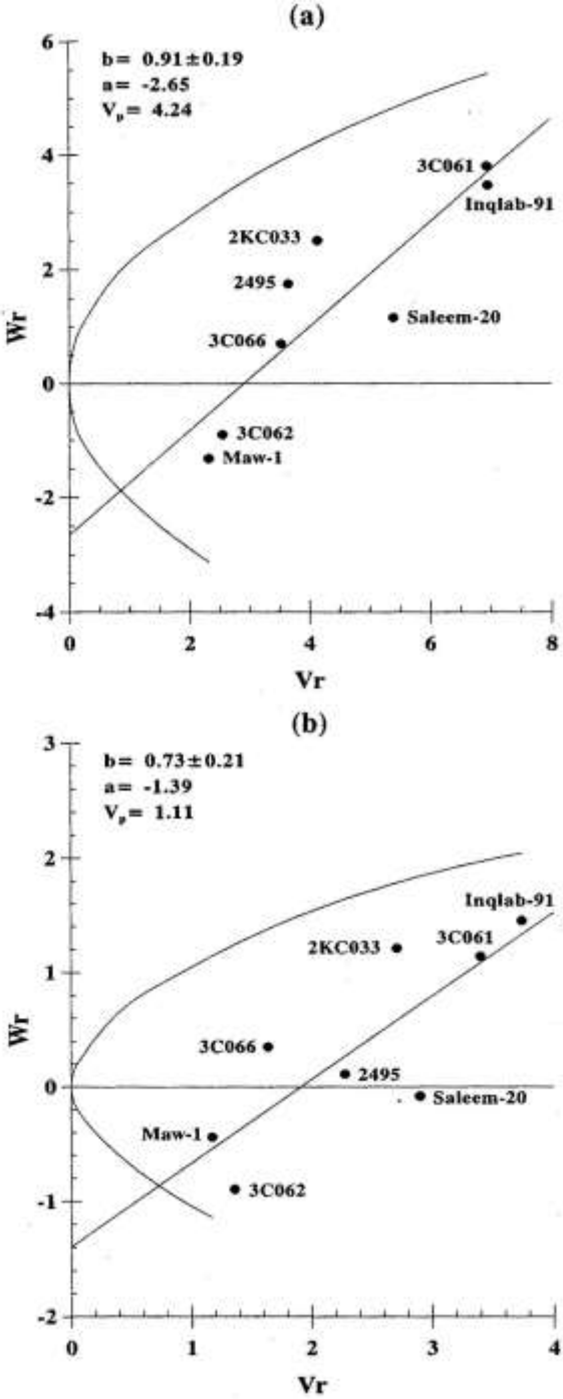

Fig. 2. Wr/Vr graph for number of spikelets per spike under (a) irrigated,and (b) rainfed conditions.

