

Pattern of inheritance in some yield related parameters in spring wheat (*Triticum aestivum* L.)

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Abstract

An experiment was conducted using 5×5 diallel crosses in wheat to evaluate five wheat genotypes and to analyze the gene action for yield and its components. Highly significant variability was observed among genotypes for various studied parameters. The additive component and non additive parts were significant for all the traits showing the importance of both these components in inheritance of the studied traits. The graphical representation showed that tiller number for each plant, height of plant, length of spike, grain number per spike and weight of 1000 grains were controlled by partial dominance with additive type of gene action. Over-dominance was observed in peduncle length, area of flag leaf and weight of grains per spike. Complete dominance was observed for spikelet number per spike and grain yield on per plant basis. Non-allelic interaction was absent for all the traits studied. The distribution of dominant and recessive genes for yield traits was also studied and noted that line 9437 being closet to the origin had maximum contribution of dominant genes for grain yield per plant. The estimates of narrow sense heritability ($h^2_{(n.s.)}$) were higher for plant height, length of peduncle and grain number per spike indicating better chance for improvement following selection procedure in these traits. The traits governed by additive genes and partial dominance should be selected in early segregating generation. In traits showing over dominance, delayed selection would be better to practice.

Keywords

Additive, Gene Action, Yield Attributes, Allelic Interaction

1. Introduction

Wheat is among the leading cereals in Pakistan (Farooq et al., 2010; Farooq et al., 2006). In Pakistan wheat is very important in terms of food security and economic stability of our country (Saeed et al., 2010).

The prerequisite for combining desirable genes in a single genotype is the evaluation of available genetic material to evaluate the genetic variability for economically important traits. The main criteria for the selection of parents, which after hybridization are likely to produce the best

recombinants for desirable traits, is the magnitude and type of gene action in a particular population (Saeed et al., 2010). Improvement in genetic material of crop plants is necessary to enhance the agricultural products in order to meet the basic needs of rapidly growing population. For this purpose information about genetics of yield and its components is of great worth for breeders for selection of parents to develop new and high yielding varieties. This is the reason for which breeding skill and successful manipulation of genetic makeup involved for expression of traits under selection has gained extreme importance. In wheat grain yield and related parameters are greatly influenced by environment (Anwar et

al., 2011). Different studies have been made to explore the inheritance of yield contributing traits. For tiller number, height of plant, weight of 100 grains and grain yield, additive effect with partial dominance was reported by Farooq et al. 2010. But Asif et al. (1999) found over dominance for weight of 1000 grains. Present study investigates genetic mechanism responsible for inheritance of traits relevant to yield in spring wheat using diallel technique developed by Jinks (1954 & 1955) and Hayman (1954 a,b). This provides an appropriate and precise mechanism of gene action of quantitative traits.

2. Materials and Methods

2.1. Location of the Experiment and Germplasm Exploited

The present study was conducted at the research area of Department of PBG, UAF, Faisalabad, Pakistan. Five wheat genotypes viz., Mairaj-08, Sehar-06, 9437, 9444 and 9451 were utilized in the study. These varieties/lines were sown in the field during rabi season 2009-10 in a two row plot of 5 meter length and cross combinations were made using diallel cross technique including direct and indirect crosses.

2.2. Statistical Design and Planting Geometry

The direct and indirect crosses with parents were planted on November 25, 2011, using the RCB design with three replicates. Each replication had 20 crosses and 5 parental lines, each line of 5 meter length. The P×P and R×R distance was maintained at 15 and 30cm, respectively. The sowing was done by using a dibble. Two seeds per hole were sown which were retained as single seedling after germination.

2.3. Measurement of Studied Traits

At maturity 10 guarded plants from every line was taken randomly and data were recorded for the traits like tillers per plant, plant height, length of peduncle, length of spike, spikelets per spike, area of flag leaf, weight of 1000 grains, grain number per spike, weight of grains per spike and yield of grains per plant. The plant height was taken from base of plant to the tip of spike excluding awns of mother shoot of selected plants in centimeter. The tillers of each genotype of selected plants were counted at maturity in each replication and average was computed. For measuring flag leaf area from fully developed flag leaves of main shoot, maximum breadth and length was measured (cm²). Data recording was done in the morning when the leaves were fully turgid. Measurement of flag leaf area was done using the function proposed by Muller (1991). At maturity the length of peduncle of main shoot of the chosen plants was measured from last node (bearing the flag leaf) to the base of spike. Spike length from selected main shoot was measured in centimeters from base of the spike to its tip without awns. The spikelet number was counted from the main spike of selected guarded plants. Spike weight of the main shoot of

each individual selected plant was weighed. Manual thrashing of main shoot was done for counting grains per spike and for measuring grain yield on per plant basis, thrashing of spikes of individual selected plants was done manually and weighed on an electronic balance. Finally average of all the traits was computed.

3. Results and Discussion

3.1. Genetic Analysis

Table 1. Mean squares of different plant parameters in a 5x5 diallel mating system cross in *Triticum aestivum* L.

Traits	Mean squares
Plant height	214.40**
Area of flag leaf	23.61**
length of Peduncle	37.34**
Tiller number for each plant	7.47**
Length of spike	1.92**
Spikelet number per spike	4.96**
Grain number per spike	61.91**
Grains weight per spike	0.18**
Weight of 1000-grain	16.51**
Grain yield per plant	1.65**

Where ** = P<0.01

The data collected for all the parameters was subjected to analysis of variance technique (Steel et al., 1997) to estimate the differences among the genotypes. Highly significant estimates were obtained among the genotypes for the parameters studied (Table-1). The traits showing significant differences were further subjected to diallel cross analysis technique devised by Hayman (1954 a,b) and Jinks (1954 & 1955). The rating of heritability was estimated as low, medium and high following Stansfield (1986).

3.2. Adequacy Tests for Additive-Dominance (AD) Model

The model of additive- dominance was employed to test the validity of the postulations underlying the genetic model, were tested by ANOVA of (Wr + Vr) and (Wr – Vr) and joint regression test, (Table 2). The coefficient of regression 'b' deviated from zero but not from one for all the parameters. This deviation indicated the occurrence of interaction among intra alleles, independent division of the genes among the parents (Shakeel et al., 2011; Farooq et al., 2011a & b). The slope of regression line proposed that all the postulates of the model of additive-dominance were fulfilled for the parameters in question (Mather and Jinks, 1982).

The estimates of mean squares for (Wr – Vr) and (Wr + Vr) (Table- 2) showed significant variation ($P \leq 0.05 - 0.01$) between the arrays (Wr + Vr) and non-significant ($P > 0.05$) variability within the arrays (Wr – Vr) were observed for most of the parameters studied except for grain number per spike which indicated the prevalence of dominance and absence of epistasis. Both the tests revealed that the genetic model for additiveness was fully fit for these traits except for

grain number per spike which exhibited partial fitness. The partially adequacy for grain number per spike may be due to the prevalence of non-allelic interaction, non-independent division of the genes in the parents and linkage as suggested by Mather and Jinks (1982). The traits, qualified one test for AD model has also been found in the studies of Farooq *et al.*, 2011 a&b.

3.3. Estimation of Components of Variation and Graphical Representation

The results of genetic components showed that the additive and non additive components were significant and positive for all the parameters indicating the prevalence of both effects in controlling the inheritance mechanism in these traits (table-3). For length of peduncle, area of flag leaf, spikelet number for each spike and grain number of each spike the values of non additive components were more than additive component D supporting the predominance of non-additive genetic effects and the estimates of $\{(H_1/D)^{0.5}\}$ was more than one thus also suggesting over dominance for these traits.