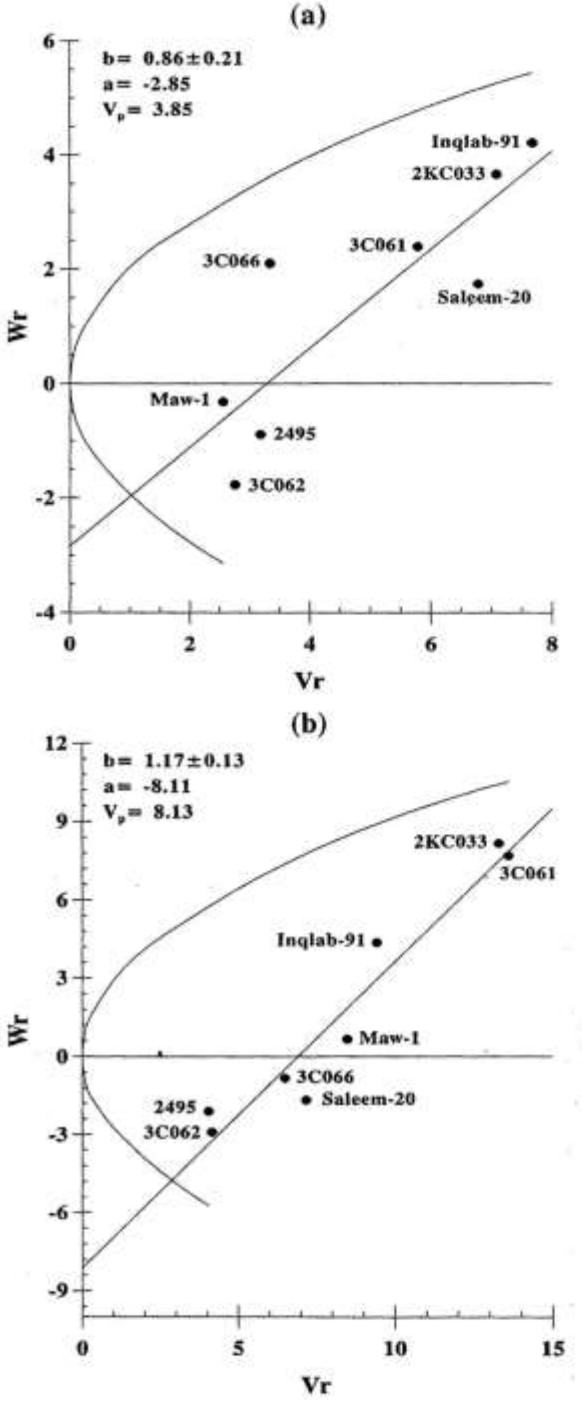

Fig. 3. Wr/Vr graph for number of grains per spike under (a) irrigated, and (b) rainfed conditions.

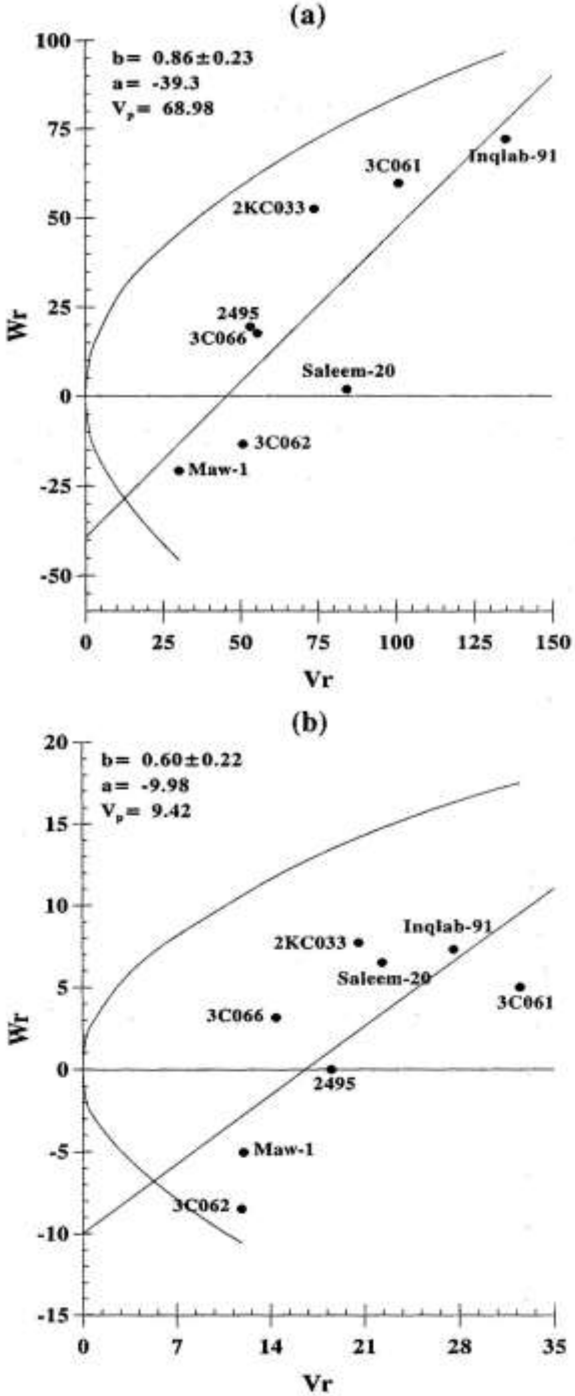

Fig. 4. Wr/Vr graph for dry weight per plant at maturity under (a) irrigated, and (b) rainfed conditions.