The positive F value showed the importance of dominant

genes and parameters showing positive sign of F indicating high ratio of dominant genes. Eight traits showed positive estimates of F while for plant height and length of peduncle this value was negative which showed less percentage of dominant to recessive alleles. The h^2 value denoting the dominance due to heterozygous loci was positive for all the traits. The positive sign of h^2 showed dominance of genes with increasing effect at most of the loci and negative sign illustrated dominance of genes with decreasing effect (Ali *et al.* 2008), but no negative sign for any of the traits was found in the current studies. Similarly, value of $H_2 / 4H_1$ ratio < 0.25 and the information, $H_1 - H_2 \neq 0$, exhibited unequal frequency of genes in the parents for traits like area of flag leaf, plant height, spikelet number per spike and grain number per spike. The traits like length of peduncle, tiller number per plant, length of spike and grain yield exhibited significant environmental influence (E) which suggested that the genetic mechanism of these traits were greatly affected by environment. According to the findings of Fehr (1978), the influence of environment and complex genetic mechanism are responsible for variation in polygenic traits like grain yield.

Table 2. Scaling test for various plant parameters in *Triticum aestivum* L.

Traits	Slope of Regression		Mean squares		Fitness of the AD model	Regression coefficient
	b_0	b_1	Wr + Vr	Wr-Vr		
Plant height	7.26**	1.53 ^{NS}	4536.63**	82.69 ^{NS}	fully fit	$b=0.82\pm0.012$
Area of Flag leaf	2.23*	1.25 ^{NS}	77.07*	9.84 ^{NS}	fully fit	$b=0.64\pm0.082$
Length of peduncle	6.24**	0.07 ^{NS}	93.26**	1.51 ^{NS}	fully fit	$b=0.98\pm0.025$
Tiller number for each plant	3.28**	0.45 ^{NS}	9.11**	0.75 ^{NS}	fully fit	$b=0.87\pm0.071$
Length of spike	20.73**	-1.43 ^{NS}	1.37**	0.003 ^{NS}	fully fit	$b=1.07\pm0.002$
Spikelet number per spike	8.87**	0.47 ^{NS}	18.98**	0.19 ^{NS}	fully fit	$b=0.94\pm0.011$
Grain number per spike	4.27*	1.71 ^{NS}	1412.48**	74.26**	Partially fit	$b=0.71\pm0.027$
Grains weight per spike	3.51*	0.46 ^{NS}	0.0013**	0.00007 ^{NS}	fully fit	$b=0.88\pm0.063$
Weight of 1000-grain	4.50*	0.27 ^{NS}	89.28**	3.47 ^{NS}	fully fit	$b=0.94\pm0.044$
Grain yield per plant	6.57**	-0.09 ^{NS}	3.82**	0.06 ^{NS}	fully fit	$b=1.01\pm0.023$

Where * = $P<0.05$ and ** $P<0.01$ and NS = Non-significant

Table 3. Estimation of genetic components of various studied parameters in *Triticum aestivum* L.

Genetic components	Traits									
	Plant height (cm)	Area of flag leaf (cm ²)	Length of peduncle (cm)	Tillers number of each plant	Length of spike (cm)	Spikelet number per spike	Grain number per spike	Grain weight per spike (g)	Weight of 1000 grains (g)	Grain yield per plant (g)
D	58.22±4.18*	11.67±1.44*	8.58±0.58*	4.45±0.34*	1.08±0.03*	3.08±0.19*	19.81±3.91*	0.02±0.004*	8.39±0.77*	1.58±0.11*
H ₁	56.21±11.29*	20.44±3.90*	12.24±1.56*	3.19±0.91*	0.73±0.08*	3.13±0.52*	24.88±10.55*	0.05±0.01*	6.09±2.09*	1.41±0.30*
H ₂	45.89±10.24*	17.12±3.53*	11.06±1.41*	3.26±0.83*	0.90±0.07*	2.92±0.47*	21.55±9.57*	0.05±0.01*	6.01±1.90*	1.40±0.30*
F	-41.14±10.44*	13.57±3.60*	-1.30±1.44	2.32±0.84*	0.81±0.07*	2.54±0.48*	2.86±9.76	0.006±0.01	6.08±1.93*	1.39±0.27*
$h^{0.5}$	21.86±6.91*	8.34±2.39*	20.55±0.95*	1.47±0.56	0.52±0.05*	4.21±0.32*	12.90±6.46*	0.07±0.01*	1.09±1.28	1.01±0.18*
E	0.45±1.71	0.41±0.59	0.15±0.24*	0.20±0.14	0.09±0.01*	0.11±0.07	0.39±1.60	0.001±0.001	0.27±0.32	0.09±0.04*
$(H_1/D)^{0.5}$	0.98	1.32	1.19	0.84	0.82	1.00	1.12	1.49	0.85	0.94
$4DH_1^{0.5}+F/4DH_1^{0.5}-F$	0.47	2.56	0.88	1.89	2.68	2.38	1.14	1.21	2.48	2.76
$H_2/4H_1$	0.20	0.21	0.22	0.26	0.31	0.23	0.21	0.26	0.25	0.25
$h^2_{(n,s)}$	0.82	0.13	0.65	0.50	0.13	0.31	0.65	0.34	0.40	0.18

Where * = $P<0.05$ and values with no star are Not-significant

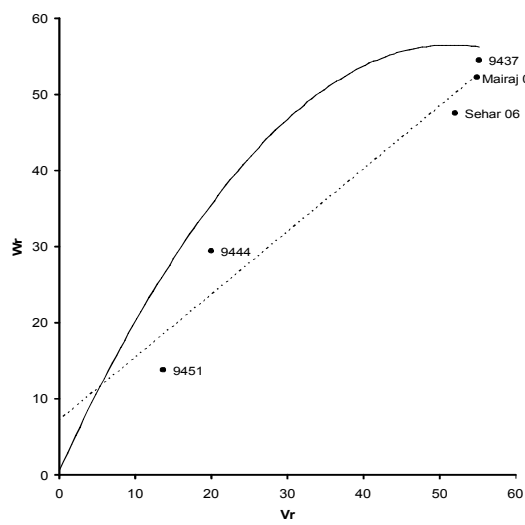


Fig 1(A).

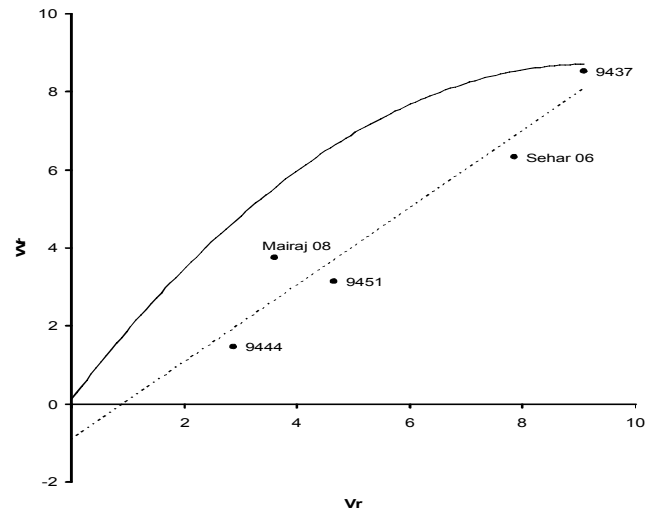


Fig 1(D).

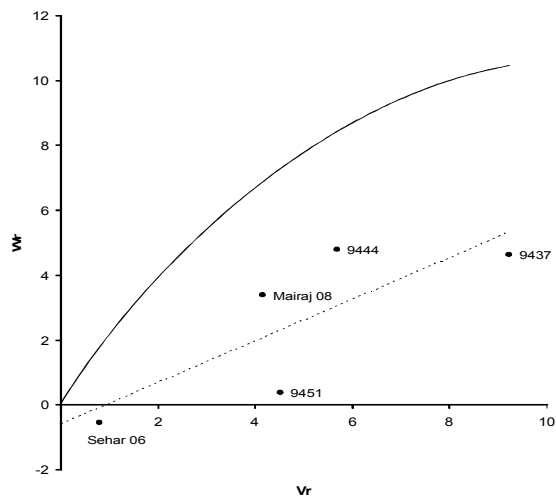


Fig 1(B).