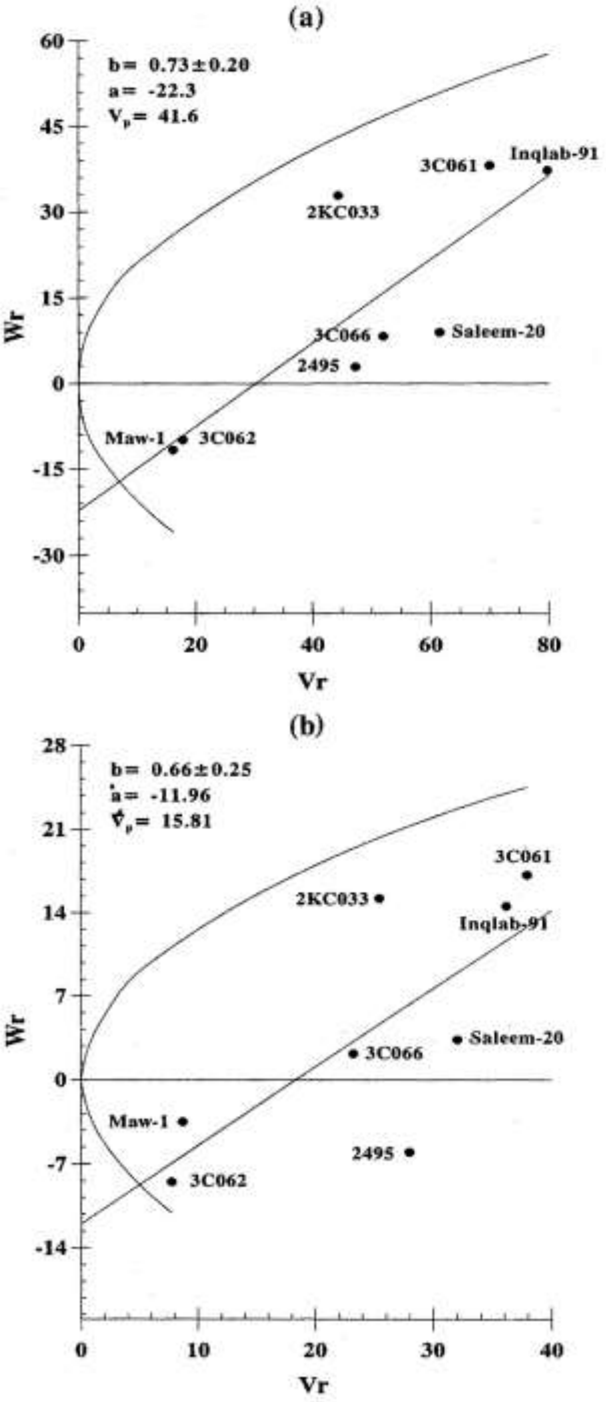

Fig. 5. Wr/Vr graph for harvest index under (a) irrigated, and (b) rainfed conditions.

Harvest index: The estimates of components of variation are presented in Tables 5 and 6. D component was found significant, which indicated the importance of additive variation in the heridity of harvest index under irrigated conditions. H_1 and H_2 were also found significant showing their important role in the expression of harvest index. Component F was non-significant displaying their unimportant role of dominant genes. The non-significant effect obtained for h^2 revealed an unimportant contribution of dominant genes toward determining harvest index. Expected environmental component of variation (E) was found non-significant. The value of $(H_1/D)^{1/2}$ is the measure of average degree of dominance (2.116) indicated over-dominance for increased harvest index. Narrow sense heritability was estimated to be 21%. D component was found significant, which indicated the importance of additive variation in the heridity of harvest index under rainfed conditions. H_1 and H_2 were also found significant showing their important role in the expression of harvest index. Component F was non-significant displaying their unimportant role of dominant genes. The non-significant effect obtained for h^2 revealed an unimportant contribution of dominant genes toward determining harvest index. Expected environmental component of variation (E) was found non-significant. The value of $(H_1/D)^{1/2}$ is the measure of average degree of dominance (2.586) indicated over-dominance for increased harvest index. Narrow sense heritability was estimated to be 15%.