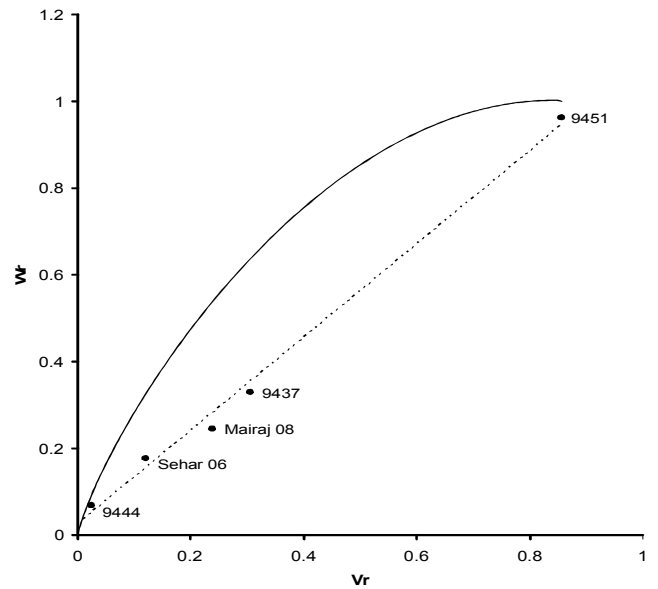


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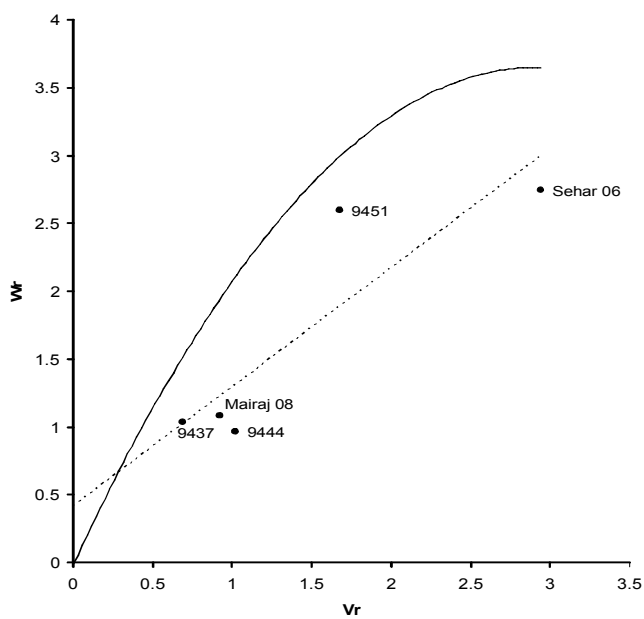


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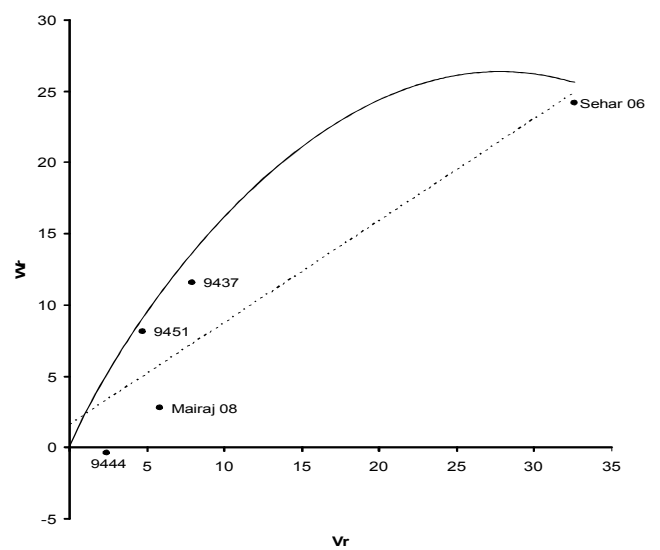