Under irrigated conditions graphical representation (Fig. 5a) disclosed an over-dominance type of gene action controlling the inheritance of harvest index with a line of unit slope and positive intercept of the regression line. Distribution of the array points in the graph indicated that MAW-1 had the maximum dominant genes for harvest index followed by 3C062 while the genotype containing the most recessive and the least dominant genes was Iinqlab-91 followed by 3C061. Under rainfed conditions graphical representation (Fig. 5b) disclosed an over-dominance type of gene action controlling the inheritance of harvest index with a line of unit slope and positive intercept of the regression line. Distribution of the array points in the graph indicated that the 3C062 had the maximum dominant genes for harvest index followed by MAW-1 while the genotype containing the most recessive and the least dominant genes was 3C061 followed by Inqlab-91. These findings are also in agreement with the findings of Golparvar *et al.*, (2004) who also found over-dominance type of gene action for harvest index. Evidence of partial dominance for harvest index was, however, reported by Srivastava & Nema (1993), Mishra *et al.*, (1996), Farshadfar *et al.*, (2000) and Sheikh *et al.*, (2000). Akhtar & Chowdhry (2006) reported additive type of gene action for harvest index. The variation in the results might be due to different genetic material used in the study and environmental effects under which genotypes were studied.

References

Akhtar, N. and M.A. Chowdhry. 2006. Genetic analysis of yield and some other quantitative traits in bread wheat. *Int. J. Agri. Biol.*, 8(4): 523-527.

Alam, K., M.A. Chowdhry and M.N. Asad. 1991. The inheritance of protein content, grain yield and yield components in bread wheat (*Triticum aestivum* L. em. Thell.). *Gomal Univ. J. Res.*, 11(1): 45-52.

Anonymous. 2007. *Agricultural Statistics of Pakistan.* Ministry of Food, Agriculture and Cooperative, Food and Agriculture Division, Economic Wing, Islamabad.

Ashfaq, M., A.S. Khan and Z. Ali. 2003. Association of morphological traits with grain yield in wheat. *Int. J. Agric. Biol.*, 5: 264-267.

Bebyakin, V.M. and N.I. Korobova. 1989. Gene interactions and combining ability effects of winter wheat varieties for yield components. *Tsitologiya i Genetika*, 23(1): 23-26.

Bull, J.K., M. Cooper, I.H. Delacy, K.E. Basford and D.R. Woodruff. 1992. Utility of repeated checks for hierarchical of data from plant breeding traits. *Field Crop Research.*, 30: 79-95.

Byrne, P.E., J. Bolanos, G.O. Edmeades and D.L. Eaton. 1995. Gains from selection under drought versua multilocation testing in related tropical maize populations. *Crop Sci*., 35: 63-69.

Chowdhry, M.A., M. Rafiq and K. Alam. 1992. Genetic architecture of grain yield and certain other traits in bread wheat. *Pak. J. Agric. Res*., 13(3): 216-220.

Farshadfar, E., M. Farshadfar and J. Sutka. 2000. Combining ability analysis of drought tolerance in wheat over different water regimes.*Acta Agronomica Hungarica*., 48(4): 353-361.

Gill, K.S., G.S. Bhullar, G.S. Mahal and H.L. Bhardwaj. 1983. Genetic systems governing yield and other characters in durum wheat. *Genetica Agraria*, 37(1/2): 105-114.

Golmirzaie, A.M., J.W. Schmidt and A.F. Dreier. 1990. Components of variance and stability parameters in studies of cultivar x environment interaction in winter wheat. *Cereal Res. Commun*., 18: 249-256.

Golparvar, A.R., M.H. Islam, F. Darvish, R. Abdulmajid and G.P. Abdollah. 2004. Genetic assessment of some morpho-physiological traits in bread wheat under drought stress conditions. *Pajouhesh va Sazandegi In Agronomy and Horticulture*, (62): 90-95.

Hayman, B.I. 1954. The analysis of variance and diallel crosses. *Biometrics*, 10: 235-45.

Khan, M.A., N. Ahmad, M. Akbar, A. Rehman and M. M. Iqbal. 2007. Combining ability analysis in wheat. *Pak. J. Agric. Sci*., 9(3): 1-5.

Khan, M.Q., K. Alam and M.A. Chowdhry. 1992. Diallel cross analysis of some morphological traits in spring wheat. *Pak. J. Agric. Res*., 13(3): 211-215.

Khan, N., M. Qasim, S. Ali and N.S. Kisana. 2004. Genotypic variation in wheat genotypes under agro-climatic conditions of Kaghan Valley. *Asian J. Plant Sci*., 3: 569-570.

Kirigwi, F.M., M.V. Ginkel, R. Trethowan, R.G. Sears, S. Rajaram and G.M. Paulsen. 2004. Evaluation of selection strategies for wheat adaptation across water regimes. *Euphytica,* 135(3): 361-371.

Kramer, P.J. 1980. Drought stress and the origin of adaptation. In: *Adaptation of plants to water and high temperature stress,* (Eds.): N.C. Turner and P.J. Kramer. pp. 7-20. John Wiley and Sons, New York.

Lonc, W. 1989. Types of gene effect governing quantitative characters in winter wheat. *Hodawla Roslin, Aklimatyazacja i Nasiennictwo, Poland,* 29(3-4): 1-11.

Mather, K. and J.L. Jinks. 1982. *Introduction to Biometrical Genetics*. Chapman and Hall Ltd., London.

Mishra, P.C., T.B. Singh, S.M. Kurmvanshi and S.N. Soni. 1996. Gene action in a diallel cross of wheat under late sowing conditions. *J. Soil and Crop,* 6(2): 128-131.

Mujtaba, S.M. and S.M. Alam. 2002. Drought phenomenon and crop growth. http://www.Pakistaneconomist.com/issue2002/issue13/i&e4.htm

Mukhtar, M.S., M. Rahman and Y. Zafar. 2002. Assessment of genetic diversity among wheat cultivars from a range of localities across Pakistan using random amplified polymorphic DNA (RAPD) analysis. *Euphytica*, 128: 417-425.

Qari, M.S., N.I. Khan and M.A. Bajwa. 1990. Comparison of wheat cultivars for stability in yield performance. *Pak. J. Agric. Res*., 11: 73-77.

Rajaram, S. 2001. Prospects and promise of wheat breeding in twenty-first century in wheat in a global environment. (Eds.): Z. Bedo and L. Lang. Dordrecht, The Netherlands: Kluwar Academic Publishers, 37-52.

Rosegrant, A.L. 1997. Wheat demanded in future. *Oxford Economic Papers*, 28: 102-117.

Sharma, J.C. and Z. Ahmad. 1980. Genetic architecture of some traits in spring wheat. *Indian J. Agric. Sci*., 50(6): 457-461.

Sheikh, S., I. Singh and J. Singh. 2000. Inheritance of some quantitative traits in bread wheat. *Ann. Agric. Res*., 21: 51-54.

Srivastava, A.N. and D.P. Nema. 1993. Graphical analysis of physiological traits and yield in bread wheat (*Triticum aestivum* L.). *Indian J. Agric. Sci*., 63(8): 479-483.

Steel, R.G.D. and J.H. Torrie. 1980. *Principles and procedures of statistics. A biometrical approach*, 2nd ed. McGraw Hill Book Co., New York.

Yadav, B., V.P. Singh and R.B. Srivastava. 1987. Gene effects for synchrony of some traits in bread wheat. *Indian J. Agric. Sci*., 57(7): 494-496.

(Received for publication 31 December 2009)