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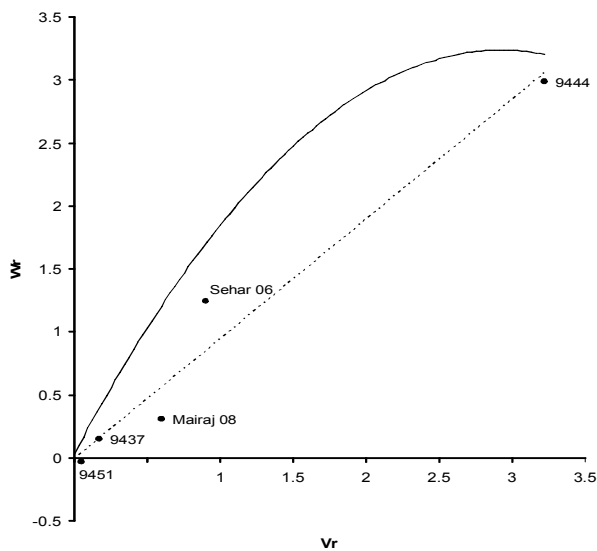


Fig 1(G).

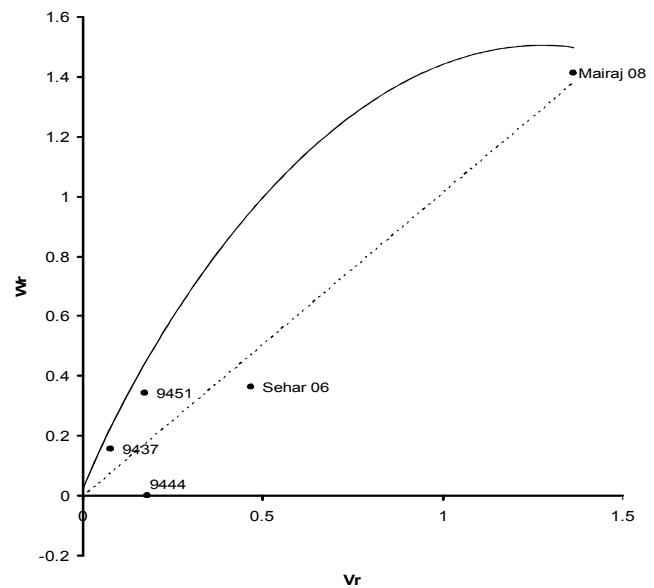


Fig 1(J).

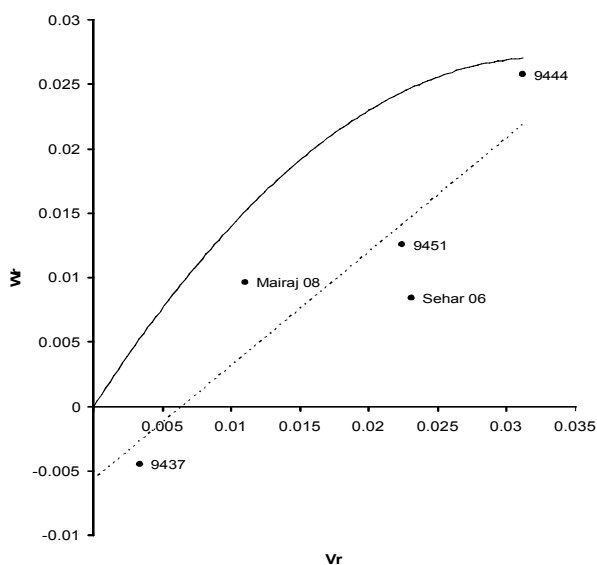


Fig 1(H).

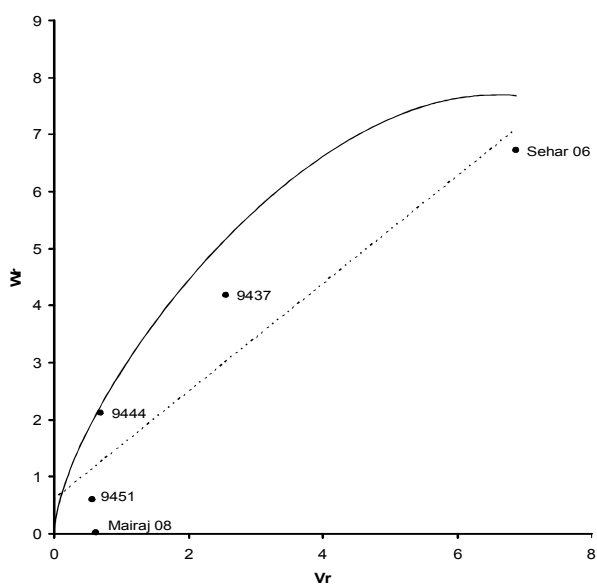


Fig 1(I).

Figure 1.(A) to 1(J). Vr/Wr graph of various plant traits in *Triticum aestivum* L.

Heritability is utilized by the plant breeders for unraveling the magnitude of genetic variability from total phenotypic variation. Selection competence for a trait under study depends on extent of genetic variation and heritability (Falconer & Mackay, 1996). The magnitude of narrow sense heritability ($h^2_{(n.s.)}$) were higher for plant height, length of peduncle and grain number per spike indicating better opportunity for improvement in these traits. Moderate estimates were found for tillers per plant and 1000 grain weight while all other traits showed low estimates. Normally the traits showing higher estimates of narrow sense heritability were controlled by additive genetic effects. Ali *et al.* (2009) and Rehman *et al.* (2009) also found higher values of heritability with additive effects of genes and low narrow sense heritability due to the prevalence of non-additive effects for yield related parameters. Both these cases have been found in the current studies.

The graphical illustration of yield relevant parameters and components of variation were presented from Fig. 1(A)-1(J). The regression line for the traits like height of plant, tiller number per plant, length of spike, grains number per spike and 1000 grains intercepted the Wr-axis above the origin point confirming occurrence of additive genetic effects with partial dominance. The results are in conformity with the research findings of Gurmani *et al.* (2007), Farooq *et al.* (2010), Yao *et al.* 2011 and Irshad *et al.*, 2012. This suggested that pedigree method could be effective for genetic improvement for these traits. For yield of grains and spikelets number per spike complete dominance was observed as the regression line intercepted the Wr-axis at the point of origin. These results are similar to the findings of Ajmal *et al.* 2011. Additive control for grain yield was previously reported at high temperature and drought (Kaur and Behal, 2010). Partial dominance with additive type of gene action was deduced for

yield (Samiulallah et al., 2010). For area of flag leaf, length of peduncle, grain number per spike and weight of grains for each spike over dominance was observed which are in accordance with the findings of Ejaz-ul-Hassan and Khaliq (2008). However, Ajmal et al., 2011 reported partial dominance for length of peduncle. The results with non-additive type of gene action and partial-dominance for spike weight are similar to the findings of Heidari et al. (2006). Later generation selection may be practiced in traits showing over dominance. The difference in genetics for a trait is due to difference in genetic material studied which had different alleles of gene(s) for controlling a trait, their allelic and non allelic interactions, variation in environment and environmental interaction with genes controlling a trait. The genetic information for the traits studied in parental varieties is prerequisite for chalking out sound breeding program and helpful in adopting the effective selection procedure in searching of transgressive segregants for the development potential genotype/varieties after hybridization.

4. Conclusion

F₁ crosses along with their parents showed significant variability thus offer sufficient possibilities for betterment in highly variable generations after crossing. The additive genetic effect were predominant for all the traits but over dominance was predominant in area of flag leaf, length of peduncle, grain weight per spike and grain number for each spike suggesting later generation selection. Plant height, tiller number per plant, weight of 1000 grain and length of spike may be improved through pedigree selection in early segregating generations.

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